



The 7th IAL Symposium 2012

Lichens: from genome to ecosystems in a changing world

9th – 13th January 2012, Chaophya Park Hotel, Bangkok, Thailand

BOOK OF ABSTRACTS

The 7th Symposium of the International Association for Lichenology

Organized by

Ramkhamhaeng University

On behalf of the International Association for Lichenology



January 2012

Lichen: from genome to ecosystem in a changing world

This book contains the abstracts of the papers for The 7th IAL Symposium 2012, The International Conference of the international Association for Lichenology on 9th – 13th January 2012 at Chaophya Park Hotel, Bangkok, Thailand. They reflect the authors' opinions and are published as presented without change, in the interests of timely dissemination.

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Welcome Message

The President of the International Association of Lichenology

Dear Fellow Lichenologist

It is a great pleasure for me to welcome you to IAL7 on behalf of the IAL Council and both the Local and Scientific Organizing Committees of the conference.

Past IAL meetings have been tremendously enjoyable and successful events and we are confident that the 7th IAL7 Symposium in Bangkok will be equally memorable. As the title of the Symposium suggests, the scientific sessions and individual contributions to them are wide ranging in topic. These reflect the tremendous influence of molecular studies on lichenology, the threats imposed by rapid man-made changes occurring to the biosphere and an ever growing interest in lichens in tropical regions.

In addition to the science, there is a rich and exciting social programme. Therefore, I hope that during this meeting you will enjoy excellent science, stimulating interaction with colleagues and a sense of community all spiced by, for the first time at an IAL Symposium, a tropical setting.

Professor Dr. Peter Crittenden

IAL President

Welcome Message

The President of Ramkhamhaeng University

Dear IAL7 Participants,

On behalf of the Lichen Research Unit at Ramkhamhaeng University, we are delighted to welcome all of you to Thailand. I am honored to know that, the 7th Symposium of the International Association for Lichenology has been held for the first time in Asia, here in Thailand. Thanks to all lichenologists from throughout the world for coming to this symposium. I hope you will soon feel very much comfortable in Bangkok, in the heart of Asia.

We are proud to know that you are giving us a great opportunity to co-hosting this important symposium with IAL. As this symposium is principally designed to provide opportunities for world-wide lichenologists to share experiences and knowledge, as well as to create co-operations to enhance researches in this field. Ramkhamhaeng University has supported, directly and indirectly, lichen research and would maintain such program to strengthening our academic capacity, including cooperation among local, regional and international scientific communities.

Apart from all the dedicated scientific program, I hope that everyone will have a chance to enjoy the wide array of social networking events, pre- and post-symposium tours. Please kindly take this great opportunity to experience our famous hospitality, excellent cuisine, rich history, culture heritage, as well as sights and sounds that are typical Thai. I hope you will have pleasant memory to take home with you.

Assistant Professor Wutisak Lapcharoensap

President of Ramkhamhaeng University

Report

Chairperson of IAL7 Organizing committee

On behalf of the local organizing committee, it is our great pleasure to welcome you to the The 7th Symposium of the International Association for Lichenology in Bangkok, Thailand.

The theme of this year ***“Lichens: from Genome to ecosystems in a changing world”*** is composed of highly achieved keynote lectures from young and senior lichenologists, oral presentations of interdisciplinary, focus sessions, as well as a poster session. I am confident that the most up-to-date worldwide research findings will be presented and discussed at this event.

Three hundred and seven abstracts from participants of over 50 countries have been submitted. One hundred and seven abstracts are assigned as oral presentations, while 183 abstracts are allocated to posters. In addition, workshops on Parmeliaceae, Graphidaceae and Tropical lichens have been well supported by international agencies and experts. Furthermore, excursions to the North, Northeast and Eastern seacoast would provide first-hand experiences on lichens, nature and culture in the tropics, which is relatively unexplored by scientific communities.

I would like to express my sincere gratitude to the speakers and all who submitted their works and attend the symposium. I hope that you will find it a thoroughly rewarding experience –, academically, professionally and socially. Finally, I hope you would be able to make the most of this lovely time of the year, either before or after the symposium.

Associate Professor Dr. Kansri Boonpragob

Chair of LOC for 7th IAL Symposium 2012

Opening Address

Chairman, The Executive Board of the National Research Council of Thailand

Dear Professor Crittenden– The President of IAL, Dr. Lumbsch- The Vice president of IAL, Assistant Professor Wutisak Lapcharoensap- The President of Ramkhamhaeng University, Distinguish IAL participants, Ladies and Gentlemen,

First of all, I would like to extend a warm welcome to all of you on behalf of The National Research Council of Thailand (NRCT), and on behalf of my own. I am delighted, this symposium is convened in Thailand, and for the first time in Asia. This symposium will be another great event which inspires and encourages scientists from different parts of the world to carry on lichen research for the benefit of the globe. The NRCT functions involve promoting and supporting cooperation among international researchers and research institutes by providing research grants to government and private sectors, coordinating with national and international organizations on research projects, as well as being a center of exchanging the research information and researchers in Thailand.

Being the part of this symposium as the main supporter of lichen research in Thailand, I am grateful to know that over three hundred abstracts from over 50 countries will be presented. I have no doubt that this symposium will be a great forum to create collaboration, exchange experiences as well as establish a lichen research network among international researchers in the near future.

Finally, I wish all symposium objectives will be accomplished and wish the participants a very fruitful and productive symposium.

Professor Dr. Thira Sutabutra

Chairman, NRCT Executive Board

IAL COUNCIL (2008-2012):

- President:** - *Peter D. Crittenden*, The University of Nottingham, UK
Vice President: - *H. Thorsten Lumbsch*, The Field Museum of Natural History, U.S.A.
Secretary: - *Jurga Motiejnaitė*, Institute of Botany, Lithuania
Treasurer: - *Christian Printzen*, Forschungsinstitut Senckenberg, Germany
Assistant Treasurer: - *Imke Schmitt*, Biodiversity and Climate Research Centre, Germany
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- *Maria Herrera-Campos*, Instituto de Biología, México
- *Kansri Boonpragob*, Ramkhamhaeng University, Thailand
- *Ana Crespo*, Universidad Complutense, Spain
Auditor: - *Ulrik Søchting*, University of Copenhagen, Denmark
Vice Auditor: - *James D. Lawrey*, George Mason University, U.S.A.
Nomination Committee: - *Gintaras Kantvilas*, Tasmanian Museum and Art Gallery, Australia
- *Lucyna Śliwa*, Polish Academy of Sciences, Poland
- *Ulrik Søchting*, University of Copenhagen, Denmark

SCIENTIFIC COMMITTEE:

- | | |
|-------------------------|-------------|
| • Achariya Rangsiruji | Thailand |
| • André Aptroot | Netherlands |
| • Andreas Beck | Germany |
| • Cecile Gueidan | U.K. |
| • Christoph Scheidegger | Switzerland |
| • Christopher Ellis | U.K. |
| • Daniele Armaleo | U.S.A. |
| • Ester Gaya | U.S.A. |
| • François Lutzoni | U.S.A. |
| • Gintaras Kantvilas | Australia |
| • Gerhard Rambold | Germany |
| • Kansri Boonpragob | Thailand |
| • Kawinnat Buaruang | Thailand |
| • Khwanruan Papong | Thailand |
| • Knut Solhaug | Norway |
| • Lucia Muggia | Austria |
| • Mats Wedin | Sweden |
| • Martin Grube | Austria |
| • Ólafur Andrússon | Iceland |
| • Olga Nadyeina | Ukraine |
| • Peter Crittenden | U.K. |
| • Pradeep Divakar | Spain |
| • Robert Lücking | U.S.A. |
| • Sarah Jovan | U.S.A. |
| • Susan Will-Wolf | U.S.A. |

Lichen: from genome to ecosystem in a changing world

- | | |
|----------------------|-------------|
| • Thorsten Lumbsch | U.S.A. |
| • Toby Spribille | U.S.A. |
| • Ulrik Søchting | Denmark |
| • Vivian Miao | Canada |
| • Wanaruk Saipunkaew | Thailand |
| • William Sanders | U.S.A. |
| • Rosemary Honegger | Switzerland |

LOCAL ORGANIZING COMMITTEE:

- Chair:** - *Kansri Boonpragob*, Ramkhamhaeng University, Bangkok
- Committee:**
- *Achariya Rangsiruji*, Srinakarinviroj University, Bangkok
 - *Chutima Sriviboon*, Ramkhamhaeng University, Bangkok
 - *Ek Sangvichien*, Ramkhamhaeng University, Bangkok
 - *Kajonsak Vongshewarat*, Ramkhamhaeng University, Bangkok
 - *Kawinnat Buaruang*, Ramkhamhaeng University, Bangkok
 - *Khwanruan Papong*, Mahasarakarm University, Maha Sarakharm
 - *Pachara Mongkolsuk*, Ramkhamhaeng University, Bangkok
 - *Pawanrat Aksornsingchai*, Ramkhamhaeng University, Bangkok
 - *Santi Wattana*, Queen Sirikit Botanic Garden, Chaingmai
 - *Sureeporn Jariangprasert* Maejo University, Chaingmai
 - *Wanaruk Saipunkaew*, Chiangmai University, Chaingmai
 - *Wetchasart Polyiam*, Ramkhamhaeng University, Bangkok

CO – HOST ORGANIZATIONS:



The Botanical Society



Chiang Mai University



Maejo University



Srinakarinwirot University



Mahasarakham University



Queen Sirikit
Botanic Garden



Biodiversity Research
and Training Program



Thai Mycological
Association

INFORMATION FOR SPEAKERS AND PRESENTERS

ORAL PRESENTATION

- Power Point slides or Acrobat PDF for presentation on a LCD projector are recommended.
- All the presentation room will be equipped with: a computer running WINDOW XP Professional operating system, with MS Office, Acrobat Reader 6.0 and a LCD video projector.
- It is recommended to use simple fonts to prepare your presentation. Fancy fonts may not always be supported by presentation computers.
- Oral presentation rooms will be equipped with the following items:
 - A laptop computer
 - An LCD video projector
 - A laser pointer
- We recommended that presenters bring their presentation files in a format compatible with one of the above applications, with the files stored in a CD-ROM or a USB thumb drive (flash disk).
- Presentation files should be uploaded into the computers at the back of presentation room at least 4 hours prior to your session. The room are opened on the following schedule:
 - Sunday 8th January 2012 from 10.00 – 18.00 hrs.
 - Monday 9th – Thursday 12th January 2012 from 8.00 – 18.00 hrs.
 - Friday 13th January 2012 from 8.00 – 16.00 hrs.
- Please arrive the presentation room at least 15-30 minutes before your presentation time in order to check attendance with the chairs of your session.

POSTER PRESENTATION

- Posters need to be on display from 9th – 13th January 2012.
- Your poster presentation code will be indicated on the poster board and the abstract / program book.
- The standard poster board size 100 (width) x 250 (height) cm. will be provided.
- Recommended size of your poster is 85 cm. x 120 cm. Posters should be in PORTRAIT layout.
- Poster rooms are Rachada 1 – 3.
- **Time for poster set up:**
 - Sunday 8th January 2012, 15.00 – 20.00 hrs.
 - Monday 9th January 2012, since 8.00 hrs.
- **Time for poster removal:**
 - Within 16.00 hrs. on Friday 13th January 2012.
- Presenters are responsible for the dismantling of their posters. Posters left behind will be disposed and are not the responsibility of the organizer.
- Self- adhesive tape will be provided for mounting your posters.

INFORMATION FOR CHAIR PERSONS

To ensure that our sessions are enjoyable, informative and fair for all speakers and members of the audience, please follow these guidelines.

BEFORE THE SESSION

- Arrive 10-15 minutes prior to the start of the session and familiarize yourself with the room layout. Introduce yourself to the room attendance staff and AV technician.
- Read the Program Update/Housekeeping Notices that will be left on the head table.
- Make decision with your co chair, who will introduce each speaker and who will keep track of the time.
- Check the content of the session
- As presenters arrive, check their attendance and advise them to keep presentation time on schedule which includes questions and discussion. It is important to keep strictly to time so that the program will not be late.
- Work out a communication signal to let presenters know that they should move to a closing slide by ringing the bell for 3 and 1 minutes left and standing up when time is over.

AT THE START OF THE SESSION

- Welcome the audience
- Inform the session time to the audience, and then introduce presenter and the title of the paper.
- Closely watch time for both the presentation and the Q&A. Suggest the audience to approach the speaker/presenters during the next break if the assigned time is over.
- Questions and discussion following the speakers/presenters should be addressed to the Chair. Have a chairman's question ready only if no questions come from the floor. Please do not leap in with your question first.
- If there are any problems during the session, seek help from the room attendance staffs.

AT THE END OF THE SESSION

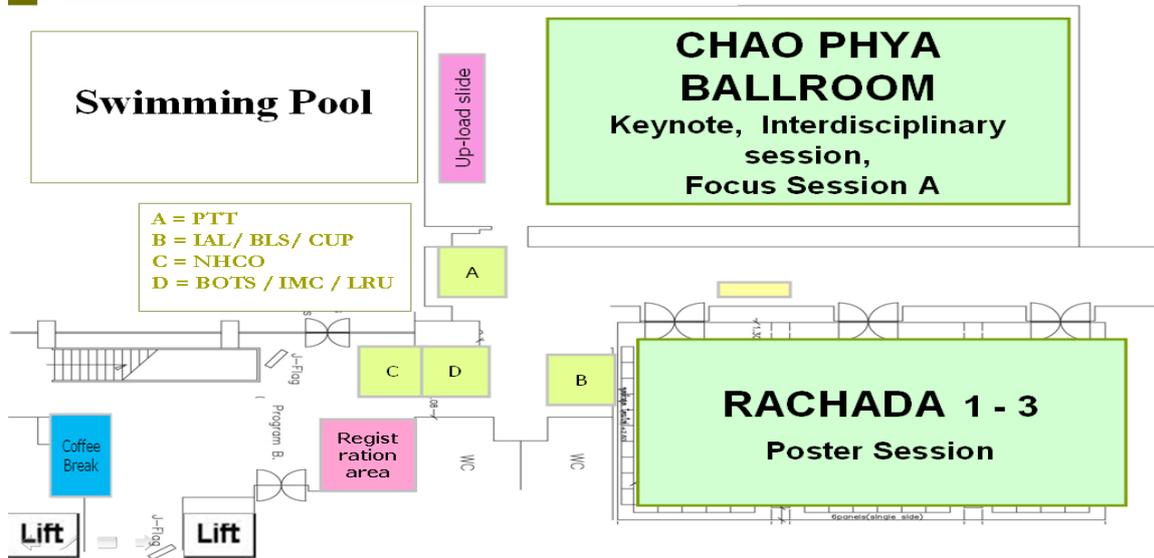
- Thank the speakers/presenters and invite applause
- Make any housekeeping announcements
- Close the session on time

SYMPOSIUM VENUE



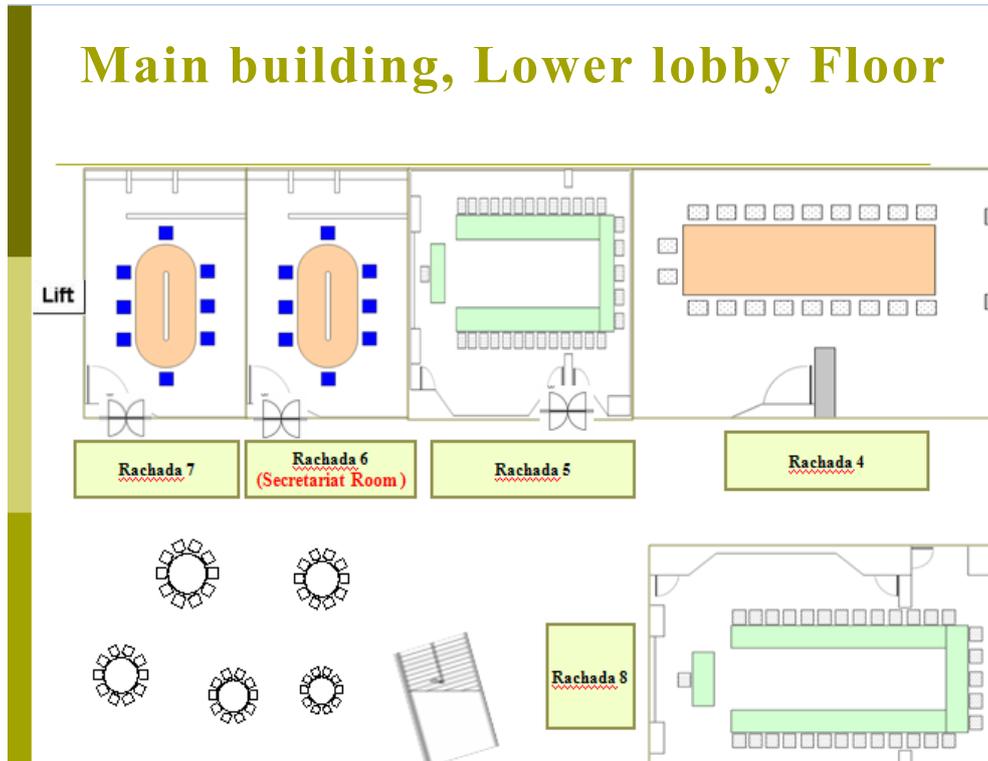
FLOOR PLAN

Main building, 2nd Floor

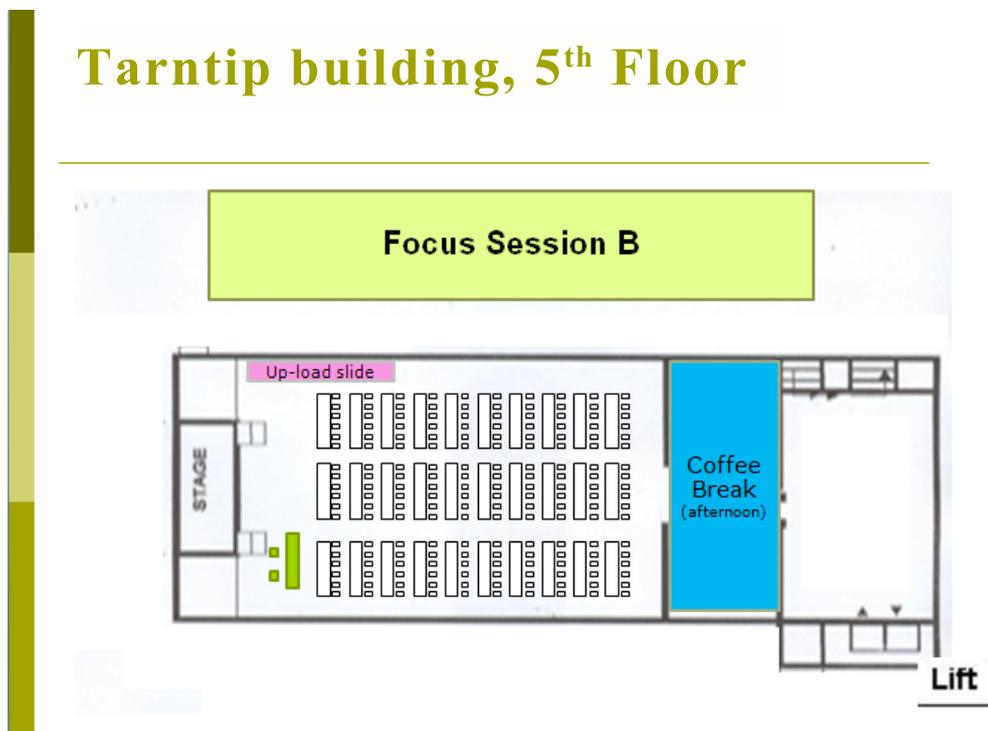


FLOOR PLAN

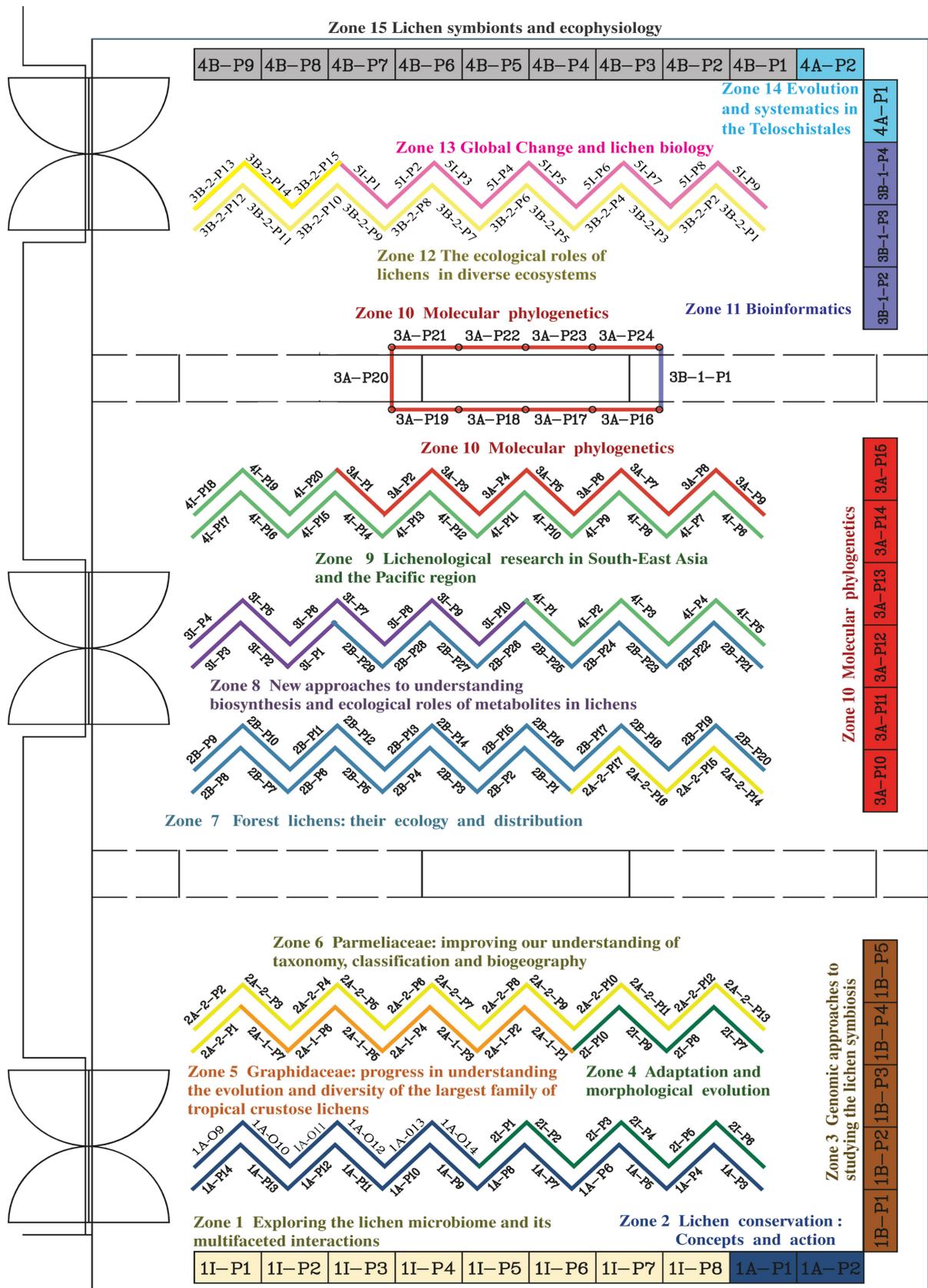
Main building, Lower lobby Floor



Tarntip building, 5th Floor



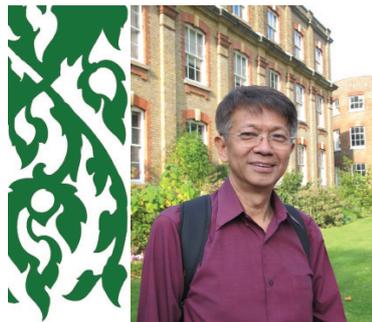
POSTER BOARD: Main building, Rachada 1 - 3



INFORMATION OF POSTER PRESENTATION BOARDS

Submission ID	Position	Submission ID	Position	Submission ID	Position	Submission ID	Position
IAL0001-00001	3A-P1	IAL0087-00001	3B-2-P5	IAL0161-00001	5I-P3	IAL0223-00001	2I-P9
IAL0004-00001	1A-O14	IAL0088-00001	4I-P7	IAL0162-00002	2B-P16	IAL0224-00001	3B-1 - P3
IAL0004-00002	2B-P13	IAL0091-00001	3A-P7	IAL0163-00001	2I-P5	IAL0230-00002	4B-P7
IAL0009-00007	1A-O12	IAL0093-00001	3B-2-P6	IAL0166-00001	3A-P11	IAL0236-00001	3I-P7
IAL0009-00009	4B-P1	IAL0094-00001	3B-2-P7	IAL0166-00002	3A-P12	IAL0238-00001	2A-2- P13
IAL0011-00001	1A-P1	IAL0095-00001	1A-P5	IAL0166-00003	3A-P13	IAL0239-00001	1B-P2
IAL0015-00001	2A-1-P1	IAL0096-00002	2A-1-P2	IAL0167-00001	3A-P14	IAL0241-00001	1A-O9
IAL0015-00002	2B-P1	IAL0100-00001	1B-P1	IAL0168-00001	2I-P6	IAL0241-00002	1B-P3
IAL0017-00001	2B-P20	IAL0101-00001	3B-2-P8	IAL0168-00002	3I-P3	IAL0242-00001	3I-P8
IAL0018-00002	1I-P1	IAL0103-00001	2A-1-P3	IAL0169-00001	4A-P2	IAL0243-00003	4I-P16
IAL0019-00001	1A-O10	IAL0103-00002	2A-1-P4	IAL0171-00001	3A-P15	IAL0244-00001	4I-P17
IAL0024-00001	4I-P20	IAL0104-00002	3A-P8	IAL0173-00001	4B-P5	IAL0245-00001	4I-P18
IAL0026-00001	4I-P1	IAL0105-00001	4I-P8	IAL0173-00002	4B-P6	IAL0246-00001	1B-P4
IAL0029-00001	4I-P2	IAL0110-00002	4A-P1	IAL0174-00003	2I-P7	IAL0247-00002	5I-P5
IAL0030-00001	3B-2-P1	IAL0110-00003	1A-P6	IAL0175-00001	3I-P4	IAL0249-00001	3I-P9
IAL0035-00002	2B-P9	IAL0111-00001	4I-P9	IAL0176-00001	3A-P16	IAL0250-00002	1A-P12
IAL0036-00001	3A-P2	IAL0113-00001	4B-P2	IAL0177-00002	2A-2- P9	IAL0252-00001	2B-P17
IAL0037-00002	4I-P3	IAL0113-00002	3I-P1	IAL0178-00002	2A-1-P5	IAL0255-00002	2A-2- P14
IAL0039-00001	4I-P4	IAL0114-00001	3A-P9	IAL0178-00003	2A-1-P6	IAL0258-00001	5I-P6
IAL0040-00005	2B-P4	IAL0114-00002	4I-P10	IAL0180-00001	3I-P5	IAL0260-00002	1I-P7
IAL0041-00001	2A-2- P1	IAL0115-00001	3I-P2	IAL0181-00001	2B-P3	IAL0261-00001	4B-P8
IAL0041-00002	2A-2- P2	IAL0120-00001	5I-P2	IAL0182-00001	2A-2- P10	IAL0263-00005	2A-2- P15
IAL0047-00001	1A-P2	IAL0124-00002	1I-P3	IAL0183-00001	2B-P11	IAL0264-00001	3B-1 - P4
IAL0056-00001	2B-P2	IAL0125-00001	1A-P7	IAL0184-00001	2B-P8	IAL0265-00001	2B-P19
IAL0057-00001	3A-P3	IAL0125-00002	1A-P8	IAL0186-00001	3I-P6	IAL0265-00002	2B-P18
IAL0057-00002	3A-P4	IAL0126-00001	3A-P10	IAL0187-00001	5I-P4	IAL0266-00001	3I-P10
IAL0057-00005	3B-2-P2	IAL0127-00001	2B-P27	IAL0189-00001	3B-2-P11	IAL0267-00001	1A-P13
IAL0057-00007	3B-1 - P1	IAL0127-00002	2B-P28	IAL0194-00001	4I-P13	IAL0270-00001	3A-P23
IAL0057-00008	2I-P1	IAL0127-00003	2B-P29	IAL0196-00001	1I-P5	IAL0275-00001	1A-P14
IAL0057-00009	3A-P5	IAL0129-00002	1A-P9	IAL0199-00001	2A-2- P11	IAL0278-00001	2B-P21
IAL0057-00010	3B-2-P3	IAL0129-00003	2A-2- P6	IAL0200-00001	1I-P6	IAL0279-00001	2A-2- P16
IAL0058-00001	2A-2- P3	IAL0131-00001	2B-P26	IAL0201-00001	3A-P17	IAL0280-00001	2I-P10
IAL0059-00002	1A-P3	IAL0131-00002	2A-2- P7	IAL0201-00002	3A-P18	IAL0281-00001	2A-2- P17
IAL0060-00001	3B-2-P4	IAL0132-00001	4I-P11	IAL0201-00003	2B-P22	IAL0282-00001	5I-P7
IAL0062-00001	2B-P24	IAL0135-00001	2B-P14	IAL0201-00004	3A-P19	IAL0284-00001	3B-2-P13
IAL0063-00001	2B-P25	IAL0136-00003	3B-2-P9	IAL0201-00008	2B-P23	IAL0285-00001	1I-P8
IAL0063-00002	2A-2- P4	IAL0137-00002	4B-P3	IAL0201-00010	3A-P20	IAL0289-00001	3B-2-P14
IAL0064-00002	1A-P4	IAL0138-00001	1A-P10	IAL0202-00002	3B-1 - P2	IAL0291-00003	5I-P8
IAL0065-00001	1A-O13	IAL0138-00002	3B-2-P10	IAL0204-00001	3A-P21	IAL0292-00001	4B-P9
IAL0065-00002	2B-P10	IAL0138-00004	2A-2- P8	IAL0204-00002	2A-2- P12	IAL0299-00002	3A-P24
IAL0068-00001	4I-P5	IAL0140-00002	2I-P2	IAL0206-00001	3A-P22	IAL0300-00001	4I-P19
IAL0070-00001	4I-P6	IAL0140-00004	1I-P4	IAL0209-00001	4I-P14	IAL0309-00002	3B-2-P15
IAL0071-00001	2B-P12	IAL0140-00005	2I-P3	IAL0211-00002	2I-P8	IAL0315-00001	2B-P5
IAL0073-00001	2A-2- P5	IAL0141-00001	2I-P4	IAL0212-00002	1A-O11	IAL0322-00001	1B-P5
IAL0078-00001	2B-P6	IAL0151-00001	2B-P15	IAL0213-00001	3B-2-P12	IAL0325-00001	5I-P9
IAL0080-00001	3A-P6	IAL0152-00001	2B-P7	IAL0219-00001	2A-1-P7		
IAL0083-00001	1I-P2	IAL0156-00001	4I-P12	IAL0219-00002	1A-P11		
IAL0086-00001	5I-P1	IAL0158-00002	4B-P4	IAL0221-00001	4I-P15		

KEYNOTE LECTURES



KEYNOTE LECTURE 1

Monday 9th January 2012

09:15 – 10:00 hrs.

Venue: Chaophya Ballroom, 2nd floor, Main Building

Professor Dr. Pranom Chantaranothai

Khon Kaen University, Thailand

E-mail: pranom@kku.ac.th

Topic: Phytogeography of Southeast Asia

Position: Professor of Botany at the Department of Biology, Khon Kaen University, Thailand

Current Academic Associate Activities:

- A Member of University Council of Khon Kaen University
- Editor-in-Chief of Thai Journal of Botany, The Botanical Society under the Royal Patronage of Her Majesty the Queen
- Honorary Research Associate, the Royal Botanic Gardens, Kew, United Kingdom

Current Research:

- Flowering plants for the Flora of Thailand Project
 - Families: Boraginaceae, Lecythidaceae, Myrtaceae, Sapotaceae and Sarcospermataceae)
 - Genera: *Phyllanthus* and *Trigonostemon* (Euphorbiaceae); *Mussaenda* and *Pavetta* (Rubiaceae); *Vitex* (Lamiaceae); *Indigofera* and *Uraria* (Leguminosae)
- Plant Diversity in Phu Phan, Phu Rua and Nam Pong National Parks, Thailand

Research Grants (Postdoctoral Research & Scholarships):

- Study of the Plant Family “Melastomataceae” at Institut für Botanik, University of Innsbruck, Austria (1991 – 1992) by Austrain Academic Exchange Service
- A Preliminary study on *Barringtonia* J.R. Forst and G. Forster of Thailand at School of Botany, Trinity College, University of Dublin, Ireland (1993 – 1994) by The International Scientific Cooperation Programme of the Commission of the European Communities Marie Curie Scheme
- A Revision of Sapotaceae in Thailand at Swedish Natural History Museum, Stockholm, Sweden (1995 – 1995) by The Swedish Institute.
- A Revision of Lecythidaceae in Thailand at Royal Botanic Gardens, Kew, United Kingdom (1999 – 1999, 6 months) by The Royal Society, UK
- The Taxonomy of *Pavetta* L. (Rubiaceae) in Thailand at School of Botany, Trinity College, University of Dublin, Ireland (2008 — 2008, 2 months) by the Commision of Higher Education, Thailand

Education:

- 1990 PhD, Trinity College, University of Dublin, Dublin, Ireland.
- 1985 BA (Poitical Science), Ramkamhaeng University, Bangkok, Thailand
- 1980 MSc (Botany), Chulalongkorn University, Bangkok, Thailand.
- 1977 BSc (Biology), Kasetsart University, Bangkok, Thailand.

PHYTOGEOGRAPHY OF SOUTHEAST ASIA

Chantaranothai P.

Applied Taxonomic Research Center, Faculty of Science, Khon Kaen University, Khon Kaen, Thailand

Southeast Asia's seasonal and tropical rainforest is four of the 25 global hotspots of biodiversity which are the Indo-Burma, Philippines, Sundaland and Wallacea hotspots. Its natural phytogeographical area comprises the mainland SE Asia and Malay Archipelago sub-region and boasts some of the largest numbers of vascular plant species in the world. Thailand has a species rich and complex biodiversity that differs in various parts of the country. The reason for the high level of species richness in Thailand is that the country is situated on the borders or at the cross-roads between four major biogeographical regions. The flora is therefore influenced by the Indo-Burmese, Indo-Chinese and Malesian elements. Seven floristic regions of Thailand are in use by botanists and the Flora of Thailand Project and more than eight forest types are recognized. A collaboration between Danish and Thai botanists was established in 1957 with the purpose of explore the natural vegetation of the country. In 1970, the first instalment of the Flora of Thailand was issued. However, Thailand is still heavily undercollected and the distributional data for most species are incomplete. At present, c. 60% of flowering plants have been studied and published. Nevertheless, the loss of biodiversity and its consequences for climate, economics, etc, are already becoming noticeable. A great deal of intensive floristic and ecological studies are still urgently needed, and also the protection and improvement of biodiversity should become the main focus of attention for the government.



KEYNOTE LECTURE 2

Tuesday 10th January 2012

09:00 – 10:00 hrs.

Venue: Chaophya Ballroom, 2nd floor, Main Building

Professor Dr. Pier Luigi Nimis

University of Trieste, Italy

E-mail: nimis@units.it

Topic: Computer-Aided identification tools: progress and problems

Position: Professor of Systematic Botany at the Department of Life Sciences of the University of Trieste

Experience:

The scientific interests of Prof. Nimis are centered on four main fields:

- Ecology - Bioindication and radioecology using lichens and bryophytes as bioindicators and bioaccumulators.
- Quantitative biogeography – multivariate analysis of plant distribution ranges in different parts of the world (Alaska-Yukon, Ontario, Siberia, Europe, Argentina).
- Lichenology - from floristics and taxonomy to vegetational and applied studies. Prof. Nimis is presently writing a lichen flora of Italy.
- Biodiversity , with emphasis on automatic generation of identification tools.

Activities:

- Prof. Nimis is member of the Editorial Boards of several international Journals . He is the coordinator of National and European Research Projects since 1991 and responsible for Lichenology within the Italian Antarctic Survey. He was Co-ordinator of the European Project KeyTo Nature from 2007 to 2010.
- Prof. Nimis was President of the Italian Lichen Society (1987-1993), Secretary of the Lichen Commission of O.P.T.I.M.A. (1993-2003), Member of the Executive Council of the International Association for Lichenology (IAL) and of the International Mycological Association, Editor-in-chief of the International Lichenological Newsletter (1997-2000), President of the International Association of Lichenology (2000-2004), and Member of the International Committee for Botanical Nomenclature
- Prof. Nimis was awarded with the small golden Panda of W.W.F. for his biomonitoring studies with lichens, with the O.P.T.I.M.A. medal (1995) for the best study on the Mediterranean flora published in 1993 (his monograph on the Lichens of Italy), and with the International Ferrari-Soave Prize for Biology from the Academy of Sciences of Turin (2009).

Academic career:

- 2009 - 2011 Dean of the PhD-School of Biomonitoring, University of Trieste.
- 1996 - 2003 Director of the Department of Biology, University of Trieste.
- 1988 - 1990 Chairman of the School of Biological Sciences, University of Trieste.
- 1986 Full Professor of Systematic Botany at the Faculty of Sciences, University of Trieste.
- 1978 a researcher at the Botanical Institute of the University of Trieste.
- 1977 Graduated with honors in Natural Sciences at the University of Trieste.

COMPUTER-AIDED IDENTIFICATION TOOLS: PROGRESS AND PROBLEMS

Nimis P. L.

Department of Life Sciences, University of Trieste, Italy

In the past, the tools for identifying organisms were printed on paper, in the form of dichotomous (rarely polytomous) keys. The constraints of a paper-printed text and the absence of computers forced most authors to organise their keys following the schemes of biological classification (keys to orders, families, genera, and finally species). Nowadays a wide array of identification tools can be generated more or less automatically starting from morpho-anatomical databases, such as single-access, multi- or free-access, and multi-entry keys. The order of couplets (choices) in an identification tool may be defined by the creator (single-access key), or may be freely selectable by the user (free-access key); a multi-entry key is an intermediate form that may combine advantages of both forms if only a small character subset is included in the multi-entry phase. In all computer-generated keys the process of identification can be made more or less completely independent from classification, with important and not always fully exploited consequences on their usability (e.g. for 'citizen science'). The new identification tools are available on a variety of media: internet, CD and DVD-Roms, printed paper, and also mobile devices such as smartphones. Furthermore, open access, an already established best practice in academic communication, puts the need of permanent cross-linking and data exchange among biodiversity data holders, while semantic markup of texts permit unprecedented increase of visibility, citations and re-use of biodiversity information; the electronic media become themselves tools and platforms for indexing, aggregating and retrieval of information, offering unique opportunities to accelerate biodiversity research and understanding. All of this is profoundly changing the way identification tools are created, where joint work among specialists and even the involvement of a large community of users (such as in the Wiki-approach) can play a much more important role than in the past. This also creates new problems as far IPRs are concerned, which need careful consideration. An exciting challenge for the next future will be the creation of computer-aided identification systems permitting an automatic integration of molecular and morpho-anatomical data.



KEYNOTE LECTURE 3

Wednesday 11th January 2012

09:00 – 10:00 hrs.

Venue: Chaophya Ballroom, 2nd floor, Main Building

Dr. Jolanta M. Miadlikowska
Duke University, United States
E-mail: jolantam@duke.edu

Topic: Novel molecular markers and their utility in molecular systematics of Fungi

Position: Research Scientist, Department of Biology, Duke University

Professional Academic Appointments:

- 2004 - present Research Scientist, Department of Biology, Duke University, Durham, NC (laboratory of Dr. F. Lutzoni).
- 2001 - 2004 Postdoctoral Research Associate, Department of Biology, Duke University, Durham, NC (laboratory of Dr. F. Lutzoni).
- 1999 - 2001 Postdoctoral Research Associate, Department of Botany, Field Museum of Natural History, Chicago, IL (laboratory of Dr. F. Lutzoni).
- 1999 - 2004 Adjunct Professor, Department of Plant Taxonomy and Nature Conservation, University of Gdansk, Gdansk, Poland.
- 1989 - 1999 Graduate Teaching Assistant, Department of Plant Ecology and Nature Protection, University of Gdansk, Gdansk, Poland. Instructor in the following courses: Systematics and Morphology of Cryptogamic Plants and Fungi, Systematics of Vascular Plants; Fundamentals of Lichenology, and Lichens as Bioindicators.
- 1987 - 1989 Technician and Research Assistant, Department of Plant Ecology and Nature Protection, University of Gdansk, Gdansk, Poland.

Research Interest:

Jolanta Miadlikowska is a systematist interested in the taxonomy, molecular systematics and evolution of lichenized fungi (with special emphasis on cyanolichens from the order Peltigerales) and their secondary cryptic associates (endolichenic fungi). She also explores the evolutionary mechanisms that shape interactions among bionts in lichen-forming associations. In her systematic work, she integrates traditional revisionary methods (morphology-, anatomy-, and chemistry-based approaches) and molecular phylogenetic tools. Recently she joined a team of mycologists exploring biodiversity, ecological role and biogeographical pattern in cryptic fungal communities associated with lichens and plants (endolichenic and endophytic fungi).

Education:

- 1994 - 1999 Ph.D. Biology (Lichenology), University of Gdansk, Gdansk, Poland.
- 1987 - 1989 M.Sc. Biology (Lichenology), University of Gdansk, Gdansk, Poland.
- 1983 - 1987 B.Sc. Biology, University of Gdansk, Gdansk, Poland.

NOVEL MOLECULAR MARKERS AND THEIR UTILITY IN MOLECULAR SYSTEMATICS OF FUNGI

Miadlikowska J. M. ¹

¹ Duke University, Department of Biology, Durham, North Carolina, United States

Although next generation sequencing methods have proven to be very successful in accelerating the process of data acquisition, development of novel molecular markers remains an integral component of the scalability of molecular systematic studies on lichen-forming fungi and associated symbionts. Existing fungal phylogenies from large-scale to species level surveys demonstrate an urgent need for novel single-copy protein-coding genes to resolve with high confidence phylogenetic relationships. For example, when using a cumulative super-matrix approach with available sequences of five frequently targeted loci for Lecanoromycetes, the resulting multilocus phylogeny was resolved but with many portions of the tree inconclusively supported, especially at deeper nodes. As part of the Assembling the Fungal Tree of Life project (AFToL 2), a comparative genomic approach was adopted to select all genes with the greatest potential to resolve the most challenging nodes of the fungal tree of life and to test their performance phylogenetically. Based on the comparison of 39 fungal genomes, 71 potentially single-copy genes were selected and a total of 243 primer pairs were designed and tested with six exemplar species representing Ascomycota, Basidiomycota and early-diverging fungi. The successful amplification and sequencing of 19 gene regions across these 6 representative taxa adds a total of about 15,000 bp per taxon, to the commonly sequenced nucLSU, nucSSU, mitSSU, MCM7, RPB1 and RPB2. The data set we generated for AFToL 2 includes 37 non-lichenized fungi for which the genomes are available and up to 26 lichen-forming members of the Lecanoromycetes, Dothideomycetes, Eurothiomycetes and Arthoniomycetes, for which the sequences were obtained from cultures of the mycobionts. Phylogenetic analyses were completed on each of the 19 novel and 8 commonly used gene regions and their multilocus combinations on the same set of taxa (including representatives of lichen-forming fungi) when possible. Phylogenetic efficiency (e.g., the level of resolution and internode robustness) and phylogenetic informativeness among all loci was compared and the utility of the novel genes in molecular systematics at various taxonomic levels is discussed. Phylogenetic performance of selected genes at the species level is shown based on a systematic revision of the genus *Peltigera*.



KEYNOTE LECTURE 4

Thursday 12th January 2012

09:00 – 10:00 hrs.

Venue: Chaophya Ballroom, 2nd floor, Main Building

Professor Dr. Jouko Rikkinen

University of Helsinki, Finland

E-mail: jouko.rikkinen@helsinki.fi

Topic: Symbiotic dispersal and lichen diversity – new insights from Cenozoic fossils and extant cyanolichens

Position: Professor of Botany, Department of Biosciences, University of Helsinki, Finland

Primary research interests and ongoing projects:

- Symbiont diversity in lichens and bryophyte symbioses. Doctoral students Katja Fedrowitz and Sanna Leppänen; graduate students Kaisa Jauhiainen and Veera Tuovinen.
- Cyanobacterial toxins in lichens and *Nostoc*-plant symbioses, Academy of Finland 2008–2011. Doctoral student Ulla Kaasalainen. In collaboration with Prof. Kaarina Sivonen <http://www.biocenter.helsinki.fi/groups/sivonen/gl.htm>.
- Palaeobiology of cryptogams preserved in amber. Graduate student Elina Kettunen. In collaboration with Dr. Alexander Schmidt <http://www.uni-goettingen.de/en/101998.html>.
- Systematics and ecology of resinicolous fungi, especially *Mycocaliciales*. Doctoral student Hanna Tuovila.
- Taita Research Station of University of Helsinki (Taita Hills, Kenya) <http://blogs.helsinki.fi/taita-research-station/>. Graduate students Mervi Laitinen and Petri Nyqvist.
- Pinkka – lajintuntemuksen oppimisympäristö ('Pinkka' – E-learning environment for biodiversity education). <http://www.helsinki.fi/pinkka/>

More details:

[https://tuhat.halvi.helsinki.fi/portal/en/persons/jouko-rikkinen\(a97cbe18-8aad-410d-b2ad-cbd23ee72268\).html](https://tuhat.halvi.helsinki.fi/portal/en/persons/jouko-rikkinen(a97cbe18-8aad-410d-b2ad-cbd23ee72268).html)

Education:

- 1999 Docent Lecturer in Botany, University of Helsinki
- 1997–1998 Post-Doctoral Fellow, Oregon State University
- 1995 Doctor of Philosophy (PhD), University of Helsinki
- 1988 Master of Science (MSc), University of Helsinki

**SYMBIOTIC DISPERSAL AND LICHEN DIVERSITY – NEW INSIGHTS
FROM CENOZOIC FOSSILS AND EXTANT CYANOLICHENS**

Rikkinen J. ¹

¹ Department of Biosciences, University of Helsinki, Helsinki, Finland

Some Paleozoic fossils may represent lichens, but their assignment to extant lineages is not possible due to their incomplete preservation, and the morphological homoplasy seen in extant lichen lineages. In contrast, during the Cenozoic numerous lichens were preserved as inclusions in amber. Some of these fossils are in excellent condition, and allow detailed comparisons with extant genera and species. Such fossils can be used for minimum age assessment of modern lichen lineages, but also offer unique evidence of evolutionary stasis in some morphological attributes, including structures that facilitate symbiotic dispersal in extant lichens. The first part of this presentation summarizes recent, previously unpublished findings from lichen fossils preserved in Baltic, Bitterfeld, and Dominican amber. Cyanobacteria participate in many types of symbioses, either serving as a source of fixed carbon and nitrogen, as in cyanolichens, or solely as a source of nitrogen, as in plant symbioses. Some strains of *Nostoc* are common symbionts in lichens and related genotypes are also found in thalloid bryophytes, cycads, and in the angiosperm *Gunnera*. Attempts to determine the strain identity of the cyanobacterial symbiont have only been made for a small fraction of all cyanolichen species. Tropical cyanolichens, in particular, have so far received very little attention. The second part of the presentation summarizes findings from ongoing studies on the genetic diversity of cyanobacterial symbionts in lichens and bryophytes. The topics touched include tripartite lichens, free-living lichen symbionts, and various community level diversity patterns in arctic, temperate and tropical environments. One unifying theme in both lines of research is the role of symbiotic dispersal in generating and maintaining biological diversity among lichen symbionts. The surprising level of genetic variation in modern lichen-symbiotic *Nostoc* may be partly explained by genetic drift in small, vertically transmitted symbiont populations. The Cenozoic lichen fossils show that such processes have had the opportunity to shape the genetic structure of lichen symbionts over tens of millions of years.



KEYNOTE LECTURE 5

Friday 13th January 2012

09:00 – 10:00 hrs.

Venue: Chaophya Ballroom, 2nd floor, Main Building

Auxiliar Professor Dr. Cristina Maria Filipe Máguas da Silva Hanson

Universidade de Lisboa, Portugal

E-mail: cmhanson@fc.ul.pt

Topic: Carbon-Water-Nitrogen relationships between lichens and the atmosphere: Tools to understand metabolism and ecosystem change

Position:

- Biologist, specialization in Ecophysiology and Stable Isotopes
- Professor at the Botany Department, University of Lisbon (FCUL)
- Researcher at Centre for Environmental Biology (CBA-FCUL)
- Member of Executive Committee of Centre for Environmental Biology (CBA-FCUL)
- Group Coordinator of Environment Functional Ecology in Centre for Environmental Biology (CBA-FCUL)
- Member of Portuguese Committee of SIBAE (Stable Isotopes Biosphere Atmosphere Exchange)

Professional Experience:

University professorship

- 1997 - present Auxiliar Prof
- 1994 - 1997 Assistant Prof
- 1991 - 1994 Assistant
- 1986 - 1987 Monitor

Portuguese Nominations:

- 2009 - present Member of Executive Committee of Centre for Environmental Biology
- 2009 - present Group Coordinator of Environment Functional Ecology in Centre for Environmental Biology (CBA)
- 2007 - 2009 Member of Executive Committee of Instituto de Ciência Aplicada e Tecnologia (ICAT)
- 1998 - 2006 Member of Scientific Committee of Center for Ecology and Plant Biology (CEBV)

International Nominations:

- 2000 - present Member of Portuguese Committee of SIBAE (Stable Isotope Biosphere Atmosphere Exchange)

Other non-academic activities:

- 2010 - present Member of Executive Committee of Portuguese Ecological Society (SPECO)

Education:

- 1997 PhD in Biology-Ecology and Systematics, University of Lisbon (UL)
- 1986 Degree in Biology, University of Lisbon (UL)

**CARBON-WATER-NITROGEN RELATIONSHIPS BETWEEN LICHENS
AND THE ATMOSPHERE: TOOLS TO UNDERSTAND METABOLISM
AND ECOSYSTEM CHANGE**

Máguas C.

Centre for Environmental Biology, Faculty of Sciences, University of Lisbon, Lisbon, Portugal

Lichens are highly diverse organisms offering a number of particular physiological and morphological characteristics, which enable the assessment of several environmental and ecological factors. Since lichens grow slowly and are strongly influenced by microclimatic conditions such as light, water, temperature, CO₂ concentration, and airborne deposition elements (i.e. nitrogen), their organic material (OM) integrates the interactions between local atmosphere conditions at their specific microhabitat over a long period. Moreover, this OM is also modeled by the continuous “equilibrium” behavior of lichens towards the surrounding atmosphere which is strongly influenced by several thallus traits such as morphology, carbon source and sink (which are mainly influenced by photosynthesis and respiration), water sources and availability time periods and nitrogen bio-availability. Indeed, our current knowledge in “biosphere-atmosphere exchange processes” lacks the understanding of these complex interactions between lichen biogenic fluxes of carbon, water and nitrogen and atmosphere. For that, tools such as the application of stable isotope techniques, may provide new insights into understanding lichen physiological and ecological processes. Due to their direct dependency on environmental conditions, lichens’ stable isotope compositions reflect changes of carbon and water as an integral over a long period and on a microenvironmental scale. Their poikilohydric nature enables them to settle under environmental conditions where higher plants are unable to survive and also to assimilate extraordinary substrates such as vapor or carbon microresources which are not commonly utilized by higher plants. Another important aspect is the need of a general framework in order to use lichen communities to evaluate and monitor complex ecosystems responses in a changing environment. Although there is an obvious local spatial scale of influence in what concerns environmental factors, which may limit the use of lichen communities to study factors associated to global change at a planetary scale, the application of spatial explicit analysis can contribute to model lichen responses to global drivers such as climate or eutrophication. The main objective of this talk is to provide an overview of past and recent insights on the interactions between local atmosphere and lichen-metabolism and functional diversity in order to a better use of lichens as tracers for biosphere-atmosphere exchange processes, and early impact indicators of global change.

AAIR LICHENS LUNCH SYMPOSIUM

Date: Tuesday 10th January 2012
Time: 12.45 – 13.15 hrs.
Room: Tarathép Hall building
Supported by: Aair Lichens Company
Abstract by: Philippe Giraudeau, Founder and Manager



DIOXINS AND FURANS IN FRANCE, RESULTS OF 10 YEARS OF SURVEYS BY THE AAIR LICHENS COMPANY, SUMMARY

Giraudeau P.

AAIR Lichens Company, 17 Rue Des Chevrettes, Carquefou, France

Nowadays, in France, environmental survey of dioxins, furans and heavy metals is compulsory for any kind of waste incinerator. In 1999, the usual methods were not accurate enough to assess the short and long-term exposition of individuals submitted to fallouts of PCDD/F in the air as well as no matrix allowed getting data linked to the average level of an industrial site, and based on periods longer than two months. Since 2000, one of the most accurate methods is the one using lichens. This method is sensitive whether the fallouts are low or high. From the beginning, the Aair Lichens Company understood the need in the utilization of this type of biomonitoring by conducting this kind of researches. However, in order to protect its invention and get enough funds for its researches, the company has patented the process. 10 years later, the results are fully recognized and the process is used by Aair Lichens for many different plant surveys with more than 85 sites being monitored. Both a partner for the government and for industrials, Aair Lichens can be capable of highlighting signatures and interferences while innovative mapping is already implemented to open new perspectives. The conference shows how much the lichen matrix is sensitive and underlines the role that Aair Lichens has been playing in France for this process could finally be recognized. Thus, the survey of dioxins and furans in lichens associates a biologic matrix to the necessity of an environmental survey that has the legitimacy of the impact on health.

KEYWORDS: lichens, PCDD/F, industries, health

Scientific Program



Monday 9th January 2012

Session: Keynote Lecturer 1 (KN1)
Date/Time: Monday 9th January, 9:20 – 10:00 hrs.
Room: Chaophya Ballroom, 2nd floor, Main Building

Lecturer: Professor Dr. Pranom Chantaranothai
Topic: PHYTOGEOGRAPHY OF SOUTH EAST ASIA

Session: Interdisciplinary Session
Topic: 1I: Exploring the lichen microbiome and its multifaceted interactions
Date/Time: Monday 9th January, 10:30 - 12:45 hrs.
Room: Chaophya Ballroom, 2nd floor, Main Building
Chairs: François Lutzoni, Martin Grube

S indicates student abstracts

1I-01: 10:30-10:45 hrs. IAL0085-00001 Page 1
LICHENICOLOUS FUNGI: DESCRIBED AND CRYPTIC FUNGAL COMPONENTS OF THE LICHEN MICROBIOME
Lawrey J., Diederich P.

S 1I-02: 10:45-11:00 hrs. IAL0274-00001 Page 1
DIVERSITY AND BIOGEOGRAPHY OF ENDOPHYTIC AND ENDOLICHENIC FUNGAL COMMUNITIES
Uren J., Lutzoni F., Miadlikowska J., Arnold A.

S 1I-03: 11:00-11:15 hrs. IAL0276-00001 Page 2
MICROBIAL COMMUNITY IN ANTARCTIC LICHENS
Park C.H., Kim K., Chun J., Jeong G., Hong S.

1I-04: 11:15-11:30 hrs. IAL0124-00001 Page 2
THE MICROBIOME OF LICHENS: STRUCTURAL AND BIOGEOGRAPHIC DIVERSITY
Berg G., Cardinale M., Grube M.

1I-05: 11:30-11:45 hrs. IAL0159-00002 Page 3
PYROSEQUENCING REVEALS PREVIOUSLY UNKNOWN PHYLOGENETIC, METABOLIC AND ECOLOGICAL COMPLEXITY WITHIN THE LICHEN MICROBIOME
Hodkinson B.P., Gottel N.R., Schadt C.W., Lutzoni F.

1I-06: 11:45-12:00 hrs. IAL0069-00001 Page 4
EVOLUTION OF PHOTOBIONT ASSOCIATIONS IN THE FAMILY VERRUCARIACEAE
Gueidan C., Thues H., Muggia L., Perez-Ortega S., Favero-Longo S., Joneson S., O'Brien H., Nelsen M.P., Duque-Thues R., Grube M., Friedl T., Brodie J., Andrew C.J., Lücking R., Lutzoni F.

1I-07: 12:00-12:15 hrs. IAL0067-00001 Page 5
PHOTOBIONT - MYCOBIONT INTERACTIONS IN THE WIDESPREAD LICHEN *CETRARIA ACULEATA*
Printzen C., Domaschke S., Fernandez Mendoza F.

1I-08: 12:15-12:30 hrs. IAL0228-00001 Page 5
GENE MOVEMENT IN THE PHOTOBIONT OF *RAMALINA MENZIESII*
Werth S., Sork V.L.

11-09: 12:30-12:45 hrs. IAL0226-00004 *Page 6*
INSIGHTS ON *TREBOUXIA* PHYCOBIONTS: COEXISTENCE OF TAXA IN A LICHEN THALLUS, MOLECULAR MARKERS, PHYSIOLOGICAL PERFORMANCES, HGT, GENOME ANALYSIS
Barreno E., Lichen Symbiogenesis Team

Session: Focus Session
Topic: 1A: Lichen conservation: concepts and action
Date/Time: Monday 9th January, 13:30-15:31 hrs.
Room: Chaophya Ballroom, 2nd floor, Main Building
Chairs: Christoph Scheidegger / Olga Nadyeina

1A-01: 13:30-13:38 hrs. IAL0133-00001 *Page 7*
LICHEN CONSERVATION: FROM ACTIONS TO CONCEPTS AND BACK
Scheidegger C., Stofer S.

1A-02: 13:38-13:53 hrs. IAL0129-00001 *Page 7*
LUNGWORT'S PATH OF LEAST RESISTANCE IS A STEEPLECHASE IN THE FOREST: SMALL SCALE GENETIC PATTERN OF *LOBARIA PULMONARIA* IN A PRIMEVAL BEECH FOREST LANDSCAPE
Nadyeina O.V., Dymytrava L.V., Naumovych G.O., Postoyalkin S.V., Scheidegger C.

S 1A-03: 13:53-14:08 hrs. IAL0162-00001 *Page 8*
***LOBARIA SCROBICULATA*, A THREATENED SPECIES: INSIGHT POPULATION DYNAMICS**
Merinero S., Martinez I., Rubio-Salcedo M.

1A-04: 14:08-14:23 hrs. IAL0149-00001 *Page 9*
FACTORS AFFECTING THE DISTRIBUTION OF SPECIES OF CONSERVATION IMPORTANCE IN THE NEW FOREST NATIONAL PARK UK
Wolseley P., Sanderson N., Thues H., Eggleton P.

1A-05: 14:23-14:38 hrs. IAL0214-00001 *Page 10*
LICHENS OF CALCAREOUS ROCKS IN FINLAND
Pykala J.

1A-06: 14:38-14:53 hrs. IAL0207-00001 *Page 11*
WINNERS AND LOSERS IN ECOLOGICAL RESTORATION: EFFECTS OF NON-INDIGENOUS HERBIVORE REMOVAL ON SAXICOLOUS LICHENS
Blanchon D., Elliott C., Ennis I., Hayward G., Galbraith M., Aguilar G.

1A-07: 14:53-15:08 hrs. IAL0248-00001 *Page 12*
LICHEN CONSERVATION IN DENSELY POPULATED AREAS: PRESSURES AND MEASURES
Sparrius L.

S 1A-08: 15:08-15:23 hrs. IAL0146-00001 *Page 12*
TRADE AND TRADITIONAL KNOWLEDGE OF LICHENS IN NEPAL HIMALAYAS
Devkota S., Scheidegger C.

1A-09: 15:23-15:26 hrs. IAL0241-00001 *Page 13*
POPULATION GENETICS AND CO-PHYLOGEOGRAPHY OF THE FUNGAL AND ALGAL SYMBIONTS OF *LOBARIA PULMONARIA* IN EUROPE
Dal Grande F., Widmer I., Wagner H.H., Scheidegger C.

1A-010: 15:26-15:27 hrs. IAL0019-00001 *Page 14*
OLD, ARTIFICIALLY DRAINED SWAMP FORESTS PROVIDE VALUABLE HABITATS FOR LICHENS: A COMPARATIVE CASE STUDY FROM ESTONIA
Lõhmus P.

Lichen: from genome to ecosystem in a changing world

- S** **1A-011:** 15:27-15:28 hrs. IAL0212-00002 *Page 15*
THE LICHEN KILLER: WHEN STONE CONSERVATION ASKS FOR NEW METHODS OF LICHEN DEVITALIZATION
Bertuzzi S., Candotto Carniel F., Tretiach M.
- 1A-012:** 15:28-15:29 hrs. IAL0009-00007 *Page 16*
THE NECESSITY FOR ESTABLISHING A DATABASE AND AN INDEX OF THE DETERIORATION OF CULTURAL HERITAGE STONEMWORK BY LICHENS AS AN AID TO CONSERVATION WORK
Favero - Longo S.E., Gazzano C., Caneva G., Cannon P., Fiorentino J., Gómez Bolea A., Grillo M., Marques J., Matteucci E., Modenesi P., Nimis P., Prieto-Lamas B., Ravera S., Roccardi A., Salvadori O., Seaward M.R., Stocker-Wörgötter E., Piervittori R.
- 1A-013:** 15:29-15:30 hrs. IAL0065-00001 *Page 17*
CONSERVATION OF LICHENS IN RUSSIAN FEDERATION: MODERN STATUS
Muchnik (Moutchnik) E.E.
- S** **1A-014:** 15:30-15:31 hrs. IAL0004-00001 *Page 18*
LICHEN CONSERVATION AS THE ELEMENT OF NATURA 2000
Dingová A., Valachovič M.

Session: Focus Session
Topic: 1B: Genomic approaches to studying the lichen symbiosis
Date/Time: Monday 9th January, 13:30-15:30 hrs.
Room: Grand Rachada Ballroom, 5th floor, Tarntip Building
Chairs: Daniele Armaleo / Ólafur Andrésón / Vivian Miao

- 1B-01:** 13:30-13:35 hrs. IAL0319-00001 *Page 19*
APPROACHING LICHENS BY UNWINDING COMPLEMENTARY GENOMES: AN INTRODUCTION
Miao V., Armaleo D.
- 1B-02:** 13:35-13:50 hrs. IAL0293-00001 *Page 19*
GENOME SEQUENCING OF XANTHORIA PARIETINA 46-1-SA22
Dyer P.S., Crittenden P.D., Archer D.B., Barry K., Foster B., Copeland A., Kuo A., Grigoriev I.
- 1B-03:** 13:50-14:05 hrs. IAL0262-00001 *Page 20*
PARTIAL GENOME OF THE PHYCOBIONT TREBOUXIA TR-9 ISOLATED FROM RAMALINA FARINACEA (L.) ACH. SEQUENCED BY 454 PYROSEQUENCING
Martínez-Alberola F., Barreno E., Marín I., Del Campo E.M., Casano L.M., Guéra A., Aldecoa R., Del Hoyo A.
- 1B-04:** 14:05-14:20 hrs. IAL0018-00001 *Page 20*
TREBOUXIA DECOLORANS - ARE THERE FUNGAL GENES IN LICHEN ALGAE?
Beck A., Divakar P.K., Zhang N., Molina M.C., Price D., Bhattacharya D., Struwe L.
- 1B-05:** 14:30-14:50 hrs. IAL0145-00001 *Page 21*
PELTIGERA LICHEN SYMBIOMES: METAGENOMICS OF A COMPLEX NATURAL COMMUNITY
Andresson O., Jónsson Z.O., Xavier B.B., Manoharan S.S., Miao V., Snaebjarnarson V., Jonsson H.
- 1B-06:** 14:50-15:10 hrs. IAL0229-00002 *Page 21*
DECODING SYMBIOSIS: THE TWO GENOMES OF THE LICHEN CLADONIA GRAYI
Armaleo D., Mueller O., Lutzoni F., Martin F., Blanc G., Merchant S., Collart F.
- 1B-07:** 15:10-15:30 hrs. IAL0172-00001 *Page 22*
LICHEN MICROBIOMES: A MULTIPHASIC APPROACH TOWARDS UNDERSTANDING DIVERSITY AND FUNCTION
Grube M., Cardinale M., Müller H., Riedel K., Berg G.

Tuesday 10th January 2012

Session: Keynote Lecturer 2 (KN2)
Date/Time: Tuesday 10th January, 9:00 – 10:00 hrs.
Room: Chaophya Ballroom, 2nd floor, Main Building

Lecturer: Professor Dr. Pier Luigi Nimis
Topic: COMPUTER-AIDED IDENTIFICATION TOOLS: PROGRESS AND PROBLEMS

Session: Interdisciplinary Session
Topic: 2I: Adaptation and morphological evolution
Date/Time: Tuesday 10th January, 10:30-12:30 hrs.
Room: Chaophya Ballroom, 2nd floor, Main Building
Chairs: Mats Wedin / Thorsten Lumbsch

2I-O1: 10:30-10:45 hrs. IAL0020-00004 *Page 23*
THALLUS ARCHITECTURE AND DOMINANCE IN *CLADINA*
Crittenden P.D., Sturrock C., Ellis C.J.

2I-O2: 10:45-11:00 hrs. IAL0185-00001 *Page 23*
PHENOTYPIC PLASTICITY IN LICHENS: INSIGHTS ON THE BIOLOGY OF THE EXTREME MODIFICATIONS IN *CETRARIA ACULEATA* (PARMELIACEAE)
Perez-Ortega S., Fernandez-Mendoza F., Raggio J., Vivas M., Ascaso C., Sancho L., Printzen C., De Los Rios A.

2I-O3: 11:00-11:15 hrs. IAL0072-00001 *Page 24*
DEVELOPMENT OF THALLUS AXES IN *USNEA LONGISSIMA*, A FRUTICOSE LICHEN SHOWING DIFFUSE GROWTH
Sanders W.B., De Los Rios A.

2I-O4: 11:15-11:30 hrs. IAL0140-00001 *Page 24*
THE *TEPHROMELA ATRA* SPECIES-COMPLEX: A CASE STUDY OF SYMBIOTIC SPECIES EVOLUTION
Muggia L., Spribille T., Perez-Ortega S., Grube M.

2I-O5: 11:30-11:45 hrs. IAL0098-00001 *Page 25*
RECONSTRUCTION OF ANCESTRAL STATES USING PHYLOGENIES: PARMELIACEAE AS A CASE STUDY
Kauff F., Divakar P.K., Lumbsch H.T., Crespo A.

2I-O6: 11:45-12:00 hrs. IAL0096-00003 *Page 25*
MORPHOLOGICAL DISPARITY AND SPECIES DELIMITATION OF LICHEN IN THE GENUS *CLADIA* (LECANORALES, ASCOMYCOTA)
Parnmen S., Rangsiruji A., Mongkolsuk P., Boonpragob K., Lumbsch H.T.

2I-O7: 12:00-12:15 hrs. IAL0075-00001 *Page 26*
MORPHOLOGICAL VARIATION, SPECIES CIRCUMSCRIPTION AND PHYLOGENETIC RELATIONSHIPS IN THE GENUS *PECCANIA* (LICHINACEAE)
Schultz M.

2I-08: 12:15-12:30 hrs. IAL0277-00001 Page 27
GOOD-BYE MORPHOLOGY, OR THREE CHEERS FOR NUANCE? MOLECULAR PHYLOGENETICS AND A POSTERIORI MORPHOLOGICAL ANALYSIS IN TWO CRUSTOSE LICHEN GENERA
Spribille T., Grube M.

Session: Focus Session
Topic: 2A-1: Graphidaceae: progress in understanding the evolution and diversity of the largest family of tropical crustose lichens
Date/Time: Tuesday 10th January, 13:30-14:30 hrs.
Venue: Chaophya Ballroom, 2nd floor, Main Building
Chairs: Robert Lücking/ Khwanruan Papong

S 2A-1-01: 13:30-13:45 hrs. IAL0178-00001 Page 28
HISTORICAL BIOGEOGRAPHY, ECOLOGY AND SYSTEMATICS OF THE FAMILY GRAPHIDACEAE (ASCOMYCOTA: OSTROPALES)
Rivas Plata E.

2A-1-02: 13:45-14:00 hrs. IAL0016-00001 Page 28
DILEMMAS IN SPECIES AND GENUS DELIMITATION IN E.G. GRAPHIDACEAE
Aptroot A.

S 2A-1-03: 14:00-14:15 hrs. IAL0033-00001 Page 29
TAXONOMY AND DIVERSITY OF LIPELLATE GRAPHIDACEAE (OSTROPALES) AT PHU LUANG WILDLIFE SANCTUARY, THAILAND
Poengsungnoen V., Mongkolsuk P., Boonpragob K., Manoch L., Kalb K.J.

2A-1-04: 14:15-14:30 hrs. IAL0283-00001 Page 29
MORPHO-CHEMOTAXONOMY OF THE GRAPHIDACEAE (SENSU LATO) LICHENS IN THE KALAHAN FOREST RESERVE OF NUEVA VIZCAYA, PHILIPPINES
Tabaquero A.L., Bawingan P.A., Lücking R.

Session: Focus Session
Topic: 2A-2: Parmeliaceae: improving our understanding of taxonomy, classification and biogeography
Date/Time: Tuesday 10th January, 14:30-15:45 hrs.
Room: Chaophya Ballroom, 2nd floor, Main Building
Chairs: Pradeep Kumar Divakar / Kawinnat Buaruang

2A-2-01: 14:30-14:45 hrs. IAL0170-00001 Page 30
MULTILOCUS PHYLOGENY AND CLASSIFICATION OF PARMELIACEAE (ASCOMYCOTA) DERIVED FROM PARSYS-10
Divakar P.K., Lumbsch T., Wedin M., Bjerke J., Mccune B., Kauff F.

2A-2-02: 14:45-15:00 hrs. IAL0177-00001 Page 31
MAKING SENSE OF CRYPTIC DIVERSITY, BIOGEOGRAPHY, AND DIVERSIFICATION IN LICHEN-FORMING FUNGI - A STUDY OF BROWN PARMELIOID LICHENS (PARMELIACEAE, ASCOMYCOTA)
Leavitt S., Chatwin W., Garcia S., Esslinger T.E., Lumbsch T.

S 2A-2-03: 15:00-15:15 hrs. IAL0272-00001 Page 31
MOLECULAR PHYLOGENETICS AND SPECIES DELIMITATION IN MENEGAZZIA (PARMELIACEAE)
Tronstad I.K., Myles B.C., Grube M., Bjerke J.

S 2A-2-04: 15:15-15:30 hrs. IAL0052-00001 Page 32
**GEOGRAPHICAL STRUCTURE OF *CETRARIA ACULEATA* POPULATIONS ALONG A WIDE
LATITUDINAL TRANSECT**
Fernandez Mendoza F., Printzen C.

2A-2-05: 15:30-15:45 hrs. IAL0198-00001 Page 33
PHYLOGENY OF THE GENUS *VULPICIDA* AND DELIMITATION OF THE SPECIES
Saag L., Mark K., Saag A., Thell A., Randlane T.

Session: Focus Session
Topic: 2B: Forest lichens: their ecology and distribution
Date/Time: Tuesday 10th January, 13:30-15:30 hrs.
Room: Grand Rachada Ballroom, 5th floor, Tarntip Building
Chairs: Susan Will-Wolf / Gintaras Kantvilas

2B-01: 13:30-13:45 hrs. IAL0040-00006 Page 34
ECOLOGICAL STUDY OF LICHENS IN THAILAND
*Polyiam W., Pangpet M., Wannalux B., Boonpeng C., Santanoo S., Pohjaroen W., Senglek S.,
Boonpragob K.*

S 2B-02: 13:45-14:00 hrs. IAL0104-00001 Page 35
**CORTICOLOUS LICHEN COMMUNITIES AS INDICATORS OF VEGETATION TYPES ALONG
ENVIRONMENTAL GRADIENTS IN KNUCKLES MOUNTAIN RANGE - SRI LANKA**
Weerakoon G.S., Mccune B., Wolseley P., Wijeyaratne S.C.

S 2B-03: 14:00-14:15 hrs. IAL0077-00001 Page 36
**OCCURRENCE AND HOST SPECIFICITY OF MACRO-LICHENS AMONG TROPICAL DECIDUOUS
FOREST OF SHIMOGA DISTRICT, SOUTHERN INDIA**
Vinayaka K.S., Krishnamurthy Y.

2B-04: 14:15-14:30 hrs. IAL0134-00001 Page 36
**EPIPHYTIC LICHEN COMMUNITIES IN BOREAL CONIFER FORESTS OF PACIFIC COAST OF
NORTHEAST ASIA (RUSSIA)**
Velikanov A., Skirina I.

2B-05: 14:30-14:45 hrs. IAL0220-00001 Page 37
USING LICHENS TO EVALUATE TASMANIAN FORESTS
Kantvilas G., Jarman J.

S 2B-06: 14:45-15:00 hrs. IAL0160-00001 Page 37
**ECOLOGICAL FACTORS AND POPULATION DYNAMICS OF *LOBARIA PULMONARIA*: IS IT AN
ENDANGERED SPECIES IN SPAIN?**
Rubio-Salcedo M., Martínez I., Merinero S., Otálora M.G.

S 2B-07: 15:00-15:15 hrs. IAL0143-00001 Page 38
**TESTING HYPOTHESES OF THE DECLINE OF THE CRITICALLY ENDANGERED *ERIODERMA
PEDICELLATUM* (PANNARIACEAE)**
Cornejo C., Scheidegger C.

S 2B-08: 15:15-15:30 hrs. IAL0130-00001 Page 38
**DIVERSITY, COMMUNITY STRUCTURE, AND SPATIAL PATTERNS OF MACROLICHENS IN A
TEMPERATE FOREST MAPPED PLOT IN SANTA CRUZ, CALIFORNIA**
Kraichak E., Carter B.E., Shaffer J., Gilbert G.S.

Wednesday 11th January 2012

Session: Keynote Lecturer 3 (KN3)
Date/Time: Wednesday 11th January, 9:00 – 10:00 hrs.
Room: Chaophya Ballroom, 2nd floor, Main Building

Lecturer: Dr. Jolanta M. Miadlikowska
Topic: NOVEL MOLECULAR MARKERS AND THEIR UTILITY IN MOLECULAR SYSTEMATICS OF FUNGI

Session: Interdisciplinary Session
Topic: 3I: New approaches to understanding biosynthesis and ecological roles of metabolites in lichens
Date/Time: Wednesday 11th January, 10:30-12:30 hrs.
Room: Chaophya Ballroom, 2nd floor, Main Building
Chairs: Lucia Muggia / Knut Solhaug

3I-01: 10:30-10:50 hrs. IAL0144-00001 *Page 39*
GAINING NEW INSIGHTS INTO LICHEN SECONDARY METABOLISM: ECOLOGICAL FACTORS TRIGGER CHEMOSYNDROMIC VARIATION WITHIN SPECIES OF THE GENUS XANTHOPARMELIA AND NOVEL TECHNIQUES TO DECIPHER THE GENETIC POTENTIAL OF POLYKETIDE BIOSYNTHESIS IN A CULTURED METABOLITE-PRODUCING MYCOBIONT
Stocker-Wörgötter E.

S 3I-02: 10:50-11:10 hrs. IAL0288-00001 *Page 40*
IDENTIFICATION OF LICHEN COMPOUNDS USING LIQUID CHROMATOGRAPHY
Fankhauser J.D., Elix J.A., Schmitt I., Lumbsch H.T.

3I-03: 11:10-11:30 hrs. IAL0153-00001 *Page 40*
SNAILS AVOID THE MEDULLA OF *LOBARIA PULMONARIA* AND *L. SCROBICULATA* DUE TO PRESENCE OF SECONDARY COMPOUNDS
Asplund J.

S 3I-04: 11:30-11:50 hrs. IAL0165-00001 *Page 41*
ACETONE-EXTRACTABLE COMPOUNDS PROTECT LICHENS AGAINST MOLLUSCS
Černajová I., Svoboda D.

3I-05: 11:50-12:10 hrs. IAL0009-00008 *Page 42*
ALLELOPATHIC EFFECTS OF LICHEN SECONDARY METABOLITES AGAINST POTENTIAL COMPETITORS FOR ROCK SURFACES
Favero-Longo S.E., Gazzano C., Piervittori R.

3I-06: 12:10-12:30 hrs. IAL0226-00001 *Page 43*
ROLE OF NITRIC OXIDE IN THE RESPONSE OF *RAMALINA FARINACEA* TO LEAD
Barreno E., Diaz-Rodriguez C., Catala M.

Thursday 12th January 2012

Session: Keynote Lecturer 4 (KN4)
Date/Time: Thursday 12th January, 9:00 – 10:00 hrs.
Room: Chaophya Ballroom, 2nd floor, Main Building

Lecturer: Professor Dr. Jouko Rikkinen
Topic: SYMBIOTIC DISPERSAL AND LICHEN DIVERSITY – NEW INSIGHTS FROM CENOZOIC FOSSILS AND EXTANT CYANOLICHENS

Session: Interdisciplinary Session
Topic: 4I: Lichenological research in South-East Asia and the Pacific region
Date/Time: Thursday 12th January, 10:30-12:30 hrs.
Room: Chaophya Ballroom, 2nd floor, Main Building
Chairs: André Aptroot / Wanaruk Saipunkaew

4I-O1: 10:35-10:45 hrs. IAL0287-00001 Page 44
THE OCEANEAN LICHEN REALM
Feuerer T.

4I-O2: 10:45-11:00 hrs. IAL0255-00001 Page 44
AN OVERVIEW OF LICHEN DIVERSITY AND CONSERVATION IN WESTERN GHATS, INDIA
Nayaka S., Upreti D.K.

4I-O3: 11:00-11:15 hrs. IAL0069-00002 Page 45
THE GENUS STAUROTHELE IN VIETNAM: SPECIES DIVERSITY AND PHYLOGENETIC PLACEMENT
Gueidan C.

S 4I-O4: 11:15-11:30 hrs. IAL0088-00002 Page 45
THE REPRODUCTIVE ECOLOGY OF *ICMADOPHILA SPLACHNIRIMA* – A RARE AUSTRALASIAN LICHEN EXHIBITING SEXUAL AND ASEQUAL REPRODUCTION
Ludwig L.R., Lord J.M., Burritt D.J., Summerfield T.C.

4I-O5: 11:30-11:45 hrs. IAL0235-00001 Page 46
lichen studies in the Cordillera region Northern Philippines - Past, Present and Future
Bawingan P.A., Lardizaval M.

S 4I-O6: 11:45-12:00 hrs. IAL0008-00001 Page 46
STUDY OF MACROLICHEN DIVERSITY BETWEEN *EUCALYPTUS*, *PINUS*, AND *ALTINGIA* TREES AT CIBODAS BOTANICAL GARDEN, WEST JAVA
Zulfikar R., Sedayu A., Arif A.

4I-O7: 12:00-12:15 hrs. IAL0037-00001 Page 47
MACROLICHEN DIVERSITY CAN BE USED AS A TOOL TO ANALYZE THE FOREST CONDITION AT HORTON PLAINS NATIONAL PARK, SRI LANKA
Jayalal R.U., Wolseley P., Wijesundara S., Karunaratne V.

Session: Focus Session
Topic: 3A: Molecular phylogenetics
Date/Time: Thursday 12th January, 13:30-15:30 hrs.
Room: Chaophya Ballroom, 2nd floor, Main Building
Chairs: Cecile Gueidan / Achariya Rangsiruji

3A-01: 13:30-13:50 hrs. IAL0273-00001 *Page 48*
THE DATING OF FUNGI AND PLANTS
Lutzoni F., Magallon S., Nowak M., Alfaro M., Mcdonald T., Miadlikowska J., Reeb V.

S 3A-02: 13:50-14:10 hrs. IAL0174-00001 *Page 48*
DIVERSIFICATION OF LICHEN-FORMING ASCOMYCETES
Nelsen M.P., Lücking R., Lumbsch H., Ree R.

3A-03: 14:10-14:25 hrs. IAL0121-00001 *Page 49*
PUNCTUATIONAL EVOLUTION AND RECENTLY ACCELERATED DIVERSIFICATION: INSIGHTS INTO THE EVOLUTION OF OSTROPOMYCETIDAE
Schmitt I., Wedin M., Baloch E., Parnmen S., Papong K., Rivas Plata E., Lücking R., Healy R.A., Lumbsch T.

S 3A-04: 14:25-14:40 hrs. IAL0143-00002 *Page 50*
MULTI-GENE PHYLOGENY DEFINES THE MONOPHYLY OF LOBARIA SECTION LOBARIA
Cornejo C., Scheidegger C.

3A-05: 14:40-14:55 hrs. IAL0044-00001 *Page 51*
DELIMITING PHYLOGENETIC SPECIES AMONG EUROPEAN TAXA OF THE GENUS USNEA
Törra T., Saag L., Randlane T., Del-Prado R., Saag A.

3A-06: 14:55-15:10 hrs. IAL0145-00002 *Page 52*
MITOCHONDRIAL GENOMES FROM THE LICHENIZED FUNGI PELTIGERA MEMBRANACEA AND PELTIGERA MALACEA
Andresson O., Miao V., Jonsson Z.O., Xavier B.B.

3A-07: 15:10-15:30 hrs. IAL0103-00004 *Page 53*
NEW APPROACHES TO INCORPORATE AMBIGUOUSLY ALIGNED SEQUENCE PORTIONS AND MORPHOLOGICAL DATA INTO PHYLOGENETIC ANALYSIS
Lücking R.

Session: Focus Session
Topic: 3B-1: Bioinformatics
Date/Time: Thursday 12th January, 13:30-14:30 hrs.
Room: Grand Rachada Ballroom, 5th floor, Tarntip Building
Chairs: Gerhard Rambold

3B-1-01: 13:35-13:45 hrs. IAL0248-00002 *Page 54*
COLLECTING, VALIDATING AND USING DISTRIBUTION DATA OF LICHENS IN THE NETHERLANDS
Sparrius L.

3B-1-02: 13:45-13:55 hrs. IAL0103-00003 *Page 55*
THE POWER OF ITS: USING MEGAPHYLOGENIES OF BARCODING GENES TO REVEAL INCONSISTENCIES IN TAXONOMIC IDENTIFICATIONS OF GENBANK SUBMISSIONS
Lücking R., Kalb K.J., Essene A.

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- S** **3B-1-03:** 13:55-14:05 hrs. IAL0160-00002 *Page 55*
EFFECTIVENESS OF THE NATURA 2000 NETWORK IN PROTECTING MEDITERRANEAN LICHEN SPECIES
Rubio-Salcedo M., Martínez I., Carreño F.
- S** **3B-1-04:** 14:05-14:15 hrs. IAL0057-00006 *Page 56*
MULTILINGUALITY IN LICHENOLOGY
Sohrabi M.
- 3B-1-05:** 14:15-14:25 hrs. IAL0202-00001 *Page 57*
DATA EXCHANGE AND PROCESSING IN DIGITAL SCIENCE INFRASTRUCTURE PLATFORMS FOR BIODIVERSITY INFORMATION
Triebel D., Hagedorn G., Rambold G.

Session: Focus Session
Topic: 3B-2: The ecological roles of lichens in diverse ecosystems
Date/Time: Thursday 12th January, 14:30-16:00 hrs.
Room: Grand Rachada Ballroom, 5th floor, Tarntip Building
Chairs: Toby Spribille

- 3B-2-01:** 14:30-14:45 hrs. IAL0119-00001 *Page 58*
ROLE OF LICHENS IN DETERIORATIVE PROCESSES THREATENING OUR STONY CULTURAL HERITAGE: CASE STUDY OF LICHEN COLONIZATION IN MACHU PICCHU (PERU)
De Los Rios A., Perez-Ortega S., Speranza M., Huallparimachi G., Wierzchos J., Galvan V., Astete F., Ascaso C.
- S** **3B-2-02:** 14:45-15:00 hrs. IAL0205-00001 *Page 59*
THE INVESTIGATION OF EPIPHYTIC LICHENS DIVERSITY IN THE NORTHEAST OF THAILAND
Dathong W., Thanee N., Saipunkaew W.
- S** **3B-2-03:** 15:00-15:15 hrs. IAL0012-00001 *Page 59*
CHANGES IN EPIGEIC LICHEN COMMUNITIES IN CALCAREOUS GRASSLANDS (ALVARS) DUE TO THE CESSATION OF TRADITIONAL LAND USE
Leppik E., Jüriado I., Suija A., Liira J.
- 3B-2-04:** 15:15-15:30 hrs. IAL0228-00002 *Page 60*
ISLAND BIOGEOGRAPHY OF *LOBARIA* SECT. *LOBARIA* IN MACARONESIA
Werth S., Cheenacharoen S., Scheidegger C.
- 3B-2-05:** 15:30-15:45 hrs. IAL0050-00001 *Page 60*
LICHEN IDENTIFICATION IN WOODLAND CARIBOU SCAT USING DNA BARCODING
Mcmullin R.T., Newmaster S.G., Fazekas A.
- S** **3B-2-06:** 15:45-16:00 hrs. IAL0136-00001 *Page 61*
ANALYSIS OF TWELVE MOLECULAR LOCI SUGGESTS HIGH PHOTOBIONT AND LOW MYCOBIONT DIVERSITY IN POPULATIONS OF *LASALLIA PUSTULATA*
Sadowska-des A., Otte J., Schmitt I.

Friday 13th January 2012

Session: Keynote Lecturer 5 (KN5)
Date/Time: Friday 13th January, 9:00 – 10:00 hrs.
Room: Chaophya Ballroom, 2nd floor, Main Building

Lecturer: Auxiliar Professor Dr. Cristina Maria Filipe Máguas da Silva Hanson
Topic: CARBON-WATER-NITROGEN RELATIONSHIPS BETWEEN LICHENS AND THE ATMOSPHERE: TOOLS TO UNDERSTAND METABOLISM AND ECOSYSTEM CHANGE

Session: Interdisciplinary Session
Topic: 5I: Global change and lichen biology
Date/Time: Friday 13th January, 10:30-12:30 hrs.
Room: Chaophya Ballroom, 2nd floor, Main Building
Chairs: Sarah Jovan / Christopher Ellis

5I-O1: 10:30-10:45 hrs. IAL0142-00001 *Page 62*
ALTITUDINAL DISTRIBUTION OF CAUCASIAN LICHENS SUPPORTS THE KEY ROLE OF CLIMATE IN HOLARCTIC DISTRIBUTION PATTERNS
Otte V., Ritz M.S.

5I-O2: 10:45-11:00 hrs. IAL0191-00001 *Page 62*
RECONSTRUCTING HISTORIC BIODIVERSITY LOSS: LICHENS AS A POWERFUL NEW ARCHAEOLOGICAL TOOL
Ellis C. J., Belinchon R., Yahr R., Coppins B.

5I-O3: 11:00-11:15 hrs. IAL0034-00001 *Page 63*
BARK ACIDITY AND LICHENS OCCURRENCE IN GOMEL, BELARUS
Tsurykau A., Khranchankova V.

5I-O4: 11:15-11:30 hrs. IAL0155-00001 *Page 63*
THE RESPONSE OF EUTROPHIC LICHENS TO DIFFERENT FORMS OF NITROGEN IN THE LOS ANGELES BASIN
Jovan S.E., Riddell J., Padgett P., Nash T.H.

5I-O5: 11:30-11:45 hrs. IAL0254-00001 *Page 64*
WHY LICHENS ARE OZONE TOLERANT? A POSSIBLE EXPLANATION FROM CELL TO SPECIES LEVEL
Tretiach M., Bertuzzi S., Candotto Carniel F., Davies L., Francini A.

5I-O6: 11:45-12:00 hrs. IAL0149-00002 *Page 65*
THE OPAL AIR SURVEY: ENGAGING THE PUBLIC WITH LICHENS
Wolseley P., Hill L., Seed L., Davies L., Power S., Hilton B.

5I-O7: 12:00-12:15 hrs. IAL0304-00001 *Page 66*
LICHENS, BRYOPHYTES AND CLIMATE CHANGE (LBCC) UTILIZING SYMBIOTA SOFTWARE
Nash T.H., Gries C., Gilbert E.

Session: Focus Session
Topic: 4A: Evolution and systematics in the teloschistales
Date/Time: Friday 13th January, 13:30-15:30 hrs.
Room: Chaophya Ballroom, 2nd floor, Main Building
Chairs: Ester Gaya / Ulrik Søchting

4A-01: 13:30-13:50 hrs. IAL0253-00001 *Page 67*
SYSTEMATICS AND EVOLUTION WITHIN THE ORDER TELOSCHISTALES AND FAMILY TELOSCHISTACEAE (ASCOMYCOTA, FUNGI) WITH A MULTI-LOCUS SUPERMATRIX APPROACH
Gaya E., Högnabba F., Ramírez-Mejía M., Holguín A., Molnar K., Fernández-Brime S., Stenroos S., Arup U., Søchting U., Van Den Boom P., Lücking R., Vargas R., Sipman H., Lutzoni F.

4A-02: 13:50-14:10 hrs. IAL0110-00001 *Page 68*
PHYLOGENY AND TAXONOMY OF THE TELOSCHISTACEAE (ASCOMYCOTA): IMPORTANCE OF MONOPHYLETIC GROUPS
Kondratyuk S.Y., Kärnefelt I., Elix J.A., Hur J., Thell A.

4A-03: 14:10-14:30 hrs. IAL0188-00001 *Page 69*
TOWARDS A NEW CLASSIFICATION OF TELOSCHISTACEAE
Arup U., Søchting U., Frödén P.

4A-04: 14:40-14:55 hrs. IAL0251-00002 *Page 69*
METABOLITE EVOLUTION IN THE LICHEN FAMILY TELOSCHISTACEAE
Søchting U., Arup U., Frödén P.

S 4A-05: 14:55-15:10 hrs. IAL0158-00001 *Page 69*
DISENTANGLING THE SPECIES DIVERSITY OF CALOPLACA TH. FR. IN CHILE
Vargas R., Beck A.

4A-06: 15:10-15:25 hrs. IAL0010-00001 *Page 70*
PHYLOGENETIC STUDIES ON SOME GROUPS WITHIN TELOSCHISTACEAE
Vondrak J., Šoun J., Řiha P.

Session: Focus Session
Topic: 4B: Lichen symbionts and ecophysiology
Date/Time: Friday 13th January, 13:30-15:30 hrs.
Room: Grand Rachada Ballroom, 5th floor, Tarntip Building
Chairs: Andreas Beck / William Sanders

S 4B-01: 13:30-13:45 hrs. IAL0174-00002 *Page 71*
ON TIME OR 'FASHIONABLY' LATE ? THE COMPARATIVE DATING OF LICHEN-ASSOCIATED EUKARYOTIC ALGAE AND THEIR FUNGAL SYMBIONTS
Nelsen M.P., Lücking R., Andrew C.J., Ree R.

S 4B-02: 13:45-14:00 hrs. IAL0112-00001 *Page 71*
PHYLOGEOGRAPHY AND GENETIC STRUCTURE OF DICTYOCHLOROPSIS RETICULATA ASSOCIATED WITH LOBARIA PULMONARIA, L. IMMIXTA AND L. MACARONESICA IN MACARONESIA
Cheenacharoen S., Dal Grande F., Werth S., Scheidegger C.

Lichen: from genome to ecosystem in a changing world

- 4B-03:** 14:00-14:15 hrs. IAL0211-00001 *Page 72*
PHOTOBIONT DIVERSITY AND RICHNESS IN LECIDEOID ANTARCTIC LICHENS FROM AN ECOLOGICAL POINT OF VIEW
Ruprecht U., Brunauer G., Printzen C.
- S 4B-04:** 14:15-14:30 hrs. IAL0097-00001 *Page 72*
HOW DO CHANGING ENVIRONMENTAL CONDITIONS AFFECT POLAR AND TEMPERATE HAPLOTYPES OF *CETRARIA ACULEATA*?
Domaschke S., Vivas M., Sancho L., Printzen C.
- S 4B-05:** 14:30-14:45 hrs. IAL0137-00001 *Page 73*
ASSESSMENT OF THE PHENOTYPIC PLASTICITY OF *UMBILICARIA DECUSSATA* ACROSS ECOPHYSIOLOGICAL STUDIES WITH SEVEN POPULATIONS WORLDWIDE.
Vivas M., Pérez-Ortega S., Pintado A., Näsholm T., Sancho L.
- S 4B-06:** 14:45-15:00 hrs. IAL0210-00001 *Page 74*
DESICCATION TOLERANCE IN THE HYGROPHILOUS LICHEN *PARMOTREMA PERLATUM* AND IN ITS ISOLATED *TREBOUXIA* PHOTOBIONT
Candotto Carniel F., Bertuzzi S., Francini A., Pellegrini E., Tretiach M.
- S 4B-07:** 15:00-15:15 hrs. IAL0195-00001 *Page 74*
PHOTOSYNTHESIS, N FIXATION AND NUTRIENT CONTENT IN THREE SPECIES OF *PLACOPSIS* FROM A SUBANTARCTIC ENVIRONMENT
Raggio Quilez J., Crittenden P.D., Green T., Pintado A., Vivas M., Sancho L.
- 4B-08:** 15:15-15:30 hrs. IAL0197-00001 *Page 75*
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11: Exploring the lichen microbiome and its multifaceted interactions

(11-O1) Submission ID: IAL0085-00001

LICHENICOLOUS FUNGI: DESCRIBED AND CRYPTIC FUNGAL COMPONENTS OF THE LICHEN MICROBIOME

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Lichenicolous fungi live exclusively inside and on lichens, most commonly as host-specific parasites, but also as broad-spectrum pathogens, saprotrophs or commensals. Over 1,800 species have been described throughout the Ascomycota and Basidiomycota, and estimates are that 3,000-5,000 species will eventually be described. Most are ascomycetes, widely distributed in 7 classes and 19 orders; fewer than 5% are basidiomycetes, but these are also diverse, representing four classes and eight orders. Since few species have been cultured or sequenced, their identity, evolutionary origin and phylogenetic position cannot always be determined with certainty. However, it appears that lichenicolous ascomycetes are common in, and probably descended from, lichens in lichen-dominated lineages, but entirely unrelated to lichens in many other groups. The origin and direction of these transitions may depend on the nature of the parasitism. Recent culture-based and culture-independent studies indicate the presence of large numbers of obligate fungal inhabitants of lichens, some of which may represent asymptomatic lichenicolous fungi. The identity, origin, and diversity of these species will become apparent as more isolates are obtained and sequenced.

(11-O2) Submission ID: IAL0274-00001

DIVERSITY AND BIOGEOGRAPHY OF ENDOPHYTIC AND ENDOLICHENIC FUNGAL COMMUNITIES

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Endophytic and endolichenic fungi occur in healthy tissues of every plant and lichen species surveyed to date. Phylogenetic analyses suggest a close evolutionary relationship between these guilds, but previous sampling has been insufficient to evaluate the distinctiveness of these symbiotrophs and has not comprehensively assessed the biogeographic and abiotic factors that structure their communities. Using molecular data (ITSrDNA-partial LSUrDNA) we examined the diversity, taxonomic composition, and distributions of 4,154 endophytic and endolichenic isolates of Pezizomycotina (Ascomycota) cultured from replicate surveys of ca. 20 phylogenetically diverse plant and lichen species in each of five North American sites (Madrean coniferous forest, Arizona; montane semi-deciduous forest, North Carolina; subtropical scrub forest, Florida; Beringian tundra and forest, western Alaska; and subalpine tundra, east-central Alaska). Our surveys reveal that these symbiotroph communities differ significantly at the species level among sites, and that different classes of Pezizomycotina dominate related hosts in different locations. Fungal communities located closer together are more similar than communities located farther apart, but differences reflect environmental characteristics more strongly than geographic distance alone. Abiotic factors such as mean annual temperature and precipitation contribute differently to endophyte and endolichenic abundance and diversity. Endolichenic fungi are distinctive relative to most endophytes of vascular plants, but genotypes occurring in lichens frequently are found in mosses as well. Overall, our study illustrates the high richness and diversity of endophytic and endolichenic fungi at a continental scale, and reveals their unique patterns of host-, climatic-, and geographic affiliation.

MICROBIAL COMMUNITY IN ANTARCTIC LICHENS

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Lichens are symbiotic association of fungal (mycobiont) and photosynthetic algal or cyanobacterial (photobiont) partners. Contribution of the two major partners has been well known, but composition and role of other components of lichen ecosystems has not been evaluated carefully. Recently, microbial community in the lichen thalli has been revealed by cultivation of microorganisms, FISH imaging, and sequence analyses. It was also suggested that bacteria, archaea and microfungi associated with lichens (microbiont) have important roles in lichen ecosystem by biodiversity and meta-proteome analyses. In the current study, microbial community composition in *Cladonia*, *Umbilicaria*, *Usnea*, and 3 crustose lichens from King George Island, Antarctica was analyzed by pyrosequencing of bacterial 16S rDNA, eukaryotic LSU rDNA, and algal ITS region of nuclear rDNA. Proteobacteria, Acidobacteria, Actinobacteria, and Bacteroidetes in bacterial community and Dothideomycetes, Eurotiomycetes and Lecanoromycetes in lichen-associated fungal community were the major phyla in the Antarctic lichen ecosystems. Microbial phylotype composition from the same or related lichen species were more closely related than those of different lichen species. Sequencing results of LSU and ITS regions of nuclear rDNA and plastid 16S rDNA of algal species indicated that each lichen thalli contain diverse photobionts. In most cases a major photobiont constituted higher than 97% of total photobiont community, but in some cases, the second major photobiont comprised upto 20% of total photobiont community. These results imply that lichen thalli is a complex ecosystem composed of lichenized fungi, diverse photobionts and microbionts such as bacteria and microfungi. It also suggests that studies for all partners of lichens are required to understand ecology and physiology of lichens.

THE MICROBIOME OF LICHENS: STRUCTURAL AND BIOGEOGRAPHIC DIVERSITY

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Lichens are traditionally considered as mutualisms between fungi and photoautotrophic species. New molecular and microscopic techniques revealed progress in the understanding of the lichen-associated microbiome. Our research during the last years revealed lichens as mini-ecosystems, which harbour highly abundant and diverse bacterial communities [1]. The analyses of samples from three lichen species (*Cladonia arbuscula*, *Lecanora polytropa* and *Umbilicaria cylindrica*) from alpine environments by a polyphasic approach showed biofilm-like structures and a high degree of species specificity [2]. Lichen-associated microbial communities consist of diverse taxonomic groups. The majority of bacteria in growing parts belong to Alphaproteobacteria [3] but there are also diverse new phylogenetic lineages as well as new species [4]. As an important driver of bacterial community the age of the thallus parts was identified: the younger growing parts of the lichens hosted bacterial communities that significantly differ from those of the older/senescing portions at the basis of the thalli. The substrate type and, to a lower extent, the exposition to the sun also affected the bacterial community structures significantly [3]. Moreover, the structure of the bacterial community was influenced by biogeographic aspects. The variation of the always dominant Alphaproteobacteria correlated with geography, whereas this effect could not be observed for *Burkholderia* or functional genes for nitrogen fixation (*nif*).

PYROSEQUENCING REVEALS PREVIOUSLY UNKNOWN PHYLOGENETIC, METABOLIC AND ECOLOGICAL COMPLEXITY WITHIN THE LICHEN MICROBIOME

11-O

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Although common knowledge dictates that a lichen is formed solely by a fungus (mycobiont) that develops a symbiotic relationship with an alga and/or cyanobacterium (photobiont), lichen-associated non-photobiont bacteria are increasingly regarded as significant players in the ecology and physiology of the lichen microbiome. For this study, 454 pyrosequencing and Sanger sequencing of cloned amplicons were conducted on lichen-associated bacteria to determine the ecological factors influencing their community composition and the metabolic functions that they perform. The 16S (SSU) rRNA gene of Bacteria was sequenced from lichen samples representing 24 genera collected from tropical to arctic environments. Comparative analyses of these sequence libraries indicate that bacterial community differences are correlated with a variety of factors, the most notable of which is photobiont-type. Metatranscriptomic libraries were made for lichens containing the two major photobiont-types (green algae [*Cladonia grayi*] and cyanobacteria [*Peltigera praetextata*]). These data reveal the diversity of functional genes in each sample, and demonstrate the fundamental differences between lichens with different types of photobionts in terms of basic carbon and nitrogen processing. Based on these functional analyses and phylogenetic results, differences in carbon and nitrogen cycling in lichens are proposed as major ecological drivers of differentiation between bacterial communities within the lichen microbiome, with secondary compounds as an alternative factor that can drastically shift the composition of bacterial communities in lichens.

EVOLUTION OF PHOTOBIONT ASSOCIATIONS IN THE FAMILY VERRUCARIACEAE

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The lichen family Verrucariaceae is well known for its unique diversity in photobionts, including some algae that are rarely or never associated with other lichens. The identity of these photobionts has been established in the past based on morphological characters, but studies have highlighted the difficulty of accurate species and genus identifications for most of these unicellular or short filamentous groups of algae with problematic taxonomy. Recent studies on Verrucariaceae, mostly focusing on peculiar algal symbionts, have therefore used molecular data to confirm the identity of these photobionts. Here, molecular data (*rbcl* and 18S) are used to confirm the identity of a taxon sampling representative of most lineages within Verrucariaceae, including some poorly known species from the tropics. Phylogenetic analyses show that a large number of species are associated with the green algal genus *Diplosphaera*. Other algal genera consist in *Auxenochlorella*, *Asterochloris*, *Dilabifilum*, *Elliptochloris*, *Heterococcus*, *Myrmecia*, *Prasiola* and *Trebouxia*. The most common lichen photobionts (*Trebouxia*, *Asterochloris*, *Trentepohlia* and *Nostoc*) are never or seldom found associated with Verrucariaceae. *Amphibious* species of Verrucariaceae show a particularly broad phylogenetic range of algal associates: they were found with algal species from the Xanthophyceae (*Heterococcus*), Ulvophyceae (*Dilabifilum*), and Trebouxiophyceae (*Diplosphaera*, *Elliptochloris* and *Prasiola*). The endolithic genus *Bagliettoa* also shows a high diversity in photobionts (*Asterochloris*, *Diplosphaera* and *Trebouxia*). In contrast, the lichen lineage including *Placidium* and *Heteroplacidium*, although colonizing different habitats (soil, bark, rock) is only associated with algal species from the genus *Myrmecia*. When studied with comparative methods, the results suggest that both habitat requirements and common ancestry were involved in shaping the current patterns of photobiont associations in Verrucariaceae. Moreover, the presence of a developed upper cortex also plays an important role in the evolution of photobiont associations in this family.

(11-O7) Submission ID: IAL0067-00001

**PHOTOBIONT - MYCOBIONT INTERACTIONS IN THE WIDESPREAD LICHEN
*CETRARIA ACULEATA***

11-O

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The fruticose *Cetraria aculeata* is an extreme example of a lichen that occupies distributional ranges across several biomes, including areas as different as e.g. the maritime Antarctic and the parameras of Central Spain. We are currently investigating how interactions with genetically different photobionts (all belonging to *Trebouxia jamesii*) may contribute to the ability of *C. aculeata* to colonize this diverse range of habitats. DNA sequences from three loci for each symbiont confirm that the most important factors shaping the genetic structure of *T. jamesii* are climate and a history of co-dispersal with the mycobiont. The genetic structure of the mycobiont is best explained by an interaction of climatic and geographical factors. Most importantly, mycobionts in the temperate region are consistently associated with a specific photobiont lineage. We therefore conclude that a photobiont switch in the past enabled *Cetraria aculeata* to colonize temperate as well as polar habitats. The genetic diversity of *T. jamesii* is highest in temperate regions and decreases significantly towards the Antarctic but less pronouncedly towards the Arctic. This indicates that climatic factors may determine which photobionts are available in a certain habitat but have a minor effect on the overall diversity of photobiont populations. Hence, the low genetic diversity of photobionts and mycobionts observed in Antarctic populations of *C. aculeata* is most likely not the result of increased selection pressure but of founder events during colonisation. Especially in largely asexual lichens such as *C. aculeata* isolation by distance is probably not the only cause of genetic structure. Rare photobiont switches that associate the mycobiont with locally adapted photobionts may also lead to genetic isolation between populations and eventually to ecological specialisation and speciation.

(11-O8) Submission ID: IAL0228-00001

GENE MOVEMENT IN THE PHOTOBIONT OF *RAMALINA MENZIESII*

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Ramalina menziesii is a widespread lichen throughout coastal and slightly inland regions of western North America in ecosystems that include desert, chaparral, oak woodland, and coniferous forest. Previously, we have found that the fungal species survived the Pleistocene glaciations in multiple refugia. Here, we assess geographic genetic variation in the photobiont of *R. menziesii* based on DNA sequence data of the nuclear ribosomal rDNA gene cluster and the rbcL gene located on the chloroplast to address three objectives. First, we investigate the spatial distribution of photobiont clades across the range of *R. menziesii*. Second, we test whether the refugial areas found for *R. menziesii* fungal genotypes show the characteristics of refugial areas in its photobiont as well (private haplotypes, high haplotype diversity). Third, we test if genetic diversity in the photobiont correlates with latitude, and with the diversity of the mycobiont. Our results indicate that the photobiont has much greater genetic differentiation across sites than the mycobiont and that the geographic patterns of genetic variation are only loosely associated with that of the photobiont. Our study provides valuable insight whether the movement of genes of lichen fungi and their photobionts exhibits congruent patterns.

INSIGHTS ON *TREBOUXIA* PHYCOBIONTS: COEXISTENCE OF TAXA IN A LICHEN THALLUS, MOLECULAR MARKERS, PHYSIOLOGICAL PERFORMANCES, HGT, GENOME ANALYSIS

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“Lichen Symbiogenesis Team” is the interdisciplinary group of Spanish scientists building on a common objective: to study the identity, genetic diversity and function of lichen phycobionts and its role in the complexity of the thalli. We are taking steps to gain insights on the knowledge of lichen symbiosis, and different approaches are being used to investigate lichen algae, especially those of the genus *Trebouxia*, in both lichenized and cultured ones. This it is doing through integration of molecular, anatomical, physiological and genome analyses. We have designed molecular markers (chloroplast, nuclear, mitochondrial) and ultrastructural methods to add precision to the circumscription of *Trebouxia* taxa, improving phylogenetic accuracy. Even, a single primer pair that can amplify a portion of the 23S rRNA gene gives a specific ortholog amplicon in a wide range of Cyanobacteria and plastid-bearing organisms, has been proposed. Our team demonstrated that in *Ramalina farinacea* two phycobionts of *Trebouxia* (TR1 and TR9) were always coexisting in a single thallus. TR1 and TR9 showed distinct physiological responses to oxidative stress caused by a ROS propagator, which produced a more severe decay in photosynthesis, photosynthetic pigments and proteins in TR1. *Ramalina fraxinea* was also investigated and phylogenetic analyses, based on new markers, indicated a high and unexpected diversification within the *Trebouxia decolorans*-like phycobionts; at least, five haplotypes and morphotypes were recognized and more than two *Trebouxia* may coexist. To understand the mechanisms involved in desiccation tolerance of lichens and their photobionts we studied dehydration rate and desiccation time in *Trebouxia* and *Asterochloris*. Our results indicate that there is an alternative mechanism of light energy dissipation during desiccation, where activation is dependent on a sufficiently slow dehydration rate. First evidence for fungal-associated NO in the regulation of oxidative stress during the early stages of rehydration - including chlorophyll photostability of the phycobionts- was provided as well as for the role of NO in the establishment of lichen symbiosis. The genomes of *Trebouxia* sp. TR-9 isolated from *Ramalina farinacea* have been partially sequenced by 454 pyrosequencing. We have identified mitochondrial and chloroplast genomes as well as interesting CO₂ concentrating or oxidative stress mechanisms among others.

1A: Lichen conservation: concepts and action

(1A – O1) Submission ID: IAL0133-00001

LICHEN CONSERVATION: FROM ACTIONS TO CONCEPTS AND BACK

1A-O

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In this address we will highlight the various instruments in Conservation Biology and discuss their applicability for lichens. We will describe some examples of species recovery programs and describe which information was most helpful to convince local and national stakeholders of the need of lichen conservation measures. We will stress the importance that data on the lichen's demography and life-cycle be communicated to the land-managers in their "language". For the facilitation of the communication between the different stakeholders, e.g. land owner, land manager, regional and national conservations agencies, and scientists, a national data Centre for lichens proved to be very important. Conservation programs were most successful when local stakeholders took the initiative and developed conservation acting plans for species or lichen communities in their area. However, this process depends on the availability of national instruments that justify local conservation measures. National Red lists are the most frequently used instruments to define threat categories and conservation priorities. Establishing national Red Lists is a very demanding scientific task and its complexity is often underestimated by scientists and funding agencies. However, Red Lists are often the most solid scientific basis available on which conservation measures can be based upon.

(1A – O2) Submission ID: IAL0129-00001

**LUNGWORT'S PATH OF LEAST RESISTANCE IS A STEEPLECHASE IN THE FOREST:
SMALL SCALE GENETIC PATTERN OF *LOBARIA PULMONARIA* IN A PRIMEVAL
BEECH FOREST LANDSCAPE**

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Lobaria pulmonaria is a widespread, but regionally threatened epiphytic lichen species with special habitat requirements to old-growth and primeval forests. The species is suffering a strong decline in managed forest landscapes in most areas of Europe and North America. Our study aimed at investigating epiphytic lichen species diversity and population genetics of *L. pulmonaria* in one of Europe's largest primeval beech (*Fagus sylvatica*) forests, situated in the Ukrainian Carpathians, the Uholka-Shyrokoluzhanskyi branch of the Carpathian Biosphere Reserve. Mountain slopes of this massif are covered by almost pure beech forests with varying altitudes from 400 to 1,500 m. occupying an area of 15,974 ha, almost 9,000 ha from which are considered to be virgin forests (Brändli & Dowhanytsch 2003). During 2009-2011 we have visited 339 plots and collected about 1,500 specimens from about 500 trees. Trees with *L. pulmonaria* were found in floodplain forests along the small streams (400-700 m alt.) and in relatively open forests on the mountain ridges close to the timberline (900-1,200 m alt.). *Lobaria pulmonaria* samples were genetically investigated with symbiont-specific microsatellite markers for myco- and phycobiont. A Bayesian analysis of the genetic population structure revealed two distinct clusters, which were distributed over the entire study area. One cluster was confined to floodplain forests and the second cluster was concentrated along the mountain ridges. On the mountain ridges, but not in the floodplain forests we found several admixed demes and a few individuals with an intermediate genotype. Intermediate genotype can be interpreted as F1 hybrid between the two different genetic clusters.

LOBARIA SCROBICULATA, A THREATENED SPECIES: INSIGHT POPULATION DYNAMICS

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1A-O

The successful conservation of a species relies on the knowledge of its biology, ecology and threats. To know the ecological, demographic and physiological status of an endangered species, it is essential do a precise diagnose of their populations. The goal of this study is to find out which are the external factors and vital processes conditioning the viability of populations of the threatened lichen species *Lobaria scrobiculata* in Central Spain. To obtain population dynamics data, we set two 50x50 m monitoring plots, corresponding to two different populations, growing in oak forests (*Quercus pyrenaica*) in Central Spain. To describe these populations, all *L. scrobiculata* individuals colonizing trees and rocks were recorded, considering variables related to individuals size, reproductive capacity, health and niche characteristics. The populations were characterized by several macro-environmental and forest structure variables. General Linear Models were carried out to find out which variables are determining the presence, abundance, thalli size distribution and reproductive capacity between trees and rocks in both populations. Currently, ca 10,000 individuals have been recorded in both populations. Of these, about a quarter of them presents asexual reproduction. GLMs results show that presence and abundance of *L. scrobiculata* are higher on trees than on rocks. Small thalli are more frequent on trees, whereas larger thalli are more common on rocks. Considering the tree model, tree density together with the tree diameter were the most important drivers determining presence, abundance and quantity of small thalli. According to the rock model, higher rock surface also promotes presence and abundance of *L. scrobiculata*, and a higher bryophytes cover favor the abundance of large thalli. Trees seem to be a more favorable habitat for the recruitment, establishment and maintenance of *L. scrobiculata* individuals. However, rocks could provide better conditions for individuals to reach a larger size. Thus, rocks may play a more important role than thought, since reproductive capacity is probably related to the individual size, as observed in other *Lobaria* species.

**FACTORS AFFECTING THE DISTRIBUTION OF SPECIES OF CONSERVATION IMPORTANCE
IN THE NEW FOREST NATIONAL PARK UK**

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1A-O

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Understanding biodiversity patterns across a landscape is vital for setting conservation priorities. In 2010 a quantitative inventory of the New Forest National Park covering c. 57,100 ha in the south of the UK was initiated in order to evaluate species distribution in a range of habitats and to provide a repeatable method with which to assess changes over time. The mosaic of woodlands, heathlands and wetlands provided an opportunity to compare ancient old-growth wood pasture with 19th century plantations of native tree species, and the effects of grazing, and isolation of sites on the distribution of lichens and saproxylic beetles, organisms that include many species of high conservation value. The sampling method followed Bioassess in using random sampling in 1 ha plots established within 6 land use types. Watercourses were sampled at 16 points along a 10 m stretch. Within woodland plots 12 random points were established from a central point and nearest trees, lignum and dead wood selected for lichen sampling using 20, 10x10 cms square quadrats. A similar method was used to sample lichens on dry and wet heathlands. For invertebrates in each 1 ha plot three sampling methods were used, pitfall trapping, Winkler bag extraction of leaf litter and hand sorting of soil pits. Results have shown that diversity and frequency of species of conservation importance in both groups is significantly related to stand age. Lichen diversity within the old growth plots occurs in stands with ancient *Quercus* trees, where grazing by a range of large herbivores maintains glades and open spaces. There are significant differences between the tree species, including between *Quercus robur* and *Quercus petraea*, an unexpected result, and indications that distance to a source of propagules has an effect on the colonization of lichens of isolated 200 year old plantations. These results are similar to those found for ground-dwelling beetles, although lichens show the patterns more clearly. The heathland plots are locally rich in lichen species that are in decline in other areas of lowland heath in Western Europe.

LICHENS OF CALCAREOUS ROCKS IN FINLAND

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1A-O

Calcareous rocks are rare and threatened habitat types in Finland. The total area of calcareous rocks is estimated to be ca. 500-2,000 hectares. Lichens of calcareous rocks in Finland have been previously insufficiently known. During the years 2003-2010 295 calcareous rocks and lime quarries have been studied, and the field work is continuing in 2011. Distribution and habitat characteristics of lichens of calcareous rocks and lime quarries are studied. The main aim is to produce data for a more precise evaluation of threat status of calcicolous lichens as well as to evaluate the need of conservation and management practices of calcareous rocks and lime quarries. Over 15,000 specimens have been collected and 137 lichens new to Finland have been determined. The total number of calcicolous lichens is ca. 280 species, which is 16% of all lichens reported to occur in Finland. The proportion of lichen species on calcareous rocks is more than 100-fold compared to the area of calcareous rocks. New localities have been found for most threatened lichens of calcareous rocks (e.g. *Nephroma helveticum*, *Peltigera retifoveata*). Five species considered extinct from Finland have been refound. The number of identified pyrenocarpous lichens is very high compared to previously known, although a large number of pyrenocarpous species still remain unidentified. Particularly *Verrucaria* is extremely species-rich, and 60 species new to Finland have been identified. Species composition of calcareous rocks differs strongly between southern and northern Finland. Many lichens on calcareous rocks have proved to very rare. Small populations are typical to many species. Shading by trees seems to restrict the occurrence of most calcicolous lichens. Lime quarries (both abandoned and those in use) are very important for many calcicolous lichens. Several rare pioneer calcicolous lichens disperse rather effectively to lime quarries. Calcareous rocks are threatened by building, mining and forestry. Conservation and management measures need to be intensified to preserve the rich lichen flora of calcareous rocks.

WINNERS AND LOSERS IN ECOLOGICAL RESTORATION: EFFECTS OF NON-INDIGENOUS HERBIVORE REMOVAL ON SAXICOLOUS LICHENS

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1A-O

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Deer were introduced to New Zealand in the 19th century and are now found over 70% of the country. The impacts on native vegetation is well known, but the effects on lichens have not been widely studied. There is only limited information available on the prevalence of lichens in the diet of deer in New Zealand, but there is some evidence that significant quantities of fungi and lichens, including species of *Pseudocyphellaria* and *Usnea* are eaten. Removal of introduced herbivores has a dramatic effect on the recovery of native vegetation, but it is not known how lichens are affected. Motu Kaikoura is a 535 ha island in northern New Zealand. It was purchased in 2004 with the aim of restoring its biodiversity. The remnant vegetation is dominated by *Leptospermum* and *Kunzea* scrub, a result of degradation by fires, farming and browsing mammals. The effects of fallow deer (*Dama dama*) have been severe, removing palatable plant species and preventing regeneration. Surveys of the vegetation found 259 native plants species remaining, some of them restricted to sites inaccessible to deer. The lichen flora is diverse with 92 species recorded. Saxicolous lichens are well represented as rocky substrates are common. The eradication of fallow deer was completed in 2008, creating the opportunity to study the effects of herbivore removal on lichen diversity and abundance. Six permanent 0.5 x 0.5 m quadrats were set up on horizontal rock surfaces to monitor any changes to saxicolous lichens over time. The percentage cover of different lichen species, mosses and grasses were determined in 2008 and each year after. Early results show an increase in annual grasses within the quadrats and a decrease in percentage cover of foliose lichens, particularly *Parmotrema* and *Xanthoparmelia* species. Fruticose lichens such as *Cladia aggregata* and *Stereocaulon ramulosum* showed smaller decreases in percentage cover. This suggests that grasses are recolonizing after herbivore removal and that this may be at the expense of some lichen species.

LICHEN CONSERVATION IN DENSELY POPULATED AREAS: PRESSURES AND MEASURES

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1A-O

Lichen populations have suffered from many threads in densely populated areas, including habitat fragmentation, air pollution and change management practices. As a result some species have become rare, whereas a small group of species is able to survive under most of these pressures. These pressures are illustrated together with successfully applied conservation measures in the Netherlands. The first example is the disappearance of epiphytic lichen populations due to changes in atmospheric pollutants and their partial recovery after air pollution reduction measures were taken. The composition of the lichen vegetation over the past 50 years reflects mainly substrate acidity preference, caused by changes in pollutant concentrations. Life history strategy and remaining pressures seem to be important factors controlling the rate of species recovery. Secondly, abandonment of traditional 19th century agricultural practices in heathland and inland dunes led to habitat loss and fragmentation of terrestrial lichen populations in those areas. Only since 25 years, conservation measures to restore inland dunes and heathlands are being taken. A recent evaluation shows best practices for conservation measures such as top soil removal, tree-removal, and re-activation of drift sands. The third example is habitat loss for coastal lichen populations confined to acid rock. In the 18th century, dykes were built to protect the Dutch coast. Imported granite and basalt rock became covered in lichens over the past 250 years. Current safety measures to improve the quality of older dykes include replacement of natural acid rock by concrete, which is unsuitable for most typical coastal lichen species, such as *Anaptychia runcinata*. To protect a part of the lichen population, rocks with rare species are taken from the dyke and placed back afterwards. Monitoring showed a considerable survival rate.

(1A – O8) Submission ID: IAL0146-00001

TRADE AND TRADITIONAL KNOWLEDGE OF LICHENS IN NEPAL HIMALAYAS

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Like different plant species, lichens are ethnobotanically important for Nepalese. To collect the data regarding the uses and trade of lichens in different parts of Nepal, field level survey was carried out during 2009-2011, using standard sets of questions. In Nepal, there are more than 525 lichen species (12% cyanobacterial and 88% green algal lichens) and around 30 species are ethnobotanically important. Apart from trade and foods, lichens are also used as spices, to treat against wounds and burns, as bedding materials and to ignite fire. Collections of some lichen species has generally increased in last few years. As example, in Banke district, the trade of lichens increased from 43.6 thousand Kg in 2009 to 199.3 thousand Kg in 2011 and such trend has seriously declined the availability of lichen species in different parts of Nepal. The amount of lichens collected in west Nepal is more for trade but in east Nepal they are collected for food and rituals. Generally, lichens are collected by adolescent or children and each collector collects from 2-10 Kg/day. Though Nepal Government has banned lichens for the export without processing, the effective implementation of such laws is currently lacking.

POPULATION GENETICS AND CO-PHYLOGEOGRAPHY OF THE FUNGAL AND ALGAL SYMBIONTS OF *LOBARIA PULMONARIA* IN EUROPE

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1A-O

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This work aims to disentangle the relevant processes shaping the genetic diversity of the eukaryotic symbionts of the epiphytic lichen *Lobaria pulmonaria* (L.) Hoffm. at the intra-population and continental scale, using fungus- and alga-specific microsatellite markers. We explored the importance of the photobiont transmission mode and of evolutionary processes (mutation, recombination) at the within-population scale. The results confirmed that *L. pulmonaria* mainly disperses vegetatively over short distances (up to 20 m). We showed that the alga is a strictly clonal organism, with mutations being responsible of its substantial genetic diversity; the fungus displayed additionally clear signal of recombination. A further population genetic study on more than five thousand thalli from more than 150 populations covering most parts of the European distribution range of the lichen showed how the predominant vertical transmission of fungal and algal symbionts can lead to high congruency in phylogeographic patterns. Statistical analyses of allele frequencies among regions and geographic centroids of non-randomly distributed alleles across Europe sustained the presence of different refugia in South Italy and the Balkans. This region is characterized by a high genetic diversity and constitutes a hotspot of geographically restricted alleles for both symbionts. Admixed populations were detected on a south-north axis indicating putative re-colonization routes from the southern refugia. This study provides necessary tools to establish conservation plans aiming to preserve the overall coevolutionary history of *L. pulmonaria* in Europe.

OLD, ARTIFICIALLY DRAINED SWAMP FORESTS PROVIDE VALUABLE HABITATS FOR LICHENS: A COMPARATIVE CASE STUDY FROM ESTONIA

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1A-O

In the boreal region, forested wetlands have been frequently drained in order to increase timber yields, while the accompanying impacts on biodiversity have received relatively little attention. At present, drained peatland forests cover 14% of the Estonian forest land, including large areas in reserves. Particularly in the nutrient-rich swamp site type, the biodiversity value of those forests is important to assess because old natural swamp forests have only survived as small remnants. I studied whether old, structurally rich drained forests can support threatened lichen species, which primary habitat swamp forests. For that, I used a fixed-area fixed-effort method to describe species richness and composition of lichens* in 20 undrained and 24 drained stands, each 2 ha in size. They represented, in a block design, 4 treatments (old-growth and mature stands; retention-cut and clear-cut plots) in 5–6 replications. The total species richness of natural and drained swamp stands was similar: 209 vs. 211 species in forests, and 176 vs. 177 in cut plots, respectively. Based on MRPP tests, the species composition of natural old-growth forests differed significantly from the other three forest stand combinations (those formed a relatively homogeneous group). However, the number of nationally protected, threatened and/or rare species** was similar or even higher in artificially drained forests compared to natural swamp forests (in total, 29 vs 27 in old-growth and 19 vs 10 in mature stands, respectively). For example, *Cetrelia olivetorum*, *Lobaria pulmonaria* and *Parmeliella triptophylla* were always found from old-growth stands, irrespective of the incidence of drainage. The availability of old deciduous trees, large snags, and logs and root plates of tree falls seems to be more crucial for most lichens than the microclimatic changes putatively attributed to drainage. Possibly, the thick carpet of mosses developing after ditching is important for holding a favorable moist microclimate. Hence, despite being developed under human impact, old artificially drained swamp forests can be considered valuable habitats for lichens in nature conservation planning.

* includes also lichenicolous and saprobic fungi traditionally treated by lichenologists

** lichenicolous fungi not included

THE LICHEN KILLER: WHEN STONE CONSERVATION ASKS FOR NEW METHODS OF LICHEN DEVITALIZATION

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1A-O

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The pros and cons of a new approach for killing poikilohydrous photoautotroph organisms that colonize outdoor stone buildings are discussed on the basis of field and laboratory data. The control of biological growth, particularly important in the field of stone conservation, largely depends on the use of biocides, that may be dangerous for the workers, the environment and the substratum. The new approach makes the most of a poorly known peculiarity of poikilohydrous organisms: they are thermo-tolerant (up to 55-60°C) when inactive for lack of water, but thermo-sensitive when hydrated and fully active metabolically. The efficacy of thermal treatments (range: 35-50°C), in parallel to applications of three commercial biocides based on quaternary ammonium cations and n-octyl-isothiazolinone, was verified in the laboratory with the biodeteriogenous lichens *Protoparmeliopsis muralis* and *Verrucaria nigrescens* at various water contents. Chlorophyll a fluorescence (ChlaF) emission were checked in treated and non-treated samples at different time intervals, from 12 h to 16 days, whereas confocal laser scan microscopy in combination with fluorescent dyes was used to assess the physiological state of photobiont and mycobiont cells. Further ChlaF measurements were carried out outdoor to evaluate the feasibility of treatments against biofilms of rocky outcrops and walls, and the behavior of phylogenetically distant groups, from cyanobacteria, to microalgae and bryophytes. The results confirm that treatments of 12-24 hours at 40-45°C are sufficient to kill all the colonizers tested so far if they are kept fully hydrated. At 35-40°C the organisms are damaged: in this case biocides at concentrations from ten to one hundred times lower than in normal applications can be used for killing them. The new protocol is simple, the field equipment is cheap, the negative effects associated with the standard biocide treatments are virtually absent, and there is no interference with the substratum. The application of thermal treatments in the tropics is also discussed.

**THE NECESSITY FOR ESTABLISHING A DATABASE AND AN INDEX OF THE
DETERIORATION OF CULTURAL HERITAGE STONEMWORK
BY LICHENS AS AN AID TO CONSERVATION WORK**

1A-0

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Conservators of cultural heritage currently lack practical tools to diagnose and quantify the impact of different (micro-)organisms on stonework, a key element in the planning and management of conservation programmes. The severity of deteriorative activity of many lichen species is well known, and thus public authorities generally opt for the physical and/or chemical removal of “disfiguring” lichens from stonework. However, in some cases these organisms may protect the substratum beneath and also have a positive aesthetic significance and biodiversity value, thus being worthy of conservation. The recently proposed Index of Lichen Potential Bio-deteriogenic Activity (ILPBA) is a numeric descriptor to measure the impact of different lichen species on the substratum, both externally and internally (Gazzano et al., 2009, *Int. Biodet. Biodegr.* 63, 836-843). A research network of lichenologists will establish a European database in order to quantify the relative damaging impacts of species and calibrate the parameter scales adopted in the index calculation so that the ILPBA and its interpretation can be effectively and appropriately disseminated to public authorities, managers and professionals engaged in conservation work. This group seeks financial support to (a) organize meetings/training schools for sharing scientific knowledge and technical skills in order to provide comparable datasets for the index validation process, (b) implement case-studies to monitor the impact of particular lichens on different substrata under a variety of climatic conditions, and (c) establish a web-site database complemented by a realistic biodeterioration index/scale suitable for use by non-scientists.

CONSERVATION OF LICHENS IN RUSSIAN FEDERATION: MODERN STATUS

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1A-O

The redlisting process nearly been accomplished in the regions of the Russian Federation. By now 81 out of 83 regions of the Russian Federation have either published regional Red Data Books or adopted regional Red lists. The 2nd edition of the Red Data Book of the Russian Federation (2008) contains 42 lichen species (in comparison with 29 species being included into the 1st edition of 1988). Significant progress has also been made in regional lichen conservation measures. Species of lichens are included into Red Data Books of 64 regions covering over 16 million km² (94.6% of the territory of Russia). 21 region have already second editions of their Red Data Books with several, major revision of species lists prior to publishing. The numbers of protected lichen species vary from 1 (Saratov, Sverdlovsk, Magadan regions) to 109 in the Republic of Karelia. Total number of lichen species (subspecies, and varieties) included into the regional Red Data Books is 583 (compared with 378 in 2004), except 85 species demanding “biological monitoring” in the Red Data Book of Murmansk region. Monitoring of redlisted lichens in several regions can be regarded as another positive trend. However some challenges still remain. The first one is the low number of lichenologists leading to uneven exploration of the lichen biota of different regions. Thus, this resulted in the absence of lichens in 19 regional Red lists as well as in rather short lists for several regions. Conflicts between experts and regional authorities responsible for adoption of the Red lists are common. The latter tending to minimize species numbers due to limited resources to support monitoring activities. The same explanation is used when species from Federal Red Data Book are proposed for exclusion from regional Red lists. Problem causing is a formal attitude of regional administrations towards preserving the territories of protected areas (except for strict nature reserves and national parks). Rare species inhabiting regional reserves and nature monuments are usually at higher risk as such protected areas are protected mainly on paper.

LICHEN CONSERVATION AS THE ELEMENT OF NATURA 2000

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1A-O

Aeolian sands in Borská nížina lowland are unique landscape in Slovakia with many semi-natural elements present. There so-called lichen steppes are presented with high biodiversity, and were therefore included in NATURA 2000 as follows: 2340 Pannonic inland dunes (alliance *Corynephorion canescentis* Klika 1931), 4030 European dry heaths (alliance *Euphorbio cyparissiacae-Callunion vulgaris* Schubert ex Passarge in Scamoni 1963), and 6260 Pannonic sand steppes (association of *Festucion vaginatae* Soó 1938). Terrain research has been carried out in the years 2009-2011 under the umbrella of the project LIFE06NAT/SK/000115. The aim of the study was to define the most optimal and the less stressed management, which should guarantee conservation of the NATURA 2000 localities. The object of the research has been to study the changing diversity and synusias of the lichens according to the different management impacts. There were six main types formed according to the growing shade to the moss and lichen layer: type 1 – open sand, type 2 – Pannonic inland dunes, type 3 – Pannonic inland dunes with oak and pine stands, type 4 – European dry heaths, type 5 – Pannonic sand steppes, type 6 – shaded places in the dense stands of oak and pine forests. There are significant differences between the types in the study area. The highest diversity, abundance and stability were reported for types 2, 3 and 4 in the Pannonic inland dunes and European dry heaths. Management included cutting the trees and cleaning by hands, little exporter with low weight or loading machine as well as spreading the surface on the open sand stands. According to the study, the effect of the machines was visible. The weakest stress for lichens is clearing after trees removal by hands or by little exporter with the low weight. Observed NATURA 2000 localities are occurred on the open poor acid sand, so the highest priority should be cutting the trees and cleaning the wood after the cutting. Data show that cutting and clearing of the stands was most important for the conservation of lichens on nutrient poor open grassland vegetation.

1B: Genomic approaches to studying the lichen symbiosis

(1B-O1) Submission ID: IAL0319-00001

**APPROACHING LICHENS BY UNWINDING COMPLEMENTARY GENOMES:
AN INTRODUCTION**

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1B-O

Lichen symbionts are unique in their near-absolute dependence on each other in nature, accompanied by occasional streaks of independence most obvious in aposymbiotic culture. This session will look at this balancing act from a genomics perspective. Superficially, the symbionts' genomes are not very different from those of their non-symbiotic fungal and algal relatives. They have not degenerated so as to produce absolute dependence between mycobiont and photobiont, but have evolved in subtle ways to cement an intimate and successful interaction while maintaining each partner's individuality. We will look not only at the general structure of several lichen genomes, but also at features connected with their functioning in the symbiosis: changes in gene families, presence of genes unique to lichens, transcriptional adaptations, metabolic adaptations, epigenetic changes. We will survey the mycobiont of *Xanthoria parietina*, two closely related *Peltigera* species and their cyanobionts, *Cladonia grayi* and its *Asterochloris* sp. photobiont, horizontal gene transfer in *Trebouxia*, and the effect of different ecological conditions on the larger bacterial communities inhabiting various lichens.

(1B-O2) Submission ID: IAL0293-00001

GENOME SEQUENCING OF *XANTHORIA PARIETINA* 46-1-SA22

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Xanthoria parietina has been chosen as a representative lichen-forming fungus for genome sequencing. This species was nominated because it has a wide distribution (being found in temperate and circumpolar regions worldwide), has a characteristic stratified thallus morphology, is amenable to axenic cultivation, and is one of the most commonly studied lichenized fungi. It can occur on a variety of substrata including rock, tree bark and man-made surfaces. To enable genome studies, ascospore progeny from an individual thallus of *X. parietina* were collected from the Peak District, UK, and grown in axenic culture to allow extraction of DNA purely of the fungal mycobiont. Sequencing of the genomic DNA by 454 and Illumina pyrosequencing technology has now been completed at the DOE Joint Genome Institute. Preliminary analysis reveals a 32 Mbp size genome (typical of pezizomycete fungi) with an estimated 10,800 genes of average size 1,505 nt encoding an average protein length of 432 amino acids. In further work, mRNA samples are being extracted from both the symbiotic (field thallus) and non-symbiotic (axenic pure culture) states of *X. parietina* prior to library construction and whole transcriptome sequencing ("RNA seq"). Arising data will be used for training of the genome auto-annotation process, and it is anticipated that comparison of transcriptome pools will yield insights into differential regulation of genes in the symbiotic versus non-symbiotic state. A multinational genome annotation group has been set up to assist with the genome annotation and analysis.

(1B-O3) Submission ID: IAL0262-00001

PARTIAL GENOME OF THE PHYCOBIONT *TREBOUXIA* TR-9 ISOLATED FROM *RAMALINA FARINACEA* (L.) ACH. SEQUENCED BY 454 PYROSEQUENCING

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1B-O

The chloroplast, mitochondrial and nuclear genomes of *Trebouxia* sp. TR-9 phycobionts, isolated from *Ramalina farinacea* (L.) Ach., have been partially sequenced by 454 pyrosequencing to analyze genome structure, repeats characterization and finding of new gene sequences compared to green algae genome databases. We show that these sequencing technologies are highly productive and generate a lot of information on phycobiont genomes. Our research group has isolated two different *Trebouxia* phycobionts (TR-1 and TR-9) that always coexist on *R. farinacea*, even in geographically distant localities. Total *Trebouxia* sp. TR-9 DNA was extracted and loaded on a ¼ GS FLX Titanium 454 pyrosequencing run. Reads were assembled with MIRA3 software; the obtained contigs were analyzed with the BLAST algorithm against *Chlamydomonas reinhardtii* P.A. Dangeard, *Chlorella variabilis* NC64A, *Arabidopsis thaliana* (L.) Heynh. and NCBI databases. We have generated 240256 reads and their average length was 579.87 bp, 75% were assembled in 20787 contigs with a total consensus of 9211887 bp and a total average coverage of 41.76. *C.reinhardtii* and *C.variabilis* NC64A proteins were used for comparative analyses against TR-9 sequences by the tBLASTn algorithm. On this way, a total of 2.799 possible homologies with both species were found (Max. Evalue: 10⁻³). A big number of *Trebouxia* sp. TR-9 sequences were obtained; and we have identified mitochondrial and partial chloroplast genomes. We also found *C. reinhardtii* flagella proteome orthologs as well as oxidative stress, glucid metabolism or CO₂ concentrating mechanisms among others. It has been determined the presence of similar repetitive sequences in 612 contigs containing mobile elements and 653 showing another type of repeated sequences. [MCINN (CGL2009-13429-C02-01/02) and Generalitat Valenciana (PROMETEO 174/2008 GVA)]

(1B-O4) Submission ID: IAL0018-00001

***TREBOUXIA* DECOLORANS - ARE THERE FUNGAL GENES IN LICHEN ALGAE?**

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Horizontal gene transfer (HGT) is widespread in prokaryotes and viruses and HGT from bacteria has contributed to yeast evolution. HGT between eukaryotes has also been recently reported. Nevertheless, very little is known about potential gene transfer between the partners in the lichen symbiosis, even though close physical proximity and symbiosis are thought to facilitate HGT. Here we used novel genome data from *Trebouxia decolorans* to investigate the possible existence of fungal derived genes in lichen algae. Phylogenomic analysis using predicted proteins from the *T. decolorans* genome returned 10,165 alignments that included other GenBank entries. These were used to infer PhyML trees of which 459 trees showed *T. decolorans* to form a monophyletic group with fungal sequences, supported at a bootstrap level $\geq 70\%$. Detailed analysis of these likely HGT candidates will be presented. The *Trebouxia* source culture was axenic and algal-fungal associations in the phylogenomic output are low (2.5%), suggesting the results are not explained by fungal contamination.

(1B-O5) Submission ID: IAL0145-00001

**PELTIGERA LICHEN SYMBIOMES: METAGENOMICS OF A COMPLEX
NATURAL COMMUNITY**

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1B-O

Genomic analyses of lichens can be carried out in two fundamentally different ways. First, by the classical approach starting with pure, usually clonal, cultures of the individual symbiotic organisms, an approach which is essentially the same as generally used in genomics. This works fine if both (or all) symbionts can be cultured. The second approach starts with field material and the symbiont genomes are analyzed simultaneously. At first sight this approach appears only slightly more complicated than with the cultured material. In the best case, there is a fairly even proportion of two genomes, and after assembly of the basic sequence reads, it is simply a matter of sorting into two bins. In practice, there are several levels of complications. First, there may be more than two major symbionts, as in the case of tripartite lichens, and they may contribute very different numbers of genomes, including variable numbers of organelle genomes. Second, as the contributing organisms are not purely clonal, there may be considerable polymorphism. This complicates genome assembly and annotation, but can also contribute information on community structure. Third, a variety of microbes are present in natural lichen communities, both on surfaces and internal. This microbiome can account for a large part of the total metagenomic DNA, and can be very disperse in terms of taxonomy and clonality. Results and methodology from the genomic sequencing and analysis of the major components of the *Peltigera membranacea* and *P. malacea* symbiotic genomes, the mycobiont, the *Nostoc* photobiont, and the microbiome, will be presented as well as major features of transcriptomic analyses from thallus, rhizines and apothecia. Use of alternative homologs and differential gene expression in the different tissues yields molecular information on the nature of this widespread symbiosis, and the genome sequence base provides a platform for a wide range of investigations, e.g. using an array of molecular markers and transcriptome sequencing of multiple samples.

(1B-O6) Submission ID: IAL0229-00002

DECODING SYMBIOSIS: THE TWO GENOMES OF THE LICHEN *CLADONIA GRAYI*

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We analyzed the genomes of the lichen fungus *Cladonia grayi* (34 Mb) and its alga, *Asterochloris* sp. (56 Mb), sequenced using DNA from the isolated symbionts grown in culture. We used several approaches to distinguish genes relevant to the lichen symbiosis from those not specifically constrained by it. One method involved searching for genes with a phylogenetic signature characterized by an early burst of positive selection followed by stabilizing selection. Another was an analysis of gene family expansion and contraction in the symbionts compared to their phylogenetic relatives. Both fungus and alga contain expanded families of novel proteins as well as of known proteins. We will focus on specific transcription factors and transporters. Finally, analyses of global transcriptional changes during early interactions between fungus and alga were combined with gene family data to further define genes relevant to symbiosis. Specific features will be discussed in detail.

LICHEN MICROBIOMES: A MULTIPHASIC APPROACH TOWARDS UNDERSTANDING DIVERSITY AND FUNCTION

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1B-O

We extend our previous research on lichen-associated bacteria to study the effects of ecological and geographic variation on composition and function of lichen microbiomes. To characterise composition of the microbiomes of individual lichens we use a polyphasic approach including SSCP fingerprinting, deep amplicon sequencing and FISH-CLSM (fluorescence in situ hybridization and confocal laser scanning microscopy). This approach revealed the composition of core and transient fractions of bacterial communities in several species of lichens. We also study the effect of lichenicolous infections on the lichen-associated bacterial communities using *Solorina crocea*. These data of lichen microbiome variation were complemented by a functional characterization of the entire lichen symbiosis using an environmental proteomics approach. We here present first data on the analysis of the metaproteome of *Lobaria pulmonaria*. The results provide new insights into the effect of geography as well as intrinsic and environmental parameters on multispecies microbial ecosystems.

2I: Adaptation and morphological evolution

(2I-O1) Submission ID: IAL0020-00004

THALLUS ARCHITECTURE AND DOMINANCE IN *CLADINA*

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The capacity of mat-forming lichens, most notably those in the subgenus *Cladina*, to dominate the ground cover over large tracts of subarctic terrain has been attributed to their specialized mode of growth. Mat-forming lichens grow acropetally (at the apices vertically upwards) while older basal regions of the thallus senesce to produce an understorey of intact and persistent litter or necromass. This basal senescence is believed to facilitate internal recycling of nitrogen and phosphorus used to fund high growth rates in the apices resulting, under steady state conditions, in deeper mats casting deeper shade. However, how thallus architecture in mat-forming lichens is adapted to promote dominance (sensu Grime) has not previously been investigated. We hypothesise that the three-dimensional multi-branched structure of *Cladina* species is an adaptation to maximise interception of light and nutrients and to generate deep zones of depletion below the “photic zone”. We have used X-Ray computed tomography to determine vertical changes in gap fraction (light interception) and leaf area index (LAI) in mats of *Cladonia portentosa* in Scottish moorland. We compare these data with field measurements made in intact lichen mats of vertical gradients in light (determined using a fibre-optic quantum sensor) and 15N capture from labelled simulated rainfall, and with laboratory measurements of vertical changes in total chlorophyll content. We discuss the results in terms of possible trade-offs between needs for maximising interception of resources to promote dominance, light capture for photosynthesis and regenerative capacity. We also compare these first measurements of LAI within *Cladina* mats with those of forest trees.

2I-O

(2I-O2) Submission ID: IAL0185-00001

PHENOTYPIC PLASTICITY IN LICHENS: INSIGHTS ON THE BIOLOGY OF THE EXTREME MODIFICATIONS IN *CETRARIA ACULEATA* (PARMELIACEAE)

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Phenotypic plasticity has been widely reported in lichens and its importance affects not only to the field of lichen ecophysiology but also to taxonomy and speciation genetics. We studied extremely modified vagrant morphs of the lichen *Cetraria aculeata* commonly found in steppe environments from Central Spain. CO₂ exchange behaviour, water relationships, anatomical and ultrastructural modifications and genetic differentiation were studied for several populations of normal attached morphs of *C. aculeata* and modified vagrant morphs. We found that normal and vagrant morphs differ in the time span they are photosynthetically active. Further, the severe modifications found in vagrant morphs have an anatomical and ultrastructural basis, with intercalary growth being the most likely responsible for the abnormal growth found in vagrant morphs. Finally, we also observed certain degree of genetic differentiation between normal and vagrant morphs; however they do not differ in photobiont use.

DEVELOPMENT OF THALLUS AXES IN *USNEA LONGISSIMA*, A FRUTICOSE LICHEN SHOWING DIFFUSE GROWTH

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2I-O

Cell wall thickening in plants is generally limited to tissues that have ceased growth. But fungal tissues in at least two lichens are known to undergo extensive diffuse growth despite massively thickened cell walls. We examined *Usnea longissima* (recently shown to elongate diffusely -- Rolstad & Rolstad 2008) in order to determine how diffuse growth shapes the morphological development of thallus axes, and how the thick cell walls of the medullary cord behave in diffuse growth. Material was examined using light microscopy, epifluorescence microscopy, SEM and TEM. Development of long axes involved continued diffuse growth of the central medullary cord, resulting in destruction of the overlying cortex, disruption of the algal layer, and stimulation of profuse lateral branch formation. At the anatomical level, fungal cells of the medullary cord repeatedly deposit layered, electron-dense wall materials that include UV-epifluorescent components, and amorphous electron-transparent substances. As older wall materials accumulate peripherally, discontinuities appear in the electron-dense layers and new branch cells grow right through the older wall layers. Layered cell wall accumulations were similar to those observed previously in *Ramalina menziesii*, although somewhat less extensive and with a greater proportion of electron-dense/UV-epifluorescent components.

(2I-O4)

Submission ID: IAL0140-00001

THE *TEPHROMELA ATRA* SPECIES-COMPLEX: A CASE STUDY OF SYMBIOTIC SPECIES EVOLUTION

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Tephromela atra is a cosmopolitan lichen species, which grows on different substrates and in different climatic conditions. It moreover exhibits a high degree of morphological heterogeneity. *T. atra* is therefore often seen as an unresolved species complex with difficult and controversial taxonomic interpretation of its infraspecific taxa. New species of the genus *Tephromela* (described from the Americas and the Southern Hemisphere in the last two decades) differ slightly by chemical or morphological characters from European *T. atra*. A previous phylogenetic study of samples from the Mediterranean revealed the presence of diverse lineages of both the mycobiont and the photobiont partners. We expanded our ongoing work on the *T. atra* species-complex to include specimens from the whole range of its geographic distribution. We perform molecular and chemical analyses and culture experiments assess geographic distribution of genetic diversity and adaptation to climatic conditions of mycobionts and photobionts in the *T. atra* species complex. Our preliminary results show that saxicolous *T. atra* are chemically homogeneous, although they represent distinct haplotype groups. We found genetic divergence between cold regions or higher elevation and lower elevations and warmer climate. Corticolous *Tephromela* samples segregate in separate clades. *T. atra* associates with green photobionts belonging to six different *Trebouxia* clades. The wider sampling confirms that specimens from higher elevation and colder region associate preferentially with *T. simplex*, whereas the most common photobionts still undescribed *Trebouxia* sp. 1 and sp. 2, seem not to be restricted only to the Mediterranean region but occur also in the Northern Europe, Chile and Peru.

(2I-O5)

Submission ID: IAL0098-00001

**RECONSTRUCTION OF ANCESTRAL STATES USING PHYLOGENIES:
PARMELIACEAE AS A CASE STUDY**

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Parmelioid lichens are a diverse and ubiquitous group of foliose lichens. Molecular phylogenetic studies have confirmed or rejected the monophyly of various genera – some newer, some older – , and others, previously believed to be unrelated, fell within single monophyletic groups. Reliable phylogenies for the parmelioid lichens enable us to further address the question of character evolution in this challenging group of lichens. Our recent study of 762 specimens using maximum likelihood and Bayesian analyses of combined datasets of up to four loci served as a starting point for a reconstruction of ancestral states for several nodes of interest. Maximum Likelihood and Bayesian Methods with the MESQUITE and BayesCharacters software packages were used, implementing and comparing binary and multistate character coding together with one- or multi-parameter models. All major monophyletic clades and subclades within the parmelioid lichens were analyzed for various sets of morphological and chemical characters, e.g. growth form, habitat, epicortex, and others. For example, for the parmelioid lichens a non-pored epicortex with pseudocyphellae and the presence of usnic acid could be reconstructed, whereas growth form and habitat remain controversial depending on the methods used for reconstruction. For most of the investigated clades, results supported with statistical significance were not conflicting between Bayesian and Maximum Likelihood methods, or between binary and multistate character coding. However, the level of statistical support varied considerably for many reconstructions. Given the considerable size and complexity of our data set, our results suggest that in such cases, a given method for reconstruction of ancestral states may be inconclusive, and results should generally be compared with other methods or models in order to achieve reliable conclusions.

2I-O

(2I-O6)

Submission ID: IAL0096-00003

**MORPHOLOGICAL DISPARITY AND SPECIES DELIMITATION OF LICHEN IN THE GENUS
CLADIA (LECANORALES, ASCOMYCOTA)**

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Phylogenetic studies of the genera *Cladia*, *Heterodea* and *Ramalinora* as well as the *Cladia aggregata* complex were carried out using the ribosomal nuclear ITS and LSU, mitochondrial SSU, protein-coding MCM7 and protein-coding GAPDH DNA sequences. Bayesian, Maximum likelihood (ML) and Maximum parsimony (MP) methods together with General Mixed Yule Coalescent (GMYC) were employed. Based on different analyses, the foliose genus *Heterodea* and the crustose genus *Ramalinora* were nested within the fruticose genus *Cladia*. For the *C. aggregata* complex, analyses based on a combined data set of nITS and protein-coding GAPDH under GMYC criteria revealed at least eleven distinct lineages. Almost all previously recognized species were intermixed within this complex. Causes of the disparity exhibited unusual morphological in this group are discussed.

MORPHOLOGICAL VARIATION, SPECIES CIRCUMSCRIPTION AND PHYLOGENETIC RELATIONSHIPS IN THE GENUS *PECCANIA* (LICHINACEAE)

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21-O

The genus *Peccania* of the cyanobacterial lichen family Lichinaceae (Lichinomycetes) contains at present approximately 12 species with a nearly worldwide distribution. Whereas the genus is very well defined by a set of correlating morphological characters it is often challenging to define proper species boundaries. The main reason for this is that the species are very uniform in thallus and fruit body anatomy. Likewise, asco- and conidiospore features are of poor diagnostic value. On the other hand, the thallus external shape and size may vary considerably among specimens of a particular species of *Peccania* or sometimes even within a single specimen. Examples of such morphologically very variable species are *Peccania coralloides*, *P. arabica* and *P. terricola*. The reasons behind the high plasticity in external morphology of the species are largely unknown. Also, variation in morphological characters such as growth form, lobe formation, branchings patterns etc. is often thought to be environmentally controlled or may change considerably according to the developmental stage of the lichen thallus under study. Finally, it is known that congruence in patterns of general growth form among lichens is often simply due to homoplasy and not because of common ancestry. For the members of the genus *Peccania* this results in rather fuzzy species circumscriptions and difficulties in species identification are notorious. Therefore, the traditional, morpho-species concepts of the species have been confronted with the results from a reconstruction of phylogenetic relationships among the species. 68 specimens of *Peccania* representing almost all described species have been studied. Secondary structure guided ITS 1+2 sequence analyses suggest that most of the species are monophyletic, this being an impressive proof for the usefulness of morphology based, traditional species circumscriptions even in critical lichen groups with a generally much reduced morphology such as the Lichinaceae. Character mappings suggest that general growth form characters like "growth form dwarf-fruticose" or "lobate-fruticose" are highly homoplasious among *Peccania* species. On the other hand, the detection of monophyletic clades was helpfull in reassessing the boundaries between morphologically variable species. Finally, the presence of cryptic species cannot be excluded in dwarf-fruticose species complex of *Peccania subnigra* and *P. fontqueriana*.

**GOOD-BYE MORPHOLOGY, OR THREE CHEERS FOR NUANCE? MOLECULAR
PHYLOGENETICS AND A POSTERIORI MORPHOLOGICAL ANALYSIS
IN TWO CRUSTOSE LICHEN GENERA**

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Recent advances in molecular phylogenetic analyses of lichen mycobionts have revealed that many taxa traditionally assumed to represent single, widespread species in fact consist of multiple, genetically distinct lineages. Consistent with a current popular trend across biological disciplines, these have been interpreted by many authors as “cryptic species”. While some authors have highlighted the usefulness of molecular markers for elucidating relationships in morphologically subtle groups, others suggest that the morphological approach itself is problematic and leading lichenologists potentially to overlook large nodes of diversity. Detection of diagnostic signal in a morphological character set requires systematic testing of congruence of a wide range of traits with identified clades. In molecular studies of mycobionts in two morphology-poor crust lichen genera, *Mycoblastus* and *Xylographa*, we recently detected numerous previously overlooked monophyletic groups that by most current measures would be called cryptic species. In some cases our results quadruple or quintuple the number of species relative to classical concepts. We tested the null hypothesis of no congruence between phenotype and genotype by scoring traditional and non-traditional morphological and chemical traits against the resulting molecular clades. In both genera, we found nearly all lineages could be reliably recognized using phenotypic characters alone. Far from being problematic, reliance on morphology underlies nearly all hypothesis-testing in current lichen molecular phylogenetics from the proposal stage to final publication. Molecular phylogeneticists have a unique opportunity to support and be supported by field lichenologists in ongoing efforts to elucidate specific problems such as photobiont effects on morphology and convergent body plan evolution in symbiosis. Together they can make meaningful contributions to lichen conservation that go well beyond the lab bench.

2I-O

2A-1: Graphidaceae: progress in understanding the evolution and diversity of the largest family of tropical crustose lichens

(2A-1-O1) Submission ID: IAL0178-00001

HISTORICAL BIOGEOGRAPHY, ECOLOGY AND SYSTEMATICS OF THE FAMILY GRAPHIDACEAE (ASCOMYCOTA: OSTROPALES)

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Graphidaceae is the second largest family of lichenized fungi and the largest family of tropical lichens, with over 1,500 accepted species. Although the family forms the most important component of tropical lichen communities, it has only recently begun to be studied in detail. Based on revisionary work undertaken by our study group for the past ten years, there is now a solid systematic concept in place, with over 50 genera currently accepted (compared to less than 15 only ten years ago). However, several clades within the family still need further studies. This applies in particular to the *Ocellularia* clade, the second largest in the family. The objective of this study was to study aspects of the natural history of Graphidaceae that go beyond a purely taxonomic revision. The research is focused on the evolution and early diversification of the family, evolution of phenotypic characters correlated with environmental parameters and their use for classification, and the phylogeny and classification of the *Ocellularia* clade. The results indicate that Graphidaceae evolved and diversified about 160–180 mya in the Jurassic, in accordance with the early evolution of modern tropical rainforests. Many of the characters used in the delimitation of genera evolved in parallel in unrelated lineages, suggesting ecological constraints as explanation. Molecular phylogeny of the *Ocellularia* clade detected several previously unrecognized lineages deserving generic status, and a formal revised classification is proposed.

2A-1-O

(2A-1-O2) Submission ID: IAL0016-00001

DILEMMAS IN SPECIES AND GENUS DELIMITATION IN E.G. GRAPHIDACEAE

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In former days, a species was what the monographer judged a good species, and a genus a handy group of species. Since cladistics was introduced in taxonomy, genus and species delimitations have become open to more universal discussions. Especially now that sequences have become available for some species (albeit still for only a minority of lichen taxa), many new classifications are proposed solely on the prerogative that a taxon should be monophyletic. This dogma needs closer scrutiny. Taxa evolve, and every monophyletic group can become paraphyletic the moment that one daughter group becomes geographically or otherwise isolated. On closer examination, nearly all groups were paraphyletic at least part of their history.

(2A-1-O3) Submission ID: IAL0033-00001

**TAXONOMY AND DIVERSITY OF LIRELLATE GRAPHIDACEAE (OSTROPALES)
AT PHU LUANG WILDLIFE SANCTUARY, THAILAND**

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Our objective was to explore the diversity and distribution of lirellate Graphidaceae occurring in seven different forest types (coniferous forest, CF; dry dipterocarp forest, DDF; dry evergreen forest, DEF; lower montane scrub, LMS; lower montane rain forest, LMRF; mixed deciduous forest, MDF; and tropical rainforest, TRF) at Phu Luang Wildlife Sanctuary. Five hundred and thirty-one specimens were collected and identified to ninety-one taxa in sixteen genera (*Acanthothecis*, *Carbacanthographis*, *Diorygma*, *Dyplolabia*, *Glyphis*, *Graphis*, *Fissurina*, *Hemithecium*, *Leiorreuma*, *Pallidogramme*, *Phaeographis*, *Platygramme*, *Platythecium*, *Sarcographa*, *Thalloloma* and *Thecaria*). Thirty-five taxa are first records for Thailand, while 17 taxa were expected to be new species to science. The highest diversity, 63 species, was found in LMS, while in LMRF (36 species), MDF (31 species), DDF (20 species) and TRF (14 species) were collected, and the lowest diversity in DEF (9 species) and CF (8 species). The genus *Graphis* showed the highest diversity with 35 species, and *Dyplolabia afzeli*, *Diorygma hieroglyphicum*, *Graphis streblocarpa*, *Pallidogramme chrysenteron* and *Phaeographis* sp. 2 are the most common species and are widespread in almost all forest types.

2A-1-O

(2A-1-O4) Submission ID: IAL0283-00001

**MORPHO-CHEMOTAXONOMY OF THE GRAPHIDACEAE (SENSU LATO) LICHENS IN THE
KALAHAN FOREST RESERVE OF NUEVA VIZCAYA, PHILIPPINES**

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Graphidaceae lichens collected from the Kalahan Forest Reserve in Imugan, Santa Fe, Nueva Vizcaya, were evaluated for their morpho-anatomical and chemical features. Taxonomic characters of thallus (cortex, texture, color), ascocarp/lirellae (morph, form, emergence, branch, color, striation, thalline margin, rim color, disc color, pruina), exciple (carbonization), hypothecium (carbonization), hymenium (inspersion), and ascospore (number per ascus, shape, septation, number of locules, length, width, color and color reaction to iodine solution) were observed and described. A total of 52 species distributed in 16 genera were identified. Two of the species are suspected to be species novae. Only three of the 52 species are thelotremoids; the rest are all graphioids. Two-way hierarchical clustering of the identified lichens showed that lirellae morphology determines major groupings while ascospore shape and iodine reaction distinguish the genera *Graphis*, *Thelotrema*, and *Glyphis*. There were significant differences in the majority of the morpho-anatomical features between the clusters. There was no significant difference in the lichen acids present in them.

2A-2: Parmeliaceae: improving our understanding of taxonomy, classification and biogeography

(2A-2-O1) Submission ID: IAL0170-00001

**MULTILOCUS PHYLOGENY AND CLASSIFICATION OF PARMELIACEAE (ASCOMYCOTA)
DERIVED FROM PARSYS-10**

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Parmeliaceae is one of the largest lichen families in lichenized fungi, containing ca. 2,500 species distributed in 84 genera. It is characterized by cupulate exciple, Lecanora-type asci and mostly simple hyaline ascospores. Taxa included in the family are morphologically very diverse e.g. crustose, subcrustose, foliose and fruticose growth forms and widely distributed. In our previous PARSYS-08 project we published a solid classification of core group parmelioid lichen and re-circumscribed several genera based on multigene molecular data. Almost all the phylogenetic relation among the divergent groups of parmelioid lichens was well resolved, however the backbone of the main clades were not resolved with confidence. Likewise parmelioids, a large number of species included in other groups of the family has also worldwide distribution and the sheer number of species makes it advisable that different research groups join forces in the study of the phylogeny of these lichens. The current project PARSYS-10 planned during an EOL meeting in 2010, and we are presenting here following results: i) elucidation of evolutionary relationship among Parmeliaceae taxa; ii) a comprehensive and coherent classification at generic level for Parmeliaceae. The following six molecular markers are included in the study, nuclear ribosomal regions, ITS and nuLSU rDNA, mitochondrial SSU rDNA, and protein coding genes RPB1, Mcm7 and tsr1. Single-gene and combined data sets were analyzed using maximum parsimony, maximum likelihood, and Bayesian methods.

(2A-2-O2) Submission ID: IAL0177-00001

MAKING SENSE OF CRYPTIC DIVERSITY, BIOGEOGRAPHY, AND DIVERSIFICATION IN LICHEN-FORMING FUNGI - A STUDY OF BROWN PARMELIOID LICHENS (PARMELIACEAE, ASCOMYCOTA)

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While many lichen-forming fungal lineages have geographically restricted distributions, there is mounting evidence that transoceanic dispersal is common within some lichen associations. However, cryptic lineages within morphologically and chemically circumscribed taxa likely confound our understanding of the role of biogeography and long-distance dispersal in many broadly distributed species. In this study we address species circumscription and biogeographic patterns in two closely related, and notoriously challenging, parmelioid lichen genera (*Melanelixia* and *Melanohalea*) with broad distributions throughout the northern Hemisphere. Using DNA sequence data from ca. 650 individuals we address current morphological/chemical species circumscriptions, identify previously unrecognized lineages, and discuss biogeographical patterns. Although many clades are largely congruent with traditionally circumscribed taxa, some morphologically indistinguishable groups (cryptic species) are recovered in multiple, distinct genetic lineages in both *Melanelixia* and *Melanohalea*. Strong nodal support and reciprocal monophyly in independent gene trees suggest long-term reproductive isolation between most lineages. While many lineages are truly widespread and support the hypothesis of common transoceanic dispersal, a limited number of clades appear to have much more restricted distributional ranges. We also estimate net diversification rates between *Melanelixia* and *Melanohalea* and calculate the difference between them. Incorporating Bayesian divergence time estimation, we explore potential explanations for differences in diversification rates and biogeographic patterns.

2A-2-O

(2A-2-O3) Submission ID: IAL0272-00001

MOLECULAR PHYLOGENETICS AND SPECIES DELIMITATION IN MENEGAZZIA (PARMELIACEAE)

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The genus *Menegazzia* has its main distribution in the Southern Hemisphere and is particularly species-rich in temperate forests in South America and Oceania and in mountainous regions close to equator. More than 70 species have been described, but species new to science are still being discovered. Recent comparative studies have also shown some formerly separated species to be conspecific, which has led to revisions of distribution maps. In this study *Menegazzia* specimens from South America, Australasia, North America, and Europe have been collected for molecular analysis to elucidate the phylogeny of this genus based on three loci (nuITS, nuLSU and mtSSU). The results suggest that the genus comprises a large proportion of endemic species and that chemistry is an important character for species delimitation. Further results will be presented, and some implications for species delimitation within the genus will be discussed.

**GEOGRAPHICAL STRUCTURE OF *CETRARIA ACULEATA* POPULATIONS ALONG
A WIDE LATITUDINAL TRANSECT**

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2A-2-O Many lichen species that occur at high latitudes are common to both hemispheres, showing a bipolar disjunct distributional pattern. The fruticose lichen *Cetraria aculeata*, as many other bipolar species, also spreads into lower latitudes, into temperate and tropical high mountains and dry temperate lowlands. With this study we aim to explore the historical and geographical processes that determined its current distribution. The geographical distribution of species has frequently been interpreted in terms of vicariance and dispersal events. The relative importance of these two processes in the evolution of a species is very difficult to partial out. In the case of bipolar lichens, and other widely distributed taxa, their distribution has been interpreted in two opposed ways: a) they had extremely large ancestral ranges, or b) they are/were able to disperse across long ranges. In this work the lichen *C. aculeata* was studied from the perspective of population and evolutionary genetics on a transect joining south and north polar regions along the Andes and the Rocky mountains. Our results suggest that this species originated in the Northern Hemisphere and advanced progressively towards the Antarctic using available patches of suitable habitats on high mountain ranges. The genetic structure of populations suggests the absence of long range connectivity between extant populations. Population size reconstructions suggest that the species underwent at least one population expansion in the past followed by a more recent contraction. It seems likely that mid and long range dispersal lead to a transient increase in population size and a subsequent increase of geographical range during the Pleistocene. Our data suggest that extant regional populations result from the concurrence of two separate processes: a) population and range expansion, and a posterior b) population fragmentation leading to the appearance of vicariant demes. The geographical extent and temporal patterns of range and population size expansions and contractions during the Pleistocene glaciations should be further explored.

PHYLOGENY OF THE GENUS *VULPICIDA* AND DELIMITATION OF THE SPECIES

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The morphological group of cetrarioid lichens (Parmeliaceae) with erect foliose/subfruticose thallus, marginal apothecia and pycnidia, and production of the *Cetraria*-type lichenan contains nearly 150 species in over 20 genera, of which c. 90 species and 15 genera form a monophyletic clade, the so-called 'cetrarioid core'. Many genera in the cetrarioid core group are narrowly defined relative to other genera in the Parmeliaceae and so the genus delimitations of cetrarioid lichens is still in focus. The genus *Vulpicida*, belonging to the cetrarioid core, consists of six species of lichenized fungi: *V. canadensis*, *V. juniperinus*, *V. pinastri*, *V. tubulosus*, *V. tilesii* and *V. viridis*. The genus is distributed in the temperate and arctic regions of the Northern Hemisphere and its species are characterized by a unique set of secondary metabolites, pinastric and vulpinic acids, that are products of the shikimic acid pathway and cause an intense yellow color of the medulla. The morphological recognition of the genus is easy due to this impressive character, but the monophyly of the genus has not been shown with confidence and the evolutionary relationships between the species have remained unclear. The delimitation of, and the relationships between, all six *Vulpicida* species using nuclear ITS and Mcm7, and mitochondrial SSU DNA sequences have been analysed. Over 100 *Vulpicida* specimens, 10–30 samples of each taxon, were analysed together with species from the cetrarioid core group. Gene trees from Bayesian and parsimony analyses are presented, as well as the coalescent-based Bayesian species trees. Morphologically similar and not easily separable *V. juniperinus* and *V. tubulosus* are divided into two clearly distinguished groups in the gene trees. However, these species are mixed in both clades, appearing polyphyletic. In contrast, they form one intermixed clade in the species tree, supporting their synonymization. *Vulpicida pinastri* appears monophyletic, while *V. tilesii* sequences also group with *V. juniperinus* and *V. tubulosus*. Two further species, *V. canadensis* and *V. viridis*, with limited North American distributions and a different shape of the pycnoconidia (citriform instead of sublageniform) appear outside the clade of the other four taxa in the multilocus trees.

2A-2-O

2B: Forest lichens: their ecology and distribution

(2B-O1) Submission ID: IAL0040-00006

ECOLOGICAL STUDY OF LICHENS IN THAILAND

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The ecological study of lichens in Thailand started in 1990. It involved using lichens to monitor air quality in Bangkok. Long term ecological projects were subsequently developed by using Khao Yai National Park as a permanent study site. It involved five main areas of concern. The first project involved the continuous use of lichens to monitor air quality in Bangkok and its environs. It consisted of species composition in low, medium and high polluted areas as well as accumulation of toxic pollutants and physiological damages of lichens transplanted to those areas. The second project involved the long term effects of different tropical ecosystems on the longevity and growth of lichens. It was found that lichens in humid tropic have shorter thallus longevity in comparison to those in temperate region. Their growth rates averaged 6.3 and 2.8 mm/year for foliose and crustose lichens, respectively. The third project involved the spatial distribution of lichens in tropical ecosystems and the vertical stratification of lichen communities. The effects of microclimate on the survival and growth of species transplanted to different ecosystems were studied. It was found that lichens originally inhabited in warm forests survive better when transplanted to cooler climates. However, in contrast, lichens initially populated in cool forests are barely able to adapt to warmer climates. The fourth project involved seasonal variations in carbon dioxide assimilation by lichens and the production of lichen substances under the conditions of varying ecosystems. Seasonal variations along these parameters were found. The fifth project involved in situ transplantation of lichens to artificial substrates to enhance the production of lichens for purposes of conservation and sustainable utilization.

2B-O

CORTICOLOUS LICHEN COMMUNITIES AS INDICATORS OF VEGETATION TYPES ALONG ENVIRONMENTAL GRADIENTS IN KNUCKLES MOUNTAIN RANGE - SRI LANKA

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Knuckles Mountain Range is a world heritage site within the central massif of Sri Lanka covering 21,000 ha and ranging from 400 to 1,900m altitude. At the higher altitudes montane and submontane forests occur giving way to disturbed secondary forests and to plantations of tea, *Acacia* and *Pinus*. This study of corticolous lichens was undertaken in all forest and plantation types in order to determine differences in assemblages and their association with environmental and microclimatic conditions, and to test for potential indicator species. Eighteen plots of 100x100 m were set up representing 8 vegetation types and 6 altitude classes. Lichen species and percentage cover were recorded in five microplots on 10 randomly selected tree trunks. Environmental parameters included bark type and pH, DBH, canopy cover and light intensity. Nonmetric multidimensional scaling (NMS) provided a graphical depiction of community relationships and habitat variables among 146 species recorded, using Beals smoothing to compensate for high beta diversity. Nonmetric-Multi-Response Permutation Procedure (MRPP) and Indicator Species Analysis (ISA) was carried to test for differences between groups and to identify species associated with the groups. The first axis of the NMS represented 33.4% of the variation in species composition coinciding with vegetation types and altitude classes. Highest diversity was recorded in montane forest including low frequency species belonging to Chlorophyceae and consistent contribution by tropical family Graphidaceae and genus *Sticta*. Rapidly invasive species were found in exotic plantations with lowest diversity. ISA indicated that forty percent of the lichen species recorded occurred frequently throughout and significant indicator values were recorded for 46 species that are exclusive to one habitat type or to one elevation class. This study has shown that lichens are potentially useful bioindicators to assess degree of disturbance and ecological continuity in the montane tropics.

2B-O

OCCURRENCE AND HOST SPECIFICITY OF MACRO-LICHENS AMONG TROPICAL DECIDUOUS FOREST OF SHIMOGA DISTRICT, SOUTHERN INDIA

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In the present investigation the diversity, distribution and host specificity of macro-lichens of tropical deciduous forests of Shimoga district, India was studied. During intensive field exploration 61 species of macrolichens classified in 23 genera and belonging to 9 families were found. The family Physciaceae is dominating with 21 species, followed by Parmeliaceae with 17 species. The corticolous lichens dominate with representing about 85% of the recorded species, while about 10% of the species were saxicolous. About 80% of the species were foliose and about 20% fruticose. Roughly 70% lichens have green algae as photobionts and 30% cyanobacteria associated as photobiont. In a heterogeneous forest land the diversity of lichens is variable as the supporting host trees provide space for different types of lichens. Some of the macrolichens were found to have a broad amplitude. This includes *Leptogium* sp., *Parmotrema tinctorum*, *P. cristiferum*, *Ramalina pacifica*, and *Usnea* sp. *Parmotrema tinctorum* had the widest amplitude and was found growing on 9 different host tree species among the selected 30 host species. The most important host species were *Terminalia paniculata*, *Spondias pinnata*, *Polyalthea* sp., *Bombax ceiba*, *Ziziphus* sp., *Delonix regia*, *Mangifera indica* but they did not occur on the bark of *Xylia xylocarpa*, *Tectona grandis*, *Lagistromia lanceolata* and *Adina cordifolia*. The pH value of the bark varies between 3.73 (*Santalum album*) and 6.84 (*Canthium* sp.). Most of the lichens prefer acidic bark and moisture content varies from *Terminalia tomentosa* (40.24%) to *Ficus racemosa* (84.27%). The lichens showed preference for certain trees mostly based on the nature of bark and its microelements and chemical composition.

2B-O

(2B-O4)

Submission ID: IAL0134-00001

EPIPHYTIC LICHEN COMMUNITIES IN BOREAL CONIFER FORESTS OF PACIFIC COAST OF NORTHEAST ASIA (RUSSIA)

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A study of lichen communities was carried out in humid boreal conifer forests on the Pacific coast of Northeast Asia. The main goal was to describe the structure of lichen communities and to reveal their relationships to ecological factors. The three most common conifer tree species in the region were chosen for lichen sampling: *Picea jezoensis*, *Abies nephrolepis* and *Pinus koraiensis*. 85 study plots were established on trunks of these trees in two main locations representing intact oldgrowth forest ecosystems. Species composition and a relative cover of each species were recorded for each plot. A total of 90 lichen species were identified. Using Ward's cluster analysis we defined 9 main lichen synusiae. Using statistical analytic tools we assessed the relationships between lichen communities and various environmental conditions, including large-scale factors (like geographic location and climate), mid-scale (forest type, relief) and small-scale factors (bark morphology, trunk aspect, height of the plot above ground). Large-scale factors proved to have the most influence on community composition, while some more local conditions showed a facultative influence, if any. Lichen species were also compared for coenotic activity (ability to dominate the communities) and frequency. *Graphis scripta*, *Menegazzia terebrata* and *Parmelia squarrosa* appeared to be the leading species in both aspects.

(2B-O5)

Submission ID: IAL0220-00001

USING LICHENS TO EVALUATE TASMANIAN FORESTS

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Lichens are a major component of forest biodiversity in Tasmania. However, using them to explore broader ecological questions such as forest history, structure and composition is very much in its early stages, unlike in Europe, for example, where the role of lichens as indicators of forest age and continuity is well-established. In Tasmania, complications arise because the lichens are still incompletely known taxonomically; the ecology and distribution of many species is likewise incompletely documented; there is a political imperative to contribute lichen information to the forest management debate, even with incomplete data; and there is only a limited understanding in the broader community of lichens themselves, their life-history and their habit ecology. Comparisons of lichens from unlogged and from harvested, regenerating forests is one way that lichens can contribute to the forestry debate. These comparisons can be undertaken in various ways; for example, using indices of diversity, comparison of species composition, or comparing abundance of particular taxa. However, these approaches do not fully take into account that species have individual responses to disturbance, different habitat requirements and different conservation status. We present a preliminary classification of Tasmanian forest lichens based on general field observations, targeted study of particular species, targeted study of particular sites, and herbarium records. This classification offers a tool whereby the ecological quality of forest sites can be evaluated.

2B-O

(2B-O6)

Submission ID: IAL0160-00001

ECOLOGICAL FACTORS AND POPULATION DYNAMICS OF *LOBARIA PULMONARIA*: IS IT AN ENDANGERED SPECIES IN SPAIN?

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The aim of this study is to describe and analyze the key variables affecting *Lobaria pulmonaria* populations, considering its ecology and population dynamics. For this purpose we defined environmental, demographic and physiological variables in two different habitats establishing 4 plots in central Spain: 2 of them in oak forests (*Quercus pyrenaica*), and 2 more in beech forests (two 1 ha, two 0.25 ha plots). All trees in each plot were georeferenced, described and marked. Location, size, status, and presence of sexual and/or asexual reproductive structures of all *L. pulmonaria* individuals in each plot were registered. Per plot, 200 individuals were randomly selected and marked. Semiannually, pictures of those 800 individuals are being taken in order to estimate potential reproductive changes and/or size variation. Monthly, we are also recording the physiological variable Fv/Fm of those 800 individuals, as a stress indicator (at noon and at predawn). Besides, 360 sampling squares (20x20cm) have also been set to find out *L. pulmonaria* establishment rates. Environmental factors determining presence, abundance, size and reproductive capability will be analyzed using Generalized Lineal Models and Generalized Lineal Mixed Models. Currently, 11680 *L. pulmonaria* individuals have been described. Trees hosting *L. pulmonaria* individuals are thicker and have rougher bark. *Lobaria pulmonaria* shows different patterns depending on forest type and among plots. One of the plots presents much lower population density than the other three (100 individuals/ha vs. 9,000 individuals/ha). Phorophytes differences were also found on height distribution pattern (individuals on beech grow grouped in the lower (<50cm) strip, but this pattern is not so remarkable on oaks), abundance (oaks have a greater number of individuals except in the low density plot), size (individuals average size is smaller on oaks) and reproductive capability of individuals (the occurrence of apothecia and soredia is slightly higher in thalli growing on beech). Moreover, differences on recruitment rate are remarkably higher on oaks than on beech trees.

**TESTING HYPOTHESES OF THE DECLINE OF THE CRITICALLY ENDANGERED
ERIODERMA PEDICELLATUM (PANNARIACEAE)**

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Erioderma pedicellatum (Hue) P.M.Jørg. is a critically endangered foliose lichen species growing exclusively on the bark of conifers. It is restricted to three disjunct geographic areas (Western Scandinavia, Atlantic Canada and Alaska). The photobiont of this lichen is the cyanobacterium *Rhizonema* sp., a rarely reported photobiont in lichen-forming fungi. Compared to most other lichen species, *E. pedicellatum*'s juvenile thalli are only rarely found and, consequently, known populations suffered a dramatic decrease during the last decades. To find causes of this decline, we tested two different hypotheses. First, we hypothesized that the availability of the free-living photobiont might limit the establishment of the lichen phenotype. Second, we studied the fungal genetic variation and populations structure. In order to test the first hypothesis, we characterized molecularly the photobiont of *E. pedicellatum* based on sequences (SSU nrRNA and RuBisCo) and investigated if several other lichen species, which form a characteristic epiphytic lichen community with *E. pedicellatum*, associate with related photobiont species in forest areas of the Avalon Peninsula (Newfoundland). Indeed, we found that *E. pedicellatum* and *Coccocarpia palmicola* (Sprengel) Arv. & D.J. Galloway share the same *Rhizonema* strain and the photobionts of other lichens of the same community are close related with this strain. Furthermore, we detected the cyanobacterial strain associated with *E. pedicellatum* in free-living populations in forest stands where neither *E. pedicellatum* nor *C. palmicola* are currently present. Thus, the photobiont of *E. pedicellatum* has a wider distribution than the lichen and the photobiont limitation hypothesis had to be rejected. For the study of fungal genetic structure of populations, we developed mycobiont-specific microsatellite markers and our results showed low variation within populations on the Avalon Peninsula. Work is ongoing to evaluate the genetic variation between populations of the Avalon Peninsula and specimens from Alaska. Ultimately, these studies will give new perspectives in the understanding of population dynamics of *E. pedicellatum*. Such data give valuable insight on how conservation strategies can be developed that guarantee the long-term persistence of this critically endangered boreal felt lichen.

2B-O

(2B-O8) Submission ID: IAL0130-00001

**DIVERSITY, COMMUNITY STRUCTURE, AND SPATIAL PATTERNS OF MACROLICHENS IN
A TEMPERATE FOREST MAPPED PLOT IN SANTA CRUZ, CALIFORNIA**

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We recorded the cover class of macrolichen species on the trunks of all woody plants with the diameter at breast height (DBH) greater than two cm in a six-hectare mixed evergreen forest plot in Santa Cruz, California, USA. Twenty nine species of macrolichens were found on 31 host species. Out of 7,984 trunks surveyed, 46.43 percent contained at least one lichen species. Species richness increased significantly with the DBH, but the rate of increase varied among species of host trees (Generalized Linear Model; $P < 0.001$). While there was no clear clustering of lichen communities based on their host species, the majority of lichen species (20 of 29) occupied 5 or fewer host species. Dissimilarity among communities was correlated with geographical distance between host trees (Mantel's Test, $r = 0.04$, $P = 0.001$). The results suggested that spatial and stochastic processes may play a more important role than niche-based, deterministic processes in assembly of lichen communities in this temperate forest plot.

3I: New approaches to understanding biosynthesis and ecological roles of metabolites in lichens

(3I - O1) Submission ID: IAL0144-00001

GAINING NEW INSIGHTS INTO LICHEN SECONDARY METABOLISM: ECOLOGICAL FACTORS TRIGGER CHEMOSYNDROMIC VARIATION WITHIN SPECIES OF THE GENUS *XANTHOPARMELIA* AND NOVEL TECHNIQUES TO DECIPHER THE GENETIC POTENTIAL OF POLYKETIDE BIOSYNTHESIS IN A CULTURED METABOLITE-PRODUCING MYCOBIONT

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The ecological role and functions of secondary metabolites, particularly medullary compounds, has been extensively discussed among lichenologists since a long time. Variations in medullary chemistry within many lichen families and genera have generated debate over the recognition of “chemical species”. A series of patterns of chemical variations have been identified as replacement-type substances, accessory-type compounds, acid deficient, acid additive strains and also the occasional presence of chemosyndromes, even overlapping chemosyndromes have been reported. In many lichen groups, which have been screened for the content of lichen substances by TLC and HPLC analyses, major compounds in a particular taxon are often accompanied by minor, biosynthetically related satellite compounds, which in turn may become predominant in closely related taxa – this is known as chemosyndromic variation. Variations in chemical composition of secondary metabolites in lichens have been used as important taxonomic characters at different levels in lichen systematic. The precise taxonomic significance of such variation has been often discussed but may be best understood a posteriori and in conjunction with other characters. Chemical analyses indicate that substantial chemical variation is possible both within a species and among closely related species. Chemosyndromic variation has been correlated with morphology (differences in chemistry co-occurring with morphological, anatomical differences), geographic variation (reproductive isolation) and also with ecology. Our recent investigations with Australian and European species of the genus *Xanthoparmelia* have mainly focused on ecological factors that may be responsible for chemosyndromic variation within Australian species like *Xanthoparmelia antleriformis*, *X. cheelii*, *X. filarszkyana*, *X. flavescensireagens*, *X. lineola*, *X. metaclystoides*, *X. substrigosa*, *X. tasmanica*, *X. flavecentireagens*, and *X. conspersa* from Europe. Distinct medullary chemistries, growth forms, and the production of vegetative diaspores have been found to have evolved independently multiple times in *Xanthoparmelia*. Chemical variation was also studied in cultured mycobionts. One mycobiont (*X. flavecentireagens*) cultured in large scale/desiccation stress that yielded a complete chemosyndrome was selected to decipher the PKS genes coding for the respective PKSs, e.g. for norlobaridone, loxodin (medullary depsidones) and usnic acid (cortical dibenzofuran).

3I-O

(3I-02) Submission ID: IAL0288-00001

IDENTIFICATION OF LICHEN COMPOUNDS USING LIQUID CHROMATOGRAPHY

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The utility of identifying lichen compounds is undeniable; whether for broad taxonomic studies or the description of new lichen species. While TLC is the most widely applied method of detection there are obvious shortcomings inherent to the method. The use of High Performance Liquid Chromatography is becoming the preferred method of lichen compound identification. We have developed a library of over 1,000 lichen compounds using herbarium material and authentic purified substances. Although not yet mainstream in many lichenologists' laboratories the use of Ultra Performance Liquid Chromatography coupled with Mass Spectrometry provides additional information is an exciting way to explore lichen chemistry. Using accurate mass measurements and statistical methods it is possible to not only identify known compounds and test their relevance to a particular taxonomic conjecture, but also to quickly identify potentially unfamiliar lichen specific secondary metabolites.

(3I-03) Submission ID: IAL0153-00001

3I-O

SNAILS AVOID THE MEDULLA OF *LOBARIA PULMONARIA* AND *L. SCROBICULATA* DUE TO PRESENCE OF SECONDARY COMPOUNDS

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Lichens are frequently grazed by various invertebrates, such as snails and slugs. However, these gastropods discriminate between the various layers of the lichen thallus. Likewise, carbon based secondary compounds (CBSCs), some of which are known to deter lichenivores, are unevenly distributed between the various layers. In this study, the degree of rejection of medullary CBSCs by gastropods is investigated. The snail *Cochlodina laminata* was offered the lichens *Lobaria pulmonaria* and *L. scrobiculata* with and without CBSCs. The secondary compounds were removed by rinsing dry thalli in acetone. The snails completely avoided the medulla of thalli with natural levels of CBSCs. However, they grazed through all layers perpendicularly after these compounds had been removed. Hence, the medullary compounds restrict feeding by gastropods to the cortical and sometimes also the photobiont layer.

ACETONE-EXTRACTABLE COMPOUNDS PROTECT LICHENS AGAINST MOLLUSCS

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It is a well-known fact that lichens produce numerous unique secondary metabolites. Various functions have been proved for them and recently a lot of evidence that one of the ecological roles, at least for some species, is protection against grazers has been gathered (eg. Pöykkö et al. 2005, Nimis & Skert 2006, Asplund et al. 2010). In our study we tested the hypothesis that acetone-extractable compounds protect selected epiphytic species of the Parmeliaceae family against lichenivorous molluscs. We chose 6 species with diverse secondary compounds – *Parmelia sulcata*, *P. saxatilis*, *Melanelixia fuliginosa*, *M. subaurifera*, *M. glabra*, *Parmelina tiliacea* and 2 species with no secondary metabolites detected by t.l.c.(Smith et al. 2009) – *Melanohalea exasperatula* and *M. exasperata*. Two species of molluscs with different ecological strategies were selected – *Lehmannia marginata* and *Cochlodina cerata*. Following the method of Solhaug and Gauslaa (2001) for acetone-rinsing and adjusting the design of Gauslaa (2005) we set an experiment - lichen thalli were cut into two halves and one of them was rinsed in acetone. The two halves were put in each of ten glass containers together with two individuals of a mollusc species. The same procedure was used for all the lichen-mollusc species combinations. Afterwards the amount of thallus consumed was calculated. A strong preference for the acetone-rinsed thallus part was observed for all the species containing secondary lichen compounds. The results are reliable at $p < 0.05$. There was no preference between thallus parts in *M. exasperatula*. Lichen species rarely found with grazing marks in the field (e.g. *P. saxatilis*) were palatable after the acetone-treatment. Moreover, species grazed frequently in the field became even more attractive. Thus, the anti-herbivore effect of secondary metabolites in lichens has been demonstrated. Differences in preference for the acetone-extracted part as well as the ability to feed on the untreated part were observed between the lichen species. This work contributes to understanding one of the ecological roles of secondary metabolites in lichens and may serve as a basis for testing further ecological consequences of predation of these lichens by molluscs.

3I-O

ALLELOPATHIC EFFECTS OF LICHEN SECONDARY METABOLITES AGAINST POTENTIAL COMPETITORS FOR ROCK SURFACES

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Lichen secondary metabolites (LSM) are known to determine allelopathic effects on soil and mycorrhizal fungi, and on the spore/seed germination and early growth stages of bryophytes and vascular plants, thus likely supporting the competition of terricolous lichens for soil surfaces. In the current study, laboratory and field assays were performed to evaluate the potential allelopathic effects of LSM against potential competitors of saxicolous lichens for rock surfaces. Usnic acid, norstictic acid and parietin, solubilized in water, water-acetone 90:10 mixture and pure acetone, were tested against microcolonial fungi (MCF: *Coniosporium apollinis*, *C. perforans*, *C. uncinatum*, *Phaeococcomyces* cf. *chersonesus*), black yeasts (BY: *Sarcinomyces petricola*), green algae (GA: *Apatococcus lobatus*, *Scenedesmus ecornis*) and cyanobacteria (CY: *Pleurocapsa minor*, *Lyngbya* sp.). The common biocide benzalkonium chloride (1%) was used as positive control. Fungal, algal and cyanobacterial colonies, cultured on standard media (MEA, *Trebouxia*-Medium, BG11), were poured with 50 µl of each solution and their areal growth was monitored for one month using image analysis (WinCAM software). Field assays on black patinas on the walls of the Roman Theatre of Aosta (NW-Italy) were also performed, using epifluorescence microscopy to check the algal and cyanobacterial sensibility. The different MCF species showed a slightly different sensibility to the different LSM solutions, but in all the cases the three metabolites in the water-acetone mixture (ca. 0.05 mM) and usnic acid in water (0.02 mM) determined the highest growth inhibition, displaying the same effects of benzalkonium chloride. On the other hand, all the LSM solutions did not significantly affect or even increased the areal growth of algal and cyanobacterial colonies. Epifluorescence observations of the treated photosynthetic microorganisms in laboratory confirmed that most of cells were still emitting a strong red fluorescence. However, in the field patinas, algal and cyanobacterial cells showed a higher sensibility to LSM, more often displaying an epifluorescence decrease in the treated areas with respect to negative controls. In conclusion, LSM may play a significant role in lichen competition for rock surfaces. LSM may be a potential resource for the MCF control on rocks, avoiding the use of human-toxic biocides.

3I-O

ROLE OF NITRIC OXIDE IN THE RESPONSE OF *RAMALINA FARINACEA* TO LEAD

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Nitric oxide is a small multifaceted molecule with a plethora of biological functions. The roles of NO in biotic and abiotic stress are especially relevant and an involvement of NO in the establishment of symbiotic relationships (i.e. mycorrhizae) has been described. Despite its relevance, NO production in lichens has only been described recently and its roles are unknown. Both pro-oxidant and antioxidant functions have been described for NO and a recent study made in our laboratories suggests that during lichen rehydration NO seems to be related with contention of oxidative damage and chlorophyll stabilization. Preliminary studies have also showed that NO is important in the regulation of oxidative damage exerted by the air pollutant cumene hydroperoxide during rehydration. The toxic mechanisms of heavy metals, such as Pb, involve both the inhibition of enzymes and the production of free radicals. The aim of the present work is to study the effect of Pb in the intracellular oxidative burst occurred during rehydration and the role of NO in the lichen *Ramalina farinacea* (L.) Ach. Intracellular ROS specific fluorescent probe, dichlorodihydrofluorescein diacetate (DCFH2-DA) has been used. ROS kinetics and chlorophyll autofluorescence have been recorded during the first minutes after rehydration. Lipid peroxidation and NO-endproducts have been quantified at different time points. NO specific inhibitor c-PTIO has been used in order to elucidate NO functions. The results show that Pb induces decreases in intracellular ROS production and lipid peroxidation during rehydration; although a decrease in chlorophyll autofluorescence has also been observed. NO inhibition during Pb-conditioned rehydration does not affect the studied parameters. We conclude that NO is not involved in lichen response to Pb. Lichen tolerance to moderate doses of Pb may be related to the induction of a compensatory response known as hormesis. [MCINN (CGL2009-13429-C02-01/02), AECID (PCI_A_I024755/09) and Generalitat Valenciana (PROMETEO 174/2008 GVA)]

31-O

4I: Lichenological research in South-East Asia and the Pacific region

(4I-O1) Submission ID: IAL0287-00001

THE OCEANEAN LICHEN REALM

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Based on 280,000 data sets of distributional, morphological, anatomical and chemical data a global biodiversity analysis is calculated. It produces six units, the Oceanian unit one of it. The pattern of floral realms differs between lichens and vascular plants, where Oceania has no independent position. The historical and ecological reasons for the deviation between these groups of organisms are explained. A similarity calculation of the Oceanian lichen checklist in relation to those of all continents results in e.g. lists of species common to the respective units and a classification of distributional patterns. The lichens of Hawaii, the most isolated island group in the world, are investigated with emphasis. An enlarged checklist of the islands based on recent collections is presented. 120 Hawaiian lichen species have been barcoded. The relation between the Hawaiian lichen biota and those of North America and Asia is investigated by molecular methods. Their phylogeography is discussed.

(4I-O2) Submission ID: IAL0255-00001

**AN OVERVIEW OF LICHEN DIVERSITY AND CONSERVATION
IN WESTERN GHATS, INDIA**

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To be precise, till date, 2,358 lichen species are recorded from India. Among eight Lichenogeographical regions of India Western Ghats (WG) and Himalayas are undoubtedly lichen diversity hotspots. WG stretches from Tapti Valley in north to the Kanyakumari in the south, and covers as many as six states with dense tropical moist broadleaf forests. A total of 1,155 lichen taxa belonging to 1,136 species, 19 infraspecific taxa, 193 genera and 54 families are reported so far from the WG. Most of these taxa (745 spp.) are recorded from Nilgiri Biosphere Reserve in Tamil Nadu. The region is dominated by crustose (727 spp.) and corticolous (986 spp.) lichens. The flora of WG contains a large number of taxa belonging to Graphidaceae (182 spp.), Pyrenocarpous (175 spp.), Parmelioid (125 spp.), Thelotremataceous (78 spp.) and Arthonioid (72 spp.) lichen communities. Further, Graphidaceae and *Graphis* are most dominant family and genus with 182 and 72 species respectively. Parmeliaceae (173 spp.), Physciaceae (118 spp.) and Thelotremataceae (87 spp.) are the other major families, while *Pyrenula* (50 spp.), *Parmotrema* (45 spp.) and *Usnea* (41 spp.) are the other important genus. The WG is represented by 266 endemic taxa and a large proportion of it includes species described in the recent years (neoendemics). This trend clearly indicates the tremendous opportunity for lichen systematics in the region. However, the lichen diversity in WG is under threat and over harvesting of economically valued species emerges as one of the major threat. The lacunae those prevents initiation of conservation measures in WG includes lack of quantitative data, inadequate ecological information, infrequent of observations, and absence of floras, checklist and threatened taxa list. Hence, gathering quantitative data at spatial, temporal and taxa levels has become a prerequisite in lichen conservation, which would help in identifying threatened taxa or vulnerable habitats.

(4I-O3)

Submission ID: IAL0069-00002

THE GENUS *STAUROTHELE* IN VIETNAM: SPECIES DIVERSITY AND PHYLOGENETIC PLACEMENT

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The Verrucariaceae is a mostly lichenized family comprising a large number of crustose saxicolous species (e.g., *Verrucaria*, *Staurothele*, *Polyblastia*, *Thelidium*). These crustose species are especially diverse on calcareous substrates, where they often are one of the main elements of the lichen flora. They are particularly diverse in the Mediterranean-type and the temperate to cold temperate climates. In the wet Tropics, they are only poorly studied so that their diversity and distribution is virtually unknown. A fieldtrip organized by the Natural History Museum in London and the Vietnam National Museum of Nature in Hanoi allowed the author to collect and study some specimens of crustose epilithic *Staurothele* from diverse localities in Northern Vietnam. The morphological study of these specimens suggests that they belong to four different species, but none of them seem to have been reported and treated in recent works on *Staurothele*. Molecular data (based on nuITS and nuLSU) show that none of these specimens are in fact *Staurothele*, but they all belong to the mostly squamulose genus *Endocarpon*. They form four to seven lineages of almost identical sequences, and are closely related to *Endocarpon diffractellum*, a species of *Staurothele* recently transferred to the genus *Endocarpon* based on molecular data. This study confirms that it is not possible to use the thallus structure as a character to differentiate the two Verrucariaceae genera with hymenial algae, *Endocarpon* and *Staurothele*.

(4I-O4)

Submission ID: IAL0088-00002

THE REPRODUCTIVE ECOLOGY OF *ICMADOPHILA SPLACHNIRIMA* – A RARE AUSTRALASIAN LICHEN EXHIBITING SEXUAL AND ASEQUAL REPRODUCTION

4I-O

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Icmadophila splachnirima grows preferentially in subalpine bogs and swamps of New Zealand (South Isl., Stewart Isl., subantarctic Islands) and South-East Australia (Tasmania, Victoria). During a summer survey of the distribution of this rare species, asexual reproduction was identified for the first time. This presentation provides results from the first year of a PhD study into the reasons for and implications of a switch from sexual to asexual reproduction in *Icmadophila splachnirima*. Preliminary results indicate that in more exposed micro-habitats, apothecial growth is reversibly arrested at an early developmental stage, always accompanied by the formation of marginal soralia. This suggests an environmentally triggered switch from sexual to asexual reproduction, possibly in response to adverse growth conditions, e.g. high-light and/or desiccation stress. This hypothesis shall be tested experimentally during the remainder of the PhD study, and the presentation will give an outline of the intended methods to achieve this, alongside with further preliminary results. A wide range of aspects relating to the species' biology and ecology will be part of this proposed work, including phytogeography, phytosociology, micro-habitat conditions, physiology, anatomy, morphology and population genetics.

LICHEN STUDIES IN THE CORDILLERA REGION NORTHERN PHILIPPINES - PAST, PRESENT AND FUTURE

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Philippine lichenology started in the 18th century when European scientists joined expeditions to the country. Meyer, Charles Gaudichard–Beaupre, Moseley, Schadenberg, and Warburg were among those who did extensive collections of lichens in the Philippines at that time. The Americans came in the early 20th century; E.D Merrill led collections from almost every part of the country. More foreign scientists came including Herre, Degelius, and Hale. Only one of the Filipino botanists, Dr. William Guezo, did serious study on lichens in the 1970's. His collections in Luzon including Benguet and Ifugao in the Cordillera Region northern Philippines resulted to new species and new records. In 1987, Andre Aptroot and Harrie collected in Baguio and Benguet that further gave new species and new records of Philippine lichens. In 1999, we started our own taxonomic study of lichens in the Cordillera Region. Presently, we have identified 130 species belonging to 37 genera distributed in 15 families in the Region. With the help of Dr. John Elix, Dr. Harrie Sipman, and Dr. Thorsten Lumbsch, our efforts resulted to new species and new records as well. We have also conducted studies on the use of lichens as indicators of environmental conditions. Our assessment of the atmospheric condition of four favorite parks of Baguio City, a prime city of the Region using epiphytic lichens as bioindicators has shown that the number of pollution tolerant species and pollution sensitive species vary significantly among them. Our study on sulfur dioxide pollution along a major road in the city also showed that the lichens, mosses, and leaves of vascular plants have no significant difference in the concentration of SO₂ accumulated within their tissues. Our lichen taxonomic study is on-going; we are also conducting biological assay of their active components and evaluating their use as bioindicator. Results we hope will support our conservation campaign for these organisms.

4I-O

STUDY OF MACROLICHEN DIVERSITY BETWEEN *EUCALYPTUS*, *PINUS*, AND *ALTINGIA* TREES AT CIBODAS BOTANICAL GARDEN, WEST JAVA

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Diversity of macrolichens on the barks of *Eucalyptus*, *Pinus*, and *Altingia* trees in Cibodas Botanical Garden was studied during November 2006 until April 2007. There were 28 species of macrolichens found on *Eucalyptus* trees (H = 3.63), followed by 22 species on *Altingia* (H = 3.4) and 17 species on *Pinus* (H = 3.09). *Usnea* spp., *Rimelia* sp., and *Parmelinella wallichiana* were the most abundant on *Eucalyptus*. *Heterodermia japonica*, *P. wallichiana*, *Physcia* sp., and *Pseudocyphellaria aurata* occurred only on *Eucalyptus*. *Usnea* sp., *Parmotrema* sp., and *Parmelia* sp. were the most abundant on *Altingia*. We found *Lobaria isidiosa*, *Lobaria* sp., *Peltigera* sp., and some Parmeliaceae that were only existed on *Altingia* trees. *Pinus* trees had *Cladonia* sp., *Usnea* sp. and *Parmelia* sp. as it top three. Note that *Everniastrum vexans*, *Leprocaulon* sp., and *Relicina* sp. only found on *Pinus*. There was no difference in term of Shanon wiener diversity index of stratum A (0 – 50 cm above ground), B (100 – 150 cm above ground), and C (200 – 250 cm above ground) on the barks of *Eucalyptus* and *Pinus*, but there was a difference in it on *Altingia*. *Usnea* sp., *Cladonia* sp., *Coccocarpia palmicola*, and *Parmotrema* sp. were the species that found on every host tree, while *Lobaria* sp., *Relicina* sp., and *Heterodermia japonica*, were the examples of species which might have substrate preference. The difference of bark texture might be one of the factors which affect the difference of macrolichen community consisting on each tree. *Eucalyptus* has the peeling bark, but mostly the peeling started from the top of the trunk. The large diameters of *Altingia* allowed foliose lichens grow with big thallus upon it. But, the rough and deeply fissured bark of *Pinus* limited the growth of macrolichens with big thallus.

**MACROLICHEN DIVERSITY CAN BE USED AS A TOOL TO ANALYZE THE FOREST
CONDITION AT HORTON PLAINS NATIONAL PARK, SRI LANKA**

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Horton Plains National Park (HPNP) is a World Heritage site that includes extensive areas of cloud forest, which occurs as continuous forest on the upper slopes, and as forest islands of different sizes interspersed in 'pathana' grassland. Preliminary investigation showed a difference in lichen communities of forest islands and of continuous forest at similar altitudes above 2,000 m. The objective of this study was to characterize macrolichen communities in forest islands and continuous forest and investigate factors affecting their distribution. Macrolichens were sampled in quadrates on tree trunks in 12 plots, 6 in forest islands and 6 in continuous forest together with environmental data and tree data. Macrolichen species were identified and their diversity and frequency used to test the relationship with phorophyte and environmental factors including light intensity. Both macrolichen diversity and their phorophyte diversity were higher in forest islands (147 macrolichen taxa) than in the continuous forest (104 macrolichen taxa). These include many new records for Sri Lanka and include new species described elsewhere. PCA analysis of macrolichen and environmental data, showed that all island plots were separated from the continuous forest plots and that this was associated with an increase in macrolichens with a cyanobacterial photobionts in the island plots. Distribution of macrolichens within both forest types was significantly correlated with light intensity, although this was not significantly different between both forest types. The results have shown that macrolichen diversity is higher in the forest islands than in the continuous forest and that this is associated with an increase in species known to be sensitive to forest disturbance and environmental change. The results suggest that external factors affect the distribution of lichens in the montane forests of HPNP. Reasons for loss of diversity and changes in montane communities will be discussed.

4I-O

3A: Molecular phylogenetics

(3A-O1) Submission ID: IAL0273-00001

THE DATING OF FUNGI AND PLANTS

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The lichen symbiosis is one of many successful interactions between fungi and plants. The omnipresence of these interdependent heterotrophic-autotrophic associations at spatial and temporal scales, and ranging from mutualism to parasitism, suggests a strongly linked coevolution of these two kingdoms. If true, major adaptive radiations of plants and fungi should be mostly synchronized. In this study we have estimated divergence time of the fungi and land plants independently and inferred the occurrence of drastic shifts in rates of diversification across both chronograms. The combination of both analytical results enabled us to determine the synchronicity of these shifts in species diversification that likely occurred during the evolution of fungi and plants. Lichen-forming ascomycetes originated during one of the most spectacular adaptive radiations of the fungi, and of the plant kingdom. The origin of ascolichens is more recent than previously expected within the context of plant evolution, and is associated with the origin and radiation of hyperdiverse endophytic and endolichenic fungi interacting symbiotically with photosynthetic cells of plants as well as photoautotrophic prokaryotic and eukaryotic cells (photobionts) found in lichens. The origin of these Leotiomyceta fungi interacting with photosynthetic cells of plants are associated with the acquisition of an ammonium transporter/ammonia permease (AMTP) gene from hyperthermophilic chemolithoautotrophic prokaryotes via horizontal gene transfer. Balanced transport of nitrogen among lichen symbionts could be essential for the establishment and maintenance of this symbiosis, especially in nitrogen limiting environments.

3A-O

(3A-O2) Submission ID: IAL0174-00001

DIVERSIFICATION OF LICHEN-FORMING ASCOMYCETES

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The disparity in species richness across fungal lineages is striking. Within the fungal class Lecanoromycetes (Ascomycota), this unevenness is especially pronounced, with the number of species per family ranging from under 15 to nearly 2,500. Here potential explanations for this imbalance, initially focusing on clade age and diversification rate, are explored. Clade age showed little correlation with clade richness, while a strong correlation was observed between net diversification rate and clade richness. A number of families, such as Parmeliaceae and Cladoniaceae, were identified as having exceptionally high diversification rates, while a number of families with low species richness, such as Gypsoplacaceae and Miltideaceae had exceptionally low diversification rates. Finally, we attempt to identify potential sources of variation in diversification rates across Lecanoromycetes.

**PUNCTUATIONAL EVOLUTION AND RECENTLY ACCELERATED DIVERSIFICATION:
INSIGHTS INTO THE EVOLUTION OF OSTROPOMYCETIDAE**

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The rates of nucleotide substitution and the rates of diversification can vary widely among clades. Analyses of such evolutionary processes may help to understand the evolution of lineages that lack a fossil record and that show remarkable phenotypic variability. We were interested in using a comparative analytical framework to analyse phylogenetic patterns of diversification and morphological disparity in the fungal subclass Ostropomycetidae. Fungi in this lineage have strikingly variable phenotypes and no fossil record. Having observed substantial branch length differences in the two major orders of Ostropomycetidae, we use a 4-locus data set of 140 species to test whether the differences in branch lengths are significant, and to estimate the contribution of punctuational evolution to the diversity in the group. Using gamma-statistics and lineage-through-time (LTT) plots we analyse the mode and tempo of evolution in these fungi. Nucleotide substitution rates differed significantly between the two major orders in the Ostropomycetidae, Agyriales and Ostropales. The test for punctuational evolution revealed a high contribution of punctuational evolution (bursts of speciation) to the evolution in Ostropales, but no such effect in Agyriales. The gamma-statistics indicated that the origins of extant lineages were clustered disproportionately late in the history of the subclass. The LTT plots show a recent acceleration of diversification in the Ostropales, but an antisigmoidal curve for the entire subclass. The antisigmoidal signal is consistent with the hypothesis of ancient mass extinction. Based on our results we develop a hypothetical evolutionary scenario for the phenotypically diverse Ostropomycetidae: after an initial radiation at the base of the clade, an ancient mass extinction led to the survival of a few phylogenetically isolated clades. Some of these clades, especially Ostropales and to some extent Agyriales, recently experienced an increase in diversification. The ancient mass extinction and subsequent radiation events in some clades may explain why Ostropomycetidae comprises fungi of vastly different life styles and morphologies. Our study suggests that comparative phylogenetic methods aid our understanding of evolutionary processes in lineages that are morphologically diverse and lack a fossil record.

MULTI-GENE PHYLOGENY DEFINES THE MONOPHYLY OF *LOBARIA* SECTION *LOBARIA*

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Lobaria (Schreb.) Hoffm. is a genus of about 80 species that is hypothesized to have originated in Eastern Asia from where taxa speciated and spread to other continents. Although Eastern Asian *Lobaria* species were comprehensively revised, our understanding of taxa delimitation remains incongruous. Traditionally, two sections are distinguished: *Lobaria* and *Ricasolia* with fusiform or acicular spores, respectively. Besides the thallus morphology and chemical compounds, the presence of apothecia and the morphology of vegetative propagules were most determinant attributes for the definition of species. While some species were separated based on combinations of several morphological and chemical characters, other taxa were described based on one distinguishing feature alone. For instance, taxa that were identical, except for the presence of vegetative diaspores, were recognized as distinct species-pairs. In our study, we focused primarily on the section *Lobaria* and we tested the monophyly of this section. For this study, we performed phylogenetic analyses with a vast sampling, mainly from Eastern Asia, and based on five genetic loci (nrITS, nrLSU, EF-1a, RPB2 and mrSSU). Additionally to morphological studies, we analyzed lichen compounds with TLC and tested key criteria in relation to the resulting phylogenetic framework. Our analyses clearly confirmed the monophyly of the section *Lobaria* and of most species within this section, but relationships among taxa belonging to the section *Ricasolia* remained inconsistent. Within the section *Lobaria*, however, different markers produced conflicting phylogenetic information for some species. In addition, some Eastern Asian taxa showed low phylogenetic resolution, thus, only concatenated analysis revealed clades, challenging however traditional systematics and the described species abundance for this region. This, in combination with the fact that these species were not monophyletic, suggests that lineage sorting is incomplete. This is the first phylogenetic hypothesis presented for the section *Lobaria* that includes an extensive sampling, and the clades recovered contrast sharply with previously defined taxa based on morphological and chemical characters. Our results demonstrate difficulties that may arise in the integration of molecular data within traditional systematics.

3A-O

DELIMITING PHYLOGENETIC SPECIES AMONG EUROPEAN TAXA OF THE GENUS *USNEA*

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The study focuses on European *Usnea* (Parmeliaceae) species with sorediate shrubby thalli, with the aim to evaluate the validity of morphology and chemistry based separation of several widely recorded species (*U. diplotypus*, *U. fulvoreaegens*, *U. glabrescens*, *U. lapponica*, *U. subfloridana*, *U. substerilis*, *U. wasmuthii*). 22 *Usnea* species, identified according to morphological and chemical characters, were studied using maximum parsimony and Bayesian analyses of ITS and beta-tubulin sequences. Pairwise maximum likelihood distances (given as number of nucleotide substitutions per site) were calculated among the ITS sequences. The distances between the haplotypes of different species (interspecific distances) and distances between haplotypes within each species (intraspecific distances) were calculated, with the aim to estimate the thresholds between these distance ranges. The analyses showed that: (a) most taxa that are morphologically well distinguished are also distinct by means of molecular characters, (b) shrubby taxa in the section *Usnea* that are difficult to determine by traditional characters, form a group of closely related but still genetically distinct species, except *U. diplotypus* and *U. substerilis* which appear polyphyletic. The branch lengths differed largely between two parts (sections *Usnea* and *Ceratinae*) of the ITS tree and thus genetic distances were calculated separately for them. In clade A (section *Usnea*), the intra- and interspecific distance ranges were considerably smaller than in clade B (section *Ceratinae*), however, the distances can be used for species delimitation in both clades. In clade A the threshold for interspecific distances is close to 0.01 s/s; in clade B the threshold is around 0.02 s/s. The interspecific distance threshold for clade A in our study is close to the according threshold established for parmelioid lichens. Our estimate for clade B is higher than in parmelioid group and within the range reported by Lumbsch (2002) for intrageneric distances in Parmeliaceae. Comparison of inter- and intraspecific genetic distances offers useful criterion for delimiting species, however, more material should be analyzed to make reliable taxonomic decisions in the genus *Usnea*. We also observed that the use of chemical characters for species determination was often complicated as the variability of secondary metabolites was higher than previously known.

**MITOCHONDRIAL GENOMES FROM THE LICHENIZED FUNGI *PELTIGERA MEMBRANACEA*
AND *PELTIGERA MALACEA***

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Mitochondrial genomes from the fungal partners of two common terricolous foliose lichen symbioses, those of *Peltigera membranacea* and *Peltigera malacea*, have been sequenced and assembled using a metagenomic approach. Annotation was facilitated by sequencing of the transcribed mitochondrial RNA. The arrangements and sequences of the two circular genomes are very similar, the major difference being the inversion and deterioration of a gene encoding a type B DNA polymerase. The roughly 63 kb genomes show all the major features found in other Pezizomycotina, such as unidirectional transcription, 14 conserved protein genes, genes for the two subunit rRNAs and for the set of 26 tRNAs used in translating the 62 amino acid codons. Both genomes encode the RNA component of RNase P, a feature seldom found in ascomycetes. The difference in genome size from the minimal ascomycete mitochondrial genomes is largely due to 17 and 20 Group I introns, respectively, most associated with homing endonucleases and all found within protein coding genes and the gene encoding the large subunit rRNA. One new intron insertion point was found, and an unusually small exon of seven nucleotides was identified and verified by RNA sequencing. Comparative analysis of mitochondrion-encoded proteins places the *Peltigera* spp., representatives of the class Lecanoromycetes, close to Leotiomyces, Dothideomyces and Sordariomyces, differing from phylogenies found using multiple nuclear genes.

**NEW APPROACHES TO INCORPORATE AMBIGUOUSLY ALIGNED SEQUENCE PORTIONS
AND MORPHOLOGICAL DATA INTO PHYLOGENETIC ANALYSIS**

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Two novel methods are presented and briefly discussed to incorporate non-DNA data into phylogenetic analysis: PICS-Ord ambiguous region coding and morphology-based phylogenetic binning. PICS-Ord is a new approach to recode ambiguously aligned sequence portions in multiple sequence alignments that have low alignment confidence, and incorporate the codes into phylogenetic analysis using a maximum likelihood approach. It works by computing pairwise distance between the ambiguously aligned sequence portions, using the distance options provided by the software NGILA, then ordinating the distance matrix by means of principal coordinates analysis (using the R `cmdscale` function), and then transforming the axis scores into integer codes. The method can handle an unlimited number of OTUs and is comparatively fast: computing an ML tree in RAxML including 100 bootstrap replicates with 700 OTUs of ITS sequences and three coded portions takes about 36 hours on a single-core PC computer. Morphology-based phylogenetic binning is a novel method to incorporate OTUs known by their morphological data only into phylogenies based on molecular data. Instead of just combining the molecular and morphological data into a supermatrix with gaps for the molecular data, the method first calculates a reference tree for all taxa for which both molecular and morphological data are known. It then computes weights for each morphological character based on its distribution in the molecular tree and the level of homoplasy displayed. These weights can be calculated using either maximum likelihood or maximum parsimony. In a third step, each OTU known by morphological data only is added to the dataset individually and its topological position in the tree computed by invoking the morphological character weights. Bootstrapping is performed to estimate the level of confidence for the topology. This is repeated for each OTU separately and gives an objective prediction for taxonomic placement of taxa even if no molecular data are available. The method is implemented in RAxML, available at <http://www.exelixis-lab.org/software.html> and <https://github.com/stamatak/>. A simple method to assess the level of homoplasy in molecular and morphological data prior to phylogenetic analysis is also discussed.

3A-O

3B-1: Bioinformatics

(3B-1-O1)

Submission ID: IAL0248-00002

COLLECTING, VALIDATING AND USING DISTRIBUTION DATA OF LICHENS IN THE NETHERLANDS

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In 2003, the Dutch Bryological and Lichenological Society (DBLS) started to compile a database with all distribution data of lichens in the Netherlands. Data sources included institutional collections, private herbaria, lichen monitoring data, published lichen inventories and field observations. In 2011 all available data was digitalized and combined into a database, comprising 0.6 million records. Most data had been collected in lichen monitoring schemes, but a vast majority of the rest had been collected by amateur lichenologists, especially saxicolous lichens and lichenicolous fungi. Amateurs are becoming the main source of distribution data of lichens, and many other species groups. Several tools have been developed to store, validate and visualize data collected by a distributed group of specialists. Web portals (e.g. www.telmeel.nl, www.observado.org) are relatively new and currently used by those who want to submit only a small number of observations at a time. Datasets in several formats received by DBLS are stored in a local MS Access database. Both web portals and local data are synchronized with the National Database Flora and Fauna, using a PostgreSQL webserver. Incoming data needs to be validated in order to keep the database free of errors as much as possible. This is done by rule-based automated validation, which decided which records are checked by a group of voluntary validators, mainly specialists. Observations of common taxa are automatically validated if a recent observation from the same locality exists. Distribution data is used for a number of applications. DBLS maintains an online atlas (www.verspreidingsatlas.nl) which displays the historical and present distribution at the scale of 5x5 km. Detailed observations are under license available for amateur lichenologists, scientists and nature conservation organizations. Data licenses are also sold to customers, including governmental organizations, ecological consultancy firms and construction and building companies, which considerably improves the conservation of lichens. The national database has recently been used to calculate trends for a new Red List, and provide distribution maps and trend graphs for several publications.

3B-1-O

THE POWER OF ITS: USING MEGAPHYLOGENIES OF BARCODING GENES TO REVEAL INCONSISTENCIES IN TAXONOMIC IDENTIFICATIONS OF GENBANK SUBMISSIONS

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We take advantage of a novel method (PICS-Ord) of recoding ambiguously aligned sequence portions in genes with variable length to assemble multiple fixed alignments of ITS sequences across large groups of taxa and analyze them using a mixed model for DNA and code partitions under maximum likelihood in RAxML. This approach allows to simultaneously align and analyze all ITS sequences of a given family and that way detecting potential problems in taxonomic identifications of GenBank submissions, as well as testing genus and species concepts. While this methodology will not recover the backbone of a family-level clade with confidence (since ITS is too variable for that purpose), it will recover supported genus and species clades. Recoding ambiguously aligned regions which otherwise would have to be removed prior to analysis add a substantial amount of resolution and support to the analysis. The method was applied to two large families of lichenized fungi, Parmeliaceae with roughly 1800 OTUs and Physciaceae with roughly 700 OTUs currently available. It was found that a substantial portion of submitted sequences have problems in terms of taxonomic identification. Some of these are clear misidentifications at species or even genus level, whereas others are caused by inappropriate taxonomic concepts. In one case, the resulting pattern suggests gene duplication as the reason for incongruence between topology and taxonomy. We suggest to using this approach routinely to screen large taxonomic groups and detect problematic sequence submissions. Unfortunately, GenBank currently lacks a system where submissions can be annotated by third parties if a problem is detected, and we urge that this problem be solved as soon as possible.

(3B-1-O3)

Submission ID: IAL0160-00002

EFFECTIVENESS OF THE NATURA 2000 NETWORK IN PROTECTING MEDITERRANEAN LICHEN SPECIES

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In the last few years, there have been an increasing number of studies on species distribution modeling. However, knowledge on the potential distribution of 'non-charismatic' species is still very scarce. In this study, we determined potential distribution patterns for 18 lichen species in Spain and evaluated the effectiveness of the Natura 2,000 network in protecting them. Models were implemented with ENFA (Ecological-Niche Factor Analysis), using presence-only data. Habitat suitability maps were obtained for each species and high suitability areas were characterized using 10 environmental variables. High-suitability area maps were overlaid with the Natura 2,000 network cover, considering the three different biogeographical regions present in mainland Spain. The studied species presented habitat requirements different from average conditions in Spain, and most of them had narrow ecological niches. Environmental constrictors were different for each model. The marginality axis was mainly linked to altitudinal variables, whereas the specialization axis was essentially related to summer precipitation and drought period. The effectiveness of the Natura 2,000 was quite low in most species. The analysis per region showed that Mediterranean lichen species growing in forests are better protected than species found in coastal, drier and warmer areas. Our results indicate that the Natura 2,000 network, a protection system based on vascular plants, does not guarantee the protection of Mediterranean lichen species. Thus, this type of gap analysis and especially the inclusion of "non-charismatic" organisms such as lichens should be considered in studies to define protected areas.

3B-1-O

MULTILINGUALITY IN LICHENOLOGY

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The Ethnologue catalogued 6,912 languages spoken in the world today, many of them exist without any developed writing systems, which brings the possibility of having them vanished or close to be extinct. At present, writing systems have been changed by using computers and telecommunication tools. Text characters or symbols in every language's writing system can be simply encoded and transformed to Unicode. Nowadays, e-learning and teaching tools are being increasingly used to enhance academic studies and appear to be most effective when based on native languages. The mother tongue is an essential condition for the development of the intellectual, moral, and physical aspects of higher education; it enhances clarity of thought, better expression of terms and regulates the knowledge gained by hearing from other sources. In order to promote 'native language'-based education in lichenology, two options of multilingual web applications are convenient and functional in both global and local scales, and are discussed. An example at a global scale is a subproject of the LIAS lichen identification system 'LIAS light' (liaslight.lias.net), being at a rather advanced state and is currently consulted by lichenologists all over the world. At a local scale, on the other hand, there is the Google-powered bilingual Iranian lichen website MYCO-LICH (www.myco-lich.com). By applying the Google Language Tool, MYCO-LICH website contents may be available in up to 40 languages. However, results are not yet fully satisfactory. In contrast, LIAS light uses highly specific terminology (e.g. concerning morphological characters and secondary metabolites), up to this time, translated by lichenologists into a total of eleven language versions (English, Chinese, Esperanto, French, Farsi (Persian), German, Hebrew, Italian, Russian, Spanish, and Turkish). For Iranian biology students and researchers, the native Persian language key with its particular right-to-left script orientation has been proved to be of considerable use. The Persian language characters were encoded in Unicode format and dynamically converted into HTML or DELTA formats. The two mentioned websites appear to be a significant contribution to the development of lichenology in countries where information flow still has to overcome linguistic barriers.

DATA EXCHANGE AND PROCESSING IN DIGITAL SCIENCE INFRASTRUCTURE PLATFORMS FOR BIODIVERSITY INFORMATION

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The digital science platforms Biodiversity Heritage Library (BHL and BHL Europe), Catalogue of Life (CoL), Encyclopedia of Life (EoL), Global Biodiversity Information Facility (GBIF), International Barcode of Life (iBOL), International Nucleotide Sequence Database Collaboration (INSDC) and JSTOR Plant Science, all are global players that among other data process and (re-)purpose lichen research data. While all these platforms capture biodiversity data, they focus on different aspects, for instance, taxonomy and classification, occurrence, morphology, molecular data, or ecology. Our contribution describes the processing of lichenological research data in some of these platforms, focusing on the technical implementation of data exchange, copyright issues, and data sharing policies and their implications for data custodians, owners, providers, and publishers. The international initiatives GBIF and CoL seek long-term business models and funding mechanisms to provide online data openly and free of charge. In the long run, GBIF depends on governmental commitments for its funding. CoL is financed by EU and other grants as well as by Species 2000, a British company limited by guarantee. These two business models are compared with that of JSTOR Plant Science, the commercial portal of the Global Plant Initiative (GPI). All three initiatives are currently discussing challenges of sustainability both with regard to data curation as well as software development for their complex portals.

3B-2: The ecological roles of lichens in diverse ecosystems

(3B-2 - O1) Submission ID: IAL0119-00001

ROLE OF LICHENS IN DETERIORATIVE PROCESSES THREATENING OUR STONY CULTURAL HERITAGE: CASE STUDY OF LICHEN COLONIZATION IN MACHU PICCHU (PERU)

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Machu Picchu is the icon of the Inca World due to its extraordinary emplacement in which the architecture harmonizes completely with its amazing natural scenic surroundings. The conservation of this sanctuary is an important task for humanity in order to preserve our cultural heritage. One important risk for its conservation is the detrimental effect of the biological colonization of its walls. This colonization is enhanced by Machu Picchu's natural emplacement in a tropical climate. Lichens are the main colonizers of its walls. Together with bryophytes, they completely cover the stone in untreated areas and are present also in areas previously treated for eliminating biological colonization. Crustose forms are the most frequently observed lichens in the emblematic constructions because Machu Picchu's caretakers mechanically remove the foliose and fruticose forms. The external effects of lichen colonization can be appreciated by simple observation, but the associated biodeterioration processes are complex, since lichen growth is usually not restricted to external zones and their effects are added to these generated by the activity of microorganisms present nearby. Hence, we have characterized the interphase lichen-lithic substrate by electron microscopy in monument samples colonized by different species in order to evaluate the differential deteriorative capacity of each one. In general, crustose species were the most important deteriorative agents due to the close interactions established between mycobiont cells and the lithic substrate. Signs of mechanical alterations can be clearly associated to their presence. Disaggregation of stone surface and detachment and separation of mica layers are phenomena frequently observed. The deteriorative lichen activity was conditioned by the physiochemical properties of the stone and the presence of endolithic microorganisms. It has been shown that there is a harmful action of lichens on Machu Picchu stone but their elimination might not always be the best strategy for preserving this monument. Only a temporary aesthetic improvement is obtained with the previous treatments because the stone is quickly recolonized. New treatments based in combination of biocide and laser cleaning are being assayed on Machu Picchu's quarry rock in order to design the best strategy to preserve this wonder world.

3B-2-O

**THE INVESTIGATION OF EPIPHYTIC LICHENS DIVERSITY
IN THE NORTHEAST OF THAILAND**

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Epiphytic lichens were investigated on 160 mango trees in 16 sampling plots in eight provinces of the Northeast of Thailand during January to December 2010 using the VDI method. The lichen species were recorded on each tree and the frequency of each species was calculated in a grid frame of 20×50 cm². Lichen specimens were collected and identified to species. The pH of bark of mango trees, which are important habitats for lichen diversity, was determined. A total of 19 families, 31 genera and 86 species were collected. The growth forms were 64.86% crustose, 34.86% foliose and 0.28% squamulose whilst foliose was not found in study areas. *Pyxine cocolos* was the highest frequency followed by *Chrysothrix xanthina*, *Lecanora leprosa* and *Graphis* sp.1, respectively. The two lowest frequencies were *Lepraria* sp. and *Graphis* sp. This investigation discovered that nine lichen species (e.g. *Phyllopsora* sp., *Parmotrema* sp., *Graphis* sp.) were found only in inside city while 15 lichen species (e.g. *Amandinea punctata*, *Buellia* sp., *Cladonia* sp., and *Pyrenula* sp.) were found only in outside city. These can be regarded as good indicators for the environment of the Northeast of Thailand. The species richness was not significantly different at the 99% significance level for outside and inside city, whilst species evenness and species index showed significant difference at the 99% significance level ($t = -1.814$ and -2.287 respectively, $p < 0.01$). Nakhon Ratchasima province showed the highest of species richness for 56.00. Analysis of Shannon Index and Species Evenness were highest in Loei province for 3.6967 and 0.71492 respectively. Sorensen's coefficient was highest in Ubon Ratchathani province for 64.71%. The measured pH of mango bark ranged from 5.33 to 5.55. The analysis of correlation between lichen diversity index and physical factors in the study area was calculated. It was found that they were significantly correlated at the 95% significance level.

**CHANGES IN EPIGEIC LICHEN COMMUNITIES IN CALCAREOUS GRASSLANDS (ALVARS)
DUE TO THE CESSATION OF TRADITIONAL LAND USE**

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Semi-natural calcareous grasslands formed on thin soil on Ordovician or Silurian calcareous sediments or monolithic calcareous bedrock are called alvars. Alvars have a limited distribution, they occur mainly on the islands of the Baltic Sea. The area of alvars is declining due to the cessation of traditional management, consisting of grazing by domestic animals. Former open grasslands grow over with junipers (*Juniperus communis*) and Scots pines (*Pinus sylvestris*). However, grazed alvars are of high conservation value as they have proved to be highly species-rich. Lichen communities on alvars are known for extraordinary lichen species composition, characterized by the coexistence of species from steppe and arctic-alpine regions. We studied the current situation of lichen communities on Estonian calcareous grasslands and evaluated the effect of increased shrub cover and ground disturbances on epigeic lichen communities, considering bedrock properties. Results show that lichen species composition and species richness on alvars is most profoundly influenced by grassland herb layer productivity: the epigeic lichen diversity increases with decreasing plant cover. Dense shrub cover is the second most important factor influencing lichen communities: lichen species composition changes and species richness decreases when the habitat is overgrown by shrubs. We also found that some areas where soil was formerly disrupted (e.g. former military areas, where soil was scraped off and old limestone quarries) could be suitable substitution habitats for endangered epigeic lichen species. These disturbed areas have similar lichen flora as in 'standard' alvar areas, where suitable conditions for alvar lichens have still been preserved.

ISLAND BIOGEOGRAPHY OF *LOBARIA* SECT. *LOBARIA* IN MACARONESIA

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Understanding why some taxa are endemic, whereas others are widespread is an important theme in evolutionary biology. Do co-distributed endemic and widespread species share biogeographic history, and do they exhibit similarities in their population structure? Here, we compare migration patterns and population structure in *Lobaria* Sect. *Lobaria* from Macaronesia, featuring two endemic and one widespread species. First, in order to determine whether the species originated in the same geographic area, we compare genetic diversity among geographic regions under the assumption that the area of origin has the highest diversity and largest number of private alleles. Second, drawing on methods borrowed from coalescent theory, we investigate bidirectional migration rates of each species among three Atlantic archipelagos and the mainland. Our results indicate that the two endemic species had clear and different centers of genetic diversity, whereas the widespread species exhibited incongruent results for different markers – its center of origin appears to be located outside Macaronesia. To conclude, the two endemic species and the widespread species had different biogeographic histories. These results imply that biological communities may be composed of species with widely different biogeographic backgrounds, even if their contemporary ranges and ecological niches overlap to a high degree.

(3B-2-O5)

Submission ID: IAL0050-00001

LICHEN IDENTIFICATION IN WOODLAND CARIBOU SCAT USING DNA BARCODING

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In Ontario, the woodland caribou (*Rangifer tarandus* subsp. *caribou*) are in peril due to declining abundance and range retraction. Conservation efforts have resulted in the designation of woodland caribou as “threatened” under the provincial Endangered Species Act and the federal Species at Risk Act. Preliminary research suggests a link between anthropogenic disturbances in vital habitat (e.g., forestry, mining, road construction, hydro development) and declining numbers in woodland caribou. One hypothesis predicts that regenerating forests do not provide sufficient supplies of high quality food to meet the energetic requirements for successful recruitment of yearlings to the breeding population. The role of nutrition is rarely considered and poorly understood partly due to the fact that nutritional hypotheses are underpinned by diet of which we know very little. We examined the winter diet of woodland caribou by barcoding dietary components from samples of feces. We amplified the ITS2 ribosomal region from extracted DNA of fecal samples of 44 caribou animals. PCR products were cloned and the insert sequenced from individual colonies. These sequences were compared with a newly created library of lichen barcodes from the region. The results showed that most of the sequences generated from the caribou fecal samples were identified as lichen fungal symbionts, primarily belonging to the genus *Cladonia*. Three lichen species, *Cladonia stygia*, *Cladonia arbuscula*, and *Cladonia mitis* are widely represented in the caribou samples, being sequenced from almost half or more of the animals sampled. *Cladonia rangiferina*, *Cladonia stellaris*, and *Cladonia uncialis* were detected in ~20–25% of animals, and the remaining lichen species were found from only 1–3 individual caribou, contributing a minor amount to the observed dietary diversity. This research suggests that caribou prefer specific species of lichens, which may be explained by palatability or variability in the nutritional value among lichen species.

3B-2-O

ANALYSIS OF TWELVE MOLECULAR LOCI SUGGESTS HIGH PHOTOBIONT AND LOW MYCOBIONT DIVERSITY IN POPULATIONS OF *LASALLIA PUSTULATA*

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The objective of this work was to estimate the genetic diversity of photobionts and mycobionts in *Lasallia pustulata*. It is our long term goal to understand the effects of climate on the selection of photobiont strains and to elucidate population dynamic processes in this lichen species. We compare the variability of molecular markers specific for the photobiont (actin, COX₂, ITS, psbJ-L, rbcL) and the mycobiont (EF1, ITS, MCM7, mtLSU, mtSSU, RPB1, RPB2, TSR1), and assess their suitability for population studies in *Lasallia pustulata* and its trebouxioid algal partner. *Lasallia pustulata* has a patchy distribution across the European continent and typically grows at elevations of 400-800 m. Occasionally it can be found at up to 2,000 m. Most populations of *Lasallia pustulata* are restricted to small islands of suitable habitat in the landscape: exposed non-calcareous boulders and cliff faces. In our study we sampled populations along a north-south gradient, including material from Norway, Germany, Poland, Austria, Spain and Portugal, and along an altitudinal gradient (0-1,700 m) at a locality in Spain. Preliminary analyses of haplotypes indicate very low genetic diversity in all fungal markers, but considerable levels of diversity in the photobiont markers. We observed that some photobiont genotypes are geographically widespread, whereas others are more locally restricted. Most populations contained several distinct photobiont haplotypes.

5I: Global Change and lichen biology

(5I-O1) Submission ID: IAL0142-00001

ALTITUDINAL DISTRIBUTION OF CAUCASIAN LICHENS SUPPORTS THE KEY ROLE OF CLIMATE IN HOLARCTIC DISTRIBUTION PATTERNS

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Distribution of many lichen species spans both Holarctic continents (Eurasia and North America). Nevertheless, it appears not stochastic, but can be assigned to certain types, which resemble those known from vascular plant species. One distribution type frequently observed in lichens is the Asa Gray disjunction (East Asia – Eastern North America), which is known from vascular plants mostly on the level of higher taxonomic units. Distributions of this type are commonly linked with extinction events during the Quaternary. Their representatives (or, in vascular plants, their close relatives) often have small isolated outposts in southeastern Europe and are considered as Tertiary relicts, which were pushed back to their current occurrences during the Pleistocene. Our study aimed to test whether occurrence of lichens of this distribution type can be explained by factors other than history. We studied the allocation of epiphytic lichens of different distribution types in the north-western Caucasus along an altitudinal gradient, which resembles a climatic gradient from warm-dry (lowlands) via warm-wet (middle altitudes) up to cold-wet summers (higher mountains). Our results show that lichens with a global distribution of the Asa Gray disjunction type clearly prefer the middle (warm-wet in summer) altitudinal belt in the Caucasus. The more pronounced the preference of the relictic areas on a global scale, the stricter the confinement to the middle altitudes in the Caucasus. Conversely, lichens that avoid the Asa Gray relictic areas on a global scale are substantially rarer or lacking at the middle altitudes of the Caucasus, occurring instead below as well as above. Species without pattern related to the Asa Gray areas do also not express an altitudinal pattern in the Caucasus. We conclude that preference or avoidance of the Asa Gray relictic areas does not need historical explanations, but can be put down to ecophysiological preferences related to the combination of moisture and temperature. This should be kept in mind also in interpreting distribution of representatives of other taxonomic groups. Also, it implies considerable distribution dynamics when climate changes.

(5I-O2) Submission ID: IAL0191-00001

RECONSTRUCTING HISTORIC BIODIVERSITY LOSS: LICHENS AS A POWERFUL NEW ARCHAEOLOGICAL TOOL

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We report the exceptional preservation of lichen epiphytes on historic wooden building materials in southern England, representing an entirely novel archaeobotanical tool. These building materials were harvested from the landscape during the pre-industrial period (< 1,750), with lichen and bryophyte epiphytes preserved intact on both bark of large timbers and smaller diameter poles and rods. By using this resource to quantify historic lichen diversity, we can demonstrate: (i) shifts in the biogeographic range of lichens across the threshold of industrialisation, and (ii) changes in epiphyte community structure, both consistent with a severe depletion in epiphyte diversity. We can robustly quantify the difference between pre-industrial biodiversity (prior to Linnaean taxonomy and a modern conservation ethic), and biodiversity and environmental indicators developed during the post-industrial period. In conclusion, modern indicators represent 'soft targets' for early-to-industrialise western regions (e.g. southern England), which may be based on the recalcitrant subset of persisting species. These results should cause the re-evaluation of conservation goals when looking for equity across developed and developing nations.

(5I-O3)

Submission ID: IAL0034-00001

BARK ACIDITY AND LICHENS OCCURRENCE IN GOMEL, BELARUS

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Bark pH might importantly determine the regional occurrence of lichen species, and specific information on the relationship between lichens and phorophyte bark pH is invaluable for bioindication and monitoring. We investigated these relationships for an urban area in the city of Gomel, the second largest city in the Republic of Belarus with a population of c. 480,000 people. We studied the composition of foliose and fruticose lichens, associated with 11 tree species, and we determined the bark pH. We found that bark acidity in Gomel exceeds the values recorded for Western European in the 1960s, by 1.5–2.5 pH units, providing new information on lichen response. Variation in bark acidity was associated with three phorophyte groups: Group 1 (pH 6–8): *Physconia distorta* and *Physconia enteroxantha*; Intermediate group (pH 4.5–6.5); Group 2 (pH 4.0–5.5): *Hypogymnia physodes*, *Evernia prunastri*, *Melanohalea exasperatula*. Regressions to explain lichen occurrence and bark acidity were calculated for contrasting indicator species: *Hypogymnia physodes* ($y = -7.76x + 52.94$; $r = 0.78$; $p < 0.01$) and *Physconia distorta* ($y = 9.38x - 43.89$; $r = 0.81$; $p < 0.01$). Using the Gomel glass factory as a site-specific case-study for increased alkalinity, we explore in detail the relationship between lichen species, their phorophytes, and the functional interaction between phorophyte pH and environmental setting.

(5I-O4)

Submission ID: IAL0155-00001

THE RESPONSE OF EUTROPHIC LICHENS TO DIFFERENT FORMS OF NITROGEN IN THE LOS ANGELES BASIN

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Epiphytic lichen communities are highly sensitive to excess nitrogen (N), which causes the replacement of native florals by N-tolerant, “weedy” eutrophic species. This shift is commonly used as the indicator of “harm” in studies developing empirical critical levels (CLE) for ammonia (NH₃) and critical loads (CLO) for N. To be most effective, empirical CLE/CLO must firmly link lichen response to causal pollutant(s), which is difficult to accomplish in field studies in part because the high cost of N measurements limits their use. For this case study we synthesized an unprecedented array of N measurements across 22 long-term monitoring sites in the Los Angeles Basin, California: gas concentrations of NH₃, nitric acid (HNO₃), nitrogen dioxide, and ozone (n = 10); N in throughfall (n = 8); modeled estimates of eight different forms of N (n = 22); and nitrate accumulated on oak twigs (n = 22). We sampled lichens on black oak (*Quercus kelloggii*) and scored plots using two indices of eutroph abundance to characterize the community-level response to N. Our results contradict two common misconceptions about the lichen-N response: 1) that eutrophs respond specifically to NH₃, and 2) that that response is necessarily dependent upon the increased pH of lichen substrates. Eutroph abundance related significantly but weakly to NH₃ ($r^2 = 0.48$). Nitrogen deposition as measured in canopy throughfall was by far the best predictor ($r^2 = 0.94$), indicating that eutrophs respond to multiple forms of N. Most N variables had significant correlations to eutroph abundance ($r^2 = 0.36 - 0.62$) as well as to each other ($r^2 = 0.61 - 0.98$), demonstrating the risk of mistaking correlation for causality in CLE/CLO field studies that lack sufficient calibration data. Our data furthermore suggest eutroph abundance is primarily driven by N inputs, not pH-- at least at the high pH values found in the basin (4.8 - 6.1). Eutrophs correlated negatively with trunk pH ($r^2 = 0.43$), exactly the opposite of results from virtually all previous studies of eutroph behavior. This correlation is probably spurious and results because HNO₃ dominates N deposition in our study region.

5I=O

WHY LICHENS ARE OZONE TOLERANT? A POSSIBLE EXPLANATION FROM CELL TO SPECIES LEVEL

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Ozone (O₃) is an important component of global change, contributing to 20th century warming. Tropospheric O₃ is constantly increasing and will continue to rise in the absence of control measures. This pollutant has direct, deleterious consequences on the terrestrial biosphere through the formation of Reactive Oxygen Species (ROS), that are particularly aggressive against cell membranes, enzymes and DNA. The data concerning the putative effects on lichens available so far are largely incomplete and rather problematic, due to differences in treatment methods, concentrations and exposure techniques. A recent field study with lichen transplants suggests that the key factor in modulating the ozone resistance of lichens is water availability, because daily rehydrated thalli can efficaciously repair O₃ damage and replenish the reservoir of antioxidants, whereas dry thalli suffer from the sum of two co-occurring stressors, desiccation and O₃. In this work the effects of O₃ on three epiphytic macrolichens with different ecology and resistance to airborne pollutants (*Flavoparmelia caperata*, *Parmotrema perlatum* and *Xanthoria parietina*) and their isolated photobionts (three species of *Trebouxia*) were verified by exposing thalli and axenic cultures in fumigation chambers and/or OTCs at different air humidity and watering regimes. Chlorophyll a fluorescence emission, antioxidants (AsA, GSH) and activity of specific enzymes (APX, CAT, DHAR, GR, POD, SOD) were measured in pre and post exposure samples, and again after 1-2 days of recovery. Histochemical techniques were used to localize ROS at cellular level by confocal microscopy, and ultrastructural modifications were studied by TEM. The results show that all the three lichens tolerate O₃ well, whereas desiccation tolerance varies in accordance to the species-specific ecology. The ozone tolerance is justified by the availability of a large pool of constitutive antioxidants that in a lichen are necessary to contrast the oxidative burst associated with the frequent dehydration-rehydration cycles to which it is naturally subjected, and oxidation occurring during the protracted desiccation.

THE OPAL AIR SURVEY: ENGAGING THE PUBLIC WITH LICHENS

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The OPAL Air Survey is part of an ongoing project to engage the public in a study of the natural world. Lichens are widespread organisms occurring in both man-made and natural habitats, and have long been used as bioindicators of environmental change. This national programme has been developed to stimulate public interest in lichens and their use as bioindicators, to allow the survey of lichens on trees in their local area and to contribute their results to an on-line website. The OPAL Air survey explores the impact of nitrogenous pollutants, largely from transport and agriculture, on selected lichen taxa in England. Participants are introduced to air quality legislation, systems used to monitor air quality and the links to the distribution and diversity of lichens on tree trunks and twigs. Three categories of lichen are distinguished: nitrogen-sensitive - *Usnea* spp., *Evernia prunastri* and *Hypogymnia* spp.; nitrogen-tolerant - *Xanthoria polycarpa*, *Xanthoria parietina*, *Physcia adscendens* and *P. tenella*; intermediate - *Melanelixia* spp., *Flavoparmelia caperata*, *Parmelia* spp. Survey packs, distributed to schools and community groups, contain an easy to follow guide with lichen images to aid identification, a workbook for recording findings and x4 magnifier. Participants were asked to record data on location, tree species and girth, indicator lichen diversity and abundance and to submit these via OPAL on the on-line database. Online identification tools are also available at <http://www.opalexplornature.org/AirSurvey>. To date, over 3,300 sites have been surveyed across England amounting to over 18,000 records of lichen on tree trunks. Nearly half of the participants state that they could not recognise a lichen before they completed the survey. Following data quality control, results were analysed statistically and showed that under increasing dry deposition of NH_x and NO_x, nitrogen-tolerant species increased and nitrogen-sensitive species decreased. However all species showed a significant relationship with historic SO₂ (1987) levels, with present day deposition of NO_x, and with mean annual rainfall. Distribution patterns of *Usnea* and *Evernia* were significantly correlated with mean annual temperature suggesting that these species may be at risk from anthropogenic climate change.

LICHENS, BRYOPHYTES AND CLIMATE CHANGE (LBCC) UTILIZING SYMBIOTA SOFTWARE

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SYMBIOTA software has been used to create along with other thematic nodes the portals: The Consortium of North American Lichen Herbaria (CNALH, <http://symbiota.org/nalichens/>) and The Consortium of North American Bryophyte Herbaria (CNABH, <http://symbiota.org/bryophytes/index.php>). Among other functions, the portals together provide access now to ca. 1.6 million collection records of lichens and bryophytes. Through new funding from the US National Science Foundation, ca. 2.3 million additional specimens will be databased from Canada, Mexico and the USA. Both groups of organisms are dominant components of arctic and subarctic ecosystems and occur extensively in boreal and other temperate to tropical ecosystems. The two portals will provide unparalleled information on distribution patterns both historically and from the present forward. For geo-referenced specimens, maps can be readily generated. As such, they will provide a major tool for assessing climate change across North America. In addition, in collaboration with LIAS (LichenizedAScomycetes) we are developing on-line keys, a prototype of which is available for the greater Sonoran Desert region for over 1,800 species. The keys are being expanded to include known arctic species. The functionality of SYMBIOTA will be demonstrated.

4A: Evolution and Systematics in the Teloschistales

(4A-O1) Submission ID: IAL0253-00001

**SYSTEMATICS AND EVOLUTION WITHIN THE ORDER TELOSCHISTALES AND FAMILY
TELOSCHISTACEAE (ASCOMYCOTA, FUNGI) WITH A MULTI-LOCUS
SUPERMATRIX APPROACH**

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The resolution of the phylogenetic relationships within the order Teloschistales (Lecanoromycetidae, Ascomycota), currently with nearly 2,000 known species and an outstanding phenotypic diversity, has been hindered by the limitation in the resolving power that a single-locus or two-locus phylogenetic studies have provided up to date. In this context, an extensive taxon sampling within the Teloschistales with more loci (especially nuclear protein-coding genes) were needed to confront the current taxonomic delimitations and to improve our understanding of evolutionary trends within this order. The present study assessed this issue using maximum likelihood and Bayesian analyses with complementary bootstrap support values and posterior probabilities based on seven loci using a supermatrix approach, and including protein-coding genes RPB1 and RPB2 apart from nuclear and mitochondrial ribosomal loci. Although the progressive addition of taxa with missing data did not dramatically affect the loss of support and resolution, the monophyly of the Teloschistales in the current sense was inconsistent, depending on the loci-taxa combination analyzed. Based on these results we propose a new, but provisional, classification for the re-circumscribed orders Caliciales and Teloschistales. We report here that the family Brigantiaeaceae and *Sipmaniella* are members of the Teloschistales in a strict sense. The position of *Cloplaca* and *Josefpoeltia* within the Teloschistaceae is confirmed by molecular phylogenetics. Within the Teloschistales, one lineage led to the diversification of the mostly epiphytic crustose Brigantiaeaceae and Letrouitiaceae, with a circumpacific center of diversity and found mostly in the tropics. The other main lineage led to another epiphytic crustose family, mostly tropical, and with an Australasian center of diversity – the Megalosporaceae – which is sister to the mainly rock-inhabiting, cosmopolitan, and species rich Teloschistaceae, with a diversity of growth habits ranging from crustose to fruticose. Additionally, we are presenting a comprehensive phylogeny for the family Teloschistaceae with new loci selected from AFTOL2, and a first exploration of the evolution of phenotypic traits and an in-depth characterization for a major taxonomic redelimitation of genera within this family.

4A-O

**PHYLOGENY AND TAXONOMY OF THE TELOSCHISTACEAE (ASCOMYCOTA):
IMPORTANCE OF MONOPHYLETIC GROUPS**

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The molecular phylogeny of the Parmeliaceae, Physciaceae, Caliciaceae and other families of lichen-forming fungi is based on polyphasic approach using up to six or seven different genes of nuclear and mitochondrial DNA. As a consequence the taxonomy of these families is now built upon correlation analysis of molecular data with morphological, anatomical, and chemical characters of robust monophyletic groups of species as well as on revision of species composition, ecological and geographical features of such monophyletic groups. Unfortunately, monophyletic groups of the Teloschistaceae are hitherto neglected. Their analysis is rather limited. So, the majority of phylogenetic analyses of the Teloschistaceae deal with small species groups (especially of *Caloplaca*) and based only on ITS1/ITS2 sequences of nuclear DNA as the main molecular tool. There are few reports of polyphasic molecular data having been used in such phylogenetic analyses. Such investigations have indicated that the currently accepted genera *Caloplaca*, *Fulgensia*, *Xanthoria*, and *Teloschistes* are polyphyletic and the delineation of *Caloplaca* and *Xanthoria* and of *Caloplaca* and *Fulgensia* is problematic. The main purpose of the present study was the comparative analysis of molecular data with morphological, anatomical, and chemical characters of selected monophyletic groups of the Teloschistaceae. Well defined monophyletic groups within species groups like those of *Caloplaca cerina*, *C. saxicola*, *C. regalis*, *C. ferruginea*, *C. variabilis* and *Fulgensia fulgens* [some of which are type species of different genera proposed in 'pre-molecular time'] are found to be distributed among other monophyletic branches of the xanthorioid lichens following analysis of nuclear and mitochondrial molecular data. As a consequence generic names proposed for the above species groups can be used together with *Caloplaca* s.str., *Teloschistes*, *Seiophora* and *Fulgensia*. However, following molecular analysis such groups/genera as *Blastenia*, *Pyrenodesmia* and the *Caloplaca saxicola*-group include far fewer species than was proposed from morphological segregation in the 'pre-molecular' period. Alternatively, molecular data confirms that the morphological defined groups (i.e. *Blastenia*, *Pyrenodesmia*, *Thamnonoma* etc.) are just as polyphyletic as the genera *Teloschistes*, *Seiophora* and *Fulgensia*.

(4A-O3)

Submission ID: IAL0188-00001

TOWARDS A NEW CLASSIFICATION OF TELOSCHISTACEAE

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The family Teloschistaceae is one of the largest families of lichen-forming fungi, probably comprising more than 1,000 species. The traditional taxonomy of genera within this family has been based on morphology, anatomy and chemistry. However, for at least twenty years this taxonomy has been known to be unnatural and with genetic data at hand this has been shown several times. However, a new delimitation of natural groups has not yet been presented for the family as a whole, but some smaller groups have been split of during the last years. We present here a first approach towards a new delimitation of genera in the family based on analyses of three loci. Some genera or groups are still not clearly delimited and problems remain in various groups, but for a large part of the family new genera can be defined.

(4A-O4)

Submission ID: IAL0251-00002

METABOLITE EVOLUTION IN THE LICHEN FAMILY TELOSCHISTACEAE

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The emerging phylogenetic structure of the large family Teloschistaceae based on DNA-data has permitted tracking the evolution of secondary metabolites across evolutionary clades. Some large clades have a very conserved set of chemical syndromes, while a number of smaller clades are characterized by synapomorphic specialized metabolite characters. New metabolites are regularly discovered in Teloschistaceae, and the structure of many compounds is yet to be clarified. At the same time several cases of metabolic losses at different levels are disclosed. The taxonomic significance of the secondary metabolites in Teloschistaceae is discussed.

(4A-O5)

Submission ID: IAL0158-00001

DISENTANGLING THE SPECIES DIVERSITY OF *CALOPLACA* TH. FR. IN CHILE

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The lichen genus *Caloplaca* is cosmopolitan and includes a high number of species worldwide, with more than 1,000 published names. In Chile, the genus has been sparsely studied, and its total number of species along the country is not completely clear. Considering morphological, chemical and molecular data, we studied the *Caloplaca* species present in the northern and central areas of Chile between 20° to 39°S. More than 1,000 specimens, both from intensive field work and herbarium material from 15 different herbaria, were studied. We registered 35 *Caloplaca* species in the study area, with the inclusion of several new species. Results from phylogenetic analysis including maximum parsimony, maximum likelihood and Bayesian inference based on ITS sequences of Chilean and non-Chilean species reveal the presence of a monophyletic clade with high support in the *Caloplaca* phylogeny that includes most of the species present in Chile.

4A-O

PHYLOGENETIC STUDIES ON SOME GROUPS WITHIN TELOSCHISTACEAE

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Investigations of four groups of Teloschistaceae provided various surprising results. (1) Within the *Caloplaca aurantia*, *C. flavescens* complex, four species were formerly recognized; two calcicolous and two coastal, from siliceous cliffs. Our data, however, indicate that they form just one phylogenetic species. *Caloplaca aurantia* and *C. flavescens* are well known and easily recognizable taxa, but they probably represent only phenotypes of a single species. These usually occur together, but marginal populations may be formed by either one of the phenotypes. (2) The species-rich group around *Caloplaca xerica* contains some species that have both sorediate and non-sorediate populations. Although both populations of one species may grow together, they have independent ecologies and distributions. In general, vegetatively reproducing populations are more abundant and more widely distributed. (3) The *Caloplaca aractina*, *C. haematites* complex contains two formerly recognized species; one corticolous, the other saxicolous. Our data show that, although the whole group is monophyletic, the corticolous and saxicolous populations do not represent homogeneous groups, but form several intermixed lineages. (4) *Caloplaca communis*, described from the eastern Mediterranean, and *C. maritima*, described from the Atlantic coast of Europe, together form a single “ring species” distributed continuously along European coasts. Distant populations differ genotypically, but populations from intermediate localities contain “intermediate genotypes”.

4B: Lichen symbionts and ecophysiology

(4B-O1) Submission ID: IAL0174-00002

ON TIME OR 'FASHIONABLY' LATE ? THE COMPARATIVE DATING OF LICHEN-ASSOCIATED EUKARYOTIC ALGAE AND THEIR FUNGAL SYMBIONTS

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How do symbiotic associations originate and evolve? Determining when associations originated, both in time and relative to the diversification of their interacting lineages, can inform about whether certain earth history events are associated with the initiation of these associations and also if transitions were contemporaneous with the evolution of an interacting lineage. Furthermore, it can shed light on the role (if any) a lineage plays in the diversification of its interacting lineage. Previous models have been put forward suggest that in contemporaneous or near contemporaneous originations, the diversification of one lineage is expected to have some impact on the evolution of its interacting lineage; contrastingly, in symbioses with largely asynchronous origins of interacting lineages, the factors driving the diversification of these interacting lineages are expected to be unrelated. Here we focus on providing a timeline for the diversification of lichen-associated eukaryotic algae, by assembling a dataset consisting of 18S and rbcL sequence data and employing a relaxed molecular clock approach, utilizing several fossil calibration points. Stem and crown ages for a number of algal lineages associating with lichen-forming fungi were obtained, and this is related to the evolution of their fungal partners.

(4B – O2) Submission ID: IAL0112-00001

PHYLOGEOGRAPHY AND GENETIC STRUCTURE OF *DICTYOCHLOROPSIS RETICULATA* ASSOCIATED WITH *LOBARIA PULMONARIA*, *L. IMMIXTA* AND *L. MACARONESICA* IN MACARONESIA.

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Macaronesia is a group of archipelagos in the North-East Atlantic Ocean near Europe and North Africa, which currently represents the largest laurel forests (laurisilva). These forests host a high diversity of habitats and species, many of which are endemic. Two laurisilva-associated lichens, *Lobaria immixta* and *L. macaronesica*, and the widely distributed *L. pulmonaria* share the same habitats and depend on the same photobiont species, *Dictyochloropsis reticulata*. We examined almost four thousand thalli from 12 islands on the archipelagos of Azores, Canary Islands and Madeira, using 13 alga-specific highly variable microsatellite loci. Discriminant analysis of principal component (DAPC), measures of genetic differentiation (DEST, FST), and Bayesian analyses detected two well differentiated groups, namely populations from Azores vs. populations from Canary Islands and Madeira. Spatial autocorrelation and other evidence indicated the absence of gene flow between the groups. These two regions were also comparably rich in geographically restricted alleles, representing a worldwide hot spot for the genetic diversity of *D. reticulata*. We also found that there was no partitioning of algal genetic structure related to the fungal host. This study provides new insights on the level of diversification of symbiotic green algae, as result of a radiation-like diversification on oceanic islands. Our findings support the hypothesis of a functional green algal-mediated guild, for which the Lobariacean fungi of the studied ecosystem are horizontally linked through sharing of photobiont genotypes.

4B-O

PHOTOBIONT DIVERSITY AND RICHNESS IN LECIDEOID ANTARCTIC LICHENS FROM AN ECOLOGICAL POINT OF VIEW

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As part of a comprehensive study on lecideoid lichens in Antarctica, we also investigated the photobiont diversity and abundance in our sample set. A phylogeny of these photobiont ITS sequences in combination with samples from Arctic, Alpine and other temperate regions reveals the presence of five, possibly even six major *Trebouxia* clades in Antarctic lecideoid lichens. Two clades are formed by members of the *T. jamesii* and *T. impressa* aggregates but for all other clades no close match of any known *Trebouxia* species could be found in the sequence databases. One genetically uniform and well supported *Trebouxia* clade was only found in the climatically unique cold desert regions of the Antarctica (preliminarily named *Trebouxia* sp. URa1). *Trebouxia* sp. URa2 and URa3 are widely distributed and abundant in the investigated areas. None of the analysed mycobionts is restricted to a particular *Trebouxia* species. *Trebouxia* sp. URa1 is preferably associated with the highly adapted Antarctic endemic lichen *L. cancriformis*. Our analysis revealed differences in the species composition of locally available photobiont pools which is clearly influenced by habitat ecology. *Trebouxia* sp. URa1 may represent an endemic photobiont species since it seems to be restricted to the Antarctic cold deserts, a habitat that has no ecological counterpart elsewhere in the world.

(4B-O4) Submission ID: IAL0097- 00001

HOW DO CHANGING ENVIRONMENTAL CONDITIONS AFFECT POLAR AND TEMPERATE HAPLOTYPES OF *CETRARIA ACULEATA*?

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Lichens are highly specialized symbiotic organisms which are able to colonize habitats with extreme environmental conditions. Our model organism *Cetraria aculeata* is common in the maritime Antarctic and throughout the Arctic. At the same time, it grows in places where competition from vascular plants is low and it can be found in arid grassland areas, maritime dunes or woodlands in temperate regions. This distribution makes it a suitable object to study ecophysiological adaptation mechanisms on an intraspecific level. Previous studies have shown that polar and temperate photobionts of *Cetraria aculeata* belong to two different genetical haplotype groups (Fernández-Mendoza et al., 2011). Here we aim at assessing the ecophysiological differences between polar and temperate populations of *C. aculeata* and to check whether they are correlated with different photobiont haplotype groups within the species. We performed gas exchange measurements at different temperatures and photon flux densities with samples collected from Antarctica, Spitsbergen, Germany and Spain. Furthermore, we transplanted thalli from these populations to Spain and Norway. By comparing photosynthetic performance, weight increase, chlorophyll content and the number of photobiont cells before and after transplantation we were able to observe physiological reactions of different genetic haplotypes to changing environmental situations.

4B-O

ASSESSMENT OF THE PHENOTYPIC PLASTICITY OF *UMBILICARIA DECUSSATA* ACROSS ECOPHYSIOLOGICAL STUDIES WITH SEVEN POPULATIONS WORLDWIDE.

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Umbilicaria decussata (Umbilicariaceae, Lecanorales) has a bipolar (arctic-alpine) distribution, appearing in many of the highest mountains in tropical and temperate regions, as well as in polar regions. This wide distribution has led us to try to understand its adaptive strategy studying its photosynthetic capacity and trying to relate it, by means of statistical modelling, with other measured parameters such as chlorophyll, ergosterol, chitin, amino acids and sugar contents, total carbon and nitrogen concentrations, as well as some climatic parameters. *Umbilicaria decussata* specimens were then collected on Mount Kilimanjaro (4,400 m.a.s.l., Tanzania), Iztaccihuatl volcano (4,300 m.a.s.l., Mexico), two localities in Chilean Andes (2,000 and 2,700 m.a.s.l.), Mount Kosciuszko (2,050 m.a.s.l., Australia), and two localities in Spain (Pyrenees, 2,600 m.a.s.l. and Sistema Central, 2,400 m.a.s.l.). Photosynthetic performance was assessed by gas exchange measurements, using an open flow system at temperatures between 0 and 25°C and light intensities ranging from 0 to 1,200 $\mu\text{mol m}^{-2}\text{s}^{-1}$. Chlorophyll was quantified by spectrophotometry according, and ergosterol, chitin, amino acids and sugars were quantified by different chromatographic methods. C and N were also measured. The most remarkable difference between populations was found in Mexican samples, which showed maximal photosynthetic yield in a dry weight basis, as well as highest ergosterol, amino acid, sugar and N content and lowest chitin to ergosterol ratio, fraction of arginine in the amino acid pool, ribitol to mannitol ratio and carbon to nitrogen ratio, revealing a more active metabolism. When all data were analysed together, C to N ratio and average temperature of the coldest month were found to be highly influential on photosynthetic potential activity, showing the importance of both metabolic and climatic variables.

(4B-O6) Submission ID: IAL0210-00001

**DESICCATION TOLERANCE IN THE HYGROPHILOUS LICHEN *PARMOTREMA PERLATUM*
AND IN ITS ISOLATED *TREBOUXIA* PHOTOBIONT**

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Desiccation is one of the most important sources of oxidative stress because it gives rise to the production of a variety of Reactive Oxygen Species. ROS are highly reactive, damaging molecules like DNA, lipids and proteins. In poikilohydrous autophototrophic organisms the production of ROS is further enhanced by light, because chlorophylls, although partially protected by structural changes at cortical and photosystem level, extinguish excitation energy not only through heat emission, but also through the direct transfer of electrons to the triplet oxygen, giving rise to the highly reactive singlet oxygen. In this study the role of light during a protracted desiccation period on the ROS production and antioxidant response was investigated. Lobes of the lichen *Parmotrema perlatum* and axenic cultures of the photobiont (a species of *Trebouxia*, putatively *T. crenulata*) were treated at different light intensities (0, 40, 120 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$) for two weeks in a desiccated state. Concentrations of H_2O_2 , SOD, GSH and GSSG were measured spectrophotometrically, and a series of confocal laser scanning microscope (CLSM) acquisitions were taken, using diclorofluorescein as a marker of the presence of H_2O_2 . After the light treatments the lobes and the cultures were kept fully hydrated at 20 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ for three days to verify whether they were able to fully scavenge the accumulated ROS and to reconstitute their original pool of antioxidants. The biochemical assays showed that concentrations of H_2O_2 changed according to the light treatments in both lobes and axenic cultures and CLSM acquisitions revealed a similar pattern. Accumulation of ROS was mostly cytoplasmic and was particularly intense at photobiont and cortical level. The comparison between lichenized and isolated *Trebouxia* based on chlorophyll a fluorescence emission revealed that the former tolerates better the desiccation stress.

(4B-O7) Submission ID: IAL0195-00001

**PHOTOSYNTHESIS, N FIXATION AND NUTRIENT CONTENT IN THREE SPECIES
OF *PLACOPSIS* FROM A SUBANTARCTIC ENVIRONMENT**

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Placopsis is a genus of tripartite crustose lichens and has its main distribution in the Southern Hemisphere. A common feature of all the species in the genus is the presence of cyanobacteria arranged in specialized structures called cephalodia, in which nitrogen can be fixed from atmosphere. It has been suggested that this nitrogen fixing capacity allows the genus to colonize barren nutrient poor habitats such as terrain recently exposed following glacial retreat. Some of species of *Placopsis* have been used for dating exposed surfaces using the technique of lichenometry. However, there are few physiological data for *Placopsis* sp., and little is known about their growth dynamics. We have studied three species in the genus (the soil/mud inhabiting *P. pycnotheca*, and the epilithic *P. perrugosa* and *P. stenophylla*) growing in the proximity of Pia Glacier, Beagle Channel, Tierra del Fuego, Southern Chile. We report the results of novel investigations in *Placopsis* into the relationships between CO_2 exchange, nitrogen fixation and total nitrogen and phosphorus content and show how these parameters are related to individual species performance. Our laboratory results suggest: (i) a strong relationship between the gas exchange data obtained and the two different ecologies of the species in the field and (ii) positive correlations between CO_2 exchange, nitrogen fixation and nutrient content. These results improve understanding of physiological interactions between the partners of tripartite lichens.

4B-O

LICHEN COMMUNITY RESPONSES TO NITROGEN (N) DEPOSITION CAN IN PART BE EXPLAINED BY THE LICHENS' SYMBIONT RESPONSES TO BOTH N AND P

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Nitrogen (N) is an important nutrient for lichens involved in many processes in both photobiont and mycobiont, but can also be excessive with many lichens disappearing as a result of anthropogenic deposition. In 2005, we initiated a long-term experiment to investigate the processes that lead to die-back of epiphytic lichen communities with increased N. We combined daily fertilization of spruce trees in an old growth boreal forest harbouring a rich lichen flora with yearly monitoring of "species" abundance, and measurements of their N-uptake, N and phosphorous (P) concentrations at five N deposition levels. In a parallel and more short-term study both N and P supply was manipulated for two of the more abundant lichens at the site, *Alectoria sarmentosa* and *Platismatia glauca*, to examine their N to P stoichiometry and their respective biont responses to both N and P. After four years, *A. sarmentosa* had decreased in abundance with increasing N, while *P. glauca* had increased at all N levels. Thallus N concentration had increased in both *A. sarmentosa* and *P. glauca* with increasing N load, and their N uptake rates were similar. Photobiont concentration had increased linearly with increased N in both species, saturating in *A. sarmentosa* in the third year at the highest N loads (25 and 50 kg ha⁻¹ yr⁻¹). However, the simulated N deposition had decreased the phosphorous (P) concentration in *A. sarmentosa*, but not in *P. glauca*. The short-term N and P manipulations showed that the photobiont growth was N-limited in both species. The mycobiont was P-limited in *A. sarmentosa* which may in part explain the decreased abundance of this species at the highest N loads. Mycobiont responses were more complex since fungal growth is also dependent on the carbon export from the photobiont, as seen in *P. glauca* where the mycobiont decreased when N additions exceeded 50 kg ha⁻¹ yr⁻¹. Our results emphasize that lichen responses to increased N loads will be dependent on the responses of its particular photo- and mycobiont to both N and P, and their relative access to P since P might mitigate the negative effects of excess N.

11: Exploring the lichen microbiome and its multifaceted interactions

(11-P1) Submission ID: IAL0018-00002

**SEASONAL DYNAMICS OF A *PHYSCIETUM ADSCENDENTIS*-ASSOCIATED
MICROBIAL COMMUNITY**

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The factors driving the diversity and structure of corticolous lichen communities have been intensely studied, but the ecology of the non-lichenized organisms in these communities remains largely unknown. For the present study, thalli of *Xanthoria parietina* and *Physconia distorta* living on a maple tree (*Acer pseudoplatanus*), where they were part of the *Physcietum adscendentis* association were sampled along with bark in spring and autumn at two expositions (WSW and SSE). The fungal community living in the lichens and on the bark was assessed by direct PCR, cloning, and screening for restriction fragment length polymorphism (RFLP). RFLP genotypes detected in the clones revealed a considerably high diversity of lichen-associated fungi, along with the primary lichen symbionts and the phorophyte. The associated fungal flora was slightly more diverse in *P. distorta* than in *X. parietina*, and the two communities differed in composition. The fungi associated with *X. parietina* appeared to be more specialized perhaps because of the high anthraquinone content of the latter species.

**TOWARDS A MOLECULAR PHYLOGENY OF LICHENICOLOUS DACAMPIACEAE
(DOTHIDEOMYCETES, ASCOMYCOTA)**

11-P

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The family Dacampiaceae comprises about 15 genera. Eight genera (*Clypeococcum*, *Dacampia*, *Ka-laalia*, *Polycoccum*, *Pseudonitschkia*, *Pseudopyrenidium*, *Pyrenidium*, *Weddellomyces*) include mainly or exclusively lichenicolous species. The family is currently classified within Pleosporales in the Dothideomycetes. However, no molecular data exist to test the phylogenetic placement of any of the lichenicolous taxa. We aim to generate a hypothesis of the phylogenetic position of lichenicolous Dacampiaceae and to test the monophyly of the group. Recent material of such inconspicuous fungi is usually not readily available for laboratory work, cultures cannot easily be obtained from obligate parasites, and it is likely that any extraction from an infected lichen specimen contains a mixture of DNAs of at least two ascomycetes. For DNA extractions we used minute portions of the samples that have been carefully prepared and cleaned under a dissecting microscope to contain as much material of the lichenicolous fungi as possible. Different PCR primer combinations for the nuclear ribosomal DNA genes were tested, and where possible directly sequenced. In many cases, as expected, mixed PCR products required sequencing via DNA cloning. It proved difficult to generate DNA sequence data of sufficient quality and quantity. We are going to report on the diversity of fungal sequences obtained from samples of lichenicolous Dacampiaceae. Our study highlights the elaborate process of obtaining reliable DNA sequence data for a larger amount of such species. The routine inclusion of sequence data in the taxonomic description for new species, as currently discussed, appears to be an extremely difficult task for these fungi. In some cases a single sequence clustering within Dothideomycetes was obtained straight away. However, despite careful preparation from some DNA extractions only sequences belonging to the host lichen could be retrieved, and in other cases cloning was necessary to separate different fungal sequences. Some sequences originated from obviously unrelated fungi, but from some extractions multiple sequences with affinity to Dothideomycetes were gathered. Therefore, multiple samples are needed to confirm the identity of a specific DNA sequence as belonging to the Dacampiaceae species in question. The phylogenetic position of some lichenicolous Dacampiaceae species will be shown.

LINKING FUNCTION WITH BIOTECHNOLOGY: THE POTENTIAL OF LICHEN-ASSOCIATED BACTERIA TO CONTROL PHYTOPATHOGENS

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Lichens are mini-ecosystems, which harbour highly abundant and diverse bacterial communities [1]. These communities are not only an important structural component of the lichen thallus; also important functions were identified [2]. One of these is pathogen defense [2]. Due to their long life, lichens have to defend themselves against a long list of ubiquitous or specifically adapted parasites. Our idea was to use this potential and to analyze the antagonistic activity of lichen-associated bacteria against *Alternaria alternata*, *Botrytis cinerea*, *Phytophthora infestans* and *Sclerotinia sclerotiorum*. The bacteria were isolated from different lichen species (*Cladonia arbuscula*, *Lecanora polytrapa*, *Lobaria immixta*, *L. pulmonaria*, *L. virens*, *Peltigera canina*, *Pseudocyphellaria aurata* and *Umbilicaria cylindrica*) from alpine environments. An impressive spectrum of antagonistic strains was selected [3]. The highest antagonistic potential was found against the ascomycetous air-borne pathogen *B. cinerea* (34.4%). The lichen with the highest overall antagonistic capacity was *Pseudocyphellaria aurata*; up to 100% of the screened bacterial isolates showed antifungal activity towards *P. infestans*. In a novel, promising approach, the bacterial strains were not directly isolated; they were caught from the bacterial community via bait plants. Using this approach it is possible to enrich plant-competent bacteria and enhance the number of bioactive isolates.

[1] Grube & Berg (2009) Fungal Biology Reviews 23:72–85

[2] Grube et al. (2009) The ISME J., 3:1105-1115

[3] Berg et al. (2011) IOBC/wprs BULLETIN, in press.

FLUORESCENCE IN SITU HYBRIDIZATION AND CONFOCAL LASER SCANNING MICROSCOPY APPROACH TO ANALYSE ALPINE SOIL CRUST LICHENS

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Biological soil crusts (BSC) are microbially dominated communities inhabiting the uppermost strata of the soil. Lichens, as distinct and colourful soil crust components of high elevations and subpolar regions, create niches for other microorganisms. In this contribution we present analyses of the structure of lichen soil crusts by using microscopic techniques (DNA-FISH and CLSM) and 3D image reconstruction. Lichen thalli were sampled above the tree-line in open habitats of the Alps, both on siliceous and calcareous substrates. We selected six squamulose and crustose lichen species for our study: *Arthrorhaphis citrinella*, *Baeomyces placophyllus*, *Diploschistes muscorum*, *Icmadophila ericetorum*, *Psora decipiens* and *Trapeliopsis granulosa*. We studied the presence and the distribution of main bacterial groups in lichen thalli and attached soil particles in the hypothallosphere. Results show that lichen species correlate with patterns of colonisation, suggesting that thalli of lichen species determine the microbial structure and that lichen soil crust communities are highly complex microbial metacommunities. Biological soil crusts substantially reduce erosion potential in sensitive habitats and thereby also contribute to higher quality of water supply.

SYMBIOTIC CYANOBACTERIA PRODUCE A SERIES OF HEPATOTOXINS IN LICHENS

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Approximately ten percent of lichens have cyanobacteria as symbiotic partners. The most common cyanobacterial genus in lichens is *Nostoc*, and recent work has shown that some symbiotic *Nostoc* strains can produce microcystins in lichen symbiosis. Microcystins and nodularins are hepatotoxic peptides produced mainly in aquatic environments by several lineages of cyanobacteria and they have been responsible for poisonings of both humans and livestock. We have screened nearly 800 cyanolichen specimens from five continents for microcystins and nodularins both by amplifying a part of the gene cluster encoding the enzyme complex responsible for microcystin production (*mcyE*) and by detecting the toxins directly from lichen specimens with LC-MS. 98 out of the 797 specimens contained microcystin synthetase genes and/or microcystins, and over 50 chemical variants of microcystins were detected. We also found nodularins in several lichens this being evidence of nodularin production in *Nostoc*. Variation in toxin production between different geographical locations and lichen species and genera was considerable, but the presence of *mcyE* gene and toxins clearly depended more on the identity of the fungal partner than the geographic origins of lichen specimens. Interestingly, the *mcyE* genes of lichen symbiotic *Nostoc* were highly diverse and the phylogenetic trees compiled from cyanobacterial *mcyE* and 16S rRNA gene sequences obtained from the same lichen samples were partly incongruent. As a whole, our results demonstrate that microcystins in lichens are not a rare phenomenon, but occur in many different lichen species all over the world.

CONTRIBUTION TO THE KNOWLEDGE OF LICHENICOLOUS FUNGI OF SPAIN

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As part of a broader study on the lichen flora of the Cap de Creus Natural Park (covering an area of 10,780 hectares in the eastern part of the Pyrenees in north-east Spain), a survey was made of the diversity of the lichenicolous fungal flora. Thirty two species of lichenicolous fungi belonging to 13 genera were identified, including four species that were new to science: *Cercidospora* sp., growing on *Caloplaca irrubescens* (distinguished from *Cercidospora caudata* s.s. by the number of spores per ascus and the host lichen species); *Lichenostigma* sp., growing on *Pertusaria monogona*, (similar to *L. rupicolae*, but with different hyphal strands structures, ascospores, and host lichen); *Llimoniela* sp. growing on *Trapeliopsis wallrothii*; and *Zwackhiomyces* sp. growing on *Endocarpon pusillum*. In addition, several other lichenicolous species were reported for the first time on the Iberian Peninsula: *Endococcus buelliae*, *Polycoccum rinodinae*, and *P. teresum*. 34 lichen taxa were found to host lichenicolous fungi, with the genera *Aspicila*, *Caloplaca*, and *Lecanora* harboring the largest number of lichenicolous species. A list for these lichen hosts is provided, with descriptions of novel associations with lichenicolous species. By adding to our knowledge of the diversity of lichenicolous fungi, this study illustrates the continuing need to investigate this little known group.

DEVELOPMENT OF COMPLEMENTARY MOLECULAR MARKERS SEEMS CRUCIAL TO DETECT THE COEXISTENCE OF DIFFERENT *TREBOUXIA* TAXA IN A SINGLE LICHEN THALLUS

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Most lichens are associated with *Trebouxia* phycobionts and some of them simultaneously include genetically different algal lineages. Recently, on the basis of anatomical and molecular analyses, it was demonstrated that in *Ramalina farinacea* (L.) Ach. two species of *Trebouxia* were always coexisting in a single thallus, even in geographically distant localities. In this work we investigate if *Ramalina fraxinea* populations may be representative of an unknown complex model of lichen symbiosis in which more than two different *Trebouxia* phycobionts can coexist as primary producers in each individual thallus. To reach this goal we made both molecular and TEM analyses. Molecular analyses based on three different molecular markers- nrITS, psbA and 23S rDNA- allowed to detect the co-existence of at least two phycobionts per thallus. One or them could be included within a *Trebouxia decolorans* complex whereas the other seemed to be very similar to one of the two coexisting phycobionts in *R. farinacea* referred as *Trebouxia* TR1 (*T. jamesii*-like) in previous works. Phylogenetic analyses based on these markers indicated a high and unexpected cryptic speciation within the *Trebouxia decolorans* complex. At least, five haplotypes and morphotypes were recognized among *T. decolorans*-like phycobionts in contrast to the very low genetic variability of the other coexisting phycobionts. Some of these haplotypes seemed to be related to the colonization of specific phorophytes. The design of an additional marker based on sequences of the psbA gene including group I introns was crucial to improve taxa recognition within the *Trebouxia decolorans* complex in combination with others. From these results we conclude that the development of complementary molecular markers may improve the recognition of different *Trebouxia* taxa within a single thallus when revising lichen symbioses models. [MCINN (CGL2009-13429-C02-01/02), AECID (PCI_A_I024755/09) and Generalitat Valenciana (PROMETEO 174/2008 GVA)]

(11-P8)

Submission ID: IAL0285-00001

GENETIC VARIABILITY OF CYANOBIONTS IN SOME *PELTIGERA* SPECIES

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In this study the variation of *Nostoc* cyanobionts was studied in members of the lichen genus *Peltigera*. Fragments of the 16S rRNA gene were analysed, as well as fragments of the NifH gene, belonging to the nitrogen-fixation gene cluster. Using DNA fingerprinting technique SSCP (Single Strand Conformation Polymorphism) we found the presence of multiple bands, indicating the non-uniformity of *Nostoc* cyanobionts incorporated in single thalli. By sequencing of SSCP bands we further characterized the multiple cyanobacterial genotypes. We are attempting to find correlating parameters for association with particular *Nostoc* strains and for their combined presence. Photobiont association in *Peltigera* seems to be more flexible than previously thought.

1A: Lichen conservation: Concepts and action

(1A-P1) Submission ID: IAL0011-00001

APPROPRIATE TECHNIQUES FOR THE TRANSPLANTATION OF LICHEN VEGETATIVE DIASPORES IN TROPICAL FORESTS IN THAILAND

1A-P

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Isidia and soredia are good sources for the vegetative propagation of lichens because they are produced in large quantities and propagation can thus be accomplished while using the least amount of lichen material. The aim of this study was to find appropriate techniques in increasing the biomass production of lichens in the tropics. Transplantation was done through spreading *Parmotrema tinctorum* isidia and *P. praesorediosum* soredia on double-sided adhesive tape (DSAT) and thereupon fixing the lichen materials on the bark of tree trunks in different types of tropical forest at Khao Yai National Park, Thailand. The survival rate of the transplanted isidia and soredia was only 9% and 8% with those transplanted to secondary forest (SF) growing into large thalli. Alternately, transplantation using *P. sulphuratum* isidia with the same materials, but fixing the DSAT on nylon nets installed at 0°, 45° and 90° inclinations was executed in SF. The highest germination rate for isidia was as much as 50% which was found on a substrate at 45° inclination two years after transplantation. Transplantation in a shaded microhabitat using *P. sancti-angelii* soredia and *P. tinctorum* isidia to a substrate at 45° inclination was performed. After three years as much as 90% of the soredia and 70% of the isidia survived and developed into young thalli. In conclusion, appropriate techniques were achieved for transplanting lichens in the tropics utilizing the least amount of lichen material. They are essential for conservation and sustainable utilization of lichens in a changing world.

(1A-P2) Submission ID: IAL0047-00001

ADDITIONS TO LICHEN BIOTA OF IRAN

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The greatly increased taxonomic understanding of Iran's lichens in the past decade is primarily due to the combined effort of both Iranian and non-Iranian scientists. As a result more than 285 lichen species have so far been recorded from northeastern Iran. As a continuation of this work further investigations were made in two reserves in Khorasan provinces (NE Iran). Eighty specimens were collected from 10 localities in Darkesh (Ala Dagh Mt.) and Tandoureh (Kopet Dagh Mt.) influenced by Euro-Siberian and Irano-Touranian phytocoria, respectively. First hand observations of these, combined with a critical literature survey, indicate four new species not previously found in Iran.

FIRST STEPS TO REVEAL THE DIVERSITY OF *LECANORA* IN BOLIVIA

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1A-P

Although Bolivia is thought to have one of the largest biodiversity worldwide, knowledge of its lichen biota is underexplored. Since several of its natural ecosystems are undoubtedly rich in lichen diversity, these soon may become endangered as in neighbouring countries. Therefore, studies aimed at establishing an inventory of this diversity are fundamental to lichen conservation in this part of South America. The present survey is focused on the genus *Lecanora* that is extremely poorly recognized in the area. Fourteen species are recorded from Bolivia (<http://botan.botany.pl/lichens-bolivia>), as compared with, for example, 124 from the comprehensively investigated Greater Sonoran Desert Region in North America. The present study, based on material collected recently from various biogeographic regions in Bolivia, has revealed many noteworthy species, many new to Bolivia (e.g. *L. cavicola*, *L. flowersiana*, *L. laxa*, *L. semipallida*, *L. stenotropa*, *L. subaurea*) and several newly reported from South America. Two species are undescribed: one closely related to *L. polytropa*, but distinguished by its anatomy and chemistry, and the other representing the *L. dispersa* group, being reminiscent of *L. semipallida*, but differing in the ITS sequence and some morphological details. Research supported by NCBI R in Poland under the LIDER Program; project no. 92/L-1/09.

(1A-P4)

Submission ID: IAL0064-00002

PRELIMINARY RESULTS OF A TAXONOMICAL REVISION OF NON-SAXICOLOUS LECIDEOID LICHENS IN SOUTHERN SOUTH AMERICA

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Lecidea sensu lato is one of the most species-rich and widespread crustose lichen groups worldwide, which is widely represented especially in extra-tropical areas. According to Zahlbruckner's catalogue 99 species of non-saxicolous *Lecidea* s. lato are known from the study area (including Argentina, Chile and Uruguay). To date taxonomy and phylogenetic studies on non-saxicolous species are largely lacking. Many specific and infraspecific names need better understanding, and the generic position of many species requires revision. Therefore, we start with a systematic revision of the poorly known group in southern South America. The taxonomic study is based on both historical and fresh collections, and considers anatomy, morphology and secondary metabolites. We show preliminary results of our work, including anatomical and morphological characters important for the taxonomy of the group, descriptions of selected species, taxonomical comments, and preliminary ecological and distributional data.

**EFFECTS OF WATER TREATMENT AND ASPECT ORIENTATION ON THE SURVIVAL OF
PARMOTREMA TINCTORUM TRANSPLANTED TO ARTIFICIAL SUBSTRATES IN THAILAND**

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1A-P

The lichen *Parmotrema tinctorum* has potential to be utilized in various ways. As such, increased production is essential to meeting future demand for this lichen. The objectives of this study were, therefore, to find appropriate techniques and microhabitats which would enhance the in situ biomass production of this lichen by means of transplantation to artificial substrates. The study was carried out by transplanting nine hundred and sixty thallus fragments of *Parmotrema tinctorum* at Khao Yai National Park. The transplanted thalli were fixed on nylon nets placed above the surface of the earth at an approximate inclination of 40°. These substrates faced the four cardinal directions in addition to those which were oriented horizontally. Three water treatments were applied to the transplanted thalli consisted of no extra water, evaporation from wet soil and spraying water over the thalli. Thirty two months after transplantation, thallus fragments which received moisture from evaporation of wet soil had higher proportion of survived thalli than those without extra water and those received spraying water over thalli accounting for 39%, 33% and 28% respectively. The transplanted thalli receiving evaporated water from the soil exhibited the highest survival rate for those on substrates facing the east at 23%, whereas those facing the south, the west, oriented horizontally, and the north exhibited respective survival rates at 19%, 21%, 19% and 18%. The thalli facing the east received more light than those facing the other cardinal directions and those oriented horizontally. The cool season showed the lowest death rate for thalli in contrast to the rainy season which showed the highest death rate caused by the accumulation of water in the nylon net substrates. In the second year of transplantation, a higher proportion of dead thalli were found comparing to the first year because numerous isidia produced by the transplanted thalli had been broken off by heavy rain. Some of them germinated and became juvenile lobules located near the original transplanted thalli. These observations are underway to facilitate optimal conditions for propagating lichens such that conservation and sustainable utilization could be implemented.

ON STUDY OF LICHEN DIVERSITY OF PROTECTED AREAS OF ESFAHAN PROVINCE (IRAN)

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1A-P

There are hitherto only data on twenty one lichen species of the genera *Acarospora*, *Aspicilia*, *Caloplaca*, *Candelariella*, *Collema*, *Glypholecia*, *Lecidea*, *Lobothallia*, *Physcia*, *Polysporina*, *Rhizoplaca*, *Rusavskia*, *Sarcogyne*, *Toninia*, and *Verrucaria*, found in the Esfahan Province of Iran (Seaward et al. 2004; Sohrabi 2009-2010 <http://www.myco-lich.com>). During 2010 special collections of lichens were done by B. Zarei-Darki in Mooteh and Karkas protected areas of the Esfahan Province, Iran. In total, more than 500 field envelopes of lichens were collected. Mooteh Wildlife refuge, with a total area a. 205,302 ha, was created in 1990 while it was as protected area since 1964. Karkas hunting-prohibited Region, with a total area a. 92,100 ha, is the protected area since 1980. Preliminary identifications of our collections show the high species diversity of both lichen-forming and lichenicolous fungi in areas mentioned. So a number of lichen taxa, i.e. *Arthonia epiphyscia*, *A. cf. hawksworthii*, *Caloplaca intrudens*, *C. scrobiculata*, *Opegrapha romsae*, *Protoparmeliopsis laatokkaensis*, *Xanthoparmelia loxodes* and *Zwackhiomyces coepulonus* are for the first time recorded for the whole Iran. The following lichen-forming and lichenicolous fungi as *Arthonia molendoi*, *Caloplaca decipiens*, *C. mogoltanica*, *C. trachyphylla*, *C. xantholyta*, *Protoparmeliopsis garovaglii*, *P. muralis*, *Muellerella pygmaea* are for the first time recorded for the Esfahan Province. The new hosts are for the first time recorded for such lichenicolous fungi as *Arthonia molendoi* and *Zwackhiomyces coepulonus*. A number of critical taxa of lichen-forming fungi of the *Protoparmeliopsis muralis*-, *Caloplaca persica*- and *C. scrobiculata*-, *Lecania ochronigra*-, and *Rusavskia elegans*- groups, as well as some representatives of the genera *Acarospora*, *Aspicilia*, *Lecanora*, and lichenicolous fungi of the genera *Zwackhiomyces*, *Cercidospora*, *Phoma*, and *Lichenostigma* are under special revision at the moment.

(1A-P7) Submission ID: IAL0125-00001

CONSERVATION BIOLOGY OF CLADONIA TRAPEZUNTICA J. STEINER

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Cladonia trapezuntica J. Steiner (lichenized fungi, Ascomycetes) rediscovered recently, was first described from North Turkey in 1909 and was never reported after. This species was collected by Handel-Mazzetti on mosses from Eseli village, which was evacuated several decades ago; today, this village is neither known from current maps nor by the local population. *Cladonia trapezuntica* is similar to *Pycnothelia papillaria* (Ehrh.) L.M. Dufour, but it differs 1) in its cushion-like growing form of the thallus, 2) by its rather temporary primary thallus (usually it is continuous in *P. papillaria*), and 3) in its growth on metal rich soil, which is rich in iron oxide followed by calcium phosphate hydroxide hydrate, calcium carbonate and barium aluminium silicate. Despite of more than 430 papers published about lichens collected from Turkey, *P. papillaria* is not known from the country. From this reason, ecology, distribution (rarity) and taxonomy of *C. trapezuntica* were studied for conservational purposes. This study was supported by The Mohamed bin Zayed Species Conservation Fund, Project number 10051505.

WHERE ARE THE TYPE SPECIMENS OF ÖDÖN SZATALA REALLY DEPOSITED?

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1A-P

Taxonomic studies based on type material are difficult if the deposition of types are not known correctly. In the case of Ödön Szatala's type specimens, several mistakes on their typification were made, since deposition of many type specimens were unknown. Ödön Szatala was usually thought to be working in his whole scientific life in the Hungarian Natural History Museum (BP). Despite of this, he was working in BP only during his last five years before his death in 1958. More than 80% of his papers were published before his time at the museum. Prior to this, he was working as an internationally respected expert on seed testing in the Royal Hungarian Experimental Institute for Seed Testing and in various stations of the same company situated in several cities. Most of 72 new lichen species, 26 new varieties and 71 new forms, described by him based on different collections, were introduced to lichenology during this period. The main problems are caused by those taxa, because the protologues do not provide any internal evidence concerning on the deposition of type materials. In this poster, we would like to present Ödön Szatala's career and share our results on his type specimens deposition. These specimens were mainly deposited in BP and W, however, other herbaria (e.g. B, CL, GB, GZU, LBL, M) could also keep some of these original materials, while no types has been seen in WU (except the isotypes in exsiccate *Lichenotheca parva*). A total of 49 critical taxa described by O. Szatala will be discussed here. This study was supported by SYNTHESYS AT-TAF-3435& HU-TAF-1103 and OTKA K81232.

**ARID LICHENS FROM THE RED DATA BOOK OF UKRAINE - ASSESSMENT,
CONSERVATION AND PERSPECTIVES**

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1A-P

A project supported by Rufford SGF was carried out in Ukraine during 2009-2011 and combined lichen floristics and community ecology. Our focus was on arid terricolous lichens in steppes because these ecosystems occupy an important part of the Ukrainian territory. However, steppe ecosystems are amongst the most disturbed areas, affected by built-up areas, mines, industries, crop farming and overgrazing. The main aim of this study was to disseminate knowledge about steppe lichens and their conservation biology to the local population, governmental and regional administrations, staff of protected areas, etc. Our activity included monitoring of terricolous lichen communities and species distribution in Ukrainian steppes. We have prepared and distributed a brochure "What do you know about steppe lichens—minute world under your foot" to school associations of young biologists and ecologists, biological faculties of universities from the main regions, administration of protected areas and Ministry of Natural Protection. Eight months later we have already received lichen specimens from schools and social organizations; also some local children`s and historic-cultural journals were interested in our project. From a scientific point of view we have collected data about historic and modern localities of terricolous lichens with relations to the steppe zone of Ukraine, including 11 species from the present edition of Red Data Book of Ukraine (2009): *Agrestia hispida*, *Aspicilia fruticulosa*, *A. vagans*, *Cetraria steppae*, *Fulgensia desertorum*, *Leptogium schraderi*, *Seiophora lacunosa*, *Squamarina lentigera*, *Xanthoparmelia camtschadalis*, *X. ryssolea*. We documented localities for 10 redlisted species, some as new, others to reconfirm records from the 19th century. In this project we described associations of terricolous lichens and clarified some taxonomically difficult species, as *Cetraria steppae* and *Xanthoparmelia ryssolea*. Our field trips and collaborations with other organizations and colleagues stimulated the establishment of new protected areas in the south of Ukraine, notably in Kherson, Donetsk, Luhansk, Odessa regions and Crimea. We assume that popularization of the lichen conservation issue will also influence the acceptance of local and regional administrations for lichen conservation.

CAUCASUS BIOSPHERE RESERVE (WESTERN CAUCASUS, RUSSIA) AS A POTENTIAL VALUABLE HOTSPOT OF LICHEN DIVERSITY IN CAUCASUS AND RUSSIA

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1A-P

The Caucasus Mountains are one of the world's biodiversity hotspots as well as one of the richest regions of Russia in this aspect. However, the Caucasus is not recognized yet as a hotspot of lichen species diversity, because the lichen flora of the Caucasus is still incompletely known. There are 1,119 species mentioned for the Northern Caucasus in the Russian lichen checklist (2010), which comprise 33% of total lichen flora of Russia. UNESCO-MAB Caucasus Biosphere Reserve (Kavkazskiy Zapovednik) is situated in the western Caucasus, which is the core of the Western Caucasus World Heritage Site. The area of the Reserve covers about 2,800 sq km of various natural ecosystems, which are about 80% of whole Great Caucasus ecosystem types. There are distinct ecological and altitudinal belts—from subtropics on the eastern Black Sea coast (30 m alt.) up to glacial and nival habitats (3,300-3,360 m alt.), with unique temperate broadleaf and mixed rainforests with annual precipitation over 2,500 mm in the most of western part of the Caucasus. High level of species endemism is character for the whole Caucasus region. Our study report 745 species of lichens and lichenicolous fungi for the Caucasian Biosphere Reserve (more than 100 are additions to the Northern Caucasus list). However our investigations covered only small part of the Reserve. Anyway we state the Caucasus Reserve has one of the richest lichen flora Reserves in Russia as compared to Pechoro-Ilych Reserve (889 sp.); Baikalskiy (719 sp.) and Laplandskiy (612 sp.). More then 130 lichens from the Caucasian Reserve are not known in other Russian Reserves and 430 species are not known in other Reserve areas of Caucasus. Nevertheless, we suppose that the actual number of species is much higher: about 1,200 lichen species could be registrated in the reserve and over 2,500 species for the whole lichen flora of the Caucasus. Therefore the Caucasus Reserve is of critical value for the total Caucasian lichen diversity conservation. The rich lichen diversity in a mountain-forested area clearly justifies a more detailed lichen exploration in the region.

FIRST ACTIONS ON A PRELIMINARY RED LIST OF VENEZUELAN LICHENS

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1A-P

Until now, no country in Latin-America has included fungi and lichenized fungi in their red lists. Efforts in fungi conservation and first attempts to create red lists have been done in Cuba, Argentina and Colombia. The conservation of lichens is strongly related to the threat upon the existing vegetation where they exist. Unfortunately in Venezuela a great extent of the natural habitats have been subject to fragmentation processes and general destruction by man. Deforestation is the main factor in the destruction of extensive natural areas with a great variety of habitats for lichens. Tropical forests are continually invaded for urban expansion and agriculture uses. In Venezuela the fragmentation and destruction of ecosystems has reached concerning levels and in some cases has reached points of no return to the original conditions. The destruction of habitats produce fragmentation of the area of distribution which affects the reproduction decreasing the capacity of perpetuation of the species in lichens and other groups. Little is known of the lichen collections in Venezuela. The project objectives include elaborating an inventory of all the existing herbaria in Venezuela outside of the country. All this information was to be introduced in a single database. The red list will be elaborated analyzing the ecological data from the database and the existing information from catalogs and checklists from Venezuela. 17 herbaria in Venezuela have lichen collections. 80% has been introduced in the database. Information from six foreign herbaria was also included. The database has nearly 50 thousand entries. An endemic species lists has been started, plus a preliminary red list for lichens. Threats to natural populations of lichens from Venezuela are being measured on the basis of particularities of geographical distribution, habitat quality and, especially, the possibilities of land transformation and in some cases of missing of large surfaces of land in natural regions of Venezuela. In the process to assigning a degree of threat the methodological approach from IUCN was followed.

(1A-P12)

Submission ID: IAL0250-00002

**TAXONOMIC STUDIES OF THE LICHEN GENUS *TONINIA*
(LECIDACEAE, ASCOMYCETES) IN ISFAHAN PROVINCE, IRAN**

1A-P

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The lichen genus *Toninia* (Lecideaceae, Ascomycetes) seems one of the well-studied genera of lichenized fungi in the world which is widely distributed especially in the temperate region, but also is presented in the arctic and subtropical regions of the world. The genus was monographed (by Timdal 1991) and so far 48 species and 9 subspecies were reported worldwide. At present, c. 13 species are known from Iran (see online checklist at www.myc-lich.com) i.e., *Toninia aromatica* (Sm.) A. Massal., *T. athallina* (Hepp) Timdal, *T. candida* (Weber) Th. Fr., *T. cinereovirens* (Schaerer) A. Massal., *T. diffracta* (A. Massal.) Zahlbr., *T. lutosa* (Ach.) Timdal, *T. opuntioides* (Vill.) Timdal, *T. physaroides* (Opiz) Zahlbr., *T. ruginosa* (Tuck.) Herre, *T. sedifolia* (Scop.) Timdal, *T. squalida* (Ach.) A. Massal., *T. taurica* (Szatala) Oxner, *T. tristis* (Th. Fr.) Th. Fr. and *T. weberi* Timdal. Some of these species seem to be broadly distributed in the world. *Toninia weberi* is known from few localities in Iran (mainly Kerman, Semnan and Tehran provinces). However, it was also reported from N. America (Colorado). Some species are widely distributed in Iran. For instance *T. candida* and *T. sedifolia* are reported from several provinces in Iran. To date taxonomic studies on the genus *Toninia* in Iran are lacking. Therefore, we start with a systematic revision of the genus *Toninia* in Esfahan province in the central part of Iran. The taxonomic study is based mainly on fresh material and compared with some well identified specimens from other regions of Iran. We show preliminary results of our work, including anatomical and morphological characters which are important for the taxonomy of the newly discovered species in the region. We also provide short descriptions, taxonomical notes, and preliminary ecological information and distribution maps for each species. The distribution maps and photographs of the species and their habitat will be appearing at the MYCO-LICH website (www.myc-lich.com).

(1A-P13)

Submission ID: IAL0267-00001

HERBARIUM OF YEREVAN STATE UNIVERSITY: LICHEN COLLECTION

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The Herbarium of Yerevan State University (YSU) has been established in 1923 by the famous Russian botanist A. Shelkovnikov. Nowadays, the herbarium consists of collections of fungi (more than 30,000 specimens of 4,500 species) and higher plants (13,000 specimens of 2,700 species). In comparison with plants and fungi, the lichen flora of Armenia is poorly studied yet. The main outstanding contributors to lichens investigation in Armenia were V. Nikoghosyan, S. Barchalov and A. Abrahamyan, whose studies are the basis for understanding lichen diversity of the country. According to First National Report "Biodiversity of Armenia" (1999) around 300 species (among them 190 species from adjacent areas of Sevan Lake) of lichens have been reported for Armenia. The purpose of this study was to catalogize and to evaluate lichen species preserved in the herbarium of YSU. In the lichen collection of the herbarium of Yerevan State University are deposited specimens collected from 1920 by A. Shelkovnikov, A. Grossgeim (1923), N. Troitsky (1929) etc. In 1960's large contribution to the herbarium has been done by M. Meliksetyan. The lichen collection contains 415 specimens from research areas of Armenia (Alaverdi, Stepanavan, Sevan, Aragats) and different countries (Russia, Georgia etc.). The lichen collection now includes 150 species belonging to 44 genera. As a result of our study, all specimens were catalogized in an electronic database (with photos). The lichen collection of the herbarium could be the basis for evaluating the lichen diversity, conservation status and listing of threatened species in the Red Book of Armenia.

LICHEN FLORA OF THE ISLAND OF LASTOVO (CROATIA, EUROPE)

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1A-P

Lastovo Archipelago (Croatia, Europe) is one of the most remote groups of islands in the Adriatic Sea, with around 30 km distance from the nearest mainland. Its isolated position together with the fact that it was a military outpost during the wars of the last century, had an exceptional influence on the preservation of the unique natural characteristics of the island. Due to the extreme beauty and large biodiversity of the islands and the surrounding marine habitats, in 2006 it was proclaimed as a Croatian Nature Park. As a part of a biodiversity project, in 2007, the Lichenology group from the Biology Students Association conducted research in the newly established park. We found 40 species on the island Lastovo, the main island of the Lastovo Archipelago; out of which, 33 species were found within the area of the Park. One of the determined lichen species *Teloschistes chrysophthalmus* (L.) Th.Fr. is listed as Near Threatened (NT) category according to IUCN categorization in the Red List of lichens of Croatia. Previous records of the lichen flora for Lastovo island date from 1938, and list a total of 55 species. We can hypothesize that some of the species previously recorded, but not found in this survey, could either be found in an inaccessible part of the island, became extinct due to the environmental changes, or were misrecorded by the previous survey. In order to enable the comparison the lichen flora with the flora with other Adriatic islands and to determine how the environmental changes influence the comparative species composition, more fieldwork and research using precise methods for assessing lichen biodiversity are needed.

1B: Genomic approaches to studying the lichen symbiosis

(1B-P1) Submission ID: IAL0100-00001

GENE EXPRESSION IN DRY AND WET THALLI OF *USNEA BISMOLLIUSCULA*

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1B-P

Symbiosis is drawing increasing attention due to its importance in the ecosystem and evolution. Among a number of symbioses in nature, the lichen is considered as one of the most successful organisms for having expanded distribution to extreme environments. The ecological success of the lichen is attributed partly to its ability to switch metabolism on and off according to the water content of thalli. In this study, we focused on metabolic differences between dry and wet thalli of *Usnea bismolliuscula* from the view point of gene expression. For the dry state, thalli kept in a natural dry condition were used, and thalli rehydrated by distilled water were used for the wet state. The thalli in the both states were exposed to white fluorescent lamp ($4.3 \mu\text{mol m}^{-2}\text{s}^{-1}$) for 1 hour. Total RNAs were extracted from the thalli of each state and differentially expressed genes between the two states were isolated by subtractive hybridization. BLASTX searches of the sequences obtained from the experiment were carried out. Possible homologs to fungal genes were detected at amino acid levels such as 6-phosphofructokinase (60% identity to *Mycosphaerella graminicola*) and heat shock protein (96% identity to *Alternaria alternata*). The results implied a shift in carbon metabolic pathway of the fungus corresponding to the water content of thalli and an induction of stress response against the low water content. The quantitative analysis of the results will be performed by RT-PCR. Alternating wetting and drying cycles are considered to be prerequisites for functioning symbioses of lichens. Therefore, examining gene expression in dry and wet thalli will shed light on the molecular basis of lichen symbioses.

(1B-P2) Submission ID: IAL0239-00001

ANALYSIS OF FUNCTIONAL GENOMICS OF LICHEN MYCOBIONT *ENDOCARPON PUSILLUM*

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The first full-length cDNA library for lichenized fungi was constructed from cultured mycobiont of the arid desert lichen *Endocarpus pusillum* Hedwig. Based on small-scale sequencing results, 111 genes of the lichenized fungi were identified for the first time. Real-time PCR showed that the size of the mycobiont genome is 39.13 Mb and the copy number of ribosomal RNA gene repeat units is 43. Genome sequencing showed that the genome is about 38.4 Mb, almost identical to the size detected by RT-PCR. 12,100 genes have been detected by large-scale identification of functional genes on before- and after-drought stress transcriptome's differential expression of *E. pusillum*, among which 5,880 genes have obvious change in sequencing signal, accounting for 48.6% of the total number of genes. Comparing to the before-drought stress transcriptome, there are 2,225 genes with up-regulation signal and 3,655 genes with down-regulation signal in after-drought stress transcriptome, accounting for 18.4% and 30.2% of the total number of genes, respectively. Up to now, 1,880 of the variational 5,880 genes have been identified as function-known genes, and 4,000 are function-unknown genes. In the following work, desiccation tolerance-related genes will be expressed in *Escherichia coli* system, and the corresponding functional proteins will be further analyzed.

ANNOTATING BIOSYNTHETIC GENE CLUSTERS IN THE *CLADONIA GRAYI* GENOME

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1B-P

We screened the genome sequence of *Cladonia grayi* for conserved protein domains of biosynthetic genes coding secondary metabolites. Here, we report the number and organization of polyketide synthase and nonribosomal peptide synthetase gene clusters.

(1B-P4) Submission ID: IAL0246-00001

TISSUE- SPECIFIC GENE EXPRESSION AND DNA CYTOSINE METHYLATION IN THE LICHEN *PELTIGERA MEMBRANACEA*

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DNA cytosine methylation (5mC) plays an essential role in the normal development of mammals and plants and is associated with various biological processes, such as silencing of transposons, regulation of gene expression during development and cell differentiation. In fungi, DNA methylation has been viewed as primarily a mechanism of genome defense (e.g. in *Neurospora crassa*), but has also been proposed to modulate transcriptional activity (e.g. *Candida albicans*). We explored the role of methylation in development of the mycobiont of the lichen, *Peltigera membranacea*, by identifying genes involved in methylation in a genome sequence assembly, by analysing Illumina-sequencing data from bisulfite-treated total metagenomic DNA of apothecia (non-symbiotic tissue) and thalli including both mycobiont and symbiotic photobionts, and correlating the results with transcriptomic data obtained by Illumina RNA-Seq. Putative homologs to most *N. crassa* genes involved in DNA methylation were found, including hpo, dim-2, and the members encoding a DCDC complex (dim-5, dim-7, dim-9, as well as cul4, ddb1 and their presumptive associated factors). Genes of the DMM complex that prevent spreading of methylation from transposons to nearby genes were also identified. Single-base resolution mapping in *P. membranacea* revealed some of the same distributional features as *N. crassa*, such as the occurrence of 5mC in all sequence contexts, and heavy methylation of transposons and repeat elements. However, a substantial fraction of the genes are also methylated in the transcribed regions (body) as in *C. albicans*, and in short regions that are depleted of G on one strand. Analysis of the RNA-Seq reads using Cufflink software revealed gene expression levels and splicing isoforms. A large number of genes showed tissue-specific gene expression and were not methylated, e.g. one of two ammonium transporter genes was strongly expressed in thalli, the other only in apothecia. lec1, encoding a lectin possibly involved in mycobiont-photobiont interaction was more highly expressed in thalli than in non-symbiotic tissues. The observation to date suggests that while one role of methylation in *P. membranacea* may be to silence transposons, additional functions, particularly with relation to gene body methylation, will be elucidated.

**A SURVEY AND ANALYSIS OF POLYKETIDE SYNTHASE GENES IN
PELTIGERA MEMBRANACEA MYCOBIONTS**

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Polyketides are a group of secondary metabolites produced by a wide range of living organisms. These compounds exhibit remarkable diversity both in terms of their structure and their biological activity. Polyketides are of great commercial interest for drug discovery since many of these compounds have desirable pharmaceutical properties and they are a source of novel antibiotics, anti-tumor and anti-cancer agents, as well as cholesterol-lowering drugs. The biosynthesis of polyketides is catalyzed by large multifunctional enzymes called polyketide synthases (PKSs) that assemble core polyketide molecules from simple starter carboxylic acid precursors and several malonyl-CoA units in a manner similar to fatty acid synthesis. Genome sequencing projects on filamentous fungi have revealed an unexpectedly large number of PKS gene clusters in their genomes, very often exceeding the number of known polyketide metabolites for a certain species. Thus, the products of many sequenced PKS clusters remain to be elucidated. Here we present a survey and analysis of PKS genes in a recently sequenced metagenome of the foliose lichen *Peltigera membranacea*, along with analysis of corresponding gene clusters, methylation and expression (RNA-Seq) data. We have identified 11 full-length PKS genes, coding for 2 non-reducing and 9 reducing PKS enzymes, including one PKS-NRPS with a truncated NRPS module. Not all deduced splice sites have been confirmed with RNA-Seq data, and some introns appear not to be spliced at all or exhibit alternative splicing.

1B-P

2I: Adaptation and morphological evolution

(2I-P1) Submission ID: IAL0057-00008

EVOLUTION OF VAGRANCY IN THE “MANNA LICHENS”

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2I-P

The vagrant growth form of lichenized fungi has evolved in several distantly related fungal lineages, including Lecanoraceae (*Rhizoplaca*), Megasporaceae (*Circinaria*), Parmeliaceae (*Cetraria*, *Masonhalea* and *Xanthoparmelia*) and Verrucariaceae (*Dermatocarpon*). This research is focused on the evolution of vagrancy among the ‘manna lichens’ as the most famous exemplar of the vagrant growth form. ‘Manna lichens’ comprise c. 17 accepted species previously treated under the genus *Aspicilia* but recently the group was entirely moved to the newly resurrected genus *Circinaria*. Therefore, no vagrant member was left in the genus *Aspicilia* (Megasporaceae) in its traditional sense. With current circumscription, the genus *Circinaria* is found to be heteromorphic, with numerous strictly saxicolous, and some true vagrant or semivagrant species. Within the ‘manna lichens’ some species are obligatorily unattached (truly vagrant), growing and reproducing without proper attachment to a substrate. Some other species are “erratic”, i.e., facultatively unattached (vagrant-crustose or semivagrant); these taxa often persist in two different growth forms, initially attached to soil or rocks and later developing a vagrant growth form. In this study, a comprehensive sampling of the genus *Circinaria* was made (c. 100 specimens), including both truly crustose and truly vagrant or semivagrant taxa. The nuITS, nuLSU and mtSSU rDNA were used as molecular markers. The datasets were analysed using parsimony and Bayesian methods. Some conclusions could be made about the relationships between truly crustose and vagrant taxa in the genus *Circinaria*. The occurrence of the vagrant growth form in several apparently unrelated lineages in the genus *Circinaria* shows interesting patterns of convergent evolution and ecological adaptation. Despite these insights, the reasons behind the high plasticity in external morphology of vagrant species still remain largely unknown.

(2I-P2) Submission ID: IAL0140-00002

ARE LONG-LIVING LICHEN THALLI AN ARENA FOR PHOTOBIONT VARIATION?

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Previous studies of symbiont selectivity in lichens often relied on the uniformity of the algal partner in individual thalli. Fingerprinting analyses of whole thallus DNA extractions, however, reveal presence of multiple *Trebouxia* strains within individuals of different species. A mixture of algal genotypes may be an adaptive advantage, because their different physiological performances can mediate tolerance to varying environmental conditions. We studied intrathalline variation of *Trebouxia* photobionts the cosmopolitan crustose lichen *Protoparmeliopsis muralis*, which has a broad ecological tolerance. We hypothesize that the lichen thallus could be an arena for combinations of the mycobiont with several algal strains, in order to promote longevity, robustness and fertility of this lichenized fungal species. We compared the photobiont diversity of marginal lobes and regenerative central outgrowths in two ecologically different localities. The single strand conformation polymorphism analysis (SSCP) and the haplotype analyses reveal the presence of different *Trebouxia* strains in the thalli. The majority of them were identified as *T. incrustata* and as “uncultured” *Trebouxia* strains, which is present as two different taxa in Czech Republic and Austria.

**A TALE OF TWO MYCOBIANTS: EXPLORING CONVERGENT EVOLUTION AND
PHOTOBIONT SWITCHING IN THE LICHEN GENUS *POLYCHIDIUM***

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The cyanolichen genus *Polychidium* (Ach.) Gray is generally considered to consist of four species, one being muscicolous, the others epiphytes. The four species share strikingly similar gross morphology but consort with different photobiont genera, namely *Nostoc* and *Scytonema*. In the past, thallus architecture has been a powerful guide in classification of lichen genera such as *Polychidium* and has often been taken to trump photobiont association and ascocarp type, but the reliability of these characters to predict phylogenetic affinity has seldom been tested. We tested the monophyly of *Polychidium* with a multilocus phylogeny based on nuclear and mitochondrial sequence data from all known Peltigerales families, and reconstructed ancestral states for specific thallus architecture and ascoma ontogeny types relative to *Polychidium* and other clades. Our working hypothesis was that if *Polychidium* were found to be monophyletic, it would suggest photobiont switching among closely related species. If however species were found to arise in different lineages, this would suggest convergent body plan and ascoma type evolution. We found that *Polychidium* consists of two species groups that arose independently in different suborders within the Peltigerales, associated with *Nostoc* and *Scytonema* photobionts, respectively. We infer from ancestral character state reconstruction that dendroid thallus architecture evolved independently in these two lineages. The independent development of similar dendroid thallus architecture in different fungal suborders with different photobionts represents one of the most extreme examples of convergent evolution documented to date in symbiotic organisms.

2I-P

**ON THE SPECIATION PROCESS IN MORPHOSPECIES:
THE EXAMPLE OF *PARMELINA PASTILLIFERA***

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The independence of the morphospecies *Parmelina pastillifera* is not questioned currently although it had been debated by authors which considered this taxon either as a synonymous with *P. tiliacea*, or as a variety of that species or as a different species. *Parmelina pastillifera* presents morphological characteristic button-like stalked isidia and grows in relatively humid oceanic regions in Europe whereas *P. tiliacea* has cylindrical isidia and grows in drier areas and shows a wider geographic distribution in Eurasia, Macaronesia and North Africa. Previous molecular phylogenetic studies have shown both taxa as sister species, although few individuals have been studied so far. The finding of individuals with intermediate morphology poses some doubts on the relationship between these taxa and their taxonomic status. Analyses with three molecular markers (nuITS, mtLSU and Elongation Factor 1), on an extensive population sampling from different localities in Western Europe, show that both species are genetically close. However the relationships between *P. pastillifera* and *P. tiliacea* cannot be directly established concatenating the three molecular markers, due to incongruence in the phylogenetic signals and the sharing of common haplotypes in the three markers. We here present an attempt to reconcile the set of gene trees with a shared species tree, using a coalescent model in order to gain a deep insight into their genetic relationships and their taxonomic status in the perspective of a speciation process.

**GENETIC DIVERSITY OF SPECIMENS AND THEIR CULTURED MYCOBIONTS
OF *CLADONIA VULCANI***

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Lichen mycobionts can be isolated by two culture methods of their ascospores or tissues (thallus fragments). The tissue culture method was described as follows. It used one or a few thallus fragments. After washing and homogenizing they were divided into segments having the size from 150 to 500 µm. The segments were placed on agar plates of malt-yeast extract (MY) medium at 18°C. After 8 months they were harvested. We previously found that cultured mycobionts obtained from podetia of *Cladonia* spp. by the tissue culture method showed the wide variety of colors and forms. Therefore, we investigated the genetic diversity distributed in specimens and their cultured mycobionts of *Cladonia vulcani* collected at four sites in the same area in Akita, Japan. We analyzed sequences of the nuclear rDNA internal transcribed spacer in each four podetia collected at four sites and decided their genotypes. It was proved that the composition of genotypes is different between each collecting site and there were a few genotypes in the same site. Consequently, we confirmed that *C. vulcani* in tested area had seven haplotypes. Besides, we divided two half parts of up- and down-sides of each four podetia collected at the same site and subjected to the DNA analysis. We found the up-side half parts and the down-side half parts were same genotype from same one podetium. Cut podetia in half lengthwise collected at four sites. The half lengthwise parts were subjected to the DNA analysis. Other parts were done to the tissue culture and were subjected to the DNA analysis. We found same genotypes between podetium and tissue culture from same one podetium. Cultured mycobionts we obtained showed three colors, violet-blue, flesh-color and brown. We supposed that the colors of cultured mycobionts were not dependent from their genotypes.

2I-P

(2I-P6)

Submission ID: IAL0168-00001

**THE YEAST-TO MYCELIAL-PHASE TRANSITIONS OF A LICHEN-FORMING
FUNGUS *UMBILICARIA MUEHLENBERGII***

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Umbilicaria muehlenbergii is the first discovered lichenized fungus with. It exists as mycelium at the symbiotic state, and as yeast at the free living state. Among the hundreds of cultures of the yeast on petri-dish in our lab, one yeast colony transitioned to mycelial-form on one plate. However, whether this transition is accidental or inevitable, and what are the factors to induce this transition are still unclear. In order to find out some clues, the present study was designed. The yeast form fungus was cultured under different conditions, including different temperatures, illuminations, with or without algae for one month. The results indicated that, the alternative temperature had a remarkable effect on the growth of the yeast and the transition to mycelial phase. Yeast grows quickly under 15°C, while did not grow at 25°C. However all yeast transitioned to mycelium under the alternative temperature (15°C 12 h/25°C 12 h). Under the alternative temperature, high density of illumination inhibited the growth of mycelium; 1 min of UV exposure increased the growth of mycelium. Co-culture with photobiont algae improved the growth of both bionts and induced the transition from yeast to mycelium. The results suggested that, the yeast-to mycelial-phase transition of lichen-forming fungus *U. muehlenbergii* is inevitable under some certain conditions such as the alternative temperature and the co-culture with photobiont. These features are relatively similar with those of some animal or plant pathogenic fungi, suggesting a close relationship or a common basis to the development of the two morphologies between lichenized fungi and pathogenic fungi.

(2I-P7)

Submission ID: IAL0174-00003

**CHARACTER STATE EVOLUTION IN THE LICHEN-FORMING LINEAGE TRYPETHELIALES
(DOTHIDEOMYCETES, ASCOMYCOTA)**

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We present a detailed phylogeny (mtSSU, nuLSU, RPB2) of the fungal order Trypetheliales. While some genera and species groups, such as *Aptrootia*, *Architrypethelium* and the *Trypethelium eluteriae* group are each recovered as monophyletic, the monophyly of a large number of genera in their current sense, such as *Trypethelium*, *Astrothelium* and *Bathelium* is rejected, forcing a re-evaluation of generic concepts in this group. As previous classification schemes were based on the evolutionary conservation of a number of morphological characters, such as ascospore septation and color, ostiole orientation and perithecial arrangement, we re-evaluated the evolution of these characters in light of phylogeny. Additionally, we examined whether morphological diversification through time was correlated with taxonomic diversification (cladogenesis), and allowed us to identify if morphological diversity is disproportionately partitioned among or within subclades within Trypetheliales.

2I-P

(2I-P8)

Submission ID: IAL0211-00002

**CRYPTIC DIVERSITY OF LECIDEOID LICHEN SPECIES (LECANORACEAE & LECIDEACEAE)
IN CONTINENTAL ANTARCTICA (ROSS SEA REGION)**

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The diversity of mainly saxicolous crustose lichens with lecideine apothecia in continental Antarctica is poorly known. Although lecideoid lichens are a diverse mixture of quite distantly related groups, they all share a similar morphology due to the ecological niche they are living in. This inconspicuous appearance not only complicates species identification but also genetic analysis because most of the biomass is growing in tight connection with rock surfaces. The limited availability of fresh samples from Antarctica in combination with the difficulties in genetic analysis is the reason why almost no reference sequences were found in public databases before the present study started. To overcome difficulties with the morphology-based species delimitations in these groups, molecular data were employed to test boundaries of the sampled species within the family Lecanoraceae (*Carbonea*, *Lecanora*, *Lecidella*, *Rhizoplaca*) and the genus *Lecidea*. Sampling was done along a north to south transect at five different areas in the Ross Sea region - continental Antarctica with more than 250 lecideoid specimens from 13 localities. The study also includes specimens from other regions in Antarctica and non - Antarctic areas. Phylogenetic analyses divide the samples from continental Antarctica into more groups than described before. Higher species diversity, higher endemism as previously thought and a more obvious classification of variable species were the results of this study. The phylogenetic estimate revealed the existence of several previously undescribed clades. Based on this phylogenetic estimate, we restudied the micromorphology and secondary chemistry of these previously unrecognized groups to evaluate the use of these characters as phylogenetic discriminators. Seven clades within the family Lecanoraceae were identified as the following species: *Carbonea vorticosa*, a previously unnamed clade of uncertain status, referred to as *Carbonea* sp. (URm1), *Lecanora fuscobrunnea*, *Lecanora physciella*, a novel species *Lecidella greenii* Ruprecht & Türk, *Lecidella siplei* and *Rhizoplaca macleanii*. Four clades were identified in the genus *Lecidea* as *Lecidea andersonii*, *L. cancriformis* as well as the novel species *L. polypycnidophora* Ruprecht & Türk sp. nov. and a second clade of uncertain status, referred to as *Lecidea* sp. (UCR1).

UMBILICARIA DECUSSATA - A PLEOMORPHIC LICHEN

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Several species pairs can be found in the Umbilicariaceae, and one taxon of a pair may produce high numbers of mitospores (“anamorphic stage”), while the other taxon exclusively develops apothecia (“teleomorphic stage”). The existence of such paired taxa may have at least three interpretations: the “taxa” represent different phenotypes of a single taxon; taxa share a close common ancestor but are now more or less reproductively isolated; taxa have attained their similarity through convergent evolution (Hestmark 1991). Morphological and molecular investigations were made to interpret the current status of the species pair *Umbilicaria decussata* – *U. polaris*. Molecular phylogeny seems to be the most appropriate tool to test the monophyly of taxa, which may be interpreted in terms of evolutionary relationships. Three data sets (nrITS, mtLSU, and nrITS+mtLSU) were analyzed using MP and ML algorithms to test the hypothesis of monophyly for the species pair. In all analyses, sequences of all *U. decussata* and *U. polaris* accessions were combined into a cluster which is well supported statistically. However, neither of the two species appeared monophyletic. According to the resulting cladograms, it is most plausible that mentioned taxa actually represent two morphotypes of one biological species, individuals of which are switched on earlier stages of ontogenesis to anamorph or teleomorph. Divergence by alternation of the reproduction mode, as shown for several species pairs (Poelt 1977; Hestmark 1991), may therefore be a result of fixing this shift in the phylogenesis and subsequent isolation of anamorph or teleomorph populations. According to this work, *U. polaris* is the teleomorph of *U. decussata*. Despite *U. decussata* and *U. polaris* being well separated morphologically, they should be treated as one species represented by two morphotypes according to the principal (anamorph or teleomorph) reproductive stage. Such a situation is well known for non-lichenized ascomycetes. Different morphs of a pleomorphic fungus may occur in different conditions (e.g. on different hosts or at different seasons). For *U. decussata*, such ecological factors as temperature and humidity may play an important role in anamorph / teleomorph switching. The investigation was supported by Russian Foundation of Basic Research (grant no. 11-04-90704).

2I-P

(2I-P10)

Submission ID: IAL0280-00001

ARTHONIALEAN CHALLENGE

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Arthoniomycetes with the single order Arthoniales (c. 1,500 species) is the largest group of mainly lichenised fungi beside Lecanoromycetes and might represent an independent case of lichenisation in Ascomycota. Most species are associated with algae of the Trentepohliales, but there are also species which form thalli with coccal green algae. Moreover, many species are non-lichenised and living either as saprobes on wood or as inhabitants (commensals to parasites) of other lichens, with different degree of host-specificity. The interrelationships of crustose species, especially of tropical taxa, are still rather unclear. There is a tremendous variation in ascomatal characters, which are otherwise used to distinguish genera or even families. We have started to explore the phylogeny of crustose Arthoniales using phylogenetic methods in more detail. The initial results reveal the non-monophyly of many genera and show also unexpected relationships. For example, Chrysotrichaceae can no longer be characterized by characters of pigmentation. Our analysis of the yet understudied Arthoniomycetes gives new insights in phenotypic and lifestyle evolution and help to refine the concept of genera.

2A - 1: Graphidaceae: progress in understanding the evolution and diversity of the largest family of tropical crustose lichens

(2A-1-P1) Submission ID: IAL0015-00001

ATM - ASSEMBLING A TAXONOMIC MONOGRAPH: THE LICHEN FAMILY GRAPHIDACEAE

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Cataloging the diversity of life is an enormous task. Of the 30 million species inhabiting this planet, only two million have been described. With a decreasing number of taxonomists, the researchers who discover and describe species, traditional approaches are not sufficient for this task. This project implements a novel approach to monographic work, cataloging all species of Graphidaceae, the largest family of lichenized fungi in the tropics, with close to 2,000 species. The ATM concept, Assembling a Taxonomic Monograph, brings together a large group of researchers from all continents, with over 50 collaborators. The goal is a series of monographs covering the entire family on a global scale. The project combines traditional methods of morphological taxonomy with the latest advances in phylogenetic research and includes a strong training and outreach component that feeds into the Encyclopedia of Life. By integration of a large group of researchers around the globe, the project works towards unified concepts that will receive broad acceptance among the scientific community and beyond. Modern electronic tools and web dissemination make the data broadly accessible and their incorporation into the Encyclopedia of Life addresses the increased public interest in biodiversity research.

2A-1-P

(2A-1-P2) Submission ID: IAL0096-00002

THE LICHEN FAMILY GRAPHIDACEAE IN THE PHILIPPINES

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Preliminary results are presented towards a monograph of the lichen family Graphidaceae in the Philippines, focusing on subfamilies Fissurinoideae and Graphidoideae. Starting with Vainio's pioneering work in the early 20th century, we revised the type material of taxa described from the Philippines. We also included material collected by Kalb and Sipman and undertook two field trips in 2007 and 2009. In addition, a local student, A. Tabaquero, is working on a Ph.D thesis project supervised by P. Bawingan. We present a list of species thus far identified from the Philippines, using a modern classification emerging from molecular studies. The composition of taxa is compared to those found on the Asian continent (India, Thailand) and in tropical Australia, and preliminary biogeographical conclusions are drawn.

PREDICTING SPECIES RICHNESS IN TROPICAL GRAPHIDACEAE BASED ON PATTERNS OF EVOLUTION AND CHARACTER CORRELATION

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2A-1-P

A numerical approach is presented to quantitatively predict the number of potentially undiscovered species within genera of Graphidaceae. The method uses a character correlation index (CCI) based on observed versus expected frequencies of pairwise character state combinations in known species of a group to estimate the degree of positive and negative evolutionary constraints in the co-occurrence of character states. These are then used to detect 'gaps' in the taxonomic record, i.e. character combinations that have not been detected in known species but are likely to occur in undiscovered ones. The method can be applied to organisms that display a modular combination of characters, that is, they are comparatively poor in characters and species are delimited by more or less free combinations of character states. This phenomenon is particularly common in Fungi, including lichenized taxa, and is here used to predict species richness in the lichen genera *Chroodiscus*, *Clandestinotrema*, *Graphis*, and *Stegobolus*, representing four distinct clades within the family. As one example, the *Graphis scripta* group was studied. A total of 42 species is known in this group and, out of a total of 240 possible character state combinations, a further 48 were found likely to represent undiscovered species, suggesting that the real species number in this group is close to 90 or about twice the number currently known. This agrees well with previous estimates for undiscovered diversity of tropical lichen species. The proposed method gives a taxonomic prediction of how such 'missing' species might look like.

(2A-1-P4) Submission ID: IAL0103-00002

PHENOTYPE-BASED PHYLOGENETIC BINNING - A QUICK TUTORIAL

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Despite the potential shortcomings of phenotype (morphological) data for phylogenetic inference, there are scenarios where only morphological data is available for systematic classification, such as phylogenetic placement of fossils or analysis of large taxonomic groups in which only a subset of species has been sequenced. Because of the frequently incongruent phylogenetic signal between morphological and molecular data, computational methods are required to (1) determine morphological site patterns that are congruent with the molecular tree (which represents the reference tree relative to any topology inferred from morphological data alone) and to (2) downweight incongruent sites, in order to improve accuracy of the phylogenetic classification of taxa for which only morphological data exist. A quick tutorial is presented here regarding a novel method called “phylogenetic binning”. We used molecular site weight calibration as implemented in the software RAxML to weight morphological characters based on their distribution on a maximum likelihood tree inferred from molecular data. We subsequently assigned morphologically defined taxa that lack molecular data to branches of the molecular reference tree, based on the morphology of the taxa included in the reference tree by means of molecular evidence. Bootstrapping was conducted to estimate support for the placement of individual taxa. We demonstrate this methodology using the lichen genera *Graphis* s.lat. and *Stegobolus* s.lat. (Ascomycota: Ostropales: Graphidaceae), which were recently shown to represent two separate, distantly related lineages each. As an example, of the 313 species of *Graphis* s.lat. included, 16 were represented by molecular and morphological data and 297 by morphology only. Using maximum likelihood and maximum parsimony site weight calibration and morphology-based phylogenetic binning, 290 of the 297 species represented by morphological data only were assigned to either *Graphis* s.str. or the segregate genus *Allographa*, with strong support (90–100%). Our results showed that assignment of taxa to clades based on morphological data substantially improved with molecular site weight calibration. Both molecular site weight calibration and branch assignment to the molecular reference tree are implemented in the RAxML 7.2.6 Windows executable and the RAxML 7.2.8 open-source code available at <http://www.exelixis-lab.org/software.html>

2A-1-P

A MEGAPHYLOGENY OF THE LICHEN FAMILY GRAPHIDACEAE

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We present an updated phylogeny of the lichen family Graphidaceae including more than 700 operational taxonomic units (OTUs) and up to three genes per OTU (mtSSU, nuLSU, RPB2). The combined dataset was analyzed under a maximum likelihood approach using RAXML, including recoding of ambiguously aligned regions with the method PICS-Ord and applying a mixed GTR and MULTIGAMMA model in RAXML. The results were used to test the current classification within the family, from subfamily to subgeneric level, and to show how well the molecular data resolve currently accepted species. The tree topology was also used to study the evolution of selected phenotypic characters that are being used in classifications within the family, such as excipulum carbonization, presence of a columella or periphysoids, ascospore types, and secondary chemistry. One of the results is that secondary chemistry is relatively uniform within larger clades and also usually constant within a species. The degree of carbonization of excipulum and columella is also species-specific, to a higher degree than previously thought. Common species such as *Ocellularia papillata* and *O. perforata* were shown to each represent several distinct species, in part not even closely related.

2A-1-P

(2A-1-P6) Submission ID: IAL0178-00003

A NEW CLASSIFICATION FOR THE FAMILY GRAPHIDACEAE (ASCOMYCOTA: LECANOROMYCETES: OSTROPALES)

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A revised classification for the emended family Graphidaceae is proposed, based on recent phylogenetic studies, including the finding that three previously separated families (Asterothyriaceae, Gomphillaceae, Thelotremataceae) are nested within Graphidaceae and in part polyphyletic. The family comprises three major clades which are here delimited as subfamilies Fissurinoideae, Gomphilloideae, and Graphidoideae. The latter is composed of three major clades which are formally delimited as tribes Graphideae, Ocellularieae, and Thelotremateae. In addition, three new genera are described to accommodate the *Ocellularia clandestina* (*Clandestinotrema*) group, the *Ocellularia cruentata* group (*Cruentotrema*) and *Myriotrema pycno-porellum* (*Pycnotrema*). Keys are provided for the species placed in the new genera.

REVISION OF THE FAMILY GRAPHIDACEAE S.L. FOR VENEZUELA, PRELIMINARY RESULTS

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The lichen family Graphidaceae, generally called “graphids” are all crustose lichens, commonly occurring in the tropical regions. The fruiting bodies are mostly linear ascomata with two parallel lines of white or black, sometimes branching, called “lirelliform”. There are generally found on barks and very occasionally on leaves. In Venezuela previous to this study only 6 genera and 22 species were known. For this project collections were done in the 9 main bioregions of Venezuela. Additionally, material from 13 separate field trips were included in the identification. Specimens from 14 herbaria in Venezuela where lichen collections are found are still being analyzed. Up to know 18 genera (*Acanthothecis*, *Anomomorpha*, *Carbacanthographis*, *Diorygma*, *Dyplolabia*, *Fissurina*, *Glyphis*, *Graphis*, *Hemithecium*, *Kalbographa*, *Leiorreuma*, *Pallidogramme*, *Phaeographis*, *Platygramme*, *Platythecium*, *Sarcographa*, *Schistophoron* and *Thallooloma*) and 177 species have been found. Within these 14 are possible new species. 133 species are officially new reports for Venezuela.

2A-1-P

2A - 2: Parmeliaceae: improving our understanding of taxonomy, classification and biogeography

(2A-2-P1) Submission ID: IAL0041-00001

THE PHYLOGENY OF *USNEA* (PARMELIACEAE) REVISITED

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Usnea is a large, cosmopolitan genus, with an estimated 500 species. Numerous species exhibit exceptional morphological plasticity, which complicate the delimitation of species. Previous studies assessing the phylogeny of the genus *Usnea* were based mainly on temperate taxa and showed a lack of support among several of the clades studied. We investigated the phylogenetic relationships of *Usnea* species based on ITS, nuLSU, RPB1 and MCM7 data, from 246 new sequences and 149 sequences downloaded from Genbank. The whole dataset comprises 87 species from across the genus, with the inclusion of several tropical and newly described species. Individual and combined datasets were analyzed using maximum likelihood and a Bayesian inference. ITS being the most complete dataset available, a comparative reconstruction of phylogenies from a strict alignment (all ambiguous sites removed), a relaxed alignment (obtained from the software G-Block), a mixed alignment of DNA and codes for ambiguous sites (calculated with PICS-Ord) and without an a-priori alignment (using BAli-phy) will be presented. The combined analysis of ITS-nuLSU-MCM7-RPB1 significantly improved the support of several clades within the phylogeny. The ITS phylogeny reconstructed with BAli-phy is concordant with the combined analysis, suggesting that ambiguous sites within ITS contain a phylogenetic signal that need to be suitably analysed.

2A-2-P

(2A-2-P2) Submission ID: IAL0041-00002

TAXONOMIC STUDIES OF NEOTROPICAL *USNEA* SPECIES (PARMELIACEAE)

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Usnea is a highly diverse genus, with an estimated 500 species from polar, temperate and tropical regions worldwide. Species are mainly corticolous and are associated with cold and humid habitats, often in correlation with the presence of fog. Numerous species exhibit exceptional morphological plasticity, which complicate the delimitation of species. Modern taxonomic revisions of the genus *Usnea* have been realized in the Northern hemisphere but very little is known about neotropical taxa. A taxonomic study of *Usnea* species, based on morphological, anatomical and chemical characters, was realized in the neotropical Andes and the Galapagos Islands. More than 50 species were delimited so far, which we estimate to represent about half of the diversity of species from this region. Several new species were discovered and the diversity of species integrates elements from North America, tropical Africa, Macaronesia and even Asia. This emphasizes the importance of examining large geographic areas to better understand global distribution patterns in this cosmopolitan genus.

VARIABILITY IN EURASIAN VAGRANT LICHENS OF THE *XANTHOPARMELIA PULLA* GROUP

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With grant support (Visegrad scholarship 61-51000067) we have studied and revised more than 400 specimens from Europe, southern territories of Russia and Central Asia. Our appraisals have shown that vagrant fruticose phenotypes from the *Xanthoparmelia pulla* complex differ from saxicolous foliose specimens of *X. pulla* s.str. by absence of apothecia and some cortex and medullar characters. These phenotypes used to be classified as subspecies of *X. pulla*, but more recently, several species have been recognized among them. Nevertheless, we have observed intermediate individuals between various phenotypes. TLC and HPLC chromatographies were used for analyses of secondary metabolites. Majority of samples, including nomenclatural types of vagrant *Xanthoparmelia pokornyi* (Körb.) O. Blanco, A. Crespo, Elix, D. Hawksw. & Lumbsch, *X. rysssolea rysssolea* (Ach.) O. Blanco, A. Crespo, Elix, D. Hawksw. & Lumbsch and *X. taurica* (Mereschk.) S.Y. Kondr. contains the stenosporic acid as the main compound; this agrees with known data from literature. However, minority of terricolous vagrant specimens have absence of stenosporic acid and possess only the gyrophoric acid and one always present unknown substance. This newly recognized chemotype does not reflect morphological characters, but it is geographically well-determined, being restricted to regions around the northern Caspian Sea. Our ITS nrDNA sequences generated from samples of various phenotypes of *Xanthoparmelia pulla* s. lat. show extremely little variability most of them are identical and others only differ in one or two substitutions. It may be interpreted as (1) the locus is too conservative to recognize phylogenetic species within the group or (2) *X. pulla* s. lat. represents only one polymorphic phylogenetic species. Similar results from six loci provided the recent study on American vagrant *Xanthoparmelia* species by Leavitt et al. (2011).

2A-2-P

(2A-2-P4) Submission ID: IAL0063-00002

GENERA *HYPOTRACHYNA* AND *REMOTOTRACHYNA* IN BOLIVIA

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The foliose lichen genera *Hypotrachyna* and *Remototrachyna* are currently represented in Bolivia by 46 and 5 species respectively. During the present study numerous species have been recorded as new to the country, including the southern most localities of *Hypotrachyna halei* and *H. partita*, the first record of *H. primitiva* for the Southern Hemisphere, and the second world locality of *H. neoscytodes*. A species of *Remototrachyna* is described as new to science. Based on anatomical and morphological characters, three species of *Hypotrachyna* have been transferred to *Remototrachyna*, the results suggesting that the latter is more diverse in the Neotropics than previously supposed; in view of the wider distribution of the genus, reconstruction of its ancestral area (previously thought to be restricted to India) requires re-evaluation. Research supported by NCBI R in Poland under the LIDER Program; project no. 92/L-1/09.

SPECIES OF GENERA *PARMELIA* IN RUSSIAN FAR EAST

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Genera *Parmelia* is presented in the south of Russian Far East by 14 species. Preliminary revision species in herbariums of the Far East (TIG, BGI, SAKH), and also LE (St.-Petersburg) has revealed a number of species which require revision. Morphological variability such species differ: *P. fertilis*, *P. adaugescens*. Last we will well distinguish only at presence apothecia since has large disputes with a thick cover. *P. fertilis* at well developed and plentiful apothecia always has poorly developed spoors. Thus the size and the form of lobes, presence adventives lobules, the size and the form pseudocyphellae vary at different samples. Stables morphological signs differ *P. omphalodes*, *P. praesquarrosa*, *P. saxatilis*. *P. squarrosa* exists in two morphological forms. Some samples have well developed marginal and laminal isidia, pseudocephellae form more less developed network. Other samples differ more extended, linear lobes, with poorly developed laminal pseudocyphellae (they are only for tops of lobes). Lobes plane to slightly concave. The tendency for isidia to be concentrated along the lobe margins. Isidia cylindrical to coralloid and longer, than at the form 1. Samples *P. laevior* also it is presented by 2 forms. There is a classical form linear lobe to 3 mm in width more often. On an island of Shikotan (Sakhalin District) the form with shorter and wide, tiled leaning lobes and thick cortex has been met. Apothecia are plentiful at two forms; the size dispute does not differ. Samples *P. sulcata* in the Far East with squarrosely rhizines and with marginal soredia. Laminal soredia thus are absent or are extremely rare. There are samples at whom the medulla C+ turns yellow, at others C –. *P. marmorata*, *P. isidioclada*, *P. pseudolaevior*, *P. fraudans* – rare lichens on south part of Russian Far East; it is necessary more quantity of samples to analyze these species. Thus the preliminary data has shown that some species of genera *Parmelia* from Russian Far East need in analysis using molecular, morphological and chemical characters.

2A-2-P

(2A-2-P6) Submission ID: IAL0129-00003

THE SPECIES OF *CETRARIA ACULEATA* GROUP (PARMELIACEAE) IN UKRAINE: IDENTIFICATION PROBLEMS

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Over 300 specimens of *Cetraria aculeata* group (*C. aculeata*, *C. muricata*, *C. steppae*) mainly from Ukraine and also from Poland, Hungary, Czech Republic, Russia, Azerbaijan, Kyrgyzstan and Turkey were studied for morphology, anatomy, chemistry, substrate specificity and geographic distribution. Previously known high level of phenotypic plasticity of these species (Kärnefelt, 1986) is confirmed upon the analyses of the specimens. Colored spot and microcrystal tests were used for norstictic acid detection in *Cetraria* specimens, but in this case they show inapplicability due to interfering components, while TLC and HPLC seem to be effective. HPLC demonstrates high variance of norstictic acid content in the studied thalli: from trace, minor, medium to major quantities which are not determined ecologically. The specimens collected from the same populations growing in the southern Russia and Ukraine regions and also Hungary may contain different amount of norstictic acid, even traces (detected by TLC as absence). Therefore distinguishing of *C. steppae* and *C. aculeata* species based on the presence/absence of norstictic acid (Kärnefelt, 1986) is considered as foundless. Taxonomic status of these southern populations (usually identified as *C. steppae*) should be investigated using specific molecular markers. Possible evolutionary and adaptive role of norstictic acid is of open question. Correct identification of *C. steppae* and *C. aculeata* species is also significant since *C. steppae* is included in the Red Data Book of Ukraine as vulnerable species.

TAXONOMIC REVISION OF THE USNIC ACID CONTAINING XANTHOPARMELIA SPECIES IN HUNGARY MORPHOLOGICAL, CHEMICAL AND MOLECULAR INVESTIGATIONS

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Xanthoparmelia is one of the major genera of foliose lichens, and its research has long tradition in Hungary starting in 1925 with Vilmos Kőfaragó-Gyelnik's taxonomic work on *Parmelia*. Following Klára Verseggy's Hungarian lichen flora (1994) and Mason E. Hale's world-monograph on *Xanthoparmelia* (1990), a modern taxonomic revision was carried out. This study consists of detailed morphological, chemical, and molecular analyses of all (appr. 500) herbarium specimens (including Gyelnik's type materials) belonging to *Parmelia* s.l. species producing usnic acid, thus having yellowish-green upper surface (i.e., *P. conspersa*, *P. hypoclستا*, *P. protomatrae*, *P. pulvinaris*, *P. subdiffluens*, *P. taractica*, and *P. tinctina*), in the main Hungarian lichen herbaria (BP, EGR, JPU, SAMU, VBI). During this revision the occurrence of seven *Xanthoparmelia* species was confirmed by morphological and chemical analyses so far, namely: *X. angustiphylla*, *X. conspersa*, *X. protomatrae*, *X. pulvinaris*, *X. stenophylla*, *X. subdiffluens*, and *X. tinctina*. Four of them (*X. angustiphylla*, *X. protomatrae*, *X. pulvinaris*, and *X. subdiffluens*) were described from Hungary by Gyelnik in the 1900s, and the main populations of *X. pulvinaris* and *X. subdiffluens* are found in Hungary. The most important morphological characteristics, e.g., the types of lobes, isidia, rhizinae, pycnidia, and the color of the lower surface were considered during the revision. Since the secondary lichen compounds are taxonomically important in this group, HPTLC and LC MS were applied to determine these substances. The molecular phylogeny of these species is not explored yet, therefore the analysis of the sequences of three molecular markers (nuclear ITS and LSU rDNA, as well as mitochondrial SSU rDNA) are being processed. Maps of the Hungarian distribution for all species were prepared. *Xanthoparmelia conspersa* and *X. stenophylla* seem to be the most widely distributed and the most frequent species. *X. protomatrae* is located mostly in the Northern Hungarian Mountain Range, and seems to be missing from most of the Transdanubian habitats. *X. subdiffluens* occurs only in a very limited area in sandy habitats of the Danube-Tisza Interfluve. The current research has been supported by the Hungarian Scientific Research Fund (OTKA K81232).

2A-2-P

PARMELIACEAE IN RUSSIA: DIVERSITY AND BIOGEOGRAPHY

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2A-2-P A total 305 species belonging to 54 genera (except for lichenicolous fungi) of the family Parmeliaceae are recorded in Russia. The epiphytic nemoral-boreal and mountain-oceanic lichens are dominant. About 30% of the species are widely distributed in the boreal mixed deciduous and light- and coniferous forests from the Baltic to the Pacific region. Whereas other more than 30% of the species have restricted distribution in the certain regions. The lowest species and genera diversity are character for the Russian Arctic (about 100 sp./30 g. of saxicolous and terricolous taxa mainly) and steppe zone of the European Russia (about 50 sp./20 g. of corticolous and terricolous taxa mainly). The highest diversity of Parmeliaceae (including 210, 177 and 153 species respectively) and also specificity (including 58, 14 and 15 species respectively, which are unknown in other regions) are typical for three regions of Russia - Far East, Southern Siberia and Caucasus. In general, the highest lichen diversity in Russia is character for regions with a suboceanic or monsoonal climate and/or in mountain regions. In mountain areas the species diversity is increases from the north to the south, whereas in flat areas there is an opposite patterns of relationship. The largest Parmeliaceae genera in Russia are *Usnea* (34 species), *Hypogymnia* (25 sp.), *Bryoria* (20 sp.), *Parmelia* (19 sp.). There are twelve genera which contain only one species: *Cetreliaopsis asahinae*, *Cornicularia normoerica*, *Everniastrum cirrhatum*, *Imshaugia aleurites*, *Letharia vulpina*, *Lethariella togashii*, *Masonhalea richardsonii*, *Oropogon asiaticus*, *Parmelinopsis afrorevoluta*, *Pseudevernia furfuracea*, *Remototrachyna koyaensis*, *Usnocetraria oakesiana*. The most widely distributed species are cosmopolites *Hypogymnia physodes*, *Parmelia sulcata*, *Vulpicida pinastri*, *Evernia mesomorpha*, *Melanohalea olivacea*, *Parmeliopsis ambigua*, *Cetraria islandica*, etc. Only two species considering as endemics to Russia: "*Catraria*" *annae* (taxonomic position is unclear) is distributed in Southern Siberia (Buryatia Republic, Zabaikalskiy krai); *Cetraria rassadiniae* occurs in the Eastern and Southern Siberia.

(2A-2-P9) Submission ID: IAL0177-00002

DIVERSITY WITHIN THE LICHENIZED GENUS OROPOGON (PARMELIACEAE)

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Molecular sequence data has revolutionized our ability to assess traditional species concepts in lichen-forming fungi. Within Parmeliaceae studies have repeatedly shown our current interpretation of morphological and chemical characters is often inadequate to accurately characterize diversity. Within this family the genus *Oropogon* has received relatively little attention since it was first proposed. However, a detailed morphological study, supplemented by chemical data from thin-layer chromatography, resulted in a dramatic, and somewhat controversial, increase in number of recognized species in the New World. Our study focuses on eight Central American *Oropogon* species with the aim to assess species diversity, the taxonomic value of putatively diagnostic morphological and chemical characters, and evolutionary relationships within this group. We reconstruct the phylogeny of this group and estimate divergence dates using molecular sequence data. Our analyses support the high degree of species-level diversity within *Oropogon*, and in contrast to many studies within Parmeliaceae, molecular data largely corroborate morphologically/chemically circumscribed taxa. Furthermore, estimated divergence dates suggest many lineages are relatively old. We reconstruct the historical demography of each species and discuss potential factors driving diversification within this group.

**PHOTOBIONT ACQUISITION, SPECIFICITY AND COEVOLUTION
IN THE LICHEN GENUS *BRYORIA***

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Lichen photobionts are assumed to coevolve with lichen mycobionts because of their close relationship. Photobionts have an essential role in lichen metabolism as providers of carbohydrates to the mycobiont. In the lichen genus *Bryoria*, the most common known photobionts belong to the coccoid green algal genus *Trebouxia*. In this study the acquisition, specificity and possible coevolution between *Bryoria* spp. and their photobionts were examined by constructing mycobiont and algal phylogenies with parsimony methods using three mycobiont loci (nuITS rDNA, GAPDH and mtSSU) and one algal locus (nuITS rDNA). According to the preliminary results the mycobionts of *Bryoria smithii*, *B. bicolor*, *B. tenuis* and *B. nadvornikiana* seem to be selective towards their photobionts implying a possible coevolutionary event in the past. All the other species included in the analyses seemed to be less selective in their photobiont acquisition. However, some geographical correlation was observed in section *Implexae* (i.e. in the group including *B. capillaris*, *B. fuscescens*, *B. implexa* s. lato, *B. lanestrís* and *B. subcana*) non-sorediate American species being more restricted in their choice of algal partners.

2A-2-P

TANGLES IN HORSEHAIR - PHYLOGENETIC STUDIES ON PENDENT *BRYORIA*

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Bryoria Brodo & D. Hawksw. (horsehair lichens) is a widespread lichen genus occurring mainly on conifers in boreal forests. The species are recognized by usually dichotomously branched thallus with slender, hairlike, gray to blackish branches, sometimes bearing soralia and pseudocyphellae. *Bryoria* is regarded as one of the taxonomically most difficult macrolichen genera due to infraspecific morphological variation, rarity of sexual fruiting structures limiting the amount of diagnostic characters, and the occurrence of putative, morphologically intermediate specimens. Especially pendent species are highly variable in morphology, giving secondary chemistry an essential role in species recognition. According to our recent phylogenetic studies on *Bryoria*, the current taxonomic status of many pendent taxa, notably in the section *Implexae* (sensu Myllys et al.), is questionable. The aim of our study is to examine with more extensive data sampling 1) the monophyly of the five taxa placed in section *Implexae*, i.e., *Bryoria capillaris* (Ach.) Brodo & D. Hawksw., *B. fuscescens* (Gyeln.) Brodo & D. Hawksw., *B. implexa* (Hoffm.) Brodo & D. Hawksw. (with five chemotypes sensu Holien), *B. lanestrís* (Ach.) Brodo & D. Hawksw. and *B. subcana* (Nyl. ex Stizenb.) Brodo & D. Hawksw., and 2) if specimens from different geographical areas are genetically isolated. We reconstruct a phylogeny for the group using four DNA regions in addition to morphological and chemical characters. Our results indicate that the taxonomic status of some species should be re-evaluated. For instance North American and European *B. capillaris* represent taxonomically distinct entities. Furthermore, some of the taxa traditionally regarded as separate species, such as *B. chalybeiformis* and *B. fuscescens*, fall into a variation range of a single species. In addition, a new undescribed North American species will be presented.

**PARMOTREMA TINCTORUM AND P. PSEUDOTINCTORUM
(PARMELIACEAE, ASCOMYCOTA) TWO SUPPORTED SPECIES**

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Parmotrema tinctorum (Despr. ex Nyl.) Hale has a tropical and sub-tropical distribution. Morphological and phylogenetic relationships have been studied in order to clarify whether the specimens from Asia could be a different species than specimens from Canarias Island. A total of 104 New sequences have been produced of nuclear ITS rDNA region and mitochondrial SSU rDNA from fifty-two specimens of *Parmotrema tinctorum* (Despr. ex Nyl.) Hale. We have included also a several related species of the genus as *P. endosulphureum* (Hillmann) Hale, *P. andinum* (Müll. Arg.) Hale, *P. internexum* (Nyl.) Hale ex De Priest & B.W. Hale and *P. nilgherrense* (Nyl.) Hale. The samples were collected from 9 worldwide locations: Canary Is., Japan, India, Nepal, Kenya, Mozambique, United States, Brazil and Costa Rica. Phylogenetic inference was performed using Maximum Parsimony analysis and Bayesian (MC) 3 tree sampling. Morphological features such as isidia, lobe morphology and upper surface maculation were studied under optical microscopy. Our results show two main conclusions: (I) All the samples from Canary Is., with some specimens from India, formed an independent well-supported monophyletic group. In contrast, some samples from India and all samples collected in Africans regions and in Japan formed another monophyletic clade with strong statistical support. (II) Two types of isidia are observed in the morphological search: a) Isidia thin cylindrical type that is mainly found on corticolous specimens. b) Isidia thick coarse type that is present on the specimens growing saxicolous. Samples bearing each type of isidia nested in two independent lineages. The samples with coarse isidia type are similar to those recognised by Des Abbayes as *Parmelia pseudotinctorum* that was considered synonym. We resurrect the name for this lineage. *Parmotrema pseudotinctorum* is distributed so far in Canary Is., Ethiopia, Guinea, Tanzania, Ivory Coast and India. The other lineage was identified as *Parmotrema tinctorum* distinctive in having thin cylindrical isidia and mainly growing corticolous, is widely distributed in tropical regions.

2A-2-P

A PRELIMINARY TAXONOMIC STUDY OF *HYPOGYMNI* (PARMELIACEAE) IN CHINA

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The genus *Hypogymnia* (Lecanorales, Parmeliaceae) mainly distributes in the Northern Hemisphere, including about 110 species worldwide according to the latest statistics from Index Fungorum by the authors. In China, 43 species have been published up to now, besides, four new species have been found and will be published soon. The number of Chinese species of *Hypogymnia* accounts for about 43% of the total. The usnic acid containing species pair *H. hypotrypa* (Nyl.) Rassad. and *H. flavida* McCune & Obermayer are endemic to China-Himalaya, the former with soredia and the latter with apothecia commonly, to validate whether it really includes two separate species, we studied the species pair based on morphology, anatomy, chemistry, biogeography, and molecular biology. The results showed that *H. hypotrypa* and *H. flavida* should be conspecific, and *H. flavida* should be treated as the synonym of *H. hypotrypa*. Based on the nrDNA ITS sequences analysis, the genus *Hypogymnia* is confirmed as a separate monophyletic clade, and *Cavernularia* should be the synonym of *Hypogymnia*. Combining phenotype and genotype analysis of *Hypogymnia* in China, we think there are three additional important characters to delimit species: pruina, dorsal perforation, and conidia. Our study also showed that the lichens of *Hypogymnia* are mainly distributed in Southwest China, constituting over 80% of the total number of the species in China. The distribution of *Hypogymnia* shows that the Southwest region as the most abundant biology diversity region is also the diversity center of *Hypogymnia*. A preliminary geographical analysis of *Hypogymnia* in China showed that they belong to six elements: Cosmopolitan element, Circumpolar element, East Asian-North American disjunctive element, East Asian-Oceanian disjunctive element, East Asian element and species endemic to China.

2A-2-P

DIVERSITY AND DISTRIBUTION OF LICHEN FAMILY PARMELIACEAE IN INDIA

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According to the recent classification of phylum Ascomycota, Parmeliaceae emerges as the largest family with about 2,500 species in the world. Parmeliaceae is distinctive in having cupulate exciple, *Lecanora*-type ascus, mostly simple, hyaline ascospores, and mainly foliose and fruticose habitat. In India Graphidaceae is the largest family with 428 species under 35 genera, while Parmeliaceae turns out to be the second largest, but most diverse family represented by 345 species distributed in 45 genera. Within the family Parmeliaceae, Parmelioid lichens are most dominant with 203 species followed by Usneoid and Cetrarioid with 74 and 43 species respectively. Among the different genera of the family *Usnea*, *Parmotrema* and *Hypotrachyna* are most prominent with 60, 51 and 38 species. The family Parmeliaceae has an extensive distribution in India; however it is heavily concentrated in north-east India with about 63% species and it is followed by western Himalayas and Western Ghats which have about 50% of the species growing in each region. In the north-east India-Sikkim (165 spp.), in western Himalayas-Uttarakhand (145 spp.) and in Western Ghats-Tamil Nadu (137 spp.) have maximum diversity. The members of Parmeliaceae grow on all substrates, however in India maximum species prefer only bark (178 spp.) while about 90 species occur either on bark or rock. Exclusive muscicolous Parmeliaceae members are absent in India, while *Allocetraria ambigua*, *Arctoparmelia subcentrifuga*, and *Hypotrachyna crenata* grow on moss as well as on bark, soil and rock. About 11% Parmeliaceae taxa (37 spp.) are endemic to India and large numbers of them (16 spp.) are found exclusively in Western Ghats region. The *Parmotrema praesorediosum*, *P. sancti-angelii*, and *P. tinctorum* found to be most common and widespread species in India. The other moderately prevalent species include *Bulbothrix isidiza*, *Canoparmelia aptata*, *C. texana*, *Everniastrium nepalense*, *Flavoparmelia caperata*, *Hypotrachyna infirma*, *Myelochroa aurulenta*, *Parmelinella wallichiana*, *Parmotrema andinum*, *P. cristiferum*, *P. hababianum*, *P. mesotropum*, *P. rampoddense*, *P. reticulatum*, *P. sacatilobum*, and *X. congensis*.

2A-2-P

(2A-2-P15) Submission ID: IAL0263-00005

HIDDEN DIVERSITY IN NORTH AMERICAN *PARMELIA*: A WORLD WAITING TO BE EXPLORED

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Parmelia s. str. comprises around 60 species, of which only 17% have been found in North America. Additional American *Parmelia* species were recently described which were hidden under widely distributed species names e. g. *Parmelia saxatilis* and *P. sulcata*. *P. mayi*, is described from the northern Appalachian mountain range (Molina et al., in press) and *P. barrenoae*, initially reported from Iberian Peninsula (Divakar et al. 2005) has recently been found in the western North America (Hodkinson et al., 2010). However, significant geographic areas remain to be explored on this continent for *Parmelia* biodiversity. In this study, we collected *Parmelia* from British Columbia (Canada) and Alaska (USA) in order to evaluate cryptic diversity and also assess the morphological variability, to determine if it could be explained as phenotypic plasticity or as segregation of new species according to operational phylogenetic criteria (Queiroz, 2007). The detailed study of the specimens allowed us to describe five different morphotypes, of which at least one should be described as a new species.

NEW APPROACH ON THE *PUNCTELIA HYPOLEUCITES* (PARMELIACEAE) COMPLEX

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The lichen genus *Punctelia* (Parmeliaceae, Lecanorales) has been object of recent studies. From the 22 species known at the time of its creation by Krog, now more than 40 species are recognized world-wide. The main features used to take species apart are presence or absent of propagules, medullar compounds, lower surface color and conidia type and size. However, some species complexes still remain. According to the pertinent literature, *Punctelia hypoleucites* (Nyl.) Krog and *P. graminicola* (B. de Lesd.) Egan. have brown lower surface, lecanoric acid as medullar compound, no propagules production and are supposed different each other by their conidia form: unciform in *P. graminicola* and filiform in *P. hypoleucites*. But the revision of the types of *P. graminicola* (ASU!), its synonym: *P. semansiana* (W. Culb. & C. Culb.) Krog (DUKE!, LSU!), and *P. hypoleucites* (H-NYL!) and its synonym *Parmelia azulensis* B. de Lesd. (US!) revealed that the lectotype of *P. hypoleucites* has unciform conidia instead of filiform as reported before, conspicuous pseudocyphellae and a lacinate thallus, while *P. graminicola* actually has unciform conidia, inconspicuous pseudocyphellae and lobate thallus. The holotype and isotypes of *P. semansiana*, and also those additional specimens studied, share characteristics with *P. hypoleucites*. As a conclusion, *P. semansiana*, before considered synonym of *P. graminicola*, proved to be a synonym of *P. hypoleucites*. For those specimens with filiform conidia which previously were treated as *P. hypoleucites*, it is more suitable to use the name *Parmelia azulensis*, which will be soon formally combined in *Punctelia*. These conclusions were also confirmed by the study of additional specimens from ASU, DUKE, F, LSU, O, SP and UCS Acknowledgements: Fundação de Amparo a Pesquisa do Estado de São Paulo – FAPESP and International Association for Plant Taxonomy – IAPT, for research support.

2A-2-P

TYPE STUDIES ON SOREDIATE *PARMOTREMA* (ASCOMYCOTA, PARMELIACEAE) WITH SALAZINIC ACID

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Parmotrema A. Massal. 1860 is one of the most diverse genus in Parmeliaceae, with about 350 species, being specially abundant in South America and other tropical areas of the world. Nevertheless, the species concepts are still unclear, and several supposed “widely distributed” species include long lists of synonyms, usually without sound justifications for the choices. Important features like the ontogeny of reproductive structures, maculation patterns, rhizinal types and conidial data are frequently overlooked. Inside *Parmotrema* there is a group of taxa that share the presence of medullar salazinic acid, and this group was selected to be revised through the types of both accepted names and synonyms. Here we discuss the sorediate taxa (27 species). The specimens were fully described and chemical substances were identified with spot tests, TLC and HPLC. Several synonyms were recognized as good species, the ontogeny of the soredia being a crucial characteristic for differentiate close taxa, as well as the conidial type, development of cilia and dimorphic rhizinae, and the maculation pattern. *Parmotrema reticulatum* (Ach.) Hale lose 10 of its 17 accepted synonyms, while to *Parmotrema subsumptum* (Nyl.) Hale the species concept is clarified. New structures were recognized as having taxonomical importance: the arbusculae (= “coralloid isidia”), present in *P. coralliforme* (Hale) Hale and *P. ramusculum* (Hale) Hale, and the botryose structures produced in *P. spinibarbe* (Kurok.) Hale. Acknowledgments: Fundacao de Amparo a Pesquisa do Estado de Sao Paulo – FAPESP and British Lichen Society.

2B: Forest lichens: their ecology and distribution

(2B-P1) Submission ID: IAL0015-00002

STUDIES ON THE LICHENIZED FUNGI OF THE FIJIAN ARCHIPELAGO

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The Fijian archipelago consists of over 300 oceanic islands and is located in the tropical south-west Pacific. Its tropical maritime climate is influenced by the south-east trade winds and together with the rugged topography and mountain ranges in the main islands that rise up to 1,300m provide suitable habitats for lichens. Habitats on the islands include cloud forests, upland tropical rainforest, lowland tropical rainforest, dry forests, mangrove forests and coastal forests. The lichen flora of Fiji is currently poorly known. Since the first paper by Krempelhuber in 1873 only a few studies have specifically focused on Fijian lichens. A recently updated checklist of Fijian lichens includes 159 species (Elix & McCarthy 2008). Recently we have started a joint project on the lichen, bryophyte and fern flora of the Fijian archipelago. After a first field trip in 2008 that resulted in 66 new records for Fiji and four new species, an additional field trip in 2011 further increased our understanding in the lichen flora of this archipelago and its floristic affinities. In this presentation we will summarize our results and compare the Fijian lichen flora to that of other Pacific islands.

2B-P

(2B-P2) Submission ID: IAL0056-00001

A PRELIMINARY INVENTORY OF THE LICHEN FLORA OF MT. KITANGLAD AND MT. MUSUAN, BUKIDNON, PHILIPPINES

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An inventory of the lichen flora was carried out in two mountains namely: Mt. Kitanglad and Musuan, Bukidnon, Philippines. Specifically, the study aimed to describe the morphology characters of the lichens; compare the floristic composition of lichen flora between study sites; and assess the conservation status of the lichen flora. Field collections of the lichens were made through alpha taxonomic methods in different vegetation types. The Biodiversity Professional was used as the statistical tool to determine the diversity status of the lichens. Taxonomic treatments include the growth forms, color, size and presence of fruiting bodies were used to identify and classify the lichens. Results of the study showed that the mountains exhibited a unique distribution pattern of the lichen species. A total of 114 species belonging to 25 genera and 12 families were observed in Mt. Kitanglad. While 39 species belonging to 16 genera and 13 families in Mt. Musuan. Both biogeographical sites revealed uniqueness on the morphology characters of the species under study. In Mt. Kitanglad, the family Lobariaceae has the most numbered species-rich, followed by Physciaceae, Parmeliaceae, Cladoniaceae, Peltigeraceae, Lecanoraceae, Usneaceae, Pertusariaceae, Thelotremataceae, Megalosporaceae, Ramalinaceae and Graphidaceae. While the family of Graphidaceae showed the most numbered species-rich, followed by Parmeliaceae, Physciaceae, Lecanoraceae, Pyrenalaceae, Lobariaceae and Thelotremataceae in Mt. Musuan. *Lobaria* sp. and *Usnea* sp. were noted as sensitive species and are extremely thriving in cold and high elevations in Mt. Kitanglad. Moreover, the study revealed floristic differences in their classificatory systems, diversity status, species composition and their ecology distribution. The overall observations on the lichen status show that the variations in morphology characters are attributed to their specific and extreme habitats.

**DIVERSITY OF LICHENS ALONG THE ELEVATION GRADIENT
AT KHAO YAI NATIONAL PARK, THAILAND**

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Environmental factors on mountain slopes influence the diversity and distribution of lichens. The aim of this study was to observe the influences of environment along a mountain slope, spanning between 100 and 1,200 m, on the diversity and distribution of lichens at Khao Yai National Park. The investigation was carried out by placing 50x10 cm quadrates on all trees with bole diameter at breast height (DBH) 4.5 cm at 130 cm above the ground in 4x4 m plots. The elevation, bark pH, the diversity and dominant of host plants, soil pH, soil moisture, organic and inorganic matters in the soil were measured at every 100 m in elevation. Observed were 141 lichen thalli from 75 species, of which crustose thalli were overwhelmingly dominant. Since most of these were sterile, the genera and species could not be ascertained. However, taxa were assigned by reference to the prominent characteristics of these lichens. The five highest important value index (IVI) were noted from *Thelotrema colobicum*, *Ocellularia* sp.2, Sterile soredia 6, Sterile non-propagule 4 and Sterile soredia 1, accounted 15.04, 12.13, 11.81, 10.80 and 10.25, respectively. Shannon's diversity index (SDI) demonstrated that the highest and subsequently lower distribution occurred at elevations 700, 1,000 and 1,200 m at the respective values of 3.05, 2.99 and 2.48. The ordination of axis 1 and axis 2 exhibited eigenvalues at 0.952 and 0.844 with a variation of 12.6 percent in the first axis. Lichen diversity was influenced by elevation, canopy cover, and the species richness of the host trees.

2B-P

SUCCESSION OF LICHENS ON SUBSTRATES IN TROPICAL FORESTS IN THAILAND

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It is well recognized lichens are pioneer species on both natural and artificial substrates. The objective of this study was to observe the establishment and growth of lichens on artificial substrates in various types of tropical forest. The study was conducted by installing four types of substrate shading net, transparent sheets, glass bottles and terra-cotta in four different types of tropical forest at Khao Yai National Park. Lichens established onto these substrates were subsequently photographed and identified during nine years of observation. After three years, eight taxa of the pioneer lichens were recognized. The thalli and reproductive structures of these lichens were virtually invisible. After five years, sixteen taxa were recognized, of which few of them had apparent reproductive structures. After nine years, many of the lichens produced fruiting bodies allowing for the identification of the genera and the species. Forty-two taxa from twenty genera were identified, including the foliicolous taxa of *Porina* spp., *Mazosia* spp., *Byssoloma* spp. and *Coenogonium* spp. The only abundant foliose thalli were *Bulbothrix isidiza*. The number of taxa was highest and sequentially lower on shading net, glass bottles, transparent sheets and terra-cotta at 20, 16, 13 and 7 respectively. The lower montane forest supported the highest number of taxa, and subsequently lower numbers were observed under tropical rain forest, mixed-deciduous forest and secondary forest at 24, 11, 11 and 8 taxa, respectively. This investigation is on-going in order to elucidate long-term influence of environmental factors on the succession of lichen in the tropical ecosystems.

BIODIVERSITY OF LICHENS IN EASTERN GHATS OF SOUTHERN INDIA

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The Eastern Ghats of southern India constitute an important biogeographic area of about 75,000 square kilometers through a chain of fragmented and distinct hill ranges. The forests in Eastern Ghats are more affected by human influence, since they experience heavy pressure on all sides, compared to Western Ghats and Himalayas. Present study deals with the distribution of lichens and environmental factors which are responsible for the growth of lichens in Yercaud hills of Eastern Ghats. Lichen distribution was noticed at 20-35 feet away from the roadsides and these were very much less at the edges of the Yercaud hills and even absent in urban areas. Yercaud hills contain (i) evergreen forest, (ii) semi evergreen forest, (iii) riparian forest and (iv) dry mixed deciduous forests at different locations. The results showed that lichens of both fruticose and crustose is very widespread and density is also high at moderate attitude areas. On the other hand, foliose species were found to be abundant in the higher altitude areas. The prevalence of many species was gradually increased towards the center of the Yercaud hills due to increased altitude level with low temperature and high relative humidity (RH). A total of 28 species belonging to 4 genera were recorded. Rainfall and maximum RH factors are positively correlated to the number of lichens whereas low temperature and maximum sunshine hours are negatively correlated. Environmental factors were correlated with lichen growth and development. Further attempts were made to correlate the existence of lichens with tree bark samples with reference to pH. The results revealed that lichen could survive well in the pH ranging from 4.4 to 5.8. pH is also one of the essential factors responsible for existence of lichens on substrata for attachment of mycobionts. Even the toxic gases were tolerated efficiently by lichen communities at pH range of 4.0 to 5.5. Existence of lichens on non-living substrata showed the most colonies observed on brick wall (36.7) followed by rock (31.3) and least in soil (13.0).

2B-P

(2B-P6)

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ASSOCIATION OF ENDOLICHENIC FUNGI WITH SOME MACROLICHENS IN CENTRAL WESTERN GHATS OF KARNATAKA, INDIA

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There are several studies on endophytic microorganisms of higher plants. Very few studies were carried out on the isolation of endolichenic fungi from the lichen thallus. This study examined some lichen species for isolation of endolichenic fungi from the internal parts to know association of endolichenic fungi within thalli of macrolichens which are commonly occur in central Western Ghats, Karnataka, India. A total of eleven lichen specimens were collected from trees of different habitats. Apparently healthy looking lichen thalli were collected in paper bags, were brought to the laboratory and isolated and identified with standard protocols. A total of 30 different endolichenic fungal species were recovered from 11 species of lichens. Twenty four species of fungi have produced fructifications in culture and have been identified to genus or species level and rest were sterile form. Higher colonization rate (59.5%-100%) of endolichenic fungi was observed among eleven lichen species in this study. Higher colonization rate was observed in *Parmotrema tinctorum* and *Ramalina pacifica* and moderate in *Cladonia fruticulosa*. Among 24 detected species most of them were belonging to Ascomycotina and all other isolates categorized as *Mycelia sterilia*. The present study revealed that the endolichenic fungi like *Chaetomium*, *Cladosporium*, *Colletotrichum*, *Fusarium*, *Phoma* and *Xylaria* spp. were frequently isolated from lichen thalli. The endolichenic fungi assist in lichen formation and growth and act as antagonistically against insect herbivores. Some endolichenic fungi can also produce bioactive substance inside lichen thalli.

THE LICHENS OF MOUNTAIN-TAIGA DARK CONIFEROUS FORESTS OF THE SOUTHERN URAL AND THE SOUTHERN SIBERIA (RUSSIA)

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Mountain-taiga dark coniferous forests are one of the most endangered ecosystems in Russia. These forests host extraordinarily rich lichen flora. The wind exposure of slopes of respective ranges of the Southern Ural and Southern Siberia may influence a specific microclimate, e.g. windward slopes have higher air humidity, supporting presence of sensitive lichens in the mountain dark coniferous forests. In addition, the lichen diversity is closely related to tree composition and age of dark coniferous forests-*Abies sibirica*, *Pinus sibirica* and *Picea obovata*. These shade-providing trees create optimal conditions for lichens, with a wide variety of microhabitats and substrates. The more xeric larch mountain forests in Southern Siberia have about half the lichen species number of the dark coniferous forests. For example, about 380 lichen species are confined to dark coniferous forests (with *Abies sibirica* and *Pinus sibirica*) of Hamar-Daban mountain range (Southern Baikal). *Abies sibirica* in Southern Baikal area has the greatest epiphytic lichen species richness (169 species from 60 genera) of any tree species. These forests provide favorable situation for a significant number of unique 'oceanic' lichen species in the continental regions of Northern Eurasia. Humid coniferous forests in Western and Eastern Sayan, Khamar-Daban (Southern Siberia) are important refuges for old-growth forest indicator macrolichens like *Sticta fuliginosa*, *S. limbata*, *S. wrightii*, *Usnea longissima* and other. *Menegazzia terebrata* and *Pyxine soredata* have been recorded for the first time in the Southern Ural Mts (Malyi Uvan) from fir-spruce forest.

2B-P

THE LICHENS FROM FAMILIES GYALECTACEAE STIZENB. AND COENOGONIACEAE (FR.) STIZENB. IN RUSSIA

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The lichen families Gyalectaceae and Coenogoniaceae are widespread in the world. They prefer humid habitats and old-growth forests and occur on different substrates (bark, rock, soil etc.). At present twenty two species are known from Russia. The most of them belong to family Gyalectaceae – twenty species. Gyalectaceae have a wide distribution in Russia: from arctic regions on the north to temperate zone and subtropics on the south. The most numerous is genus *Gyalecta*. It is represented in the country by fourteen species: *G. derivata* (Nyl.) H. Olivier, *G. flotovii* Körb., *G. foveolaris* (Ach.) Schaer., *G. friesii* Flot ex Körb., *G. geoica* (Wahlenb. ex Ach.) Ach., *G. jenensis* (Batsch) Zahlbr., *G. kukriensis* (Räsänen) Räsänen, *G. liguriensis* (Vězda) Vězda, *G. nigricans* Vain., *G. peziza* (Mont.) Anzi, *G. subclausa* Anzi, *G. titovii* Gagarina, *G. truncigena* (Ach.) Hepp, *G. ulmi* (Sw.) Zahlbr. in Engl. et Prantl. Two more genera from Gyalectaceae are known from Russia: *Belonia* Körb. – *B. mediterranea* Nav.-Ros. & Llimona, *B. russula* Körb. ex Nyl., *B. herculina* (Rehm in Lojka) Keissl. in Rabenh., and *Pachyphiale* Lönnr. – *P. carneola* (Ach.) Arnold, *P. fagicola* (Hepp in Arnold) Zwackh, *P. ophiospora* Lettau ex Vězda. Coenogoniaceae species occur in the world mainly in tropical areas. In Russia only two species from the family have been found. They are *Coenogonium pineti* (Schrad. ex Ach.) Lücking & Lumbsch in Lücking et al. and *C. luteum* (Dicks.) Kalb & Lücking.

EPIXILIC LICHEN SUCCESSION ON DEADFALL IN MOUNTAIN FORESTS

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Epixilic lichen succession was studied in Buryatia Republic (Russia) in conifer forests with *Abies sibirica* Ledeb., *Pinus sibirica* Du Tour, *Larix gmelinii* Rupr. and *Pinus sylvestris* L. on Khamar-Daban and Ikatsky ranges on 700 – 2,300 m above sea level. Deadwood was separated by origin: cutting and natural residue. 55 lichens species were listed for deadwood on plots. Author found four lichen succession stages corresponding with wood decaying stages. I stage of wood decay includes epiphytic (from live trees) fruticose lichens sinusia. *Usnea fragileszens*, *Usnea subfloridana*, *Bryoria furcellata*, *Tuckermanopsis ciliaris*, *Hypogymnia physodes*, *Evernia mesomorpha*, *Evernia esorediosa* occurred on bark. When xylotrophic fungi of Aphilophorales order appear, I stage fast proceeds to II-III stages of decay. Lichens composition has low change with adding such species as: *Mycoblastus affinis*, *Vulpicida pinastri*, *Imshaugia aleurites*, *Parmeliopsis ambigua*, *Japewia torniensis*. II stage of decay – bark peeled off, wood partly loses hardness, branches stay (Klimchenko, 2005) attend with epiphytic lichens elimination, primary thalli of genus *Cladonia* species and an admixture of *Lecanora saligna*, *L. symmicta*, *Trapeliopsis granulosa* appearing. *Calicium* species thalli are highly abundant on dry wood (*C. denigratum*, *C. trabinellum*, *C. glaucellum*, *C. lenticulare*). Not all species are in contact; they do not form sinusia, rather are similar to new succession. Crustose hygromesophylic species *Micarea melaena*, *M. prasina*, *Bacidia subincompta*, and other, typical for moist decaying wood soon replacing competitive fruticose lichens with primary thalloma, such as *Cladonia digitata*, *C. macilenta*, *C. botrytes*, *C. deformis* (III stage). At this point dense epixilic species society forming, sinusia proper. In next stage species composition richness increasing as wood decomposition finishes. IV stage wood decaying–wood lost structure, gone to dust. In this time on deadwood surface ground layer accumulate, deadwood overgrown with mosses and fruticose lichens species, typical for soil appearing: *Cladonia amaurocraea*, *C. arbuscula*, *C. rangiferina*, *C. stellaris*. Thus, epixylic lichens held to overall succession pattern with full species replacement and ended with wood decaying. Deadwood, although relating their origin to live trees, by substrate characters differ from the live phorophyte. The investigation was supported by Russian Fund of Basic Research (grant 10-04-00337-a).

2B-P

**A FIRST SURVEY OF LICHEN DIVERSITY IN THE NATIONAL PARK “MESHCHERSKY”
(RYAZAN’REGION,CENTRAL,RUSSIA).**

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The National Park “Meshchersky” (further NP), established in 1992 occupies over 100,000 ha in two districts of Ryazan region. The NP territory belongs to the south-taiga forest subzone and is flat lowland with sandy dune elevations and paludal bottoms; the mean height varies between 80 and 120 meters above sea level. The climate is moderately continental, and the average annual temperature is +4°C with July to be warmest. The average annual precipitation is 560 mm. Forests occupy 61,051 ha with dominating pine and birch forest (62% and 32% respectively); spruce occupies only 2%, oaks, aspens, black alders, willows account for 1% each. Pioneer inventorial studies of NP lichen diversity were carried out in 2009-2010. 119 lichen species (including traditionally analyzed fungi) were recorded. The most common are the following 15 species: *Chaenotheca ferruginea*, *Cladonia cenotea*, *C. chlorophaea* agr., *C. fimbriata*, *C. rangiferina*, *Hypocenomyce scalaris*, *Hypogymnia physodes*, *Lecanora albellula*, *L. symmicta*, *Parmelia sulcata*, *Parmeliopsis ambigua*, *Physcia aipolia*, *Pycnora sorophora*, *Scoliciosporum chlorococcum*, *S. sarothamni*, *Vulpicida pinastris*, *Xanthoria parietina*. All the species noted basically inhabit tree bark and wood (except those in the genus *Cladonia* which grow more often on the soil or mosses at trunk bases or decaying brushwood). Among rarely occurring lichen species which may serve as indicators of relatively undisturbed old-age forest communities are *Calicium trabinellum*, *Chaenotheca stemonea*, *Cladonia parasitica*. To rare or occasionally occurring lichens in the middle belt of European Russia belong *Baeomyces rufus*, *Catinaria atropurpurea*, *Chaenothecopsis pusilla*, *C. savonica*, *Lecanora fuscescens*, *Psilolechia lucida*, *Thelocarpon laureri*. Lichenological investigations in the NP remain necessary, as only relatively small sample areas of the territory have been surveyed so far. Probably, no more than 75% of the lichen biota has been described up to now.

2B-P

DIVERSITY OF EPIPHYTIC LICHENS IN PRIMEVAL BEECH FORESTS OF THE CARPATHIAN BIOSPHERE RESERVE (UKRAINE)

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2B-P The species richness and composition of epiphytic lichens were evaluated on trunks of *Fagus sylvatica* in primeval beech forest stands of the Carpathian Biosphere Reserve (Ukraine). A total 327 forest sampling plots were investigated. On each sampling plot we observed lichens on different age classes of trees with a special focus on veteran trees. The environmental variables such as development stage of forest, canopy closure, northing, easting and inclination of the slope and natural and anthropogenic forest stand disturbances, were measured on each sampling plot. More than 195 lichen species have been listed so far. Crustose lichen species are amongst the most frequent species and include *Phlyctis argena* (95.1%), *Graphis scripta* (91.4%), *Pyrenula nitida* (87.2%) and *Lepraria lobificans* (78.6%). The highest number of lichens was recorded on beech trees, which grow near the subalpine timberline in mature or overmature forests. Young forest stands have the lowest number of lichens (up to 5). In mature or overmature forests at the bottom of valley or on the lower part of the mountain slopes an characteristic lichen richness of 6-14 species was observed while on the upper part of the mountain slopes and on mountain ridges 15-25 lichen species were recorded per each plot. We found 12 lichen species which are included in the Red Data Book of Ukraine (2009) e.g. *Belonia herculina*, *Gyalecta truncigena*, *Heterodermia speciosa*, *Leptogium saturninum*, *Lobaria amplissima*, *L. pulmonaria*, *Melanohalea elegantula*, *Nephroma parile*, *N. resupinatum*, *Pannaria conoplea*, *Parmeliella triptophylla* and *Parmotrema perlatum*. Primeval beech forests were found to shelter a relatively low average species richness but to harbour a high number of rare and endangered epiphytic lichen species.

(2B-P12) Submission ID: IAL0071-00001

LICHEN FLORA OF ILAM PROVINCE, SOUTH WEST IRAN AND ITS BIOGEOGRAPHICAL SIGNIFICANCE

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Ilam province, part of The Zagros Mountains, contain several ecosystems. Prominent among them are the forest area. From the whole 160 lichen species of this area, 114 species are recorded as new to Ilam province, and two species, *Lecanora sulphurata* (Ach.) Nyl. and *L. klauskalbii* Sipman are new to Iran. It is very probable that The Zagros Mountains forest steppe harbour an interesting lichen flora, but so far they have been hardly explored. A regional specialty may be the species *Pyrenula subelliptica* (Tuck. in Lea) R.C. Harris, which is mainly known from eastern North America and appears to be restricted in the Old World to the Euxinio-Hyrcanian region, as suggested by Some other North American element as *Lecanora juniperina* and *L. percrenata* and a tropical element as *Pyrgidium montelicum* (Beltr.) Tibell and the recorded new species of *Megaspora rimisorediata* Valadbeigi & A. Nordin are indications for the lichenological significance of this region.

**THE IMPACT OF FOREST MANAGEMENT ON CHANGES IN COMPOSITION
OF TERRICOLOUS LICHENS**

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The study focused on the dry acidophilous Scots pine forests with rich lichen and mosses layer in Borská nížina lowland (SW Slovakia) comparing to the Bory Tucholskie (NW Poland). There so-called lichen and moss forests Dicrano-Pinion (Libbert 1933) Matuszkiewicz 1962 are present, famous for their biodiversity of lower plants flora (cryptogams). Between years 2006 and 2011 each type of vegetation was studied by 1 large phytosociological sample (400 m²) and 10 micro-samples (0.25 m²) made on 35 localities. Vegetation types were divided based on their decline of management impact. The first type of secondary vegetation called *Pleurozio schreberii-Pinetum* (Slovakia) in managed forests with 140 micro-samples was observed. On the second type of secondary vegetation called Cladonio-Pinetum (Slovakia) stands 110 micro-samples were studied in protected forests, where forest management was limited. The third type was natural typological Cladonio-Pinetum Juraszek 1928 forests in Bory Tucholskie National park (Poland) where 100 micro-samples were used for comparison. Using the TWINSpan, CANOCO (CCA, DCA), JUICE and Ecological values of lichens for analysing the data, the results show that forestry has a considerable negative effect on diversity and synusias of lichens. Diversity of lichens in different forests was as follows: 15 species in managed, 25 in protected and 28 in natural forests. The highest number of lichens which are tolerant to anthropogenic impact are in managed forests as well as those are able to colonize soil with the higher pH, thicker A0 and humus layers. Thermophilous taxa occur mainly in natural and protected forests. There were mostly species which are characteristic for climax and stable communities.

2B-P

THE VERTICAL GRADIENT OF EPIPHYTIC LICHENS IN CONIFEROUS FOREST CANOPIES

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The vertical gradient of epiphytic lichens was studied in coniferous forests in Estonia, northern Europe; lichens were recorded in height ranges from tree bottom to the top. (1) All lichen species were recorded in three spruce (*Picea abies*) and three pine (*Pinus sylvestris*) sample plots in a relatively unpolluted area. (2) Macrolichen species were recorded in four spruce and four pine plots in different distances from oil shale power plants, sources of alkaline dust pollution. Altogether 70 trees were sampled. In unpolluted sample plots, acidophilic lichen species dominated in species composition. Several species, e.g. *Hypogymnia physodes*, *Platismatia glauca* and *Pseudevernia furfuracea*, were frequent across the height ranges, while the occurrence of many species changed with height. Some lichens, e.g. *Micarea melaena*, were recorded mainly in the lower part of tree trunks; but for example *Cladonia* species that are also usually associated with trunk bases grew on decorticated branches in pine canopies too. Many species, e.g. several *Usnea* species growing mainly on spruce branches, were added with the height. Upper canopy had a distinct lichen composition with high frequency of *Melanohalea exasperatula* and *Scoliciosporum chlorococcum* on both tree species. In polluted areas, lichens growing in upper canopy were clearly more affected by dust deposition. Lichen species composition changed with both distance from the pollution sources and height in the canopy. The proportion of dust indicator species, e.g. *Physcia adscendens*, *P. dubia*, *P. stellaris*, *Xanthoria parietina* and *X. polycarpa*, was highest in the treetops in the sample plot located closest to the pollution sources, whereas there were no dust indicators in the lowest height range. The results confirm that the occurrence of many species changes vertically on trees. Therefore, the total lichen species richness on trees is significantly underestimated when only the first meters near the ground are studied. In addition, upper canopy lichens proved to be more informative dust indicators compared to lower canopy lichens in relatively dense coniferous forests.

2B-P

(2B-P15) Submission ID: IAL0151-00001

ENVIRONMENTAL FACTORS INFLUENCING THE DIVERSITY AND THE COMPOSITION OF THE EPIPHYTIC LICHEN COMMUNITIES IN MANAGED FORESTS OF SOUTHERN BELGIUM

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Lichens are widely used as indicators of environmental changes caused by air pollution, climate change and forest management. The establishment of a baseline of the lichen vegetation and subsequent monitoring is one way to investigate the effects of those changes. The diversity and composition of the epiphytic lichen communities in 30 forest plots in ecologically diverse and managed forests of Wallonia (southern Belgium) were investigated in relation to 22 environmental variables used to characterize those forest plots: 10 abiotic environmental variables, two variables related to tree species and 10 lichen ecological indices based on the lichens. ANCOVA and RDA revealed that increasing light, moisture and bark pH have a positive influence on the lichen diversity while the key factors affecting the species composition in the different forest types are light, moisture, temperature and eutrophication.

**WHICH ENVIRONMENTAL FACTORS ARE CONDITIONING LICHEN SPECIES DIVERSITY
IN *PINUS NIGRA* FORESTS?**

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Forest structure alteration modifies light intensity and water availability. Considering that these are the main factors determining lichens growth, we aim to quantify the effect of environmental variables on the diversity and floristic composition of epiphytic communities at a regional scale. We sampled 91 patches of *Pinus nigra* subsp. *salzmannii* forests in two mountain systems in Spain (Meridional Iberian System and Betic Range). We recorded presence/absence data in 15 trees per patch. The selected environmental variables were: forest structure (canopy cover, and mean DBH), climatic and orographic (area, annual rainfall, summer rainfall, temperatures, altitude and slope) and landscape (patch area and type of surrounding matrix). Generalized Linear Models (GLMs) were used to determine the effect of the environmental variables on the species richness and Caliciales richness. We used Canonical Correspondence Analysis (CCA) to study how these variables influence the distribution of epiphytic lichens. The results showed that species richness mainly depends on factors related to the mountain system, forest structure, annual rainfall and altitude, whereas landscape variables did not show any significant influence. In the specific case of Caliciales, the richness was only and strongly conditioned by forest structure, above all by the presence of mature trees. In these Mediterranean pine forests, epiphytic lichen diversity is highly related to the type of historical and current forest management, which leads to a variation in habitat quality for these organisms. To preserve these epiphytic communities, we suggest avoiding tree felling in the mature and best-preserved forest patches. Nevertheless, we propose the selective logging as a more appropriate type of forest management in the less mature forest patches. This study is being funded by Dirección del Medio Natural, Comunidad Autónoma de Castilla-La Mancha (POII09-0286-4849), and we thank the Ministerio de Educación for a FPU fellowship (Formación de Profesorado Universitario) to the first author of this work, Sonia Merinero.

2B-P

ECOLOGY, DIVERSITY AND ALTITUDINAL DISTRIBUTION OF CORTICOLOUS LICHENS IN MOUNT KENYA TROPICAL MONTANE FOREST

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Documenting the biological diversity is an obligation to all countries that have ratified the Convention on Biological Diversity (CBD) with an aim of developing national strategies for its conservation and sustainable use. However, for many tropical countries knowledge on the diversity and distribution of many groups of organisms is still inadequate. In Kenya, lichens are among the most understudied groups with many regions of the country waiting to be surveyed. The majority of undiscovered species are believed to occur in the tropics where inventories are either incomplete or lacking for many regions. Kenya is estimated to have between 1,500 and 2,000 species of lichens. However, to date only about 700 species have been documented; of these 628 are macrolichens as documented in the current edition of *Macrolichens of East Africa* and on an existing online checklist. Therefore, more than half of the projected lichen diversity remains undiscovered with the majority of the little known being crustose species. These predictions are evident in our preliminary data from the study of Mt Kenya forests that aimed at comparing the diversity of lichens among forests types with contrasting moisture and altitude gradients. Preliminary results indicate that various forest types in Mt. Kenya are rich in lichens. From this study alone, more than 100 species have been added to the current checklist of Kenyan lichens. Ten of these species are probably new to science and further work is ongoing to evaluate their identity. Initial analyses of ecological data indicate higher diversity in the moist forest types than the drier forests. Conversely lichen diversity was higher in mixed forests in lower and higher elevations, but interestingly less in middle elevation mixed forests, as well as the bamboo zone. Mt Kenya forests are therefore endowed with diverse and rich lichen communities that corroborate with its unique physiographic and environmental gradients.

2B-P

(2B-P18)

Submission ID: IAL0265-00002

LICHENS OF PURGATORY AND RIDGES MOUNTAINS: FURTHER EXPLORATIONS IN THE UWHARRIE MOUNTAINS OF NORTH CAROLINA, USA

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The Uwharrie Mountains is an ancient range of isolated peaks (monadnocks) formed ca. 500 mya from the eruptions of a chain of volcanic islands in shallow seas that reach SSW-NNE in the Piedmont ecoregion of south central North Carolina, USA. We present the results of a recent survey focused on the lichenized fungi of two monadnocks: Purgatory Mountain and Ridges Mountain, in a continuing effort to document the lichen diversity of the Piedmont of North Carolina. We sampled three habitats: Basic Oak-Hickory Forest over basic rock, Piedmont Monadnock Forest over basic rock (both on Ridges Mountain), and Piedmont Monadnock Forest over acidic rock (Purgatory Mountain), using 20×50 m rectangular plots. In each plot we collected representatives of every lichen taxon we could find, recording the substrate each found on. Canopy cover was also recorded in each plot, using a spherical densiometer, to investigate influence of light exposure on the lichen biotas. The Basic Oak-Hickory Forest plot was sampled specifically to compare its lichen biota with that in the same forest type studied in Mason Farm Biological Reserve, 80 km east, in 2008, as well as to contrast with the other plots of this study. After species determination, we performed a Non-Multidimensional Scaling (NMS) and Cluster analyses to evaluate the impact of canopy openings (light availability) and particularly rock pH (using only samples collected in rock substrate) in the formation of lichen communities. Our results show that from a total of 157 samples collected, 100 lichen species were found in Ridges and Purgatory Mtns combined (~35-53 spp. per plot). The combined biota is 56% crustose, 29% foliose and 8% fruticose. We found 28 species new to the Uwharrie Mountains, including *Xanthoria parietina*, reported here as new to North Carolina. Our findings also show differences in the lichen community based on canopy opening and substrate type and pH (for those collected on rock), as expected.

2B-P

(2B-P19)

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LICHENS, LICHENICOLOUS FUNGI AND ALLIED FUNGI OF TURNIPSEED WAKENATURE PRESERVE, NORTH CAROLINA, USA

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Turnipseed Preserve in eastern Wake County, North Carolina was surveyed of its lichen diversity in 2009-2011 as part of an assessment toward its designation as the first WakeNature Preserve in recognition of its important ecological resources by the local stakeholder group WakeNature Preserves Partnership. Lichen diversity in this Outer Piedmont/Fall Line preserve was sampled in open fields, forests and rock outcrops including granitic flatrocks, a globally rare natural community that is dominated by lichens and bryophytes. A total of 170 taxa in 75 genera were catalogued, representing 38 families with 12 new state records. Noteworthy finds include: 1) the state-listed rare *Canoparmelia amabilis*, 2) the recently-described *Acarospora janae*, and 3) Lichenotheliaceae, a family newly reported for North Carolina represented by the lichenicolous fungus *Lichenostigma cosmopolites* and the rock-inhabiting fungus *Lichenothelia scopularia*, the latter newly reported for eastern North America. An evaluation of pollution-sensitive and tolerant taxa suggests the area to be somewhat compromised by the ambient air pollution with most pollution-tolerant species in more exposed habitats and pollution-sensitive ones in shaded forests.

IS LICHEN SPECIES RICHNESS LINKED TO LAND COVER PATTERN AT LARGE SCALES IN FORESTS ACROSS THE USA?

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We studied the response of Lichen S, an index of lichen species richness, to five land cover metrics in six large regions of the coterminous USA. We found in an earlier study that climate and pollution explain 20-40% of variation in Lichen S in these same regions. Lichen S is number of macrolichen species from timed samples of fixed-area forested plots, using data from a national USA forest inventory. Our questions were 1) is land cover correlated with Lichen S across large regions, 2) is land cover correlated with climate and air quality, and 3) does inclusion of land cover variables improve analyses of Lichen S response? Our analysis tools, correlation and linear regression with ranked data, gave robust results comparable across regions, at some cost of lower statistical power. In three western USA regions strong correlations between climate and land cover suggest climate is more important to explain Lichen S. In three eastern USA regions we found an effect of land cover on Lichen S independent from climate and pollution. We found response of Lichen S to land cover was mostly stronger as size of area evaluated around a plot increased, with much variability between regions. Percentage of nearby area forested was the single most useful land cover metric, though no single land cover variable or response model was best in all regions. We found that climate, pollution, and land cover together explain 30-47% of variation in Lichen S at least for eastern USA; an improvement from the previous study. Several follow-up studies are suggested.

2B-P

COMPARISON OF THE DIVERSITY OF *GRAPHIS* SPECIES IN DIFFERENT VEGETATION TYPES IN MEXICO

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Patterns and processes leading to the heterogenous distribution of biodiversity can be studied altitudinally, latitudinally, in different environments and with different degrees of anthropogenic disturbance, and focusing on different taxa. In this study we investigate the ecogeographical distribution of the genus *Graphis* (Graphidaceae). This genus exhibits a wide tropical distribution and high species diversity, with over 300 accepted species. We compared the species diversity and composition of *Graphis* in Mexico in two contrasting ecosystems: the Tropical Rain Forest in Los Tuxtlas, Veracruz and the Tropical deciduous forest in Chamela, Jalisco. For each site, the *Graphis* species, the pH bark and DBH of the colonized phorophytes, and seasonal fluctuations in light and evaporation were recorded along ten points each within three 450 m transects, considering both the canopy and the understory. Alpha, beta, and gamma diversity were calculated. The structure of *Graphis* communities for each ecosystem was analyzed using X2 and Kruskal Wallis ANOVA, as well as cluster and NMS analyses. The highest species diversity was found in the canopy of the tropical rain forest, where constantly high values of light and evaporation were recorded during the two seasons. On the other hand, in the Tropical deciduous forest, the number of species was lower, and no correlation with environmental parameters was. At both sites, a low correlation was found between species diversity and bark pH and DBH of the trees.

**DIVERSITY, ECOGEOGRAPHY, AND SYSTEMATICS OF THE LICHEN
GENUS *STICTA* IN COLOMBIA**

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Sticta is one of the genera of macrolichens most frequently collected in the highlands of the tropics. In their 2008 checklist, Sipman and colleagues cited 26 species for Colombia. The present work is a taxonomic revision of the genus for this country. As main result, at least 68 species are recognized, which possibly more than 30 being new species, along with several new reports and new combinations. One of the most striking cases is the segregation of at least ten new species which were traditionally included in the broad concept of *S. fuliginosa*, but morpho-anatomical and molecular analysis demonstrated that they are not only different species but also not even closely related. A similar case is the *S. weigellii-beauvoisii-carolinensis* complex. These species are morphologically similar but show subtle differences in their reproductive structures and other characters such as the cyphellae. This species complex compares to species from North America, but molecular data separate the species in different clades. With respect to the general taxonomy of *Sticta*, novel characters are added to complement the already known features to facilitate the recognition of species groups and species. These include a new classification for cyphellae, tomentum, the shape of isidia, phyllidia and lobules, as well as the cells at the base of the cyphellae. Our results indicate that the greater diversity of the group is found in the Andean regions above 2,000 m, the paramo regions being the richest in diversity. It was found that the proportion of species with cyanobionts far exceeded the number of species with chlorobionts, especially in the paramo regions. Therefore, quantitative sampling was conducted in the paramo area and it was shown that species with cyanobionts may contribute substantially to the nitrogen cycle in paramo ecosystems due to their ability to fix atmospheric nitrogen. Many of the species of *Sticta* found in Colombia are more widely distributed in the Neotropics, and therefore the results can be at least partially applied to a region spanning from southern Mexico to northern Bolivia and Peru.

2B-P

MICROLICHENS OF COLOMBIA: A FIRST APPROACH INCLUDING NEW RECORDS

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This is the first joint paper of the Grupo Colombiano de Liquenología (GCOL). We present an updated, illustrated list of crustose microlichens for Colombia, mainly based on collections by the first and last authors in the “Llanos” and the areas surrounding Bogotá (Cundinamarca), with additional material gathered by participants of the second NSF Tropical Lichen Workshop in Tolima in 2010 and specimens studied by several undergraduate and graduate thesis students during the course of 2009 to 2011. Due to its geographic situation connecting Central with South America, as well as its size and diversity of ecosystems, Colombia is considered one of the five countries with the highest lichen diversity in the Neotropics, together with Mexico, Venezuela, Bolivia, and Brazil. The microlichens identified in the studied material substantially increase our knowledge of the Colombian lichen biota, although much remains to be done to achieve a more complete picture of its diversity. Among the many new records for the country are: *Gassicurtia coccinea* (Fée) Marbach, *Laurerea purpurina* (Nyl) Zahlbr., *Ocellularia polydisca* (Redinger), *O. fumosa* (Ach.) Müll. Arg., *Trypethelium platystomum* Mont., *Cryptothecia effusa* ((Müll. Arg.) R. Sant., *Opegrapha heterospora* Vain., *Cresponea flava* (Vain.) Egea & Torrente., and *Phlyctis brasiliensis* Nyl. Many species are documented with images and their ecosystem and habitat preferences are indicated.

2B-P

(2B-P24)

Submission ID: IAL0062-00001

LICHENICOLOUS FUNGI FROM BOLIVIA, MAINLY FROM ANDEAN FORESTS

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The lichenicolous fungi of Bolivia have not been studied in detail and to date only 20 species have been reported from there. During several expeditions to Bolivia, the authors obtained a large number of lichenicolous fungi, of which 59 species have so far been identified, with five new to science; 47 taxa are recorded for the first time from Bolivia, some of which are also new to the Southern Hemisphere or South America. The richest habitats, including Yungas and Tucumano-Boliviano montane vegetation, are in the Andean forests. Several additional species belonging to critical groups are under study and many more species are expected to be discovered in Bolivia. This research received support from the National Centre for Research and Development (NCBiR) in Poland under the LIDER Programme for 2010-2013 (no. 92/L-1/09).

(2B-P25)

Submission ID: IAL0063-00001

TOWARDS A MONOGRAPH OF FOLIICOLOUS LICHENIZED FUNGI OF BOLIVIA

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Bolivia, a landlocked country of South America with an area of 1,098,581 km², has an impressive variety of forest vegetation which provides suitable biotopes for foliicolous lichens. Prior to the author's fieldwork between 2004 and 2011, the country's lichen biota had not been investigated comprehensively. As a consequence, a large collection of foliicolous lichens of c. 8,000 specimens has formed the basis of a monograph, including descriptions of all taxa, identification keys and iconography. To date, almost 300 species have been recognized, including several species new to science and numerous records new to Bolivia. Work on the collection is still in progress, therefore the number of known species and particular species distribution have yet to be determined in order to recognise patterns in the main forest ecosystems in Bolivia. Research supported by NCBI R in Poland under the LIDER Program; project no. 92/L-1/09.

(2B-P26)

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NEW SPECIES AND INTERESTING RECORDS OF TROPICAL FOLIICOLOUS LICHENS

2B-P

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Though foliicolous lichenised fungi occasionally occur in temperate region among Mediterranean, sub-tropical or even oceanic circumstances, their highest diversity is reached in the tropical regions. Folii-colous lichens grow in various types of rainforests. There is a huge variation in species number and composition depending on forest types and altitude. For these lichens microclimatic conditions on and near leaves, various characters of the substrate leaves are very important, just like macro- or mesoclimatic conditions affecting on their surrounding forests. Knowledge on this field increased considerably in the last decades, however some groups are still poorly known, even more to do on their lichenicolous fungi. Therefore studying collections from Central and South America and East Africa we concentrate on these less investigated taxa. During our study of Pilocarpaceae we discovered species new to science which are currently under description (e.g., *Calopadia* sp., *Fellhanera* spp.), others (belonging to *Bacidina*, *Eugeniella*, *Fellhanera*) represent new records for their distribution. Also several new records of noteworthy lichens were found in further taxonomic groups. Among species of lichenicolous fungi, *Keratosphaera antoniana* Flakus, Farkas & Lucking has been described as new recently and it is presented with more details here. Our results additionally to its taxonomic value, represent contributions to a better knowledge on distribution and supply data for further ecological investigations. Research supported by the Hungarian Scientific Research Fund; OTKA K81232.

LICHENS FROM THE BRAZILIAN AMAZON: NEW TAXA AND INTERESTING RECORDS

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Brazil is considered one of the most diverse country in the world, comprising two major tropical forest blocks, the Atlantic rainforest and the Amazon. The Caxiuanã National Forest, in the Brazilian Amazon, is situated in the municipalities of Melgaço and Portel (1°37'S /51°19'W and 1°54'S/51°58'W) in the micro-region of Furos, in the bay of Caxiuanã, between the Xingu and Tocantins rivers, occupying an area of about 300,000 ha. The National Forest comprises several vegetation types, including non-flooded (terra firme forest with islands of savanna-like and secondary forest) and flooded forest (várzea and igapó), being the terra firme forest the predominant type. On the frame of a recent inventory of the lichenized mycota from the Caxiuanã National Forest, at the Ferreira Penna Research Station, in the Brazilian Amazon, two new taxa are described as new and four new combinations are presented: *Ampliotrema megalostoma* (Müll. Arg.) Cáceres & Lücking comb. nova, *Graphis brachylirellata* Cáceres & Lücking spec. nova, *Malmidea leucogranifera* Cáceres & Lücking spec. nova, *Ocellularia conformalis* (Kremp.) Cáceres & Lücking comb. nova, *Redingeria microspora* (Zahlbr.) Cáceres & Lücking comb. nova, *Sarcographa megistocarpa* (Leight.) Cáceres & Lücking comb. nova. Type material and duplicates will be deposited in F and URM Herbaria.

2B-P

(2B-P28)

Submission ID: IAL0127-00002

MANGROVE AND RESTINGA LICHENS FROM NORTHEASTERN BRAZIL

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Mangroves are found in tropical and subtropical tidal areas, which include estuaries and marine shorelines. Brazil contains approximately 26,000 km² of mangroves, 15% of the world's total of 172,000 km². It is possible to understand the importance of mangroves from the functions it plays in the environmental balance. It is known that, besides protecting the coast, this phytogeographic formation works as a climate regulator and true pollutants filters. In the state of Sergipe, the mangroves occur in the estuaries of the major rivers: Real, Sergipe and Vasa-Barris. In some cases, we also find Restinga vegetation associated with mangroves areas, as in the present study. Studies on the lichen diversity on mangroves are very scarce in Brazil as a whole, and nothing has been done until the moment in Mangroves from Northeast Brazil. This study aims to survey the diversity of lichens in mangrove areas in the state of Sergipe and also on the surrounding Restinga vegetation. Samples were collected in April 2010 and the first area visited is located in Santo Amaro das Brotas (10°46'43"S/37°03'30"W), a municipality in eastern Sergipe, 13 km from Aracaju, the state capital. Lichens were collected using hammer, knife, paper envelopes and GPS. Thallus morphology was examined using a Leica EZ4 dissecting microscope. Sections of thalli and ascomata were cut by hand with a razor blade and examined with squash preparations in water, KOH and Lugol's solution. A total of 99 samples have been analyzed so far, and 35 species are here reported, of which 18 are new records for the state of Sergipe and two new records for Brazil, namely *Gassicurta bellardii* (Sipman) Marbach and *Stirtonia alboverruca* Makhija & Patw.

**LICHENS FROM SERRA DE ITABAIANA NATIONAL PARK, AN ATLANTIC RAINFOREST
RELICT IN SERGIPE, BRAZIL**

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The Atlantic rainforest in Sergipe, the smallest Brazilian state with an area of ca. 21,910 Km², is almost nonexistent. The devastation of the natural areas has been taking place for a long time and the current vegetation cover (only 0,1% of the original area) is restrict to very small forest remnants, like islands surrounded by sugarcane plantations and pastures. The Serra de Itabaiana National Park, located 50 km from the coast and the state capital, Aracaju, is the most important Atlantic rainforest remnant in Sergipe. Studies on the lichenized fungi from Serra de Itabaiana have been incomplete so far. This ongoing research project on the Serra de Itabaiana, a very unique vegetation, aims to estimate the lichen diversity present on the area and thus reinforce the current conservation policies for this atlantic rainforest relict. The lichens have been collected during five field trips which took place in October 2002, then recently in January, April, May, and December 2010, using opportunistic and quantitative sampling protocols. Thallus morphology was examined using a Leica EZ4 dissecting microscope. Sections of thalli and ascomata were cut by hand with a razor blade and examined with squash preparations in water, KOH and Lugol's solution. A total of 300 samples have been analyzed so far, and ca. 65 species are here reported, of which 11 are new records for the state of Sergipe and one a new records for Brazil: *Chapsa platycarpoides* (Tuck.) Breuss & Lücking.

2B-P

3I: New approaches to understanding biosynthesis and ecological roles of metabolites in lichens

(3I - P1) Submission ID: IAL0113-00002

CHEMICAL ANALYSES AND MOLECULAR STUDIES OF SELECTED CETRARIOID LICHENS (PARMELIACEAE) AND THEIR CULTURED MYCOBIANTS

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Lichens produce a great variety of primary (intracellular) and secondary metabolites (extracellular); a considerable number of them has not been structurally identified and are still recognized as “unknowns”. In this study, three cetrarioid lichens, e.g. *Cetraria ericetorum*, *C. islandica* and *Flavocetraria nivalis*, were chosen for molecular and chemical investigations. HPLC and TLC analyses have to be complemented by mass spectroscopic methods. In further series of experiments, the fungal symbionts of the selected lichen thalli were isolated by means of the modified Yamamoto-method and sub-cultured on different nutrient media. By using electronically adjustable culture chambers, a number of environmental conditions were tested to provide best growth reactions for the three selected lichen fungi. For identification of the cultured fungal isolates and the three voucher specimens, DNA-analyses were performed by using the primers ITS1F and ITS4 for the PCR-reactions to amplify the internal transcribed spacer 1 region, 5.8S region, and the internal transcribed spacer 2 region of genomic rDNA. The sequencing was accomplished by MWG Biotech AG (Germany) and Macrogen Inc. (Europe). The identities of the lichen and fungal sequences were examined via Blastn search of the NCBI GenBank. Consequently, the mycobiont of *C. islandica* was grown aposymbiotically for the first time. Finally, the mycobiont cultures were investigated by using similar chemical analyses as mentioned before for the original lichen thalli and differences in the metabolite compositions were documented. Regarding *C. islandica*, which was previously found to contain biologically active substances, the chemical constituents of the “crude” lichen extract, could be of high interest for future pharmaceutical applications.

3I-P

**ANTIOXIDANT AND ANTIMICROBIAL ACTIVITY OF *PARMELIA SAXATILIS*
ETHANOL EXTRACT**

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The aim of this study was to evaluate the antioxidant and antimicrobial activity of ethanol extract of *Parmelia saxatilis* (L) Ach. *P. saxatilis* originated from Tara Mountain (Serbia) was used for the study. 4.5 g of air dried sample was extracted by stirring with 30-fold higher volume of 70% ethanol at 30°C for 72 hours and filtering through Whatman No. 4 filter paper. The obtained ethanol extract was evaporated at 40°C to dryness, redissolved in 96% ethanol (antioxidant test) and 5% DMSO (antimicrobial test), respectively, to a final concentration of 20 mg/ml. Antioxidant capacity was determined spectrophotometrically by methanol solution of DPPH at 517 nm and compared with commercial antioxidant, BHA. The concentrations of phenol and flavonoid compounds in the extract were measured spectrophotometrically by Folin-Ciocalteu reagent at 740 nm and ethanol/aluminium nitrate/potassium acetate mixture at 415 nm, respectively. Antimicrobial capacity of the extract was evaluated on 5 bacterial and 8 fungal species. Tests were carried out by various extract dilutions, in triplicate. Six extract concentrations ranged from 10 mg/ml to 0.312 mg/ml, obtained by double dilutions, caused decrease of DPPH free radical-scavenging in the range from 79.76% to 14.76%. Defined EC₅₀ value was 1.81 mg/ml. The tested extract concentrations had good antioxidant activity compared to BHA one (92.61%). The amount of total phenol compounds was ranged from 193.95 µg/ml (10 mg/ml) to 30.10 µg/ml (0.312 mg/ml). The total flavonoid content was less, ranged from 134.48 µg/ml (10 mg/ml) to 1.90 µg/ml (0.312 mg/ml). Scavenging effect directly correlates with the different phenol content ($r^2 = 0.9981$) and less with flavonoid content ($r^2 = 0.6634$). The extract showed insignificant antibacterial activity, while antifungal activity was absent. The growth of *Escherichia coli*, *Enterococcus faecalis* and *Pseudomonas aeruginosa* was inhibited by the highest extract concentration (10 mg/ml), while *Klebsiella pneumoniae* and *Staphylococcus aureus* were more sensitive (1.25 mg/ml and 2.5 mg/ml, respectively).

3I-P

**ACETYLCHOLINESTRASE INHIBITORY AND NEUROPROTECTIVE EFFECTS OF
BIRULOQUINONE, ISOLATED FROM LICHEN-FORMING FUNGUS *CLADONIA MACILENTA***

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Alzheimer's disease (AD) is the most common type of dementia in aging population. At present, acetylcholinesterase (AChE) inhibitors are the first group of drugs approved by the Food and Drug Administration to treat mild to moderate AD. In present study, one AChE inhibitor, biruloquinone, was isolated from the extract of lichen-forming fungus *Cladonia macilenta*, which showed the most potent AChE inhibitory activity in previous screening experiment. The IC₅₀ and inhibitory kinetic assay suggested biruloquinone is a mixed-II inhibitor on AChE, with the IC₅₀ value of 27.1 µg/ml (83.1 µM). The molecular modeling results indicated that biruloquinone is supposed to bind AChE through the stable H-bond with two active sites of the protein. The neuroprotective effects of biruloquinone on the H₂O₂ and β-amyloid-induced cell injuries were also evaluated. The results indicated that biruloquinone remarkably improved the viability of the injured cells at 1 to 25 µg/ml. The protective effects are proposed to be related to the potent antioxidant activities of biruloquinone. These results implied that biruloquinone has the potential to be used as multi-functional anti-AD agent.

**EFFECT OF SUGAR ON SECONDARY METABOLISM IN CULTURED
LICHEN MYCOBIONT OF *CLADONIA RAMULOSA***

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Lichens produce peculiar secondary metabolites known as lichen substances. However, cultured lichen mycobionts tend not to produce lichen substances. To investigate the influence of sugar on the secondary metabolism in lichenized fungi, 125 strains of mycobiont were cultured on malt–yeast extract medium (MY, control), MY medium with 20% sucrose (S20) and Lilly–Bennett medium (LB). After three or six months, lichen substances were produced on S20 medium by four species, while only one species *Cladonia ramulosa* produced lecanoric acid (LA) after one-month culture on LB. Addition of sugar alcohols on LB medium decreased LA levels. The LA level was elevated on LB with fructose, suggesting that polyketide biosynthetic pathway was regulated by sugars or was involved in sugar metabolisms. Two partial cDNAs of *C. ramulosa* polyketide synthases (CrPKS1 and CrPKS2) were cloned and used for RT-PCR analyses. The levels of CrPKS1 transcript began to accumulate and reached a maximum level at 12 days after transferring to LB medium with fructose, prior to LA production at 16 days. It is hypothesized that CrPKS1 products synthesize lecanoric acids and that fructose plays a key role in control of symbiotic/non-symbiotic metabolism in *C. ramulosa* mycobionts.

**HETEROLOGOUS EXPRESSION OF POLYKETIDE SYNTHASE GENES
OF LICHEN *CLADONIA METACORALLIFERA***

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Lichens produce unique polyketide secondary metabolites including depsides, depsidones, dibenzofurans, and depsones. The biosynthesis of these compounds is governed by polyketide synthase (PKS), but the mechanism via which they are produced has remained unclear until now. Heterologous expression in a surrogate host provides an alternative approach for functional analysis of lichen polyketide biosynthesis. Cultured mycobiont of *Cladonia metacorallifera* producing a large amount various polyketide were used to isolate and characterize polyketide synthase genes. The CmPKSs showed greatest homology with uncharacterized genes from filamentous fungi and composed exclusive clades in reducing and non-reducing PKSs. We construct subclones using spliced full length cDNA of CmPKS1 and CmPKS35 for stable expression in the filamentous fungus *Aspergillus nidulans*. There are 10% efficiency of single copy inserted transformants about CmPKS1 and CmPKS35. We are expecting the new polyketide product by LC-MS and HPLC analysis.

ANTIOXIDANT CAPACITY OF *PSEUDOEVERNIA FURFURACEA* EXTRACT

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Evaluation of the antioxidant capacity of ethanol extract of *Pseudoevernia furfuraceae* (L.) Zopf. was the aim of this study. *P. furfuraceae* originated from Tara Mountain (Serbia) was used for the study. 5.5 g of air dried sample was extracted by stirring with 30-fold higher volume of 70% ethanol at 30°C for 72 hours and filtering through Whatman No. 4 filter paper. The obtained ethanol extract was evaporated at 40°C to dryness, redissolved in 96% ethanol to a final concentration of 20 mg/ml. Antioxidant capacity was determined spectrophotometrically by methanol solution of DPPH at 517 nm. Antioxidant activity of the tested extract concentrations were studied in comparison to commercial antioxidant, BHA. The concentrations of phenol and flavonoid compounds in the extract were measured spectrophotometrically by Folin-Ciocalteu reagent at 740 nm and ethanol/aluminium nitrate/potassium acetate mixture at 415 nm, respectively. Tests were carried out by various extract dilutions, in triplicate. Six extract concentrations ranged from 10 mg/ml to 0.312 mg/ml, obtained by double dilutions, caused decrease of DPPH free radical-scavenging in the range from 90.04% to 21.39%. Defined EC₅₀ value was 1.85 mg/ml. The tested extract concentrations had strong antioxidant activity compared to BHA one (92.61%). The amounts of total phenol compounds were ranged from 61.53 µg/ml (10 mg/ml) to 5.540 µg/ml (1.25 mg/ml), while at lower extract concentrations these compounds were missed. The total flavonoids content was significantly higher, ranged from 240.13 µg/ml (10 mg/ml) to 62.97 µg/ml (0.625 mg/ml), while at the concentration of 0.312 mg/ml their presence was not noted. Although, antioxidant activity had some value at the concentration of 0.312 mg/ml, it could be concluded that other compounds were responsible for it. Scavenging effect directly correlates with the different flavonoid content ($r^2 = 0.9641$) and less with phenol compounds content ($r^2 = 0.6826$).

3I-P

ANTIFUNGAL ACTIVITY AGAINST PLANT PATHOGENIC FUNGI FROM CRUDE EXTRACT OF *USNEA PULVINULATA*

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Usnea pulvinulata contains various secondary metabolites such as usnic acid, diffractaic acid, menegazziaic acid, norstictic acid, protocetraric acid, salazinic acid and ursoric acid. This study tested the inhibition of crude extracts of *U. pulvinulata* from absolute water, acetone, ethanol and methanol against 6 plants pathogenic fungi such as *Colletotrichum gloeosporioides* (banana anthracnose, cultivated banana anthracnose, chili anthracnose, *Dendrobium* anthracnose and mango anthracnose), *Colletotrichum capsici* (chili anthracnose and papaya anthracnose), *Curvularia lunata* (dirty panicle disease of rice), *Diplodia* sp. (leaf blight of *Dendrobium*), *Fusarium moniliforme* (bakane disease of rice) and *Pestalotiopsis guepinii* (leaf blight of *Guava*). The crude extract of *U. pulvinulata* from acetone showed the highest inhibition against all six plants pathogenic fungi. Ethanol and methanol crude extracts can be antifungal against plant pathogen fungi. The crude extract from absolute water, however, did not inhibit the tested fungi.

DIFFERENT STRATEGIES TO ACHIEVE Pb-TOLERANCE IN THE TWO *TREBOUXIA* PHYCOBIONTS OF THE LICHEN *RAMALINA FARINACEA*

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Ramalina farinacea L. (Ach.) has a relatively high tolerance to Pb (Branquinho *et al.*, 1999). On the other hand, our group demonstrated that this lichen contains two *Trebouxia* phycobionts (provisionally named TR1 and TR9). TR1 and TR9 showed distinct physiological responses to oxidative stress caused by a strong ROS propagator, which produced a more severe decay in photosynthesis, photosynthetic pigments and proteins in TR1. Antioxidant enzymes were decreased by oxidative stress in TR1, but increased in TR9. Since Pb toxicity is caused by enhanced ROS formation, we hypothesized that TR9 phycobiont would be relatively more Pb-tolerant than TR1. Therefore, in the present study we searched for physiological differences between isolated TR1 and TR9 under Pb exposure by analyzing the extracellular and intracellular Pb accumulation, photosynthetic pigments and chlorophyll fluorescence parameters. Additionally, the detoxification response to Pb was estimated by several important antioxidant enzymes: glutathione reductase (GR), superoxide dismutase (SOD), ascorbate peroxidase (APx) and catalase. As expected, extracellular Pb increased with the augment of Pb in both TR1 and TR9. However, TR9 immobilized significantly more metal than TR1 at extracellular level. The intracellular Pb uptake followed an opposite trend to that observed for the extracellular Pb, being approximately three times higher in TR1 than in TR9. However, photosynthetic pigments were not strongly affected by the presence of Pb within cells in either TR1 or TR9, since it was not observed any pigment decay higher than 10% (respect to controls). Accordingly, photosynthetic electron transport was not affected by the presence of Pb, as evidence by absence of PSII photoinhibition and the lack of effect on the Φ PSII in both phycobionts. Control levels of GR, SOD and APx were significantly higher in TR1 than in TR9. However, Pb induced the three enzymes in TR9 while it had no effect on TR1, so that antioxidant activities were quantitatively similar in both phycobionts under Pb treatments. In conclusion, each algal species seem to have acquired similar levels of Pb tolerance through the integration of distinct morphological, biochemical and physiological features. [MCINN (CGL2009-13429-C02-01/02), AECID (PCI_A_I024755/09) and Generalitat Valenciana (PROMETEO 174/2008 GVA)]

3I-P

AMYLOLYTIC ACTIVITIES OF SOME THERMOPHILIC MYCOBIONTS ISOLATED IN NIGERIA

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A total of 16 species of fungi were isolated from 3 locations viz:-two refuse-dump sites and palm kernel stack in Ibadan, Nigeria. Out of the 16 isolates obtained at 45°C incubation temperature, 9 were found to be thermotolerant while the other 7 were found to be thermophilic. The thermophilic and thermotolerant fungi were separated from the others by incubating at a low temperature of 12 °C at which the thermotolerant fungi grew, while the thermophilic did not grow at this temperature. All the fungi (thermophilic and thermotolerant) were screened for possible antimicrobial activities using different media sources. However, none of the screened organisms showed sign of antimicrobial activity by having no clear zone of inhibition against the test organisms. The test organisms used were *Bacillus subtilis* and *Staphylococcus aureus*. The conditions necessary for the production of extracellular amylase enzyme of thermophilic fungi isolated were determined using a stationary liquid medium of starch-yeast extract. Amylases were produced by all the thermophilic fungi. The amylase activities of all the fungi used were determined at pH 6.9. The peak activities for the enzyme (amylase) were shown to be at 45°C. The possible use of extracellular enzymes from these fungi for various purposes is discussed.

PHYCOBIONTS IN SUSPENSION: METHODS OF QUANTIFICATION

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The quantification of phycobiont concentration in suspensions is usually performed under the microscope by means of hemocytometric chambers. This method is time consuming and the presence of phycobiont clusters increases experimental error. Future advances in phycobiont biology require rapid and precise surrogate methods. Optical density (OD) has long been used in microbiology since it is simple and rapid. Chlorophyll autofluorescence can be used as a measure of cell number, a widespread method in green algae research. Finally, the use of specific stoichiometric fluorescent probes, such as Hoechst, allows precise quantification of DNA. Fluorometric methods are extremely sensitive and very low concentrations can be detected. Furthermore, the use of microplates and plate-readers can greatly assist in this task, since tens of low volume samples can be measured simultaneously. The aim of this work is the study of different surrogate methods for the quantification of phycobiont suspensions. Two axenic strains, *Asterochloris erici* Ahmadjian (SAG 32.85 = UTEX 911), and *Trebouxia* sp.(TR9) isolated from *Ramalina farinacea*, were studied. Suspensions were grown in 3NBBM (16:8 h light:dark) at 20°C and 15°C, respectively. A Fuchs-Rosenthal hemocytometric chamber was used for cell counts. OD (650 nm) was measured in fresh 100 µl-aliquots with an Anthos 2010 plate-reader. Chlorophyll autofluorescence (λ_{exc} 485 nm, λ_{em} 635 nm) and DNA-bound Hoechst fluorescence (λ_{exc} 360, λ_{em} 465 nm) were measured in a TECAN SPECTRAFluor Plus plate-reader. Frozen 200 µl aliquots were used for fluorometric methods. Chlorophyll samples were thawed and directly measured, DNA samples were previously lysed in a DNA buffer. The results show that OD gives reproducible, rapid results, using low volumes. However, its sensitivity is the lowest. Chlorophyll autofluorescence is rapid and sensitive but requires the availability of a fluorometer, as DNA quantification, that also needs a short sample processing. However, both OD and chlorophyll autofluorescence may be affected by changes during phycobiont cell cycle (i.e. debris, cluster/cell size, metabolism). We conclude that the measurements studied may be used as surrogates of cell number but the limitations of each method must always be considered. [MCINN (CGL2009-13429-C02-01/02), AECID (PCI_A_1024755/09) and Generalitat Valenciana (PROMETEO 174/2008 GVA)]

4I: Lichenological research in South-East Asia and the Pacific region

(4I-P1) Submission ID: IAL0026-00001

**THE LICHENS FAMILY PHYSCIACEAE (LECANORALES, ASCOMYCOTA)
IN THAILAND**

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Members of the lichens family Physciaceae were collected from sixteen provinces and eleven forest types in Thailand and taxonomically identified in the period between 1995 and 2010. They were classified under the rubrics of nineteen genera and one hundred twenty-eight species. Nine taxa of foliose and twenty-six taxa of crustose lichens were newly described in Thailand. In addition, nine taxa of foliose and twenty-seven of crustose lichens are expected to be identified as new species previously unknown to science.

(4I-P2) Submission ID: IAL0029-00001

**IN VITRO ANTIPROLIFERATIVE ACTIVITY OF LAURERA SPECIES (TRYPETHELIACEAE,
PYRENULALES) CRUDE EXTRACTS AGAINST FOUR HUMAN CANCER CELL LINES**

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4I-P

Laurera species is a common genera of crustose lichens in Thailand, which has been reported to produce antifungal compounds and photoprotective secondary products. The chemical constituents of several lichens have been shown to have biological and pharmaceutical activity including antibacterial, antifungal, anti-proliferative and cytotoxic activity. The aim of this study is to investigate in vitro antiproliferative activity of *Laurera* species crude extracts with different solvents of increasing polarity. Four crustose lichen species, *Laurera benguelensis*, *L. madreporiformis*, *L. meristospora*, and *L. subdiscreta*, were extracted successively with chloroform and methanol using maceration process. The cytotoxic activity of the eight lichen extracts was evaluated in vitro using four human cancer cells: KB (human epidermoid carcinoma), HepG2 (human hepatocellular carcinoma) HeLa (human cervical carcinoma) and MCF-7 (human breast carcinoma) and a non-cancerous cells, Vero (African green monkey kidney cells). The inhibition of cell proliferation by crude extracts was determined by MTT colorimetric assay and g/ml. The crude chloroform extract of the four $\mu 30 \leq$ active standard value at IC_{50} crustose lichens showed against four human cancer cells (KB, HepG2, HeLa and g/ml, μ MCF-7) at the IC_{50} values of 0.3-11.0, 0.49-24.0, 0.59-19.0 and 0.9-35.5 respectively, whereas the methanolic extracts had weak activity (IC_{50} vales of g/ml) but exhibit low toxicity with normal cell than other crude μ 14.5-100 g/ml). Therefore, the non-polar lichen compounds μ extracts IC_{50} vales of 45-59 showed higher antiproliferative and cytotoxic activity than polar lichen compounds. Purification and identification of the bioactive components from these active lichens are under investigation.

ANZIA MAHAELIYENSIS AND ANZIA FLAVOTENUIS, TWO NEW SPECIES FROM HORTON PLAINS SRI LANKA

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The genus *Anzia* includes c. 34 accepted species worldwide, occurring mainly in subtropical to tropical mountains at altitudes between 1,000 to 4,000 m in both the northern and the southern hemispheres. During a study of epiphytic lichens in Horton Plains National Park in Sri Lanka, the first author collected specimens of two taxa of *Anzia* for further study at the Natural History Museum, London. Morphological and anatomical observations and HPTLC analyses of these two specimens suggested that they are new to science and will be validly published in a forthcoming paper in the *Lichenologist*. In order to assess their phylogenetic relationship to each other and to other species of *Anzia*, molecular analysis was undertaken and a phylogenetic tree constructed using six published ITS sequences from 5 species of *Anzia* as well as ITS sequences from other Parmelioid genera as outgroups including *Pannoparmelia angustata* (formerly included in *Anzia*). The most likely tree shows that both new species cluster within the well-supported genus *Anzia*, and are genetically distinct from each other and from other sampled species of *Anzia*. They form a monophyletic group together with *A. hypoleucoides*: the first one, *Anzia flavotenuis* sp. nov. is most closely related to *A. hypoleucoides* and the second one *A. mahaelyensis* sp. nov. is sister to these two species. Both *A. hypoleucoides* and *A. flavotenuis* contain lobaric acid but the former lacks the yellow pigment and does not have isidia. The species in the other well-supported group within *Anzia* (*A. colpodes*, *A. colpota*, *A. formosana* and *A. opuntilla*) contain divaricatic acid except for *A. formosana* which contains anziaic acid, also present in *A. mahaelyensis*. Morphologically, *A. mahaelyensis* is characterised by a white single-layered medulla and pale tipped isidia and *A. flavotenuis* by a two-layered medulla with the upper layer yellow and the lower part white, a central chondroid axis and isidia with brown-black tips. As traditionally delimited based on morphology, these two new species would belong to two different subgenera, but our molecular results show that they belong to the same lineage and suggest that these two subgenera are not monophyletic.

4I-P

OPTIMIZATION FOR SECONDARY METABOLITES PRODUCTION FROM TROPICAL LICHEN MYCOBIONTS

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Lichens are resources for novel compounds with many of them having importance in medicine and other fields. Intact lichens cannot be cultivated but their mycobionts can be axenically grown in laboratory from ascospore discharge or tissue culture techniques. Frequency of spore discharge, germination and colony development were varied among tropical lichen species. Mycobiont cultures from stock at The Lichen Research Unit, Ramkhamhaeng University (RAMK) were screened for their abilities to produce biological activities. Among these four mycobiont species; *Graphis* sp., *Graphina albissima*, *Ocellularia punctulata* and *Pyrenula kurzii* were selected regarding their potential to produce metabolites with antimicrobial activities. From 7 different media for stimulation of growth of mycobionts, Malt-Yeast Extract medium was chosen for its superior performance and used for further experimentation. The mycobionts were grown on both solid and liquid media and the secondary metabolites produced under various conditions were examined. Static and shake liquid cultures with various supporting materials were examined for growth of mycobionts, however in these conditions growth rate were higher but the metabolites produced were lower in both number and quantities. Another way to culture the mycobionts was solid medium and was also considered an easier method and mycobionts were grown for period of 27 weeks at room temperature, cells and pieces of agar block were removed at intervals and extracted with methanol. Chemical profiles detected by Thin Layer Chromatography (TLC) indicated that the metabolites produced increased gradually during 9-15 weeks of incubation under these conditions. Comparison of pH between acidic, neutral and alkaline conditions for growth of these mycobionts showed that the optimize pH for all of them was at neutral pH. Some lichen substances absorb ultraviolet light and protect the algae from too intensive irradiation, in order to induce metabolite production in mycobionts cultures, both short and long wavelength UV light were investigated. The results indicated that the number of spots on TLC plates were decreased, however the conditions in this experiment were not entirely suitable. Scale up for high numbers of cell mass and secreted metabolites were done and further studied on the chemical structures of new chemical compounds were investigated and are discussed.

4I-P

(4I-P5)

Submission ID: IAL0068-00001

LICHEN DIVERSITY «HOT SPOT» IN KRONOTSKY NATURE RESERVE, KAMCHATKA

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Primeval old-growth spruce forests in vicinity of Levaya Schapina River (Kronotsky Nature Reserve, Eastern Kamchatka) were investigated. The area appeared to be exceptionally rich in lichens, particularly spruce epiphytes: more than 130 lichen species were recorded on bark of *Picea ajanensis*. The most important finding is a population of *Erioderma pedicellatum*. The species was rather abundant on twigs of old spruces, where it grew together with *Lobaria pulmonaria*, *L. scrobiculata*, *Nephroma helveticum*, *Ramalina thrausta*, *Sticta limbata* and other species. At least thirty lichen species found near Schapina are known as indicators of undisturbed old-growth forests, among them *Arthonia zwackii* (new for Russian Far East), *Usnea longissima* (extremely rare in the North of Russian Far East), *Pseucyphalaria crocata* and *Schismatomma pericleum* (new for the North of Russian Far East).

CHEMICAL STUDIES ON TWO LICHENS OF THE GENUS *ERIODERMA* FROM MALAYSIA

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Chemical studies on two lichens, *Erioderma phaeorhizum* var. *in* *lat.* and *Erioderma tomentosum* Hue, collected from Brincang, Cameron Highlands Malaysia were carried out. The structure of the compounds isolated from both lichens were elucidated by chromatographic, spectroscopic, microanalysis methods and unambiguous synthesis. Two new depsidones, hypophysciosporin [methyl 2-chloro-3,8-dihydroxy-1,4,6,9-tetramethyl-11-oxo-11H-dibenzo[b,e] [1,4] dioxepin-7-carboxylate] and 3-*o*-methylhypophysciosporin [methyl 2-chloro-8-hydroxy-3-methoxy-1,4,6,9-tetramethyl-11-oxo-11H-dibenzo[b,e] [1,4] dioxepin-7-carboxylate], have been isolated from *Erioderma phaeorhizum* together with eight known depsidones, vicanicin, isovicanicin, norvicanicin, *o*-methylvicanicin, eriodermin, argopsin, granulatin and physciosporin. In addition the chroman, vitamin E acetate, has been isolated from *Erioderma tomentosum*, the first reported occurrence of this compound in a lichen. The other compounds which have been isolated from this lichen were the depsidones, vicanicin, norvicanicin and argopsin, and the depside, atranorin. The minor unknown compounds have been isolated from *Erioderma phaeorhizum*. The structure of the first compound is related to 3-*o*-methylhypophysciosporin while the second compound is related to vitamin E. Biosynthesis pathway of these metabolites is proposed. Possibly it involves secondary modification of the simplest β -orcinol depsidone, hypoprotocetraric acid, via several stages of enzymatic reactions involving oxidation, *o*-methylation of hydroxyl and carboxyl groups, decarboxylation and chlorination.

REDISCOVERY OF A FORGOTTEN LICHEN GENUS WITH UNIQUE CONIDIOMATA FROM NEW ZEALAND

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A peculiar lichen with unique conidiomata from southern New Zealand, *Nukaia cupulifera*, is described as new to science. The conidiomata closely resemble apothecia of a gyalectoid lichen but in section reveal their conidiomatal nature, owing close resemblance to the campylidia of the family Pilocarpaceae. The new taxon is closely related to and congeneric with a lichen described in 1955 as *Ephelidium heardense* C.W. Dodge & E.D. Rudolph, but differs in certain anatomical and chemical details. Unfortunately, the generic name *Ephelidium* C.W. Dodge & E.D. Rudolph cannot be used, although it was accepted in Species Fungorum and the Checklist Of The Lichens Of Australia And Its Island Territories, because it is a later homonym of the unrelated, non-lichenized, phytopathogenic ascomycete genus *Ephelidium* C. Spegazzini from 1921. We therefore introduce the replacement name *Nukaia* for this peculiar taxon. A structure apparently similar to the conidiomata of *Nukaia* was described in 1890 by Müller Argoviensis as "orthidium"; unfortunately, the specific material was not cited and was not found in the G herbarium, so we are unable to evaluate whether a similar or congeneric lichen is involved. It seems, however, unlikely, since Müller Argoviensis described this structure from a foliicolous lichen growing in the Atlantic rain forest of Brazil. The generic position of *Nukaia cupulifera* was tested using ITS sequence analysis, which places it in Ramalinaceae but not within any of the known genera of that family.

**MORPHOLOGICAL AND ANATOMICAL CHARACTERISTICS OF DISCOLICHENS
AT PHU LUANG WILDLIFE SANCTUARY (PLWS), LOEI PROVINCE**

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In the period between August 2005 and June 2010 discolichens were collected from tree bark and rocks at Phu Luang Wildlife Sanctuary (PLWS). The specimens were collected in seven types of forest growth, viz., coniferous, Dry Dipterocarp and Dry Evergreen Forests in addition to Lower Montane Rain Forest, Lower Montane Scrub, Mixed Deciduous Forest, and Tropical Rain Forest. Subsequent to collection, the discolichens were identified on the basis of morphological and anatomical characteristics. Characteristically, the members of this group of lichens are disc-shaped with colored apothecia. The apothecial margins also contain algae (lecanorine apothecium) or algae are absent (lecidine apothecium and biatorine apothecium). In respect to the ascospores of the discolichens examined, they were found to be variable in size, shape and type, with the type being from simple, transversely septate or muriform. It was also found that chemical characteristics were very important, particularly at the family and genus level. In terms of taxonomic identification, they were found to be classifiable under the rubrics of eleven families and fifteen genera. The fifteen genera to which they belonged were *Bacidia*, *Bellemerea*, *Brigantiaea*, *Caloplaca*, *Catillochroma*, *Haematomma*, *Lecanora*, *Lecidella*, *Letrouitia*, *Malmidea*, *Maronina*, *Megalospora*, *Micarea*, *Ramboldia* and *Vainionor*. Finally, a total of fifty species were identified.

USNEA IN INDONESIAN TRADITIONAL MEDICINE

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Usnea spp. is one of lichens used as a traditional medicine called Jamu for at least 1,000 years in Indonesia. It grows in the forest at high 800 m above sea levels. Exploitation and destruction of forests have caused these lichens to be a rare species. The ethnolichenology study have been made for knowing the diversity of *Usnea* and use these species by local people in Priangan. Taxonomic study of beard moss (*Usnea* spp.) at Priangan was carried out by using morphological, anatomical and chemical characters. The survey have found the 11 (eleven) species in Pine forest at Priangan area. Only 3 species have been used as traditional medicine and preservation of nira from Arenga catechu. The 25 formula of jamu have been sold in market was used *Usnea*.

ANTIMICROBIAL ACTIVITY OF LICHEN-FORMING FUNGI FROM GENUS *TRYPETHELIUM*

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The genus *Trypethelium* is a widely distributed crustose lichen in tropical areas especially in dry dipterocarp forest. Some metabolites produced from this lichen genus exhibited biological activity. Ascospore discharge technique was performed for isolation of lichen mycobionts from lichen thalli which were collected from various locations in Thailand. Thirty-eight of the selected mycobiont cultures were grown on Malt-Yeast-Extract medium at room temperature for 12 weeks. The restriction fragment length polymorphism (RFLP) analysis based on internal transcribed spacer (ITS) region technique was used to select 18 mycobionts as representative for further studies of secondary metabolite production. Cells of these mycobionts were harvested and extracted for substances by methanol and concentrated by rotary evaporator subsequently. Primary chemical analysis was detected by Thin Layer Chromatography with CH₂Cl₂: MeOH (10 : 0.2) as solvent system. The substances from mycobiont isolate number KY 418 exhibited 13 spots which represented a higher number than others. Furthermore, the potent antimicrobial activities from this isolate were evaluated against represented microorganisms; bacteria *Escherichia coli* and *Staphylococcus aureus*, yeast (*Candida albicans*) and a filamentous fungus (*Aspergillus niger*) by bioautography. Inhibition against *E. coli* was exhibited from spots at Rf value 0.12 and 0.56 respectively. In case of *S. aureus* the result showed that the compound from spot Rf value 0.12 inhibited the test microorganism. A clear zone from antifungal activity against *C. albicans* was recorded from spot Rf value 0.09 but the inhibition of *A. niger* spore germination occurred from compounds with long range Rf values. To compare chemical substances produced by this mycobiont with lichen substances from thalli of *Trypethelium eluteriae*, another TLC with solvent system A; toluene : dioxane : acetic acid (180 : 45 : 5) was tested for comparison of Rf value. The substances produced by the mycobiont displayed 11 spots whilst 10 spots were found from lichen thalli. The same Rf value from both were 0.14 which may be siphulin or cryptostitic acid. Rf values of 0.44 and 0.55 from the mycobiont should be evaluated for secalonic acid and emodin respectively.

4I-P

(4I-P11) Submission ID: IAL0132-00001

**A FIRST ASSESSMENT OF THE LICHEN BIODIVERSITY IN NEORA VALLEY NATIONAL PARK,
EASTERN HIMALAYA, INDIA**

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Neora Valley National Park is one of the pristine ecosystems of the Eastern Himalayas with its amazing biodiversity, and home for many rare and endangered, plants, animals and birds. The national park spreads over an area of 88 sq km bordering Sikkim and Bhutan under Kalimpong sub-division of the Darjeeling district of West Bengal state. The valley is of great ecological interest and values about 60% of its total area being primeval forest making this one of the best preserved biomes of the country. The park provides shelter and protection to various species of wildlife included in the Red Data Book. Floristically the park is rich, it shows the occurrence of 812 species of Angiosperms under 468 genera and 138 families, 4 species of Gymnosperms under 4 genera and 3 families, and 48 species of Pteridophytes under 26 genera and 18 families. The diverse phorophytes (tropical to alpine), both exposed and unexposed rocks along rivers, streams and hilly slopes and the humus rich soil support a rich growth of all kinds of lichens in the park. The investigation of over 800 specimens collected between 2007 and 2010 from the area reveals the occurrence of 160 species under 63 genera and 35 families. This includes 6 new species, 10 new records for India, 14 new records for Himalaya and 27 new records for the state of West Bengal. Of the total 160 taxa, 61 are crustose, 80 foliose and 19 fruticose. Analysis of the data reveal family Parmeliaceae shows highest generic as well as species diversity with 13 genera and 41 species followed by Graphidaceae with 6 genera and 18 species. Among the genera *Hypotrachyna* is the largest with 18 species followed by *Heterodermia* (12 species), *Lecanora* (10 species), *Graphis* (9 species) and *Cladonia* (6 species). Fourteen families are represented by 1 species each and thirty genera by 1 species each. The undisturbed primary forests from Chaudaphery to Rechilla, Mullkharka to Rechilla, Chaudaphery to Doley and Doley to Aloorbari show rich in lichen diversity unlike to other reserve forests particularly in the low altitudes.

4I-P

(4I-P12) Submission ID: IAL0156-00001

**TAXONOMIC STUDY OF THE GENUS *PORPIDIA* (PORPIDIACEAE, ASCOMYCOTA)
FROM CHINA AND SOUTH KOREA**

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The crustose lichen genus *Porpidia* Körber is a saxicolous lichen widely distributes in China and South Korea, it is a genus segregate from the large classical genus *Lecidea*. There has no systematic study ever been done in these two countries, this is the first revisionary study of the genus in this region. 12 species are confirmed in this study, including two new species from China (*Porpidia* a and b), one new record to South Korea (*P. macrocarpa*) and three new records to China (*P. flavicunda*, *P. soredizodes* and *P. thomsonii*). Brief description of each new species and new record is presented with the morphological, anatomical and chemical characters. A key to all the known species is also provided.

DISTRIBUTION OF HAEMATOMMA SPP. IN JAPAN

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We collected specimens of *Haematomma* spp. while investigating the lichen biota in Miyazaki Prefecture on the island of Kyushu. *Haematomma* spp. are attractive because of their reddish apothecia. However, there have been a few description related this genus in Japan. Now, seven taxa, *H. africanum*, *H. fauriei*, *H. persoonii*, *H. puniceum* subsp. *pacificum*, *H. puniceum* subsp. *puniceum*, *H. puniceum* subsp. *esoredioatum* were listed in Japanese species (Harada et al. 2002), based on papers of Sato (1941) and Asahina (1964). Staiger & Kalb (1995) reported only three Japanese *Haematomma*, *H. africanum*, *H. fauriei* and *H. persoonii*. Our and herbarium's specimens were examined by morphological, anatomical and chemical studies. Constituents of thalli were identified by HPLC with a photodiode-array detector. *H. collatum* and *H. accolens* are here reported for the first time from Japan. *H. collatum* is distributed in islands of Honshu and Kyushu in a warm temperate zone. *H. accolens* is found in only Miyazaki Pref. *H. fauriei* and *H. persoonii* were also identified. *H. fauriei* is distributed in a cool temperate zone; on the other hand, *H. persoonii* is done in a warm temperate zone. *H. puniceum* subsp. *pacificum* and *H. puniceum* subsp. *puniceum* were not recognized. It is supposed that these two species may be mistaken with *H. collatum*. Consequently, we confirmed five species, *H. accolens*, *H. africanum*, *H. collatum*, *H. fauriei* and *H. persoonii* in Japan.

**CONCENTRATION OF RADIOISOTOPES IN LICHENS BEFORE AND AFTER
FUKUSHIMA NPP ACCIDENT IN JAPAN**

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After the earthquakes and tsunami, and the following disaster at the Fukushima Nuclear Power Plant (NPP) on March 11, 2011, high concentration of radioisotopes, i.e., radiocesium (¹³⁷Cs, ¹³⁴Cs) and radioiodine (¹³¹I) has been reported from eastern Japan. Most reports came from atmosphere, surface soil, water and vegetables, and by far none of such investigations have been devoted to fungi. Fungi, especially lichens and mushrooms are known to accumulate radioisotopes from surrounding environment. We therefore investigated the concentrations of radioisotopes (¹³⁷Cs, ¹³⁴Cs, ¹³¹I) in lichens and mushrooms collected in Tsukuba city (ca. 170 km south of the Fukushima NPP) and adjacent area using a low background gamma-ray detector. In order to evaluate the values, we also measured those radioisotopes of herbarium lichen specimens which were collected before the Fukushima NPP accident. Radioisotope concentrations of lichens within the campus of University of Tsukuba were as follows. *Phaeophyscia spinellosa* growing on horizontal surface of concrete: ¹³⁷Cs, ¹³⁴Cs, ¹³¹I = ND, ND, ND on February 19, 2010; 12641±279, 12413±285, 8436±207 (Bq/kg fresh weight) on April 26, 2011; 14876±314, 13197±256, ND on June 30, 2011. *Dirinaria applanata* growing on trunk: 3558±129, 3219±105, 3438±103 on April 26, 2011. *Physcia orientalis* growing on trunk: 20553±339, 18049±248, ND on June 30, 2011. Lichens tend to accumulate the radioisotopes except ¹³¹I as the days go by. The results from mushrooms within the campus were variable and generally showed less concentration of radioisotopes than lichens. However, it is surprising in that lignicolous mushrooms (e.g. *Schizophyllum*: 5719±202, 5506±194, 8681±463 on April 26, 2011) have significantly higher concentration of radioisotopes than ectomycorrhizal mushroom (e.g. *Russula*: ND, 130±30, ND on April 26, 2011). With the herbarium specimens of *Parmotrema tinctorum* collected around Fukushima Prefecture, all values of radioisotopes were ND on September 16, 2008, but 506±90 of ¹³⁷Cs was detected from the sample collected on December 5, 1964. The latter is probably derived from the fallout of nuclear tests.

4I-P

(4I-P15)

Submission ID: IAL0221-00001

TAXONOMIC STUDY ON THE LICHENS OF “LECIDEA GROUP” FROM WESTERN CHINA

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The genus *Lecidea* (s. lat., sensu Zahlbruckner 1926) is one of the largest lichen genera and has an extraordinary wide circumscription accepting more than 1,350 taxa in the rank of species. However, in the past several decades many obviously unnatural units have been excluded based on the structure of the ascomata, especially the nature of the hamathecial tissues, ascus apical structures, and exciple. Our work focuses on “*Lecidea* group”, the genera and species which have crustose to squamulose thallus containing protococcoid algae, dark to black apothecia without a thalline margin, and 8 simple, colourless spores per ascus. During our taxonomic study of “*Lecidea* group” from Western China, we found 15 new records for the country: *Amygdalaria continua* Brodo & Hertel, *Carbonea vorticosa* (Flörke) Hertel, *Lecidea berengeriana* (A. Massal.) Nyl., *L. confluens* (Weber) Ach., *L. cyrtidia* Tuck., *L. diducens* Nyl., *L. lapicida* var. *pantherina* (DC.) Ach., *L. promiscens* Nyl., *L. pseudaglaea* Hertel, *L. tessellata* var. *caesia* (Anzi) Arnold, *Lecidella bullata* Korber., *L. nashiana* Knoph & Leuckert, *Porpidia flavicunda* (Ach.) Gowan, *P. soredizodes* (Lamy) J.R. Laundon and *P. thomsonii* Gowan. Brief description of each species is presented with the morphological, anatomical and chemical characters.

(4I-P16)

Submission ID: IAL0243-00003

**DETERMINATION OF IRON (Fe) AND ZINC (Zn) CONTENTS IN SOME LICHENS
IN NONGSOUNG DISTRICT, MUKDAHAN PROVINCE, THAILAND**

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This research was to study the concentration of Fe and Zn contents in thallus of *Dirinaria picta*, *Laurera benguelensis*, *Parmotrema tinctorum* and *Pyxine coccifera* from Nongsoung District, Mukdahan Province. Atomic Absorption Spectrometry (AAS) technique was used to determine amounts of metals in corticolous lichens. The high concentration of Fe were found in *Pyxine coccifera* and *Dirinaria picta*; 0.959 mg g⁻¹ and 0.853 mg g⁻¹, respectively. In other hand, Zn concentration was low such as *Parmotrema tinctorum* 0.293 mg g⁻¹, *Laurera benguelensis* 0.213 mg g⁻¹. The trace element absorption in lichens thallus can be used for bio-monitoring of air pollution.

(4I-P17)

Submission ID: IAL0244-00001

**MEASURING NITRATE AND SULFATE DEPOSITION IN LICHENS AFTER TRANSPLANTATION
TO POLLUTED SITES IN BANGKOK, THAILAND**

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The ion chromatography was performed to measure nitrate and sulfate deposition in lichens transplanted to public parks around Bangkok city. The inorganic anions in lichens were separated and quantify by using column IonPac AS12A and suppressed conductometric detection with ASRS-300 (4 mm). The eluent was a mixture of 2.7 mM Na₂CO₃ and 0.3 mM NaHCO₃ by isocratic elution. The chromatographic conditions were validated in terms of detection limit, precision and linearity. It was found that the detection limit of nitrate and sulfate were 0.014 mg/L and 0.019 mg/L respectively, and precision in seven repetitions (%RSD) of two ions were more than 2.5% at concentration lower than 1 ppm and less than 0.6 % at concentration higher than 1 ppm. The linearity was obtained by correlation coefficient (R²) better than 0.998. The results found that the amounts of nitrates and sulfates in transplanted lichens from eleven public parks had increasing tendency with exposure time in Bangkok during 19/9/2010 to 5/2/2011. However, the amount of both ions in the last sampling period 20/4/2011, declined in all public parks because of rain before samples were collected. Nevertheless these amounts were still higher than those at Khao Yai National Park and the control site. No correlations, R² below 0.3, were found between nitrate and sulfate from CS, KY, BS and SP, whereas the other sites had R² higher than 0.5.

4I-P

**QUANTITATIVE DETERMINATION OF SECONDARY METABOLITES IN LICHEN
PARMOTREMA TINCTORUM BY HIGH-PERFORMANCE LIQUID CHROMATOGRAPHY**

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Lichens produce secondary metabolic products for auto-protection against adverse environment which vary among habitats. Precise determination of lichen products is essential to enhance our understanding on production and roles of lichen novel products, which have extensive implication on sustainable utilization in several aspects. The aim of this work was to quantify orsellinic acid, methyl orsellinate and lecanoric acid in lichen *Parmotrema tinctorum* using HPLC system of HP1100 binary pump. The separations were carried out on a Hypersil C18 column (250 millimeters x 4.0 millimeters, 5 micrometers) under gradient elution and UV detection. Two mobile phases, methanol and 1% phosphoric acid were employed. The chromatographic method was validated, which the result showed that the method was suitable for quantitative analysis. Orsellinic acid, methyl orsellinate and lecanoric acid used for making standard calibration curve were prepared in the laboratory by solvent extraction and purification were then performed by column chromatography. The lichen samples were collected from five forests at Khao Yai National Park, which were Dry dipterocarp forest, Tropical rain forest, Dry evergreen forest, Lower montane forest and Secondary forest. These forests situated at different attitude which vary in environmental surrounding. Lichen substances were extracted at room temperature with acetone, filtered and evaporated to dryness. The residues were then dissolved by methanol in exact volume using benzoic acid as an internal standard. The solution samples were filtered through 0.45 micrometers syringe membrane before injection to HPLC. The amount of orsellinic acid, methyl orsellinate and lecanoric acid in lichen samples collected from five forests were evaluated and compared.

NOTES ON OCCURRENCE OF CYANOLICHENS IN INDIA

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Cyanolichens constitutes a separate group of lichenized fungi having cyanophycean algae either alone or along with a chlorophycean primary photobiont. Cyanolichens in India are represented by 200 species belonging to 28 genera and 10 families, which is about 8.6% of the total lichen flora of the country. Out of the total about 10% of them are bipartite and 3 to 4% are tripartite. *Leptogium*, *Collema*, *Sticta* and *Lobaria* are the most common epiphytic cyanolichens which also grow occasionally on rock and soil. Similarly, *Peltigera* and *Stereocaulon* are the dominant genera growing on soil. Collemetaceae is the most common and widely distributed family and it includes 67 species under 3 genera. However, Lichinaceae is the most diverse family as it includes 13 species within 8 genera. Altitudinal distribution clearly showed that most of the cyanolichens preferred subtropical (700–1,500 m) to temperate (1,500–3,500 m) regions while alpine region hosted limited number of 30 species. Among all lichenogeographic regions western Himalaya exhibits the concentration maximum number of cyanolichens wherein a total of 111 species recorded. A wide range of cyanobionts are found in Indian cyanolichens. The filamentous forms with heterocyst include *Dichothrix*, *Nostoc*, *Scytonema*, *Calothrix* and *Stigonema* while the common unicellular forms are *Anacystis*, *Gloeocapsa*, *Chroococcus*, *Aphanocapsa* and *Xanthocapsa*. The highest diversity of cyanobiont is recorded in the family lichinaceae represented by *Chroococcus*, *Gloeocapsa*, *Nostoc*, *Scytonema* and *Stigonema*. Cyanobiont in the lichen usually determines the consistency and growth form of the cyanolichens leading to formation of crustose, squamulose, foliose and dimorphic habits. It is now well established that cyanolichens require liquid water for their metabolic activity. Hence, they act as an indicator of shady, wet and moist habitats. In India it is observed that cyanolichens prefer to grown in least disturbed environments. These qualities of cyanolichens make them excellent biomonitors and can be utilized for environmental monitoring in relation to various anthropogenic disturbances and climate change.

4I-P

PHYSICIACEAE OF PANAMA

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During a fieldtrip to Panama in February-March 2010 by the first author, lichens were collected from all kind of substrata, in lowland, coastal- and upland areas in the provinces of Bocas del Toro, Chiriqui, Coclé and Panama. All material is deposited in the private herbarium of P. van den Boom. Lichen morphology was examined by standard techniques using stereo and compound microscopes. Chemical constituents were identified by TLC and HPLC. The most recent checklist of lichens of Panama is published online by Feuerer (2008). Some groups such as the foliicolous lichens and the lichenicolous fungi (Etayo 1997) and the Thelotremataceae (Hale 1978) are rather well known in that country. However, concerning the Physciaceae only a few genera are reported and even a few species are known of the wide and widespread genus *Buellia* s. l. (Marbach 2001). An annotated list including c. 45 species of Physciaceae is presented in this study. Among them many are new records for Panama or constitute interesting and rare neotropical species (e.g. *Cratiria americana*, *Gassicurtia rufofuscescens*, *Stigmatochroma kryptoviolascens*) and some are certainly new species (e.g. *Cratiria* aff. *lauricassiae*). The best represented genus is the macrolichen *Heterodermia* with c. 15 species.

3A: Molecular phylogenetics

(3A-P1) Submission ID: IAL0001-00001

MOLECULAR PHYLOGENY REVEALS OVERLOOKED DIVERSITY WITHIN THE JELLY FUNGI GROWING ON BEARD-LICHENS.

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The genera *Usnea* and *Protousnea* (beard lichens) are home to a substantial diversity of lichen-inhabiting fungi. Several of these fungi induce the formation of conspicuous galls or deformations on the host-lichen thallus and, in particular, galls formed by basidiomycetous taxa exhibit a considerable variation in size, shape and colour. Basidiomycetes growing on beard lichens are currently represented by the genera *Biatoropsis* (1 species: *B. usnearum*), *Cystobasidium* (1 species: *C. usneicola*) and *Tremella* (3 species: *T. nashii*, *T. santesonii* and *T. stevensiana*). Previous works confirmed the placement of the genus *Biatoropsis* within the Tremellales, but the phylogenetic position of other Tremellales growing on *Usnea*, and the systematic placement of *Cystobasidium usneicola* (currently in Cystobasidiales) have never been tested by molecular methods. We use a taxon sampling covering Asia, Australia, Europe, North America and South America, and two different data sets of nuclear and mitochondrial ribosomal DNA markers to study the phylogenetic relationships of these taxa in a broader scale (nSSU, 5.8S, and nLSU) and to tackle species delimitation aspects (ITS1, 5.8S, ITS2 and mtSSU). Possible co-evolution patterns with their *Usnea* and *Protousnea* hosts are discussed.

(3A-P2) Submission ID: IAL0036-00001

HOW MANY GENERA ARE HIDDEN WITHIN *BUELLIA* SENSU LATO?

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The lichen genus *Buellia* forms the core of the *Buellia* clade within the family Physciaceae. This clade contains crustose to squamulose and microfoliose forms with apothecia or mazaedia, including the bulk of the former Caliciales and the genera *Dirinaria* and *Pyxine*. The crustose forms with apothecia have traditionally been classified as *Buellia* sensu lato, but genera such as *Amandinea* and *Hafellia* were subsequently segregated and, eventually, Marbach in 2000 proposed a new classification recognizing a large number of genera especially for tropical epiphytic species, such as *Baculifera*, *Chrismofulvea*, *Cratiria*, *Gassicurtia*, and *Stigmatochroma*. We tested the proposed classification using a combination of mtSSU, nuLSU, and ITS data. For that purpose, we assembled nearly 200 sequences of Physciaceae focusing on *Buellia* sensu lato, including 70 sequences newly generated from tropical epiphytic species. As a result, most of the genera proposed by Marbach are supported, but a more thorough revision is required to accommodate other species currently retained in *Buellia* sensu lato. We discuss the problem of typification of *Buellia*, since the current typification makes *Buellia* and *Hafellia* congeneric and the name *Buellia* s.str. applicable to the group of species currently classified under *Hafellia*.

A PHYLOGENETIC ANALYSIS OF THE UMBILICATE *ASPICILIA* (MEGASPORACEAE, ASCOMYCOTA) BASED ON NU-ITS AND NU-LSU SEQUENCE DATA

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The genus *Aspicilia* is the largest genus in the family Megasporaceae and includes a number of morphologically distinct groups of species (e.g., umbilicate, subfruticose, crustose). One of the smallest groups consists of the two umbilicate species *A. caesiascens* Pisút and *A. oxneriana* O. B. Blum that are characterized by the presence of central strands in their thalli, the lack of secondary substances and that they are attached to rocks. Currently the phylogenetic relationships of the two umbilicate taxa are poorly understood. Our aim was to reconstruct the phylogeny of these two species to test whether certain characters found only in *Aspicilia* (such as umbilical growth form) have evolved repeatedly or only once. We used the nuITS and nuLSU rDNA as molecular markers. Convergent evolution of the umbilicate growth form was revealed by molecular data in Megasporaceae. Our analysis shows that *A. caesiascens* with small spores, eight spored asci and a subhymenial algal layer form a monophyletic group that is placed in the genus *Lobothallia* s.lat. Further, *A. oxneriana* that has larger spores, 1-4 (6) spored asci and lacks a subhymenial algal layer form a monophyletic group and nests within the genus *Circinaria*. The variability and taxonomic importance of particular features in both species are discussed. Two new combinations in the genera *Circinaria* and *Lobothallia* are necessary. A key and distribution maps to the species present in Iran and the Central Asia are provided.

CURRENT STATUS OF THE PHYLOGENY OF THE FAMILY MEGASPORACEAE

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The family Megasporaceae (Pertusariales, Lecanoromycetes, Ascomycota), as currently circumscribed, includes five genera (*Megaspora*, *Lobothallia*, *Aspicilia*, *Sagedia*, and *Circinaria*) and ca. 300 species world-wide. Species of the family are lichenized with chlorococcal algae. While the majority of species grow on rocks (mainly crustose forms, but include several subfoliose, to umbilicate taxa), others are commonly found on soil, including subfruticose (erratic or vagrant) specimens, and a limited number of species grow on bark and wood. Representatives from this family are found in diverse habitats, including: maritime habitats, open forests, semiarid steppes, and very hot deserts. Earlier studies have shown that the speciose genus *Aspicilia* sensu lato is a polyphyletic. For example, *Aspicilia* s. str. (*A. cinerea* group), *Sagedia* s. str. (*S. zonata* group) and *Lobothallia* s. lat. (including *L. farinosa* and *L. recedens*) correspond to well-supported monophyletic lineages within Megasporaceae. Many 'manna lichen' species have been moved to *Circinaria*, but our preliminary results shown that the genus is composed of two major lineages: a group of strictly saxicolous species, containing aspicilin and without pseudocyphellae (*C. contorta*, *C. calcarea*, *C. cupreogrisea*, *C. leproscens*, and *C. gibbosa*) and a group including both vagrant and saxicolous taxa, with pseudocyphellae but without aspicilin (so far called 'manna lichens' or sphaerothallioid lichens). In addition, we assessed the relationship of some representatives from corticolous and terricolous species, including *A. uxoris*, *A. tibetica*, *A. cerspiana*, and *A. mansourii*, using a combined dataset from two nuclear ribosomal loci (ITS and LSU). Our result shown that *A. uxoris* group is also other generic-level monophyletic group within traditional *Aspicilia* s. lat., and sister to *Lobothallia* s. lat.

**A PHYLOGENETIC STUDY OF THE *ASPICILIA INTERMUTANS* COMPLEX
(MEGASPORACEAE)**

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The genus *Aspicilia* A. Massal. was recently redefined and distinguished from the closely related genera *Circinaria*, *Lobothallia*, *Megasporea* and *Sagedia*. *Aspicilia* s.str. (sensu Nordin et al. 2010) is defined by a set of morphological characters such as exclusively crustose, sometimes radiating thallus, 8-spored asci, ellipsoid to rarely globose spores, sized 10–30 x 8–20 µm. The conidia length is rather variable (11–40 µm). Aspicilin is absent and substictic acid a unique substance in the genus, though present only in few species. Following the new generic circumscription the taxonomic position of many species in *Aspicilia* has to be confirmed. The aim of our study is to examine the *Aspicilia intermutans* complex, basing on extensive sampling in a limited area. 18 Heteromorphic specimens from two Greek islands were investigated to get an impression of the variation within populations, and compared with specimens from NW Iran and southern France. The analysis uses the nuITS molecular marker, chemistry and several morphological characters. A phylogenetic analysis was performed using the parsimony method (program TNT). Our results indicate that some morphological characters traditionally used to circumscribe *Aspicilia* species such as chemistry and ascomata and conidiomata structure led to the formation of non-monophyletic groups. A minor part of the specimens previously recognized as *Aspicilia intermutans* were found to be distributed across the *Aspicilia* s.l. tree and seem to represent taxonomically distinct entities, most likely including undescribed species.

**CORTICIALES ALLIES OF LICHENIZED/LICHENICOLOUS BASIDIOMYCETES:
PHYLOGENY AND CHARACTER EVOLUTION**

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Corticiales is a poorly investigated order of basidiomycetes which have been largely neglected in mycological inventories due to their inconspicuous fruiting bodies and difficulties in their identification. Predominantly consisting of saprotrophic corticioid fungi, the order also harbours a few lichenized/lichenicolous species. While Corticiales fungi play various ecological roles in terrestrial ecosystems, yet they have very similar morphological characteristics, with little external variation, rendering their taxonomy and generic delimitations problematic. Lichenicolous taxa appear as teleomorph or exclusively anamorph members. In this study, we attempted to make a comprehensive sampling of the order, with representatives from all ecological guilds and nutritional modes present in the Corticiales, including lichenized and lichenicolous taxa. To examine the circumscription of genera and the phylogenetic relationships among the species, we analyzed nuclear and mitochondrial sequence data with maximum parsimony and Bayesian methods and also studied morphological and ecological characters. We believe a well-resolved taxonomic backbone for Corticiales is essential before making evolutionary assessments. Our study yields a refined family arrangement for this order and recognition of a number of genera and species new to science. All lichen associates (lichenized and lichenicolous species) of Corticiales are shown to be accumulated in the newly circumscribed family Corticiaceae s.s., leaving the bulk of saprotrophic species in the two corticioid families Punctulariaceae and Vuilleminiaceae. Some conclusions are made about the relationships between fertile and anamorph taxa. For instance, the lichenicolous anamorph *Marchandiomyces corallinus* is shown to be a close relative of the teleomorphic corticioid genus *Marchandiopsis*. We consider the justifications towards the occurrence of more than one nutritional guild in a single genus, and its evolution in the Corticiales.

3A-P

GENUS AND SPECIES CONCEPTS IN *DICTYONEMA* S. L.

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Dictyonema sensu lato is a large, pantropical genus of basidiolichens that produces crustose to foliose thalli lichenized with cyanobacteria and corticioid to stereoid basidiocarps. There are thought to be more than 20 species in the genus, but species concepts are currently not well established. The most widely used concepts are those of Parmasto (1978), who adopted a relatively wide species concept, emphasizing thallus anatomy and treating morphological differences largely as phenotypic variation. Consequently, his monograph synonymized several different taxa under key names such as *Dictyonema pavonia* (*Cora glabrata*) and *Dictyonema sericeum*. Recent investigations in our labs have begun to use DNA sequences obtained from hundreds of Neotropical specimens, including extensive collections from the Galápagos Islands, to elucidate relationships of *Dictyonema* species and their close relatives. Molecular phylogenies based on nuLSU and nuITS rDNA sequences have resolved five distinct generic lineages within Parmasto's concept of *Dictyonema* sensu lato: *Cora*, *Corella*, *Dictyonema* s.str., *Cyphellostereum* and the monospecific *Acantholichen pannarioides*. The entire group includes very different morphotypes and photobiont interactions, although all species form lichenized associations with a scytonematoid Rhizonema photobiont. In *Dictyonema* s.str. and *Cyphellostereum*, the cyanobacteria maintain their filamentous structure, while in *Cora*, *Corella*, and *Acantholichen*, the cyanobacterial cells assume a "chroococcoid" shape. Based on our phylogenetic reconstructions, we are now able to recognize important characters for delimiting genera and species, including color of the thallus, presence of a hypothallus and/or prothallus, growth form, texture of upper and lower surfaces, presence and shape of basidiocarps, and anatomical features of the cyanobacteria and fungal sheath cells. Based on these results, we conclude that the collective species *Dictyonema glabratum*, *D. sericeum*, and *D. phyllogenum* represent about 25 to 30 different species.

(3A-P8)

Submission ID: IAL0104-00002

NEW MOLECULAR DATA ON PYRENULACEAE FROM SRI LANKA REVEAL TWO WELL-SUPPORTED GROUPS WITHIN THIS FAMILY

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The lichen family Pyrenulaceae is an important element of the epiphytic lichen flora in wet tropical forests. It mainly comprises crustose and corticolous species associated with the green algal genus *Trentepohlia*. This family belongs to Pyrenulales (Eurotiomycetes), an order characterized by perithecial ascomata of ascohymental origin with fissitunicate asci and septate to muriform ascospores. Pyrenulaceae is a large family with 11 genera and c. 230 known species. As with many other crustose corticolous tropical groups of lichens, molecular data is lacking for most species, mainly due to difficulties in recovering good quality genomic DNA from herbarium specimens. The few existing molecular studies including species of Pyrenulaceae have looked at the phylogenetic placement of families and genera traditionally classified within the order Pyrenulales, but none so far have focused on phylogenetic relationships within Pyrenulaceae. The sampling of fresh specimens from different localities in Sri Lanka allows us to assemble a preliminary molecular dataset (ITS, nuLSU and mtSSU) to investigate relationships within the family Pyrenulaceae. The taxon sampling includes *Anthracothecium nanum*, *Pyrgillus javanicus* and 19 taxa of *Pyrenula* (among which 6 are from Sri Lanka). Preliminary results show with strong support that all taxa sampled divide into two major clades. One clade includes *Anthracothecium australiense*, *A. prasinum*, *Pyrenula chlorospila*, *P. macrospora*, *P. nitida*, *P. pseudobufonia*, *P. quassiaecola* and *P. thelomorpha*. The other clade includes all taxa from Sri Lanka, viz. *Pyrenula aspistea*, *P. mamillana*, *P. masariospora* and *P. finitima* (= *P. subcongruens*) as well as *Pyrenula cruenta*, *P. laevigata*, *P. subpraelucida* and *Pyrgillus javanicus*. Results suggest that the presence or absence of pseudocyphellae is correlated with these two clades.

3A-P

(3A-P9)

Submission ID: IAL0114-00001

CRYPTIC DIVERSITY IN *TRYPETHELIUM ELUTERIAE* IN THAILAND

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The diversity of tropical crustose lichens is poorly known. In a project to better understand the diversity of Trypetheliaceae in Thailand, we isolated mycobionts of 38 samples from different locations within the country. ITS polymorphism analysis using the ITS-RFLP technique divided the samples into 12 groups. We generated ITS and mtSSU rDNA sequences of 1-3 representative of each group. The concatenated data set was analyzed using maximum likelihood and Bayesian approaches. The phylogenetic estimate suggests that at least nine *Trypethelium* species occur in Thailand. The phylogenetic analysis also revealed the presence of three distinct clades within a morphologically-circumscribed *Trypethelium eluteriae*. This is another indication of the presence of cryptic species within crustose tropical lichenized fungi and shows the importance of including molecular data in circumscribing species to fully understand the diversity of lichen-forming fungi. Additional studies are in progress to identify ITS barcoding gaps among species and to develop a barcoding identification system for Trypetheliaceae in Thailand that can be used throughout south-east Asia. Further, studies on morphology of mycobiont cultures and growth patterns of mycobionts are shown to provide phylogenetically important information.

PHYLOGENETIC RELATIONSHIPS OF LICHENIZED AND NON-LICHENIZED CALICIOID FUNGI AND THE EVOLUTION OF THE MAZAEIDIUM WITHIN ASCOMYCOTA

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Calicioid or mazaediate fungi constitute a very heterogeneous assemblage of diverse fungi sharing the presence of prototunicate asci and the production of a mazaedium. These mazaediate fungi were once treated as an order of Ascomycota (Caliciales) but many are now known to be nested within Arthoniomycetes, Eurotiomycetes and Lecanoromycetes, thus, confirming the high polyphyly of the group. In this study we utilize multi-gene phylogenetic analyses (based on nuLSU, ITS, mtSSU, RPB1 and mcm7) of all major mazaediate groups to study the evolution of the mazaedium, and we focus particularly on the remaining mazaediate families of unclear position within the Ascomycota.

(3A-P11) Submission ID: IAL0166-00001

IDENTITY OF *ENDOCARPON PULVINATUM*, THE ONLY SUBFRUTICOSE VERRUCARIACEAE

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Endocarpon (Verrucariaceae) comprises lichenized species which are characterized by a squamulose or subfruticose thallus, muriform ascospores and the presence of hymenial algae. *Endocarpon pulvinatum* was described by T. Fries from Norway in 1861 and is distributed in the northern part of Scandinavia, Central Europe, Iceland and on higher altitudes in North America. The species is unique in Verrucariaceae with its subfruticose habitus, bearing some resemblance to the rare North American species *Endocarpon tortuosum*. Phylogeny of Verrucariaceae is being scrutinised at present and several new genera have been proposed such as *Atla*, *Hydropunctaria* and *Wahlenbergiella*. Phylogenetic analysis have indicated that some of the present genera within Verrucariaceae are polyphyletic although there has not been any indications until now that *Endocarpon* could be polyphyletic. Five loci were sequenced (ITS, nuLSU, mtSSU, RPB1 and Mcm7) from few specimens of *E. pulvinatum* collected in Iceland. Phylogenetic analyses were conducted in order to reveal the placement of *E. pulvinatum* within the Verrucariaceae. The results indicate that *E. pulvinatum* does not belong to *Endocarpon* but should rather be placed in *Staurothele*, a crustose genus which shares muriform spores and presence of hymenial algae with *Endocarpon*.

3A-P

PHYLOGENY OF MARINE VERRUCARIACEAE BASED ON MULTILOCUS ANALYSES

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Verrucariaceae comprises mainly crustose lichens although some of its members can be squamulose, foliose or even subfruticose. Lichenicolous lifestyle is furthermore found in this family. The genus *Verrucaria* was for long suspected to be polyphyletic, which was confirmed with molecular methods by Gueidan et al. (2009). Several species of *Verrucaria* s. lat. do occur on intertidal cliffs and rocks. Some species are also inundated most of the time. Two new genera, *Hydropunctaria* and *Wahlenbergiella*, include these maritime species. In Iceland 12 species of *Verrucaria* s. lat. have been reported growing in maritime habitats. Two of those species belong to *Hydropunctaria* (*H. amphibia* and *H. maura*) while other two species belong to *Wahlenbergiella*, (*W. mucosa* and *W. striatula*). Five loci were sequenced (ITS, ncLSU, mtSSU, RPB1 and Mcm7) from more than 30 maritime specimens, mainly collected from the North Atlantic coast of Iceland in order to reveal the generic affinities of the maritime species of *Verrucaria* s. lat. occurring in the North Atlantic. Furthermore several specimens were included from coastal habitats of the southern hemisphere (Antarctica, Chile and Tasmania) to determine their phylogenetic relationships. Phylogenetic analyses revealed that most of the maritime species belong to *Wahlenbergiella*, *Hydropunctaria* on the other hand seems to comprise mainly species growing in freshwater habitats except for *H. amphibia*, *H. maura* and the Mediterranean species *H. adriatica*.

DERMATOCARPON ARNOLDIANUM AND D. INTESTINIFORME IN CENTRAL EUROPE

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Dermatocarpon arnoldianum and *D. intestiniforme*, which have been proposed to be synonyms of *D. miniatum*, were studied and compared to other specimens of the *D. miniatum* complex. The synonymization were based on material from the Nordic countries and partly from North America while material from Central Europe has not been studied earlier concerning the delimitation of the two taxa. *Dermatocarpon arnoldianum* was described from northern Norway by Degelius in 1934 while *D. intestiniforme* was described by Körber from Central Europe in 1859 as *Endocarpon intestiniforme*. The purpose of this study is to reveal whether the two names represent monophyletic taxa that can be recognized by morphological characters. Phylogenetic analysis based on four loci viz. ITS, LSU, RPB1 and Mcm7 were conducted. Eight specimens of the two species from the Alps were sequenced for the study and compared to 46 other specimens belonging to the *D. miniatum* complex from different locations world-wide. Substantial variation were detected in the sequences, especially in the ITS. Morphological study was conducted and comparison made with type material of both taxa. The results indicate that *D. arnoldianum* auct. in the Alps is an undescribed taxon, different from the Norwegian type, while the identity of *D. intestiniforme* is more questionable.

(3A-P14) Submission ID: IAL0167-00001

DNA BARCODING OF LICHENIZED FUNGI *MICAREA* AND *VERRUCARIA* SHOWS HIGH IDENTIFICATION SUCCESS

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Our project focuses on DNA barcoding and on taxonomy of approximately 500 deficiently known crustose lichens in Finland. In addition, our aim is to clarify the distribution, habitat requirements and threat status of these species. We are focusing on the genera *Micarea* and *Verrucaria*, but we are also barcoding *Arthonia* spp., *Lecania* spp. and *Lecanora* spp. Identification in these groups is often difficult with morphological characters. During our project we have created DNA barcodes for approximately 400 specimens and 180 species. Our results show that the ITS region is a useful barcode for the identification of these crustose lichens. The taxonomic status of some species should be re-evaluated. Several species are recorded as new to Finland.

(3A-P15) Submission ID: IAL0171-00001

TAXONOMIC REVISION OF *CLADONIA CARIOSA* GROUP (CLADONIACEAE) BASED ON PHENOTYPIC AND MOLECULAR DATA

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The *Cladonia cariosa* group, which includes *C. acuminata* (Ach.) Norrl., *C. cariosa* (Ach.) Spreng and *C. symphycarpa* (Flörke) Fr., is monophyletic (Stenross *et al.* 2002). The species within the group are characterized by having a persistent primary thallus and an ascyphose secondary thallus. *Cladonia acuminata* differs morphologically from *C. cariosa* and *C. symphycarpa* in having sorediate podetia, unbranched or dichotomically branched near the tips (Ahti, 2000). However, it is difficult to distinguish *C. cariosa* from *C. symphycarpa*. The characters used to differentiate these taxa from one another are the squamule size and the amount of podetium fissures, which are more abundant in *C. cariosa*. The species delimitation is further complicated by frequent lack of podetia in *C. symphycarpa* which led to use the chemical variation to distinguish *C. cariosa* from *C. symphycarpa*, but it was found that they share several chemotypes (Harris, 1975; Culberson *et al.* 1993; Piercey-Normore, 2003; Burgaz & Ahti, 2009; Bültmann & Lünterbusch, 2008). The aim of this study is to elucidate the species boundaries within *C. cariosa* group. Three loci were used for species delimitation: ITS rDNA, rpb2 and ef1 α . Maximum likelihood and Bayesian methods of phylogenetic reconstruction were employed. Transversal sections of the squamules stained with lactophenol blue solution were made to study the cortex structure, and the squamules surfaces were observed by Scanning Electron Microscopy. The phylogenetic analyses showed four strongly supported monophyletic lineages within *C. cariosa* group. These lineages are chemically variable, which restricts the taxonomic value of the chemical characters. Some micro-morphological differences in the cortical surface of the different phylogenetic lineages were found.

3A-P

(3A-P16)

Submission ID: IAL0176-00001

FOCUS ON THE WORLD CLADONIACEAE

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Cladoniaceae, with its c. 550 species and more than 10 genera, is one of the largest and most diverse families of lichen-forming fungi. The species comprise a significant component of numerous terrestrial ecosystems around the world, such as the boreal forests and the white sands of the Amazonas. *Cladonia* is the largest genus of the family, including approximately 500 species. There has been an enormous effort devoted to the Cladoniaceae. The Finnish E.A. Vainio published the first monograph of the family in the late 19th century. His work was followed by numerous regional treatments and revisions by various authors. Currently, a full size world monograph of the Cladoniaceae is under preparation by Stenroos & Ahti, and a new phylogeny is about to be completed. Our immediate goal is to produce a more accurate classification for the family. We compiled a preliminary data set of about 550 taxa representing over 250 species from around the world. At this point, ITS rDNA, IGS rDNA, EF1- α , and RPB2 regions were used as molecular markers. Phylogenetic analyses using both conventional parsimony (program TNT) and direct optimization (POY) were performed. The results enable a preliminary outline for classification. Further, we will use the phylogeny, once completed, for clarifying character evolution, for instance. We will also attempt to estimate the age and biogeographical origin of the Cladoniaceae.

(3A-P17)

Submission ID: IAL0201-00001

STICTA FULIGINOSA (LOBARIACEAE): SPECIES OR MORPHOTYPE?

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3A-P

The lichen genus *Sticta* is one of the largest genera of macrolichens, with possibly well beyond 100 species. Recent taxonomic and phylogenetic studies have indicated that the species concept in the genus is generally too broad: what has been recognized as “species”, such as *S. damicornis* or *S. weigellii*, comprise indeed several, in part unrelated lineages. One of the most striking examples of a morphotype species is *S. fuliginosa*, the most widely distributed and most commonly collected species with a supposedly cosmopolitan distribution. In virtually all treatments, any material having broad, rounded lobes with isidia on the surface rather than the margin is identified with the name *S. fuliginosa*. In the course of a revision of the genus *Sticta* in Colombia, we found that this concepts includes very distinctive morphotypes, differing in upper surface structure, lobe thickness, and the shape of the tomentum and cyphellae on the underside. Preliminary, we have identified roughly ten different species that would fit into a broad concept of *S. fuliginosa*. Molecular studies do not only confirm this revised concept but also show that several of these species are not closely related to *S. fuliginosa* but fall within other groups. Thus, the traditional concept of *Sticta fuliginosa* is that of a morphotype, rather than a group of closely related, cryptic species. This is in accordance with similar findings in other morphotype-based species complexes, such as *S. damicornis* and *S. weigellii*, which also include several, partially unrelated species lineages.

DIVERSITY AND PHYLOGENY OF THE GENUS *LOBARIELLA* (LOBARIACEAE)

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The lichen genus *Lobariella* is characterized within the family Lobariaceae by a white-tomentose underside lacking cyphellae, pseudocyphellae, and veins, but instead having pseudocyphellae on the upper surface, resembling those of *Parmelia*. For some time, the genus was considered to include five species: *Lobariella botryoides* (Yoshim. & Arv.) Moncada & Lücking, *L. crenulata* (Hook. in Kunth) Yoshim. (type species), *L. exornata* (Zahlbr.) Yoshim., *L. pallida* (Hook. f.) Moncada & Lücking, and *L. subexornata* (Yoshim.) Yoshim. The latter four species have a green photobiont, whereas *L. botryoides* has cyanobacterial photobiont. In the frame of a survey of Lobariaceae in Colombia and adjacent areas, we came across three further, undescribed species of this genus: *L. sipmanii* Moncada, Betancourt & Lücking, with cyanobacterial photobiont and otherwise morphologically intermediate between *L. crenulata* and *L. pallida*; *L. soledians* Moncada, Betancourt & Lücking spec. nova., similar to *L. botryoides* but with marginal soredia rather than laminal isidia becoming sorediate, and *L. flavomedullosa* Moncada, Betancourt & Lücking spec. nova, close to *L. crenulata* but with pale yellow medulla. A molecular phylogeny based on nuclear ITS confirms the validity of these species and also suggests that *Lobariella* should be retained at the generic level, along with further division of *Lobaria* s.lat. into three to four additional genera. *Lobariella* is an exclusively neotropical genus and found at mid to high elevations in rain and cloud forest as well as paramo. *Lobariella botryoides*, *L. pallida*, *L. sipmanii*, and *L. soledians* are more characteristic of upper montane cloud forest and paramo vegetation, whereas the other four species, all with green photobiont, are more typically found in montane rain and cloud forest. Each of the eight recognized species is illustrated and a key to all species is presented.

**TYPE AND NOMENCLATURAL STUDIES IN NEOTROPICAL SPECIES OF
THE GENUS *STICTA* (LOBARIACEAE)**

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Sticta is one of the largest, yet least studied macrolichen genera. The available treatments focus on extratropical regions including North America, southern South America, Europe, Australia, and New Zealand. No modern revision exists for the Neotropics and most of the type material on which names for neotropical material are based has not yet been studied. This applies in particular to names described by Nylander and others based on material collected in Colombia and adjacent areas mainly by Lindig, but also by other historic collectors. As part of a revision of the genus *Sticta* in Colombia, we present results from type studies of neotropical taxa, with some unexpected conclusions. Among the most intriguing cases are the names *Sticta laciniata* (Sw.) Ach. and *S. laciniata* var. *dilatata* Nyl., comprising common green morphotypes. The first was considered illegitimate, as its basionym, *Lichen laciniatus* Sw., is a later homonym of *L. laciniatus* Huds. Therefore, a separate species, *S. laciniosa* D. J. Galloway., was described for this taxon. However, under ICBN Art. 58.1, *Sticta laciniata* is to be considered a replacement name for *Lichen laciniatus* and is legitimate, cited correctly as *S. laciniata* Ach. *Sticta laciniata* var. *dilatata* is cited in Zahlbruckner's Catalogus as basionym of both *S. boliviana* Nyl. and *S. granatensis* Nyl., interpreting the citation of the name *S. laciniata* var. *dilatata* in two different publications by Nylander in 1861 and 1863 as referring to two different taxa. However, in 1863, Nylander referred to the name established in 1861, for which in 1874 he introduced, cryptically, the new name *S. boliviana*. This name is legitimate, even if it includes the type of *S. laciniata* var. *dilatata* and there was no need to establish a replacement name at the species level, because priority does not apply to names at different ranks. Therefore, *S. dilatata* (Nyl.) Vain. [raising *S. laciniata* var. *dilatata* to species rank], is to be considered a homotypic synonym of *S. boliviana*. *Sticta granatensis*, on the other hand, and contrary to Zahlbruckner's interpretation, is not based on *S. laciniata* var. *dilatata*, but was established separately with a different type.

3A-P

THE *STICTA WEIGELII* COMPLEX (LOBARIACEAE): TROPICAL TAXA ADD ANOTHER LEVEL OF COMPLEXITY

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The correct application of the name *weigeli* is one of the great mysteries in the lichen genus *Sticta*. Traditionally, most material with a cyanobacterial photobiont, non-pedunculate thalli, and marginal isidia has been named *Sticta weigeli* by a variety of authors. In a molecular phylogenetic study, McDonald and co-authors in 2003 restricted the application of the name to specimens with cylindrical isidia and a K+ yellow medulla. This was confirmed by Galloway in 2006, after having studied the type material. In the course of a survey of the genus *Sticta* in Colombia and Costa Rica, it was found that material which fitted the concept of *S. weigeli* belonged to a larger number of different morphotypes, separated chiefly by lobe configuration, color of the upper and lower side, cyphellae morphology, and type and color of the isidia. In a parallel study, it was also discovered that the K-reaction of the medulla depended, in part, on the way material was collected and dried: specimens kept moist for a prolonged time or dried in a plant press or with heat tended to have a K+yellow medulla, even if thallus portions of the same specimens which had been air-dried exhibited a K-negative medulla. It was therefore clear that neither the molecular study performed by McDonald et al. nor the description of the type material provided by Galloway was sufficient to elucidate the correct application of the name *weigeli*, and we restudied the type to assess characters such as lobe configuration, coloration, and type of isidia. It was found that the name *weigeli* applies to a clade of tropical specimens that has a much branched thallus with canaliculate, dark brown lobes, delicate, cylindrical to coralloid, brown-black isidia, and a dark brown tomentum on the underside throughout.

**HOW MANY SPECIES ARE THERE IN *RHIZOCARPON GEOGRAPHICUM* GROUP?
A PHYLOGENETIC STUDY OF THE COMPLEX**

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The *Rhizocarpon geographicum* group described by Runemark (1956) includes currently almost 24 yellow pigmented species with I+ blue reacting medulla and muriform ascospores. The taxonomy of the group has only suffered minor changes during the last 50 years. However, species delimitation within the group is still a highly problematic issue. We studied the inter- and intraspecific variation in the *R. geographicum* group using the results from two sets of characters: anatomic-morphological and molecular characters. In a global view, we compared the results with a possible eco-geographic pattern. Specimens of 14 species from high altitudes in the Iberian Peninsula (100 samples) were studied in detail to clarify the phylogeny of morphological species under a molecular framework. More than 20 morphological and chemical characters were statistically studied. 150 specimens included in the *R. geographicum* group from 14 locations distributed worldwide (North-Pole, Europe, America, Asia, Oceania and South-Pole), as well as other closely related taxa, were investigated in order to shed light on the biogeography of the group. Molecular data were obtained from ITS region of nuclear ribosomal DNA and mitochondrial LSU for the mycobiont. Phylogenetic inference was performed using Maximum Parsimony methods and Bayesian (MC) 3 tree-sampling. Our results showed that: (I) All the specimens studied and previously classified as members of the *R. geographicum* group formed a monophyletic clade, supported by high bootstrap and posterior probability. (II) Morphological characters traditionally used in the identification of species were proved to be highly plastic and inconsistent, leading to a fuzzy taxonomy within this group. The morphological variability observed could be due to the plasticity of the characters and their adaptation to different micro-ecological conditions. (III) We suggest that the genus *Rhizocarpon* needs a thorough review based on a combined morphological and molecular data: our results have shown that *R. superficiale* species is not included in the subgenus *Rhizocarpon* s. str. and is closer to the subgenus *Phaeotallus*. (IV) The *R. geographicum* group includes several well-supported clades that show a bipolar distribution pattern; many samples are distributed in highly distant geographical areas. (V) Molecular data also showed a high genetic diversity within the studied populations.

3A-P

PHYLOGENETIC POSITION OF THE CRUSTOSE *STEREOCAULON* SPECIES

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Species traditionally included in the genus *Stereocaulon* (lichenized ascomycetes) are characterized by a dimorphic thallus that consists of a crustose primary thallus and a fruticose secondary thallus (pseudopodetia). However, six crustose species lacking a fruticose secondary thallus are currently included in the genus. Four of these have been included in molecular analyses and their inclusion in the genus was supported. Whether the crustose growth form is a plesiomorphic or apomorphic feature within *Stereocaulon* has remained unresolved due to contradictory placements of the crustose species in earlier studies. The aim of the present study is to clarify the position of the crustose *Stereocaulon* species by adding molecular data, especially of the crustose species not included in earlier analyses, i.e. *Stereocaulon nivale* and *S. plicatile*. The inclusion of *S. plicatile* in the genus is particularly interesting as it is the only species in the genus with submuriform to muriform ascospores. Phylogenetic relationships were examined using ITS1-5.8S-ITS2 and β -tubulin sequences in parsimony analyses. The results show that the crustose species do not form a monophyletic entity and suggest that the crustose growth form is a plesiomorphic feature within *Stereocaulon*. The inclusion of the newly sequenced *S. nivale* and *S. plicatile* in *Stereocaulon* is confirmed as these species are nested in the genus. The nested position of *S. plicatile* indicates an independent gain of the submuriform to muriform spore type within the genus.

(3A-P23)

Submission ID: IAL0270-00001

MULTILOCUS-BASED PHYLOGENY AND SPECIES RECOGNITION WITHIN THE COSMOPOLITAN *PELTIGERA NEOPOLYDACTYLA-DOLICHORHIZA* COMPLEX

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The *Peltigera neopolydactyla-dolichorhiza* complex is broadly distributed, growing in boreal and temperate regions from northern Norway to southern Chile, as well as in tropical mountains. Observed morphotype and chemotype variation within this complex suggested the presence of multiple undescribed species. This was confirmed based on a preliminary phylogeny using the ITS region, where *P. neopolydactyla* and *P. dolichorhiza* are not distinct monophyletic species, but rather form a complex assemblage of several species, with some well-known species, such as *P. hymenina*, nested within that species complex. A comprehensive molecular phylogenetic study and a taxonomic revision of this complex are urgently needed. We first generated single-locus and multilocus phylogenies for the entire section Polydactylon (which includes the *P. neopolydactyla-dolichorhiza* complex), using traditional ITS and nuLSU markers, as well as new protein-coding loci from the AFTOL project. Using 454 generated sequences spanning the entire genome of two species, we are developing primers to amplify and sequence intergenic spacers to enhance species recognition within this complex. We will assess species delimitation in the *P. neopolydactyla-dolichorhiza* complex by applying a pluralistic approach e.g., phylogenetic and population genetic methods. A detailed study of morphological and chemical characters is conducted to determine their correlation with genetically inferred species.

**SIMPLE TECHNIQUE FOR ON SITE IDENTIFICATION OF *PYXINE COCOES* (Sw.) NYL.,
A FOLIOSE LICHEN, BASED ON GENOSENSOR**

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A simple technique for an on-site identification of *Pyxine cocoes* (Sw.) Nyl., a foliose lichen, based on variable sequence domains within the internal transcribed spacer (ITS) region had been developed. This technique involved an isothermal DNA amplification of 84 nucleotides fragment of target ITS element for DNA signals multiplication at 63 °C for 2 hours and a signal detection via visual fluorescence signals simultaneously using DNA binder. Results of the detection can be observed with unaided eye within 2 hours without the need of thermocycler and gel electrophoresis. DNA signals were detected only from *Pyxine cocoes* but not from *Chrysothrix xanthina* Kalb. and *Parmotrema tinctorum* (Nyl.) Hale. The detection limit was at 50 copies of target DNA domains per reaction, equally to 25 cells. This constitutes a basis for a simple and accurate detection of target lichen species, suitable for field application.

3B - 1: Bioinformatics

(3B-1-P1)

Submission ID: IAL0057-00007

MYCO-LICH: A NEW TOOL FOR DEVELOPMENT OF IRANIAN MYCOLOGY-LICHENOLOGY

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The MYCO-LICH (www.myco-lich.com) web application is a new information system, aimed to facilitate and promote biodiversity studies in mycology and lichenology in Iran. This website is powered by Google Apps and has two main directions: educational and research. MYCO-LICH serves as a repository of modern descriptions, distributions maps and illustrations of the lichenized and non-lichenized fungi of Iran. Some important information presented in the lichenology part of the website include: history of Iranian lichenology, national, provincial and regional level checklists, photo gallery at provincial and regional levels, collection of identification tips and keys, information and photos from the expeditions and explorers, information on the Red List of threatened species, glossary and information on vernacular names of lichens in Iran and list of proposed vernacular names for promoting discussion by the public, list of herbaria where Iranian specimens are deposited, collectors of Iranian lichens and maps for their visited spots, and related material and bibliographic resources on Iranian lichens. In order to stimulate and accelerate the floristic studies, all records new to Iran are published as e-records and are listed under the national checklist. The new e-records are published as RSS feed, readable by all kind of RSS or Feed Readers. Moreover, our online catalogue of the lichen family Megasporaceae including 'manna lichens' of the world is growing, descriptions and distribution maps of some species are now available online. The mycological part is under development, and is aimed to host pictorial checklist of Iranian wood-inhabiting fungi, as well as online catalogue of wood-inhabiting basidiomycetes of the Caucasus region. MYCO-LICH provides an educational section where several useful links and material are accessible. The aim of this section is to visualize the methodology in studying lichens and fungi: specimen handling at the herbarium, equipment used in the field and laboratory, HPLC, TLC, DNA extraction, spot test, and UV test. There are also several useful cross links to some databases and scientific journals with lichenological and mycological contents and courses and Power-Point slides provided by lichenologists who voluntarily made them available for public use.

3B-1-P

**INDEXS - AN ONLINE THESAURUS FOR STANDARD BIBLIOGRAPHIC DATA
ON EXSICCATAE IN BOTANY AND MYCOLOGY**

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So-called exsiccatae (singular: exsiccata) are series of published, uniform and numbered sets of preserved specimens distributed together with printed labels. These series have informative titles and are usually accompanied by printed booklets with labels ('schedae'). The nomenclatural status of these printed matters with regard to the effective publication of names is treated by the International Code of Botanical Nomenclature (Art. 30.4). Over 2,000 plant and fungus exsiccatae have been issued since the end of the 18th century, with more than 20 million specimens distributed in varying numbers of duplicates to institutions worldwide. Typically, exsiccatae are devoted to thematic subjects, such as medicinal plants, or material from 'exotic' countries, for example WIRTGEN, Herb. Deutsch. Arzneipfl. or KALB, Lich. Neotrop., SMITH, Pl. Guatem. Others are restricted to particular taxonomic or ecological groups, e.g., LINTON & LINTON, Brit. Willows; SMITH, Diatom. Spec. Typ.; LUNDQVIST, Fungi Fimicoli Exs. During the 19th century, well-known series, such as SCHIMPER, Iter Abyssin., were managed and sold by trade companies. Some 1,000+ exsiccatae contain vascular plants, c. 700 fungi and lichens, c. 500 bryophytes, and c. 250 algae. More than 50 exsiccatae projects are currently active, usually as part of the regular exchange programs of the publishing institutions (e.g., ALLEN & PURSELL, Maine Mosses; TRIEBEL, Microf. Exs.). Frequently, the specimens of exsiccatae sent out to herbaria are not preserved in the original context, but instead split and inserted in the receiving institution's main collection. To support the digitalization of exsiccata material, the Botanische Staatssammlung München has established an online thesaurus database 'IndExs'. It aims at a complete catalogue of all series worldwide, offering standard abbreviations and bibliographic details as well as additional data and images for recognizing exsiccatae and facilitating their databasing. With the help of IndExs, data capture during retro-digitalization becomes more efficient because exsiccatae specimens can be assigned to known series, with all accompanying information already including in IndExs. Since 2001, we have provided search and download options via an internet interface (<http://indexes.botanischestaatssammlung.de>). A SOAP web service is running. IndExs is powered by Diversity Workbench (http://www.diversityworkbench.net/Portal/DiversityExsiccatae_Information_Models).

3B-1-P

**FLORISTIC DATA AND SPECIES ACCUMULATION CURVES: A CASE STUDY FROM THE
CATALOG OF ALASKAN LICHENS**

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With large databases of specimen identity and locality now available online, it is tempting to use this data to infer biodiversity statistics and ecological patterns for lichens. Whether floristic data can be used reliably for measures of species diversity, abundance and range is limited due to sampling error. Most data on lichen occurrence comes from ad hoc collection schemes, which vary greatly in intensity, collector ability and taxonomic focus. These informal collections do not provide accurate measurement of abundance, making most estimates of species richness unreliable. However, it may be possible to estimate how many species have gone undetected in a given region via species accumulation curves. In this study, species accumulation curves are built from a heterogeneous data set, a database of published Alaskan lichen collections. The curves are fitted to three different models and the data set is further partitioned by region and macro- and microlichens. The reliability of the species curves is compared to species richness estimates of smaller, intensively sampled areas of Alaska.

**CHARACTERIZATION OF THE MATING-TYPE LOCI IN *LOBARIA PULMONARIA*
AND IMPLICATIONS FOR CONSERVATION**

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A large proportion of lichen-forming ascomycetes are known to reproduce sexually. One key factor governing the sexual reproductive mode in ascomycetes is the presence or absence of mating-type (MAT) genes represented by two alternative idiomorphs, Mat1-1 and Mat1-2 genes. However, in fungi other than ascomycetes more than two idiomorphs may be present. The genes encoded by the MAT locus are putative transcription factors thought to control sexual development and to regulate the expression of downstream, mating-type-specific genes. Although there is little sequence similarity among MAT genes from different genera, the encoded DNA binding proteins have conserved motifs, e.g., the α box in Mat1-1 and the HMG domain in Mat1-2. In spite of the high occurrence of sexual reproduction, mating systems of lichens remain poorly understood. However, a detailed study of sexual reproductive strategies is required for understanding evolutionary traits and population genetics of lichen-forming fungi. The aim of the present study was to determine the organization of the MAT locus in the putatively heterothallic species *Lobaria pulmonaria* L. (Hoffm.) in order to gain insights into the genetic basis of its reproductive strategies and sexuality. Targeting conserved motifs of MAT genes with degenerate PCR followed by inverse PCR and TAIL-PCR, we identified MAT genes and their flanking regions in *L. pulmonaria*. Our study further included the development of real-time PCR to detect MAT loci in European and Asian *L. pulmonaria* populations. These markers were used to infer the relation between fertility, genetic diversity and the occurrence of MAT genes, especially in strongly fragmented and geographically isolated populations where the low numbers of ascospores could be due to lack of mating partners.

3B - 2: The ecological roles of lichens in diverse ecosystems

(3B-2-P1) Submission ID: IAL0030-00001

THE EFFECTS OF ATMOSPHERIC POLLUTANTS IN BANGKOK PUBLIC PARKS ON THE PHYSIOLOGICAL PROCESSES OF THE LICHEN *PARMOTREMA TINCTORUM* (NYL.) HALE

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The capacity of lichens to absorb and accumulate atmospheric pollutants, and their physiological responses has been used to monitor air quality extensively. However, this aspect is less studied in the tropics where rain is intense and where industrialization and urbanization are now expanding apace. Accordingly, the objectives of this study were to assess air quality in Bangkok public parks by investigating the effects on physiological processes by air pollutants absorbed and accumulated in transplanted lichens. The lichen *Parmotrema tinctorum* (Nyl.) Hale was gathered from an unpolluted control site at Khao Yai National Park and transplanted into ten public parks in Bangkok. Transplantation was also conducted at the control site and a rural area at Ban Sang. The photosynthetic rate, chlorophyll content, chlorophyll a fluorescence, and phaeophytin were measured before transplantation, and then 45, 140, and 210 days after transplantation. The amounts of the fluoride ion (F⁻), chloride ion (Cl⁻), nitrate ion (NO₃⁻), sulfate ion (SO₄²⁻), phosphate ion (PO₄³⁻) and oxalate ion (C₂O₄²⁻) absorbed and accumulated in the thalli of the lichens were analyzed at the aforementioned periods. The results show that the photosynthetic capacity of the transplanted lichens at all polluted sites substantially declined, particularly after 140 days of transplantation. Correspondingly, the amounts of ionic air pollutants increased in the thalli. However, 210 days after transplantation the photosynthetic rates of the lichens obviously recovered, while the amounts of ionic substances in the thalli decreased. This was a consequence of the heavy rain that occurred during this period. Applications of the Pearson product-moment correlation coefficient method yielded high positive correlations between photosynthesis, chlorophyll a fluorescence, and chlorophyll content. However, negative correlations were found to hold between chlorophyll degradation and all air pollutants, with the exception of C₂O₄²⁻. The rates of the photosynthesis and chlorophyll a fluorescence parameters for the transplanted lichens exhibited the highest negative correlations with Cl⁻, NO₃⁻ and F⁻ which ranged from 0.897 to 0.64. Lower levels of negative correlations were shown for SO₄²⁻ and PO₄³⁻. This study demonstrated diverse air quality at ten Bangkok public parks assessed by lichens.

3B-2-P

LICHENS AND STONE SURFACE DECAY OF THE TOMB OF CYRUS IN PASARGADAE (FARS PROVINCE, IRAN)

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The cultural heritage of Iran comprises of a large number of historical stonework, including decorative and monumental art, dating back from pre-Islamic to contemporary eras. Many of the ancient monuments are exposed to chemical, physical and biological agents, which cause their degradation gradually. One of the most important monuments is Pasargadae (a city in ancient Persia) and the tomb of Cyrus the Great (559-530 BC), which is the second largest archaeological site in Iran after the imperial palace complex of Persepolis. Today, Pasargadae and the Tomb of Cyrus are listed by UNESCO as a World Heritage Site. The grave which is built of large pieces of calcareous rock is located in an open, sun-exposed area. The exposed rock faces of the tomb are colonized by different species of lichenized and non-lichenized fungi, as well as of a few mosses and green algal species. In 2005, most of the growing lichens on the grave were photographed and a relatively small number of lichen samples (ca. 20) were collected for identification in the laboratory. In this study more than 10 species of lichens were found to grow on the grave. The interesting lichenized fungi are *Acarospora cervina* A. Massal., *A. laqueata* Stizenb., *Anaptychia desertorum* (Rupr) Poelt, *Caloplaca biatorina* (A. Massal.) J. Steiner, *C. decipiens* (Arnold) Blomb. & Forssell, *C. erodens* Tretiach, Pinna & Grube, *Candelariella* cf. *vitellina* (Hoffm.) Müll. Arg., *Lecanora crenulata* Hook, and some other poorly developed thalli of *Acarospora* sp., *Aspicilia* sp., *Lecanora* sp., *Rinodina* sp., and *Verrucaria* sp. were also detected. The climate of the study area is suitable for xerophilic lichens and fungi, therefore the saxicolous lichens with crustose growth forms are dominant on the rock surfaces of the tomb.

(3B-2-P3) Submission ID: IAL0057-00010

LICHENS AROUND THE TANGIVAR STONE INSCRIPTION, KURDISTAN, IRAN

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Lichens play major roles in the biodeterioration of stone substrata, both physically and chemically. Their function as biological agents in soil development is indisputable. They are capable of damaging stone inscriptions within a relatively short time-scale. Some important ancient rock drawings and stone inscriptions in Iran are located in natural environments (often in the mountains). Many of them were colonized by several lichen species which are aggressive damaging the monuments. One of the recently observed monuments is the Tangivar stone inscription which is located in (Kurdistan, 50 km SE of Sanandaj, 10 km S of Palangan, Tangivar, with altitude 1,200 m, and GPS information: 35° 0' 14" North, 46° 37' 34" East). The Tangivar monument is positioned on a high cliff c. 30 m. above the ground surface. To avoid damaging monuments the collecting of lichen specimens was prohibited by the local authorities. Therefore, the most common species growing around the monuments were observed and c. 20 specimens were collected from rocks surrounding the monuments where it is permitted. Our results show that several species that may cause grave damage to the monument, including *Acarospora interrupta*, *A. laqueata*, *A. cervina*, *A. aspera* s.l., *Caloplaca decipiens*, *Lobothallia praeradiosa*, *Placocarpus schaeferi*, and *Polysporina urceolata*. Some of the critical specimens that need further study are *A. aff. farinosa*, *Aspicilia* cf. *syriaca*, *Caloplaca* cf. *biatorina*, *Candelariella* sp., *Lecanora* gr. *muralis*, *Thallinocarpon* sp., and *Placidium* sp. Some color photographs of these species are presented on the MYCO-LICH website (www.myco-lich.com).

ECOLOGICAL DIVERSITY OF *VERRUCARIA* S.LAT. (VERRUCARIACEAE)

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Verrucaria s.lat. includes crustose, areolate and placodioid species characterized by immersed or sessile perithecia often covered by an involucrellum, with simple and colourless ascospores, without paraphyses and with paraphyses. Species of *Verrucaria* s.lat. grow on calcareous or siliceous rocks, or occasionally on soil and bark, or parasitically on other lichens; foliicolous species have been discovered in the tropics. They develop in terrestrial or aquatic freshwater and maritime habitats. During a critical revision of *Verrucaria* s.lat. in Poland (2006-2011), a total of 57 species were accepted (including newly reported taxa) belonging to seven genera currently distinguished within *Verrucaria* s.lat.: *Bagliettoa* (4 species), *Hydropunctaria* (3), *Parabagliettoa* (3), *Placopyrenium* (3), *Verrucaria* (38), *Verrucula* (4) and *Verruculopsis* (2). These genera have diverse habitat preferences and play an important role in a variety of ecosystems. The genus *Bagliettoa* contains species growing on calcareous or mortar substrates sufficiently exposed to the sun, in low to moderate eutrophic environments. They are saxicolous, calcicolous, xerophilous, photophilous, and slightly to moderately nitrophilous species. The genus *Hydropunctaria* comprises saxicolous, hydrophilic (aquatic or amphibious), non-calcareous species, colonizing either marine or freshwater habitats. *Parabagliettoa* is composed of species growing on calcareous rocks, in both moderately sunny and shady sites. Species of *Placopyrenium* often grow parasitically, especially at young developmental stages, or later parasymbiotically on lichen hosts growing on different substrate types, often on both calcareous and siliceous rocks. *Verrucaria* species occur on various rocks, rarely on bark or soil, in terrestrial, maritime or freshwater habitats. *Verrucula* contains exclusively parasitic species growing on thalli or rarely on apothecia of lichens containing anthraquinones. *Verruculopsis* is another mostly parasitic genus, but in Poland only its non-parasitic members have been recorded on vertical to horizontal surfaces of rocks in sunny and exposed places. This project was supported by the Ministry of Education and Higher Education in Poland (2010-2013), grant no. N N 304 170539.

(3B-2-P5)

Submission ID: IAL0087-00001

PRELIMINARY SURVEY OF LICHEN DIVERSITY ON STONE MONUMENTS IN NAKHON RATCHASIMA PROVINCE, THAILAND

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3B-2-P

The objective of this study was to investigate saxicolous lichens on stone monuments in Nakhon Ratchasima province, during May to July 2011. The total of 135 specimens were collected from eight sites: Prasat Khonburi, Prasat Pha Kho, Prasat Hin Phi Mai, Prasat Hin Phanom Wan, Prang Ku, Prasat Muang Sema, Prasat Muang Khak and Prasat Muang Khorat at the elevation 130-200 meters above sea level. Four physical factors on lichens were measured; temperature (31-35 °C), humidity of air (46-59%), light intensity (27,333-61,833 lux) and pH of substrates (6.1-7.7). The samples were identified into 11 families, 17 genera and 22 species. Seventeen genera of lichens were *Pyxine*, *Physcia*, *Dirinaria*, *Hyperphyscia*, *Chrysothrix*, *Amandinea*, *Dimelaena*, *Diploschistes*, *Lecanora*, *Parmotrema*, *Peltula*, *Porina*, *Bacidia*, *Lepraria*, *Leproloma*, *Caloplaca*, and *Buellia*. *Pyxine* and *Caloplaca* were commonly found in all eight sites.

SEASONAL VARIATIONS IN PHYSIOLOGICAL PROCESSES AND LICHEN SUBSTANCES IN *RELICINA ABSTRUSA* IN THE TROPICAL FORESTS OF THAILAND

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Lichens produce secondary metabolic products for protection against adverse environmental conditions. As such, there are a variety of potential uses of lichen products. Accordingly, the objectives of this study were to investigate seasonal variations in the physiological processes and the quantities of secondary metabolites produced in tropical lichens. The current investigation was conducted using the lichen *Relicina abstrusa* whose habitation is in the canopy of the tropical rain forest (TRF) and in the dry evergreen forest (DEF) at Khao Yai National Park, Thailand as a model. Photosynthesis, chlorophyll fluorescence and quantities of lichen products were analyzed during the cool, hot and rainy seasons. The photosynthetic rates of the lichen in DEF were higher than those in TRF in all three seasons. However, photosynthetic rates were at their highest during the rainy season and comparatively lower in the cool and hot seasons. Values for the photosystem II (PSII) quantum yield and the Fv/Fm coincided with carbon assimilation rates. Norstictic and usnic acids which were major products of this lichen varied between sites and among seasons. Norstictic acid was produced in larger quantities than usnic acid in both TRF and DEF in all three seasons. Both lichen substances were synthesized in the highest quantity during the rainy season, and subsequently at lower quantities in the hot and cool seasons in TRF and DEF with the exception of norstictic acid in DEF. These results demonstrated that the production of lichen secondary metabolites was not always correlated with photosynthetic capacity. *R. abtrusa* in DEF produced the highest amount of norstictic acid in the hot season when photosynthetic capacity was at its lowest. This implies that lichens primarily allocate carbohydrates so as to produce lichen substances that are protective against adverse environmental conditions even when carbon dioxide assimilation is low. However, it is necessary to conduct long term and extensive investigations in order to elucidate how external stimuli affect the synthesis of secondary metabolites of other lichens in various kinds of forests in the tropics.

(3B-2-P7) Submission ID: IAL0094-00001

VARIATIONS IN THE GROWTH RATES OF LICHENS OVER THE COURSE OF A LONG-TERM INVESTIGATION IN THE TROPICAL FORESTS AT KHAO YAI NATIONAL PARK, THAILAND

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Long term monitoring of the growth of lichens in five types of tropical forests in Thailand was conducted between 1999 and 2010 at Khao Yai National Park. The objectives of this study were to observe (1) the longevity of lichen thalli in a tropical climate; and (2) variations of the growth rates of lichens in various types of tropical forests under different climate. A total of 73 species with 306 thalli were monitored, of which 45 were crustose and 28 were foliose species composing of 146 and 160 thalli, respectively. After twelve years only 23% of the observed thalli remained intact with 32% of the crustose and 14% of the foliose lichens. The largest proportions of intact thalli of both crustose and foliose were observed under dry dipterocarp forest conditions at 58% and 31%, respectively. The average growth rate for crustose lichens was 2.8 mm/year with a range between 0.29 and 7.89 mm/year, whereas those of foliose lichens was 6.36 mm/year with a range between 0.11 and 17.43 mm/year. Lichens in the five forest types differed in average growth rates. The lowest rate was observed under dry evergreen forest and with the highest growth rate being noted under tropical rain forest. In contrast, the growth rate of foliose lichens varied from 1.24 to 14.53 mm/year with the lowest rate being found under tropical rain forest and the highest rate measured under lower montane forest. Average growth rates of the crustose lichens measured after two, four, six, eight, ten, and twelve years, respectively, fluctuated at 1.30, 2.46, 2.52, 2.59, 2.03 and 2.28 mm/year, while those of the foliose thalli were 6.04, 5.58, 4.78, 5.89, 6.24 and 6.36 mm/year. This study demonstrated that lichen thalli in a sunny and dry habitat in the tropics live longer than in shady warm-wet places. Variations in the growth rates at differing ecosystems and over the years reflected variability of climatic conditions. These results require amplification and must be further addressed for the sake of conserving biodiversity under a changing climate.

(3B-2-P8) Submission ID: IAL0101-00001

LICHENS AS BIOMARKERS FOR DEW AMOUNT AND DURATION IN THE NEGEV DESERT

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3B-2-P

We studied the lichen diversity on cobbles at 18 stations located within four aspects of a second order drainage basin near Sede Boqer at the Negev Highlands, Israel where dew was found to be the main water source for lichens. At each station 10 cobbles were randomly chosen and the lichen composition and structure were investigated and compared to the dew amount and duration that characterize each station. The stations were grouped into 5 clusters that showed a close link with the dew moisture regime. Lichen distribution pointed to species which can serve as biomarkers for dew amount and especially for dew duration. The data implies that lichens can provide information regarding the dew regime at meso-habitats where no microclimatic data are available.

ASSESSING VARIABILITY OF MOLECULAR MARKERS FOR POPULATION STUDIES IN MYCOBIANTS AND PHOTOBIONTS: A CASE STUDY USING *LASALLIA PUSTULATA*

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In this study we assess the variability of the following markers: Photobiont: ITS rDNA, actin, RBCL, COX, PSB; Mycobiont: ITSrDNA, mtSSU, mtLSU, RPB1, RPB2, MCM7, TSR1 and EF1. We report variability of these markers within *Lasallia pustulata* collected from different populations across Europe. Additionally, we checked for diversity of fungal ITS rDNA copies using 454 pyrosequencing of ITS amplicons. This study revealed a number of different ITS haplotypes within a single specimen.

(3B-2-P10) Submission ID: IAL0138-00002

PECULIAR BIODIVERSITY OF LICHENS IN THE DAGESTAN REPUBLIC (RUSSIA)

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On grounds of lichenofloristic surveys, the Dagestan Republic is one of the least-known parts of Russia as well as the Caucasus Mountains. Due to its diverse geomorphology and altitudinal range, it harbors a species-rich mosaic of xerophilous to alpine vegetation; e.g. mountainous dry pine forests, mesophytic deciduous forests, steppes and semi-deserts. Vascular plants are rather well-known and comprise c. 3,000 species, including 73 local endemics. Nevertheless, only 63 lichen species were known before our investigations. Our study increased the number of known lichens and lichenicolous fungi to 460. Within 3 years (2009-2011), 415 species of lichens and lichenicolous fungi were recorded within 15 square kilometers in the Gunib plateau (42°24'N, 46°55'E, 1,450-2,335 m) in Intermontane Dagestan. It has higher lichen biodiversity in a relatively small space than anywhere else in Russia. More than 100 recorded species were previously not known from Caucasus and 29 species are new to Russia. More than 80% of the species (345) were present in two vegetation types: (1) pine forest with *Pinus kochiana* and (2) birch forest; both types together occupy only c. 3 square kilometers of the territory. Northern slopes with dense deciduous forests have the highest diversity of cyanolichens, 39 species. The major epiphytic diversity was observed on bark of *Betula* in well-preserved forests, 128 species. Terricolous species were recorded mainly above 1,900 m. The majority of saxicolous lichens was found on vertical, sun-exposed limestone rocks, in both xeric and humid conditions in altitudes 1,500-2,335 m. The lichen flora of the Gunib plateau has a high proportion of temperate-oceanic and boreal elements among epiphytic lichens; but montane-continental and arctic-alpine elements prevail among saxicolous and terricolous lichens. Our preliminary data show that the lichen flora of Dagestan is related to the floras in Armeno-Iranian and Central Anatolian floristic provinces within the Irano-Turanian region. In conclusion, we estimate more than thousand lichen species occurring in Dagestan.

3B-2-P

GEOGRAPHICAL ASPECTS OF SYMBIONT DIVERSITY IN THE GENUS *NEPHROMA*

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Patterns of symbiont diversity in cyanolichens are important for the deeper understanding of ecological processes affecting these species, such as dispersal, establishment, and symbiont selectivity. We studied the diversity of *Nephroma* (Peltigerales, Ascomycota) mycobionts within a global, phylogenetic framework and investigated the genetic diversity of their associated *Nostoc* photobionts. Fungal genotypes were based on the Internal Transcribed Spacer region (ITS) of ribosomal DNA (rDNA), while cyanobacterial diversity was based on nucleotide differences in the tRNA^{Leu} (UAA) intron. The full data set included over 250 mycobiont and over 350 photobiont sequences, of which over 140 were obtained from the same lichen specimen, respectively. Our sampling was focused on the northern hemisphere, but we also included some material from South America and New Zealand. The study illustrates the phylogenetic structure for the genus *Nephroma* in the northern hemisphere and shows that several clades are variable and likely consist of several species. Our results provide evidence that several lichen-forming fungi of the genus *Nephroma* associate with sequence identical *Nostoc* haplotypes over a global scale (Europe – Asia, or Europe – North America). All bipartite species share *Nostoc* genotypes with one or more species, while tripartite species are not monophyletic within *Nephroma* but use entirely different photobiotic strains. Geographic mosaic patterns in symbiont selectivity were identified for two species, showing relatively higher selectivity locally compared to globally. Such patterns indicate habitat preferences of particular symbiont combinations but also a possible founder effect. We conclude that species of the genus *Nephroma* are selective in their association with symbiotic partners. Particular symbiont associations are linked to geographical areas, and several lichen-forming fungi of this genus share sequence identical photobionts over a global scale. More studies on photobiont sharing in lichen communities are needed to further identify how and where lichen species acquire their symbiotic partners.

**LICHEN COMMUNITIES ON *TSUGA HETEROPHYLLA* IN COLD RAINFORESTS:
WHAT DRIVES COMPOSITION AND RICHNESS?**

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Epiphytic lichen communities in southeast Alaska are known to be among the richest of any high latitude, conifer-dominated region in the world. However, little is known of the local gradients that cause some lichen communities to be especially rich and others poor, and what causes local spikes in richness of cyanolichens. Understanding species distribution and richness concentration patterns is important since lichens are used for air quality and forest health monitoring. Epiphytic crust lichens were studied on 114 branches of *Tsuga heterophylla* trees at 19 different localities in low elevation boreal rainforests in the vicinity of Juneau, Alaska. Branches of equal cut-point diameter and controlled for overall collective twig mass were taken from different heights above the ground and in different light exposure situations with replication, and substrate element chemistry was determined by spectrometric analysis. Species richness was significantly correlated with a nutrient gradient (N content and C/N ratio as well as Zn content). A principal components analysis of species composition against quantified environmental gradients revealed a gradient between cyanolichen-dominated branches and those dominated by chlorolichens. This gradient was likewise primarily explained by the C/N ratio as well as tree and branch age and significant gradients in the content of Zn and other metals and cations. The results reinforce the importance of nutrient regimes and forest age structure in determining composition but suggest that cation gradients (such as Ca, Mg) ascribed importance for local enrichment of cyanolichen communities in inland regions may not explain as much variability in cold coastal rainforests.

**MICROLICHEN COMMUNITY STRUCTURE AS A WAY TO COMPREHEND TROPICAL DRY
FOREST REGENERATION**

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The tropical dry forest is the most extensive ecosystem in the neotropics, and at the same time, one of the most endangered ones in the world. As a result, some studies aim to understand its regenerating process. The objective of this project was to comprehend the importance that lichen communities have in the succession process. For this, we analyzed the microlichen species cover in 204 trees at 4 levels of disturbance, ranging from 6 years after agricultural use to pristine areas, all on the Mexican Pacific coast. We found more than 120 lichen species. The best represented families were Arthoniaceae, Pyrenulaceae, Roccellaceae and Graphidaceae. Our analysis suggest that the lichen cover and richness recovers faster than expected, been the 18 years old forest statistically equal to the pristine areas. Nonetheless, the lichen community structure was completely different. Using an ordination analysis (NMS) we were able to distinguish the mature forest from all the levels of disturbance. We also found some lichens that can be used as indicators species of disturbance or conserved areas, mainly in the genera *Pyrenula* and *Arthonia*, as well as several new species. Using multivariate methods we analyzed the preference of species groups to some microenvironmental factors such as relative light intensity, phorophyte specificity and pH. Lastly we discuss the application of our results in conservation issues.

STUDY OF ANTIOXIDANT AND ANTICANCEROUS ACTIVITY OF *RAMALINA LACERA* FOR BIOMEDICAL APPLICATION

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Highly reactive free radicals and oxygen species are present in biological systems from wide variety of sources. These free radicals may oxidize nucleic acids, proteins, lipids or DNA and can initiate degenerative disease may include chronic diseases like heart and cancer diseases. Antioxidant compounds such as phenolic acid, flavonoids and terpenoids in food samples play an important role as a health-protecting factor. Among the plant kingdom, lichens are very important in terms of production of bioactive compounds. They are symbiotic organism of both fungus and algae. It has the enormous biomedical applications leads to effective drug molecule preparation against particular target. Attempts were made to study the anticancerous and antioxidant activities using *Ramalina lacera*, a fruticose lichen. Sequential extraction of 7 g with 100 ml of five different solvents like chloroform, acetone, ethyl acetate, ethanol and water was carried out using a Soxhlet extractor for 12-15 cycles. The extractive value recorded was 18.2, 23.8, 10.2, 73.2 and 37.4 mg/g of dry lichen sample, respectively. Among the different solvent systems tested, ethyl acetate was found to be best in terms of rapid extraction of bioactive substances from lichens which were recorded as 73.2 mg/g of dry lichens. Further, extracts were subjected to DPPH antioxidant activity to measure the scavenging abilities against free radicals at different time intervals. The results revealed that ethyl acetate and ethanol extracts showed the inhibition of radical as 70.4% and 84%, respectively, whereas acetone did not show any activity against free radicals. Aqueous and chloroform extracts showed least inhibition activity of 15% and 1.74%, respectively. We conclude that bioactive antioxidant molecules mainly present in ethyl acetate and ethanol extracts. Both these extracts were subjected to study the efficacy against MCF-7 and Hela cancer cell lines. Ethanol extracts showed the better IC₅₀ than ethyl acetate extract and it was found to be 40µM against Hela cell lines whereas MCF-7 cell line was 30µM.

(3B-2-P15)

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FUNCTIONAL AND STRUCTURAL ROLE OF LICHEN BIOTA

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3B-2-P

It is well known that the ecological (systemic) role of lichen biota in communities is determined by the symbiotic character of lichens. In ecological communities, lichens perform as one of the first visible components of highly complex ecosystems. At least three important processes are initiated by lichens: accumulation of organic material as a result of photosynthesis on initially life-free surfaces, chemical (biochemical, biogeochemical) transformation of substrate matter, and accumulation and transformation of matter deposited from atmosphere (both dry and wet). Four main peculiarities comprise the following: symbiotic photosynthesis, remarkable self-surface of lichen thalli, passive and active accumulation of water and minerals through atmospheric moisture, active penetration of hyphae into substrate surface and bounding of airborne dust particles by hyphae. Substrate conditions change under the natural weathering (rock surfaces) or ageing (tree bark) processes or under the human impact (environment pollution s.l.). A specific group of substrates are man-made materials. In this case, some processes initiated by natural agents are the same as in natural substrates. Very often, man-made substrates change in different ways, mainly through oxidation, alkalization, or some other chemical or physical destructive processes. Lichens as complex organisms (systems) perform several biospheric functions of living mater, such as a gas function, two types of concentration functions, an oxidation-reduction function, an acidification-alkalization function, and a biochemical function.

5I: Global Change and lichen biology

(5I-P1)

Submission ID: IAL0086-00001

LICHENS IN HYPERTROPHICATED ENVIRONMENT - FOREST AFFECTED BY GREAT CORMORANT COLONY

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Piscivorous birds are an important agent, transferring nutrients from aquatic ecosystems to the terrestrial habitats by depositing food scraps, egg shells, feathers, dead bodies of birds and large amounts of nutrient-rich excrements, thus dramatically influencing soil nutrient balance and changing plant cover. The continental subspecies of the great cormorant (*Phalacrocorax carbo sinensis*) is an alien bird that spreads in the coastal forests of the Baltic region. The largest and oldest cormorant colony in Lithuania was studied for its influence on various components of pine forest ecosystem, lichens among them. Epiphytic and epixylic lichens were investigated on all available substrate groups in forest parts under varying degree of bird colony influence. Cormorant colony activities dramatically changed lichen communities transforming them into species-poor nitrophilic assemblages with prevailing two highly nitrotolerant lichens, that often formed monospecific communities on bark (*Phaeophyscia orbicularis*) or vertical wood surfaces (*Xanthoria candelaria*) in the centre of the colony, not used for nesting by now. Total lichen desert and depauperated communities of lichens typical to pines coincided with the most active nesting zone and its outer (expansion) edge respectively. Outside the colony, acidophilic and neutrophilic lichen communities prevailed. Distribution of lichen community types in the studied area coincided with numbers and abundance of eutrophic and alien vascular plant species in lower forest vegetation layers. Changes in lichen species numbers, composition, abundance and substrate colonization correlated with significant alterations of substrate chemistry. Content of nitrogen in pine bark in the colony centre up to 1.5 times exceeded bark N outside the colony, content of phosphorus - up to five times, bark pH in the colony centre reached 7.5-8, while outside the colony it was 3.5-6. Lichen desert in the part of the colony with highest concentration of nests was apparently related to extremely high pH levels of bark during the nesting period and to colony development dynamics: too short time span between die-away of acidophilic and establishment of nitrophilous species. The research was funded by the Research Council of Lithuania, grant No. LEK-23/2010.

(5I-P2)

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NOCTURNAL HYDRATION INCREASES LICHEN GROWTH RATES

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The aim of this experiment was to understand how hydration events during periods of light and darkness influenced viability and growth in *Lobaria pulmonaria* and *L. scrobiculata* under controlled conditions. The study was motivated by a need to develop optimal conditions for lichen growth during short-term experiments. In total 400 thalli of each species were grown in growth chambers for 14 days at a 12 hrs photoperiod with 100 $\mu\text{mol photons m}^{-1} \text{s}^{-2}$ light intensity at four diurnal temperature regimes: 25°-20°C, 21°-16°C, 13°-8°C, and 6°-1°C during which the highest temperature in each regime was given during day, and the lowest during night. The samples were given two different treatments: 50% of the thalli were moistened twice a day to keep them continuously wet, whereas 50% were moistened only once early. The latter treatment kept the thalli moist during the light periods, but dry during all dark periods. Chlorophyll a fluorescence (CaF) was assessed before and after the experiment to quantify possible stress due to treatment, and growth rates were quantified in terms of biomass (dry weight) and thallus area increments. In general, both species showed higher growth rates (dry mass and area) and higher values of photosynthetic efficiency, Fv/Fm when they were permanently moist. This suggests that nocturnal respiration may enhance the conversion rate of photosynthates into thallus extension and thus, at least in short term, boost lichens growth. Furthermore, the growth chamber temperature strongly influenced growth rates for both species. However, *L. pulmonaria* had a higher optimal temperature for growth (21-16°C) than *L. scrobiculata* (13-8°C).

(5I-P3)

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LICHENS AS BIO-INDICATORS OF AMMONIA CONCENTRATION IN FLANDERS

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Monitoring of ammonia through its effects on biodiversity using epiphytic lichens is well established in some countries, e.g. the Netherlands. The present study investigated the feasibility of using epiphytic lichens for bio-monitoring ammonia concentrations in Flanders (Belgium), with particular focus on the classification of concentrations above or below the WHO-norm of 8 $\mu\text{g}/\text{m}^3$ (critical level for vegetation). Secondary aim was to find a simple yet sufficiently accurate method that could even be applied by non-specialists of lichens. Air concentrations of ammonia were continuously measured for 13 months by passive samplers at 100 points at different distances to the northeast of a live stock farm. Lichens were studied on (6-) 10 oaks or poplars at the same points. Results indicate that it is possible to develop a bio-monitoring network based on a small selection of lichen species, particularly in order to distinguish between minimum ammonia levels below or above the WHO-norm.

5I-P

**NITROGEN DRIVES LICHEN COMMUNITY CHANGES THROUGH
THE DIFFERENT SPECIES RESPONSES**

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Nitrogen (N) deposition has increased globally over the last 150 years and further increase is predicted in the future. N is an important nutrient for lichens, involved in many processes in both the photobiont and mycobiont. However, N can also be excessive, with many lichens and lichen communities disappearing with increased deposition. We initiated a long-term experiment aiming at understanding the underlying dynamic processes that lead to altered structure and die-back of epiphytic lichen communities with increased N load. The aim was to study how the N deposition would affect the epiphytic lichen community composition in a naturally N poor boreal forest. This was done by daily fertilization (during the growing season) of spruce trees with a rich lichen flora at five N levels (0.6, 6, 12.5, 25 and 50 kg N ha⁻¹ year⁻¹) during four consecutive growing seasons (2006-2009), and yearly monitoring of changes in abundance of crustose, foliose, and pendulous lichens. Change in lichen abundance on each branch was recorded each autumn and 2005 before the treatments started. The simulated N deposition caused significant changes for *Alectoria sarmentosa*, *Bryoria* spp. and *Hypogymnia physodes*. *A. sarmentosa* increased over time in the lower two levels of N, remained stable at intermediate levels, and decreased at the higher levels. The abundance of *Bryoria* spp. showed a positive response to 6 kg N, but negative to 12.5 kg N and higher loads. *Hypogymnia* spp. decreased over time for all treatments except in 12.5 kg ha⁻¹, where it only decreased during the first treatment year and then increased after 2007. The abundance of *Platismatia glauca* increased over time, independent of treatment. Our results show that four years of simulated N deposition caused an alteration of the epiphytic lichen community. As we hypothesized, responses to the treatments differed among species, reflecting their different N optima. The results indicated that decreased stability of the lichen thalli, due to altered phytobiont:mycobiont ratio or parasitic fungal attacks, might be causing the decline of *A. sarmentosa*, and that competitive interactions were not important for changes in species abundance during the first four years.

**HOW MUCH DOES LICHEN DIVERSITY INDICATE GLOBAL CHANGE?
ASSESSING THE USE IN BEECH FORESTS**

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Mediterranean forests undergo the consequences of global change. The effects are much related to climate drivers (global warming and changes in rain regimes) and human activities (e.g., changes in land use, forest management). Despite changes on Mediterranean communities have been documented from a long term, current alterations happen faster and more severe. Some communities are dramatically affected, challenging their ability to overcome. Beech forests can be included within forests communities menaced by global change within Mediterranean areas, which represents their southern boundary range. They thrive under specific climatic conditions, characterized by higher rain regime. The convergence of a diminution of precipitation and a rise in temperature would restrict suitable areas for *Fagus sylvatica*; thus limiting the development of well established forests. In addition, agricultural activities are also limiting and, sometimes, reducing their former area. Changes on forest communities affect all the levels, being more noticeable on the most sensitive components, namely lichens. Lichen diversity is being used to assess environmental quality on forests. Several components of lichen diversity, mainly referring to biotype, eutrophication, humidity requirements, pH of the substrate, have been included to study beech forest quality from the North-eastern Iberian Peninsula. Lichen diversity and functional groups will be analysed and related with environmental parameters, including climate and land use change. A first group of lichen species is distinguished, composed by crustose biotype, mainly with *Trentepohlia* as photobiont, mesotrophic, and hygrophytic to mesohygrophytic and neutrophilous. This group of species is found in all the analysed forest and will represent the climax community on *Fagus sylvatica* trees. Changes in the conditions of forests, such openings or proximity to agricultural areas, determine the irruption of a second group of species characterized by foliose biotype, trebouxoid algae as a photobiont, eutrophic, mesohygrophytic to xerophytic and basophilous. The future predictions on climate change, reducing the area suitable for *Fagus sylvatica* in the area, will lead to the replacement of beech forests to pine or oak forests, promoting a shift on lichen community with an increase of the second group of species.

SURVEYING LICHEN BIODIVERSITY ON *ROYSTONEA REGIA* IN AN URBAN ENVIRONMENT

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Lichen biodiversity is often used to assess air quality and ecosystem health within non-urban environments. This project, however, looks at the diversity and abundance of foliose, fruticose, and crustose lichens on a particular substrate, *Roystonea regia*, comparing a university campus versus a botanical garden in the middle of a metropolis. The particular substrate was chosen for two main reasons; first, it is distributed throughout the study area, being exposed to a variety of levels of impact, and second because its large smooth trunks provide an ideal location for discovering and identifying discrete lichen species. *Roystonea regia* is found in Cuba, Florida, the Bahamas and the Yucatan Peninsula, and specimens thereof are often imported from and transferred between these various locations. It is thus likely that lichen species unique to these other subtropical areas have made their way to south Florida on a royal palm tree. Trunks are surveyed from the base of the tree to 1.6m. It is acknowledged that not surveying the higher portion of the trunk may have overlooked some lichen species only occurring there. Lichens are primarily identified via morphology. Some collecting will be made, if identification cannot be easily done with morphology, if the specimen seems to be new to the area [and if there is enough of it that a small collection will not hurt its population], or if the particular lichen species is being found in a unique circumstance requiring further investigation. Ideally molecular work will be performed on lichen species found, however this component of the project will not be complete by January 2012. Lichen diversity is assessed using coefficient of community and a set of other similarity indices. It is hypothesized that overall lichen diversity per substrate will increase from areas with high impact [foot traffic and automobile traffic] and low moisture, to areas with low impact and high moisture [nearby lake or pond].

(5I-P7)

Submission ID: IAL0282-00001

LICHEN FLORA OF THE RIVER ZRMANJA (CROATIA, EUROPE)

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River Zrmanja is a representative karst river in northern Dalmatia, characterized by a rich and unique flora and fauna. Part of the area belongs to the Nature Park "South Velebit" and along its inflow Krupa with numerous waterfalls, cascades and rapids forms habitat of particular importance for endemic species, such as *Degenia velebitica*. Furthermore, river canyon with its sandbanks and sandy dunes is one of the greatest natural resources of Croatia. As a part of a student project entitled "Biodiversity research of River Zrmanja 2010" maintained by Biology Students Association, Lichenology group carried out the research in the wider area of the River Zrmanja and conducted inventory of lichen flora. During our field research 76 species were found and could be distributed in 18 families. Among these species there are 3 that are recorded on the Red List of lichens of Republic of Croatia. These are *Lobaria pulmonaria* (L.) Hoffm., *Pseudevernia furfuracea* (L.) Zopf and *Teloschistes chrysophthalmus* (L.) Th.Fr. Presence of these species some of which are extremely sensitive to air pollution is conceivable evidence of ecological preservation of this region of Croatia. As the last lichenological research of this area and the majority of the data gathered, contain imprecisely described locations, age over 50 years, therefore lichenological studies are of great importance for this region. We are willing to provide more fieldwork and research in order to gather this specific data for assaying lichen biodiversity, also to conduct comparison of species of the similar habitats and to determine impact of the environmental changes to the lichen flora.

5I-P

ESTABLISHMENT OF A FREQUENCY-BASED EPIPHYTIC LICHEN BIO-MONITORING SCHEME TO EVALUATE ATMOSPHERIC NH₃ POLLUTION IN THE UK

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Following declines in atmospheric SO₂, concerns have arisen over the impact of atmospheric inorganic nitrogen (N) concentrations on ecosystems. Atmospheric N pollution is typically dominated by oxidised forms in urban areas and reduced forms in rural ones, with the main source of reduced N being NH₃ from animal by-products. Lichen species associated with the Xanthorion parietinae alliance are typically observed to colonise affected areas, and previous studies have shown that epiphytic lichens can be used as effective bio-indicators of N pollution. An example of this is the UK-tested Lichen Acidophyte Nitrophyte (LAN) scoring system. However, a review of suitable indicator species for use in a UK-based bio-monitoring scheme is required for numerous reasons. These include the lower background NH₃ concentrations in the UK, the confounding influence of climate, temporal-spatial fragmentation of potential indicators resulting from previous SO₂ perturbation and ease of lichen species identification by non-specialists. Lichens were surveyed on trunks and branches at 28 sites across the UK, following an established technique. A shortlist of indicator species was produced specific to NH₃ concentrations in air from an indicator species analysis undertaken in PC-Ord. These species were used to test the efficacy of a simple frequency-based version of the LAN scoring system, which reduced levels of subjectivity and species bias inherently present in an abundance-based surveying technique. Individual indicator species were given no weighting in the Frequency-based LAN (FLAN) to further offset any potential geographical bias resulting from the more species-poor regions that were adversely affected by SO₂ pollution in the past. Correlation and regression analyses were used to evaluate relationships between the scoring system and potentially confounding variables, including other N forms, deposition rates, climate and phorophyte species. The findings of the study suggest that the FLAN technique may prove a fast and effective means of epiphytic bio-monitoring for atmospheric NH₃ in the UK, by using a limited number of easily identifiable lichens. NO₂ was observed to be a confounding factor, but the established similarity in effects of NO₂ and NH₃ on lichen communities suggests the technique may be transferable to urban areas.

LICHEN FUNCTIONAL DIVERSITY AS A TOOL FOR ASSESSING THE FIRST EFFECTS OF CLIMATE CHANGE: DEVELOPING AN EARLY-WARNING ECOLOGICAL INDICATOR

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Climate change is one of the greatest challenges facing conservation and it is predicted that its impact will be most significant in the Mediterranean region due to increased temperatures and reduced precipitation. There is a need to have tools for monitoring and even anticipate the subtle changes that will occur due to climate change. We used lichen functional diversity with the aim of detecting climate change conditions both in space and time. This was done in southern Portugal, in a region characterized by a Mediterranean climate but with heterogeneous conditions in terms of humidity and precipitation: the coastal areas have higher humidity due to the predominant northwest winds that come from the sea, whereas the inner areas of this region is much dryer and can be classified as semi-arid. Lichen biodiversity was divided in groups of hygrophyte or xerophytes lichens classified on the bases of expert knowledge. They were also divided on the basis of the genus of the alga involved in the symbiosis and also according to their growth form. An index of lichen abundance, Lichen Diversity Value (LDV) was calculated using a standard methodology. The results have shown that the functional groups related to water requirements and growth forms were significantly correlated with macroclimatic changes in space. The LDV also showed a response to temperature variance over time, in a 5 year interval. Surprisingly, we found that the number of lichen species with photobionts of the genus *Trentepohlia* has been increasing along time in the semi-arid area and this was well related to the increasing levels of relative humidity. Therefore, lichen functional diversity showed to be a good candidate for an ecological indicator for the early effects of climate change.

4A: Evolution and Systematics in the Teloschistales

(4A-P1) Submission ID: IAL0110-00002

MOLECULAR PHYLOGENY AND RECENT TAXONOMY OF ASIAN *RUSAVSKIA ELEGANS* COMPLEX AND CLOSELY RELATED GASPARRINOID LICHENS (TELOSCHISTACEAE, LICHEN-FORMING FUNGI)

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Xanthoria elegans (Link) Th.Fr., with narrow and convex lobes, in contrast to wide and plane thalline lobes of *Xanthoria parietina* (L.) Th.Fr. was recognized at the end of the 18th century. The *X. elegans* group including 12 species was segregated from the genus *Xanthoria* as a separate genus, *Rusavskia* S. Y. Kondr. & Kärnefelt, in 2003 based on morphological and anatomical data (Kondratyuk & Kärnefelt 2003). Later it was shown that the *Rusavskia elegans* group including *R. elegans* (Link) S.Y. Kondr. & Kärnefelt, *R. soredata* (Vain.) S.Y. Kondr. & Kärnefelt, *R. papillifera* (Vain.) S.Y. Kondr. & Kärnefelt and *R. digitata* (S.Y. Kondr.) S.Y. Kondr. & Kärnefelt, forms a robust monophyletic branch in the family Teloschistaceae according to molecular data (Fedorenko et al., 2009, 2011). *Rusavskia elegans* is frequently misidentified, and even gene bank sequences ascribed to *R. elegans* in fact belong to the *Caloplaca saxicola* group. About ten morphologically similar to *R. elegans* lichen groups shown to form separate robust monophyletic branches in the phylogenetic tree of the Teloschistaceae (Kondratyuk et al. in prep.). Among them there are the following: *Rusavskia resendei* (Poelt) S.Y. Kondr. & Kärnefelt, showing also similarity to *Xanthoria parietina* group, as well as the gasparrinoid (=placodioid) species groups *Caloplaca saxicola*, *C. regalis*, *C. aurantia*, *C. trachyphylla*, *C. elegantissima* etc. Results of phylogenetic analyses based on nuclear and mitochondrial DNA, and new morphological and anatomical data, on groups mentioned above will be illustrated. Their taxonomic status will be especially discussed. New Asian species of the *Rusavskia elegans* group and closely related groups of gasparrinoid lichens, i.e. *C. trachyphylla* (Tuck.) Zahlbr., *C. mogoltanica* S.Y. Kondr. & Kudratov, *C. scrobiculata* H. Magn.), as well as taxa of *C. persica* (J. Steiner) M. Steiner & Poelt and *C. intrudens* H. Magn. groups will be presented. Financial support of the State Agency on Science, Innovation and Information of Ukraine (417/2011) is appreciated.

4A-P

**OBLIGATE AND OTHER LICHENICOLOUS FUNGI ON *XANTHORIA PARIETINA*
AS A CONTRIBUTION TO THE TAXONOMY OF THE TELOSCHISTACEAE**

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Due to nitrogen pollution *Xanthoria parietina* is a vastly spreading macrolichen at least in Europe. Therefore, the thallus surface area available for infection by lichenicolous fungi is dramatically increased. Based mainly on Central European material the diversity of lichenicolous fungi invading either thalli and/or ascomata of *Xanthoria parietina* has been investigated. The aim of the study was to elucidate if a macrolichen becoming so common and dominant in epiphytic lichen communities has an influence on the regional diversity and commonness of its lichenicolous fungi. So far 27 species are known to be able to live on *Xanthoria parietina*, placing this common macrolichen among the lichen species with an astonishingly rich fungus flora. Fourteen fungi are known from their teleomorphic state and can therefore be classified by their phenotypic characters. The taxonomic position of the anamorphic fungi is so far only partly resolved. Various fungal orders contribute one to several members to the xanthoriicolous fungus diversity (number of affiliated taxa in brackets): Pleosporales (5), Hypocreales (4), Arthoniales (3), Capnodiales (3), Verrucariales (2), Lecanorales (1), Dothideales (1), Atheliales (1), Liceales (1), Corticiales (1) and further anamorphic fungi (5). Five taxa exhibit a narrow host spectrum and appear to be restricted to the *Xanthoria parietina* group, six species appear to be host-specific at the family level. Nine species are obligately lichenicolous fungi with a broad host spectrum, whereas seven taxa are facultatively lichenicolous, hence about 60 percent belong to the omnivorous element. Various degrees of host specificity of the xanthoriicolous fungi may also be used to support or reject phylogenetic reconstruction models of Teloschistales. Whereas some species such as *Teloggalla olivieri*, *Xanthoriicola physciae* and *Pyrenochaeta xanthoriae* have been present in every richer collection, others, like *Hainesia xanthoriae*, appear to remain rare even in a *Xanthoria parietina*-dominated landscape.

4B: Lichen symbionts and ecophysiology

(4B-P1) Submission ID: IAL0009-00009

A QUANTITATIVE EVALUATION OF BIOCIDES EFFICACY THROUGH THE COLOUR BASED IMAGE ANALYSIS OF ALGAL CHLOROPHYLL EPIFLUORESCENCE

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Epifluorescence microscope observations are applied in the field of stonework conservation to semi-quantitatively evaluate the efficacy of biocide treatments on epilithic photoautotrophic organisms, including lichens. In the current study, dominant lichen species on the marble and calcschist balustrade of the Savoy Castle in Govone (NW-Italy) were investigated for their sensitivity to the common biocide benzalkonium chloride (BZC). Five species (*Aspicilia contorta*, *Caloplaca citrina*, *Candelariella aurella*, *Protoparmeliopsis muralis*, *Verrucaria* gr. *nigrescens*) were assayed with different concentrations (0.5%, 2.5%, 5.0% BZC in isopropanol-water 1:1 mixture), application methods (brushing, spraying) and number of applications (one or two, spaced one week apart). Epifluorescence observations were performed 8 and 16 days after the treatments. Three representative images per sample (three samples per species per treatment) were analyzed (a) semi-quantitatively, an expert eye defining the algal sensitivity according to a 5-level arbitrary scale, and (b) quantitatively, using colour-based image analysis (WinCAM software). For each image, we determined the hue, saturation and intensity co-ordinates (colour model HSI) of the epifluorescence of six algal cells arbitrarily chosen using a grid. A high linear fit was detected between the semi-quantitative data and the hue measures. Spraying gave better results than brushing. Single and double treatments with 2.5% and 5.0% BZC showed similar efficacy, and this latter was only slightly higher than that of two applications of 0.5% BZC. *A. contorta* and *P. muralis* were highly sensitive to all the BZC concentrations, while *C. citrina*, *C. aurella* and *V. muralis* showed some resilience also to 5.0% BZC. In conclusion, the image analysis approach allows the quantitative/statistical comparison of the efficacy of different treatments avoiding the subjective step of the expert evaluation, suggesting that its application could extend to the non-expert personnel involved in restoration programs. A comparison of image analysis results with measurements on the functionality of the photosynthetic process (Chl-a F) of the treated thalli could allow, in the future, the definition of the range of hue values corresponding to active and inactive algal cells. This step may further increase the potency of this diagnostic tool and support a progressive reduction of excessive biocide dispersion in the environment.

4B-P

**MOLECULAR EVOLUTION OF LICHENIZED TRENTEPOHIALES COLLECTED
IN DIVERSE HABITATS**

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The order Trentepohliales is best known as free-living, sub-aerial algae growing in humid situations and on varied substrata. Nevertheless, this algal group is as well associated with many ascomycetous fungi of the humid tropics, forming lichens. The present study is dealing with trentepohlioid photobionts of different lichen species from various collection sites in Europe, Australia, Central- and South America. Due to the fact of poor understanding and deficient knowledge of the phylogenetic relationships within the lichenized order Trentepohliales, their taxonomy is currently in urgent need of revision. To achieve molecular data for the phylogenetic relationships between the trentepohlioid photobionts from the various collection sites mentioned above, we performed DNA analyses with especially and newly designed primers. Therefore, the lichenized algae of selected lichens were isolated according to a modified Yamamoto-method using thallus fragments. The isolation or culturing was performed on different nutrient media, e.g. Bolds Basal Medium, Woods Hole MBL, and optimal Haematococcus Medium. To enhance the biomass production, the culture methods and conditions were altered referring to the origin of the lichens, collected in tropical or temperate climatic regions. The DNA of the cultured trentepohlioid algae were extracted by using a modified CTAB-method and DNA analyses were accomplished with universal primer to amplify the genomic 18S rDNA, the genomic ITS region and the rbcL region of the chloroplast DNA to maintain sequences for the primer-design. Accordingly, these special trentepohlioid primers were used for further molecular analyses by using the algal DNA of the lichen thalli. The identifications of the obtained sequences from the algal cultures and the corresponding lichen thalli were carried out by NCBI BLAST alignment. The maximum likelihood trees of the different Trentepohliales-sequences were computed with the programs MrBayes and BEAST. Results indicate that the growth of the cultured photobionts is highly polymorphic depending upon the composition of the used nutrient media. Moreover the algal cells produce different levels of carotenoid contents (e.g. astaxanthin), which are deposited once as ellipsoidal bodies or small spherical droplets. Phylogenetic trees representing all investigated species from tropical and temperate habitats are presented.

**COMPARISON OF FLUORESCENCE ACTIVITY IN POPULATIONS OF
LASALLIA PUSTULATA AND L. HISPANICA IN THE FIELD AND UNDER LAB
CONDITIONS ALONG A SEASONAL GRADIENT**

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Lasallia pustulata and *L. hispanica* (Umbilicariaceae, Lecanorales) are the two only species of this genus present in Iberian Peninsula. They often share distribution, although *L. hispanica* can stand harder conditions, being able to colonize higher altitudes in Iberian mountains. We have chosen a locality near Madrid, in Central Spain, where the two species coexist, to test the consistency of fluorescence field and lab measurements. For that purpose, we have measured the evolution of PSII quantum yield once a month during a whole year in field conditions, and then we have collected three thalli of each species to repeat these measurements after two days of acclimation to lab conditions (namely, 12h 100 $\mu\text{mol m}^{-2}\text{s}^{-1}$ / 12 h darkness, 10°C, spraying once a day with spring water), trying to minimize the influence of previous climatic episodes in fluorescence performance. The comparison between both systems shows a common pattern of evolution along the year. However, we could observe differences that reflect the influence of previous days weather in the results, showing a highly plastic response of Chl a.

**PHOTOBIONT SELECTIVITY AND SPECIFICITY IN CALOPLACA SPECIES IN A FOG
INDUCED LICHEN COMMUNITY IN THE ATACAMA DESERT, NORTHERN CHILE**

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Little is known about the nature of the association between mycobionts and photobionts in isolated communities. Here we studied the photobiont diversity of different *Caloplaca* Th. Fr. species in a fog induced community in the Atacama Desert. We compared nrDNA ITS sequences of both symbionts, photobionts and mycobionts, along with morphological characters of the different lichen thalli, to investigate the diversity and to assess the degree of selectivity and specificity of photobionts species in a community of *Caloplaca* species. Specimens of 6 species (*C. orthoclada* Zahlbr., *C. fernandeziana* Zahlbr. and 4 undescribed species) were sampled in an altitudinal gradient in a coastal reef with strong fog presence, 60 km south of Iquique, Chile. The photobiont species in this community belonged to two species of the genus *Trebouxia*, *T. arboricola* Puymaly s.l. and *T. gigantea* (Hildreth & Ahmadjian) Gaertner. Most of the fungal species were lichenized with photobionts belonging to different haplotypes of *T. arboricola* s.l., although specimens of two species (*C. orthoclada* and *C. sp. 1*) were related to representatives of *T. gigantea* as well. These results indicate that members of the genus *Caloplaca* in northern Chile have a moderate selectivity and appear to be selective to members of the *Trebouxia arboricola* group. Also, an altitudinal variation in *Trebouxia* haplotypes was observed at high altitudes, which had higher water availability given a higher fog condensation and precipitation. This may suggest that short-term ecological factors, as altitude and water availability could result in local specificity and specialization as a product of local adaptation.

LICHENIZED FUNGI PROVIDE AN IDEAL OSMOTIC SPACE BY ADJUSTING THEIR OWN CELLULAR OSMOLARITY DIFFERENTLY FOR CHLOROBIONTS OR CYANOBIONTS

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Lichens are organisms resulted from symbioses between a fungus and either a green alga or a cyanobacterium. They are known to exhibit extreme tolerance of desiccation. Their all metabolic activities are stopped in drought condition and rapidly recovered in re-hydration. We investigated the responses of photosystem against dehydration using chlorolichens (*Ramalina yasudae* and *Parmotrema tinctorum*), cyanolichens (*Collema subflaccidum* and *Peltigera degenii*), a cephalodium-possessing lichen (*Stereocaulon sorediiferum*) that has a green-algal part and a cyanobacterial part within the same thallus, a green-algal photobiont (*Trebouxia* sp.), an aerial green alga (*Trentepolia aurea*), and a terrestrial cyanobacterium (*Nostoc commune*). The response of photosystem to dehydration shown by cyanolichen was almost the same as that shown by a terrestrial cyanobacterium. The cyanolichen was more sensitive to dehydration than the chlorolichen or the chlorobiont. We found that the differences in response to dehydration were closely related to cellular osmolarity; osmolarity was comparable between cyanolichen and cyanobacterium and between chlorolichen and green alga. Furthermore, in the cephalodium-possessing lichen, the osmolarity of cephalodia and effect of dehydration on cephalodia were similar to those of cyanolichen. Responses of its green-algal part within the identical thallus were similar to those of chlorolichens. This indicates that photobionts retain their original properties as free-living organisms, such as their ability to combat water loss, even after lichenization. More importantly, symbiont fungi adjust their osmotic pressures for the sake of their green-algal or cyanobacterial partners; providing suitable osmotic environments to combat desiccation. We conclude that the lichen symbiosis involves a mutual partnership rather than a commensalism. Inspired by these results, we conducted three-dimensional image analysis by X-ray microtomography, and we will also discuss on the morphology related to photosynthetic environments of green-algal and cephalodia parts of a *S. sorediiferum*.

LICHEN ASSIST THE DROUGHT-INDUCED NPQ OF THEIR PHOTOBIONT BY ARABITOL

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Lichens have remarkable drought tolerance, and such ability enables them to survive in extreme environments that frequently fall in desiccation. We have investigated their highly effective thermal dissipation mechanism of excess light energy in photosystem II under drought conditions that is detected as non-photochemical quenching (NPQ). Drought-induced non-photochemical quenching (d-NPQ) plays a very important role in photosynthetic organisms inhabiting in extreme drought sites, because excess light under drought condition induces accumulation of 3chl* and the resulting 3chl* generates reactive oxygen species (ROS). ROS causes photoinhibition and injures cells leading to cell deaths. Recently, it was reported that the d-NPQ related energy transfer from PSII to a fluorescence quencher, F740, and an energy dissipation within 30 fs in dehydrated lichens. However, we found that photobiont *Trebouxia* sp. lost these abilities and became more sensitive against light stress once they had been isolated from a lichen body *Ramalina yasudae*. This phenomenon indicated the presence of physico-chemical interaction between the mycobiont and photobiont. We analyzed the water-soluble materials obtained during the isolation process of *Trebouxia* from *R. yasudae*, and found that a pentane-1, 2, 3, 4, 5-pentol (D-Arabitol) was the major component. Therefore, we measured time-resolved fluorescence spectra and analyzed decay-associated spectra (DAS) of *R. yasudae*, isolated *Trebouxia* and arabitol-treated *Trebouxia*. As a result, isolated *Trebouxia* didn't show d-NPQ but arabitol-treated *Trebouxia* showed d-NPQ and energy transfer from PSII to F740 as in lichen. Based on these results, we can conclude that accumulated arabitol in lichen thalli accelerate energy dissipation in photobionts under drought conditions leading to the protection of them from photoinhibition.

EARLY DEVELOPMENT OF TEMPERATE FOLIOSE LICHENS ON COVER SLIPS

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Lichen developmental biology is of special interest because at least two genomes are involved in morphogenesis. Yet little is known about this process, in part because lichens grow slowly and are notoriously difficult to culture in laboratory conditions. As well, most surfaces used for lichen growth have been difficult to image. We attempt to document lichen development by placing soredia from foliose temperate lichens *Parmelia sulcata* and *Physcia adscendens* onto plastic cover slips and growing them outdoors (in Canada 133 km north-east of Toronto) for a period of 15 months. The cover slips allowed non-destructive imaging of live developing lichens as well as preparation for light and electron microscopy. Only soredia seeded on cover slips in May (as opposed to August or January) successfully developed. These samples were analyzed after 6, 10 and 15 months. Well-developed attachment hyphae were seen by 6 months (November), while lobules (early lichen thallus) were detected after 10 months. In other words they developed between November and March, Ontario, Canada's coldest time of the year. This adds weight to previous inferences that temperate lichens are more developmentally competent at cold temperatures. In terms of morphology, the hyphae and lobules varied considerably between species, raising the possibility that lichen species or at least genera may be identifiable at an early point in the development process. Considering spatial patterns, soredia were often found in clumps. Most development occurred on the periphery or outside of the soredial clumps. It was only after 15 months that soredia inside clumps began to form more attachment hyphae and lobules with higher frequency. The delayed development inside clumps suggests these soredia experience lateral inhibition or a lack of nutrients. Microscopic examination suggested that the upper cortex forms after the lower cortex and that it forms in patches. Overall, we have shown that foliose temperate lichens can be cultured on cover slips, presenting a method where development may be observed in identified lichen species. The cover slip technique may be useful for a variety of culture studies including biomonitoring for conditions conducive to lichen development.

EFFECTS OF UVR (A-B) IN CHLOROPHYLL A FLUORESCENCE OF *SEIROPHORA VILLOSA* AND *RAMALINA PUSILLA* AND THEIR ISOLATED PHYCOBIANTS

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The lichens *Seirophora villosa* (Ach.) Frödén and *Ramalina pusilla* Le Prévost grow on twigs of shrubs and small trees in coastal dune ecosystems of the Mediterranean area. However, *S. villosa* grows in microhabitats directly exposed to solar radiation, where *R. pusilla* does not develop, suggesting a better adaptation to ultraviolet radiation. These two species may be a good model to understand the acclimation of lichens to different types of irradiation. For this reason, we decided to analyze the responses of these lichens and their phycobionts both lichenized and in culture. *R. pusilla* and *S. villosa* were collected in Es Trenc (Mallorca, Spain) on *Juniperus turbinata* Guss. and *Pinus halepensis* Miller. Phycobionts were isolated and grown on cellulose-acetate discs on agar 3NBBM. The thalli were previously acclimated in growth chambers for 3 days with cycles of 12 h light and 12 h darkness at 17°C. UVA and UVB fluorescent lamps (Philips) was used and located at a precise distance from the samples. The UVA and UVB treatments were done independently. The photosynthetic activity was calculated using the fluorometer DualPam (Walz). The chlorophyll a fluorescence (C_{la}) measurements were performed after 7, 14 and 28 days (12/12 day/night cycles at 17°C). Algal discs were exposed to UV during 1 h, 2 h, 6 h and 24 h. In *S. villosa*, maximal PSII quantum yield (F_v/F_m) decline during irradiation time with UVB in both thalli and isolated phycobionts. UVA radiation seems to have low effect on the thalli of *S. villosa*, and damage was only observed in cultured phycobionts after 24 h of exposure. The experiments with *S. villosa* showed protection of the algae within the thallus, against UVA and UVB radiation. In *R. pusilla* a significant effect on F_v/F_m was observed after 7 days UVA exposure in thalli and 6 h in its isolated phycobionts. Our results show that the phycobionts of *S. pusilla* are more sensitive to UV radiation than *S. villosa*. [MCINN (CGL2009-13429-C02-01/02), AECID (PCI_A_I024755/09) and Generalitat Valenciana (PROMETEO 174/2008 GVA)]

BLUE LIGHT SCREENING REDUCE BLUE LIGHT PHOTOSYNTHETIC EFFICIENCY OF CYANOLICHENS COMPARED WITH CHLOROLICHENS

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Cyanolichens have phycocyanins that mainly absorb light in the green part of the spectrum. Thereby, phycocyanins enhance the absorption of light transmitted through a canopy. The combination of phycocyanins and chl a may thus improve photosynthesis in shaded forest sites. We compared the chlorolichens *Lobaria pulmonaria* and *Peltigera leucophlebia* with the cyanolichens *L. hallii* and *P. praetextata* by measuring light response curves for photosynthetic CO₂ uptake, O₂ evolution, as well as photosystem II efficiency in blue, green and red light, respectively. Maximal photosynthetic CO₂ uptake was slightly higher for both cyanolichens than for the chlorolichens in green light. In red light there was no difference in maximal CO₂ uptake, whereas both cyanolichens had substantially lower photosynthesis in blue light. The same trend occurred for photosynthetic O₂ evolution. Apparent electron transport rate (ETR) did not differ between red and green light in any of the species. For the cyanolichens, ETR showed no sign of light saturation in blue light, indicating that little blue light absorbed is used in photosynthesis. Reflectance spectra showed that green light was less reflected in the cyanolichens, which may partly explain the slightly higher cyanobacterial photosynthetic CO₂ uptake in green light. However, low reflectance of blue light for all lichens cannot explain the reduced photosynthesis in cyanolichens in blue light. Transmittance of light through the combined cortex and photobiont layer showed that also the blue light was efficiently absorbed. Screening was estimated indirectly by comparing chlorophyll fluorescence ratios between chlorophyll fluorescence excited with blue and red light. Much lower blue/red ratios occurred in the cyanolichens *L. hallii* and *P. praetextata* than in the chlorolichens *L. pulmonaria* and *P. leucophlebia*, indicating that screening of blue light in the cyanolichens inhibited blue light from reaching the photosynthetic apparatus. The UV and blue light absorbing compound scytonemin in cyanobacteria and in some lichens was suggested as a candidate for screening. HPLC analyses showed that *L. hallii* contained some scytonemin that partly may explain the blue light screening, whereas *P. praetextata* contained no scytonemin. Therefore, the mechanism for blue light screening and low blue light photosynthesis in cyanolichens remains unknown.

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