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Hyde KD[1,2,3], Abdel-Wahab MA[4], Abdollahzadeh J[5], Abeywickrama PD[6], Absalan S[7,2], Afshari N[7,2], Ainsworth AM[8], Akulov OY[9], Aleoshin VV[10,11], Al-Sadi AM[12], Alvarado P[13], Alves A[14], Alves-Silva G[132], Amalfi M[15,16], Amira Y[17], Amuhenage TB[2,3], Anderson JL[18,102], Antonín V[19], Aouali S[20], Aptroot A[21], Apurillo CCS[2,3,22], Araújo JPM[23], Ariyawansa HA[24], Armand A[2,3], Arumugam E[25], Asghari R[2,3], Assis DMA[26], Atienza V[27], Avasthi S[28], Azevedo E[29], Bahkali AH[30], Bakhshi M[31], Banihashemi Z[32], Bao DF[33], Baral HO[34], Barata M[35], Barbosa FR[36], Barbosa RN[26], Barreto RW[37], Baschien C[178], Belamesiatseva DB[39], Bennett Reuel M[40,41], Bera I[2], Bezerra JDP[42], Bezerra JL[43], Bhat DJ[30,44], Bhunjun CS[2,3], Bianchinotti MV[45], Błaszkowski J[46], Blondelle A[112], Boekhout T[47], Bonito G[48], Boonmee S[2,3], Boonyuen N[49], Bregant C[50], Buchanan P[51], Bundhun D[2,3], Burgaud G[52], Burgess T[53], Buyck B[54], Cabarroi-Hernández M[55], Cáceres MES[56], Caeiro MF[29], Cai L[58], Cai MF[59], Calabon MS[60], Calaça FJS[61,62], Callalli M[63,64,65], Camara MPS[66], Cano-Lira JF[67], Cantillo T[68], Cao B[69], Carlavilla JR[70], Carvalho A[71], Castañeda-Ruiz RF[72], Castlebury L[73], Castro-Jauregui O[55], Catania MDV[74], Cavalcanti LH[75], Cazabonne J[76,77], Cedeño-Sanchez ML[79,278], Chaharmiri-Dokhaharani S[2], Chaiwan N[80], Chakraborty N[81], Chaverri P[82,83], Cheewangkoon R[84], Chen C[2,3,127], Chen CY[85], Chen KH[86], Chen J[181], Chen Q[87], Chen WH[88], Chen YP[89], Chethana KWT[2,3], Coleine C[90], Condé TO[91], Corazon-Guivin MA[92,93], Cortés-Pérez A[55], Costa-Rezende DH[94], Courtecuisse R[95], Crouch JA[96], Crous PW[97], Cui BK[98], Cui YY[99,100], da Silva DKA[26], da Silva GA[26], da Silva IR[101], da Silva RMF[26], da Silva Santos AC[26], Dai DQ[1,*], Dai YC[98], Damm U[103], Darmostuk V[104], Daroodi Zoha[105], Das K[106], Das K[107], Davoodian N[108], Davydov EA[109], Dayarathne MC[110], Decock C[111], de Groot MD[112,113], De Kesel A[15], dela Cruz TEE[40], De Lange R[112], Delgado G[116], Denchev CM[117], Denchev TT[117], de Oliveira NT[26], de Silva NI[7,118], de Souza FA[119], Dentinger B[120], Devadatha B[121,122], Dianese JC[123], Dima B[124], Diniz AG[26], Dissanayake AJ[89], Dissanayake LS[125], Doğan HH[126], Doilom M[127], Dolatabadi S[128], Dong W[127], Dong ZY[127], Dos Santos LA[131], Drechsler-Santos ER[132], Du TY[1,2], Dubey MK[133], Dutta AK[134], Egidi E[135], Elliott TF[136], Elshahed MS[137], Erdoğdu M[138], Ertz D[15,16], Etayo J[139], Evans HC[140], Fan XL[141], Fan YG[142], Fedosova AG[143], Fell J[144], Fernandes I[145,146,102], Firmino AL[147], Fiuza PO[148], Flakus A[104,339], Fragoso de Souza CA[150], Frisvad JC[151], Fryar SC[152,102], Gabaldón T[153,154,155,156], Gajanayake AJ[2,3], Galindo LJ[170], Gannibal PB[157,158], García D[159], García-Sandoval SR[160,161], Garrido-Benavent I[27], Garzoli L[163], Gautam AK[164], Ge Z-W[99], Gené DJ[166], Gentekaki E[2,3], Ghobad-Nejhad M[167],

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Corresponding Author: Qiang Li – e-mail – LQ@mail.qjnu.edu.cn,
Dong-Qin Dai – e-mail – cicidaidongqin@gmail.com

Giachini AJ[168], Gibertoni TB[26], Góes-Neto A[169], Gomdola D[2,3], Gomes de Farias AR[2], Gorjón SP[171], Goto BT[172], Granados-Montero MM[173], Griffith GW[174], Groenewald JZ[97], Groenewald M[97], Grossart HP[175,176], Gueidan C[177], Gunarathne A[2,3], Gunaseelan S[25], Gusmão LFP[179], Gutierrez AC[180], Guzmán-Dávalos L[55], Haelewaters D[15,112,182,183], Halling R[184,185], Han YF[186], Hapuarachchi KK[187], Harder CB[188], Harrington TC[189], Hattori T[190], He MQ[69], He S[2,3,99], He SH[98], Healy R[192], Herández-Restrepo M[97], Heredia G[193], Hodge KT[194], Holgado-Rojas M[195,196,197], Hongsanan S[198,199], Horak E[200,201], Hosoya T[202], Houbraken J[97], Huang SK[203], Huanraluek N[2], Hur JS[204], Hurdeal VG[2,3], Hustad VP[205], Iotti M[206], Iturriaga T[194], Jafar E[207], Janik P[104], Jany JL[52]Jayalal RGU[209], Jayasiri SC[210], Jayawardena RS[2,3,211], Jeewon R[212,213], Jerônimo GH[324], Jesus AL[324], Jin J[214], Johnston PR[51], Jones EBG[216,30], Joshi Y[398], Justo A[218], Kaishian P[219], Kakishima M[220], Kaliyaperumal M[25], Kang GP[222,223], Kang JC[224], Karakehian JM[115], Karimi O[2,3], Karpov SA[225], Karunarathna SC[227], Kaufmann M[228], Kemler M[229], Kezo K[25], Khyaju S[2,3], Kirchmair M[230], Kirk PM[8], Kitaura MJ[232], Klawonn I[233], Kolarik M[234], Kong A[235], Kuhar F[236], Kukwa M[237], Kumar S[238], Kušan I[239], Lado C[240], Larsson KH[241,242], Latha KPD[243], Lee HB[253], Leonardi M[206], Leontyev DL[244,245], Lestari AS[2,3,246], Li CJY[2,3,99], Li DW[247], Li H[2,3,127],Li HY[248], Li L[249,2,3], Li QR[250], Li Q[1,*], Li WL[89], Li Y[98], Li YC[99,100], Li YX[2,3,127], Liao CF[2,3,127], Liimatainen K[8], Lim YW[255], Lin CG[256], Linaldeddu BT[50], Linde CC[257], Linn MM[2,3], Liu F[69], Liu JK[89], Liu NG[258], Liu S[98], Liu SL[69], Liu XF[1,,3], Liu XY[260], Liu XZ[261], Liu ZB[98], Lu L[2], Lu YZ[249], Luangharn T[2], Luangsa-ard JJ[49], Lumbsch HT[263], Lumyong S[7,264,265], Luo L[2,3,99], Luo M[127], Luo ZL[33], Ma J[2,3,129,249], Machado AR[26], Madagammana AD[2,3], Madrid H[268], Magurno F[269], Magyar D[270], Mahadevan N[271,272], Maharachchikumbura SSN[89,273], Maimaiti Y[274], Malosso E[26], Manamgoda DS[275], Manawasinghe IS[127] , Mapook A[2], Marasinghe DS[2], Mardones M[277], Marin-Felix Y[278], Márquez R[279], Masigol H[280], Matočec N[239], May TW[281], McKenzie EHC[51], Meiras-Ottoni A[26], Melo RFR[26], Mendes-Alvarenga RL[26], Mendieta S[283], Meng QF[284,2,3], Menkis A[285], Menolli N Jr[286], Mešić A[239], Meza Calvo JG[288], Mikhailov KV[10,11], Miller SL[289], Moncada B[290,291], Moncalvo JM[292,293], Monteiro JS[294,295], Monteiro M[296], Mora-Montes HM[297], Moreau PA[298], Mueller GM[299], Mukhopadyay S[2,3], Murugadoss R[25], Nagy LG[300], Najafiniya M[301], Nanayakkara CM[130], Nascimento CC[286,302], Nei Y[303], Neves MA[304], Neuhauser S[230], Niego AGT[305], Nilsson RH[306], Niskanen T[307], Niveiro N[308], Noorabadi MT[2], Noordeloos ME[309], Norphanphoun C[2,366], Nuñez Otaño NB[310], O'Donnell RP[311], Oehl F[312], Olariaga I[313], Orlando OP[314], Pang KL[315], Papp V[316], Pawłowska J[317], Peintner U[230], Pem D[2,3], Pereira OL[318], Perera RH[2,319], Perez-Moreno J[320], Perez-Ortega S[321], Péter G[322], Phillips AJL[323], Phonemany M[2,3], Phukhamsakda C[2], Phutthacharoen K[2,3], Piepenbring M[221], Pires-Zottarelli CLA[324], Poinar G[325], Pošta A[239], Prieto M[326], Promputtha I[7], Quandt CA[327], Radek R[328], Rahnama K[329], Raj KNA[330], Rajeshkumar KC[331], Rämä T[332], Rambold G[333,334], Ramírez-Cruz V[55], Rasconi S[335], Rathnayaka AR[2], Raza M[274,58], Ren GC[336,337], Robledo GL[338], Rodriguez-Flakus P[104,339], Ronikier A[104], Rossi W[206], Ryberg M[340], Ryvarden LR[341], Salvador-Montoya CA[342], Samant B[343], Samarakoon BC[2,3], Samarakoon MC[84], Sánchez-Castro I[344], Sánchez-García M[345], Sandoval-Denis M[97],

Santamaria B[112], Santiago ALCMA[26], Sarma VV[346], Savchenko A[347], Savchenko K[348], Saxena RK[349], Scholler M[350], Schoutteten N[112], Seifollahi E[2], Selbmann L[90,351], Selcuk F[352], Senanayake IC[162,353], Shabashova TG[39], Shen HW[33], Shen YM[354], Silva-Filho AGS[286], Simmons DR[355], Singh R[356], Sir EB[357], Song CG[98], Souza-Motta CM[26], Sruthi OP[331], Stadler M[278], Stchigel AM[67], Stemler J[359,360,361], Stephenson SL[362], Strassert JFH[363], Su HL[2,3,99], Su L[364], Suetrong S[365], Sulistyo B[112], Sun YF[98], Sun YR[366,2,3], Svantesson S[367,368,] Sysouphanthong P[2], Takamatsu S[369,202], Tan TH[2,222,223], Tanaka K[370], Tang AMC[371], Tang X[2,3,372], Tanney JB[373], Tavakol NM[2], Taylor JE[374], Taylor PWJ[375], Tedersoo L[376,47], Tennakoon DS[118,7], Thamodini GK[12], Thines M[38], Thiyagaraja V[379,84,2], Thongklang N[2,3], Tiago PV[26], Tian Q[89], Tian WH[89], Tibell L[380], Tibell S[380], Tibpromma S[1], Tkalčec Z[239], Tomšovský M[381], Toome-Heller M[382], Torruella G[153,154], Tsurykau A[385,386], Udayanga D[275], Ulukapi M[352], Untereiner WA[387], Uzunov BA[388], Valle LG[389], Van Caenegem W[112], Van den Wyngaert S[390], Van Vooren N[391], Velez P[392], Verma RK[393], Vieira LC[26], Vieira WAS[394], Vizzini A[395], Walker A[2,3], Walker AK[396], Wanasinghe DN[379], Wang CG[98], Wang K[69], Wang SX[399], Wang XY[99,100], Wang Y[366], Wannasawang N[2], Wartchow F[276], Wei DP[372], Wei XL[58], White JF[266], Wijayawardene NN[1,254], Wijesinghe SN[2], Wijesundara DSA[400], Wisitrassameewong K[262], Worthy FR[99,100], Wu F[98], Wu G[99,100], Wu HX[165], Wu N[2,3,89], Wu WP[191], Wurzbacher C[251], Xiao YP[252], Xiong YR[2,3,127], Xu B[127], Xu LJ[401], Xu R[208,149], Xu RF[2,3,99], Xu RJ[2,3,99], Xu TM[98], Yakovchenko L[383], Yan JY[6], Yang HD[2,3,384], Yang J[2], Yang ZL[384], Yang YH[2,3,127], Yapa N[397], Yasanthika E[2,3],, Youssef NH[137], Yu FM[2,3,384], Yu Q[358], Yu XD[89], Yu YX[89], Yu ZF[401], Yuan HS[282], Yuan Y[98], Yurkov A[178], Zafari D[215], Zamora JC[114], Zare R[31], Zeng M[2,3,384], Zeng NK[267], Zeng XY[366], Zhang F[2,3,377], Zhang H[217], Zhang JF[57,378], Zhang JY[2,3,249], Zhang QY[98], Zhang SN[89], Zhang W[6], Zhang Y[98], Zhang YX[127], Zhao CL[187], Zhao H[98], Zhao Q[384], Zhao RL[69], Zhou LW[69], Zhou M[98], Zhurbenko MP[143], Zin HH[2,3], Zucconi L[231]

[1] *Centre for Yunnan Plateau Biological Resources Protection and Utilization, College of Biological Resource and Food Engineering, Qujing Normal University, Qujing, Yunnan 655011, P.R. China*
[2] *Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand*
[3] *School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand*
[4] *Department of Botany and Microbiology, Faculty of Science, Sohag University, Sohag 82524, Egypt*
[5] *Department of Plant Protection, Agriculture Faculty, University of Kurdistan, P.O. Box 416, Sanandaj, Iran*
[6] *Beijing Key Laboratory of Environment Friendly Management on Fruit Diseases and Pests in North China, Institute of Plant Protection, Beijing Academy of Agriculture and Forestry Sciences, Beijing 100097, People's Republic of China*
[7] *Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand*
[8] *Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3AE, UK*
[9] *V.N. Karazin Kharkiv National University, Svobody sq., 4, Kharkiv, 61022, Ukraine*
[10] *Belozersky Institute for Physico-Chemical Biology, Lomonosov Moscow State University, Moscow, 119992, Russian Federation*
[11] *Kharkevich Institute for Information Transmission Problems, Russian Academy of Sciences, Moscow 127051, Russian Federation*
[12] *Department of Plant Sciences, College of Agricultural and Marine Sciences, Sultan Qaboos University, AlKhoud 123, Oman*
[13] *Dr. Fernando Bongera st., Severo Ochoa bldg. S1.04, 33006 Oviedo, Spain*
[14] *Centre for Environmental and Marine Studies (CESAM), Department of Biology, University of Aveiro, 3810-193 Aveiro, Portugal*
[15] *Meise Botanic Garden, Department Research, Nieuwelaan 38, BE-1860 Meise, Belgium*

[16]*Fédération Wallonie-Bruxelles, Service Général de l'Enseignement Supérieur et de la Recherche Scientifique, rue A. Lavallée 1, BE-1080 Bruxelles, Belgium*
[17]*REMA – Núcleo Ressacada de Pesquisas em Meio Ambiente, Universidade Federal de Santa Catarina, Departamento de Microbiologia, Campus Universitário – Trindade 88040-970 Florianópolis – SC – Brasil*
[18]*Department of Aquatic Sciences and Assessment, Division of Microbial Ecology, Swedish University of Agricultural Sciences, Lennart Hjelms väg 9, 756 51 Uppsala, Sweden*
[19]*Moravian Museum, Dept. of Botany, Zelný trh 6, CZ-659 37 Brno, Czech Republic*
[20]*Forest Pathology and Mycology Laboratory, Forest Protection Division, National Forest Research Institute, Algiers 16032, Algeria*
[21]*Laboratório de Botânica / Liquenologia, Instituto de Biociências, Universidade Federal de Mato Grosso do Sul, Avenida Costa e Silva s/n, Bairro Universitário, CEP 79070-900, Campo Grande, Mato Grosso do Sul, Brazil*
[22]*Center for Research in Science and Technology (CReST), Philippine Science High School-Eastern Visayas Campus, 6501 Palo, Leyte, Philippines*
[23]*Institute of Systematic Botany, The New York Botanical Garden, Bronx - NY 10458 USA*
[24]*Department of Plant Pathology and Microbiology, National Taiwan University, Taiwan*
[25]*Centre for Advanced Studies in Botany, University of Madras, Guindy Campus, Chennai 600 025, Tamil Nadu, India*
[26]*Department of Mycology, Federal University of Pernambuco, Recife, 50740-600, Brazil*
[27]*Departament de Botànica i Geologia, Facultat de Ciències Biològiques, Campus de Burjassot, Universitat de València, ES-46100 Burjassot, València, Spain*
[28]*School of Studies in Botany, Jiwaji University Gwalior, Madhya Pradesh, 474011, India*
[29]*Centro de Ecologia, Evolução e Alterações Climáticas (CE3C), and Centro de Estudos do Ambiente e do Mar (CESAM), Faculdade de Ciências, Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal*
[30]*Department of Botany and Microbiology, College of Science, King Saud University, P.O. Box 2455, Riyadh 11451, Saudi Arabia*
[31]*Iranian Research Institute of Plant Protection, P.O. Box 19395-1454, Agricultural Research, Education and Extension Organization (AREEO), Tehran, Iran*
[32]*Department of Plant Protection, College of Agriculture, Shiraz University, Shiraz, Iran*
[33]*College of Agriculture and Biological Science, Dali University, Dali 671003, Yunnan, P. R. China*
[34]*Blaihofstraße 42, D–72074 Tübingen, Germany*
[35]*Centro de Ecologia, Evolução e Alterações Climáticas (CE3C), Faculdade de Ciências, Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal; Departamento de Biologia Vegetal, Faculdade de Ciências, Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal*
[36]*Universidade Federal de Mato Grosso - UFMT, Instituto de Ciências Naturais, Humanas e Sociais, Av. Alexandre Ferronato, 1200, Setor Industrial, CEP: 78.557-267, Sinop, Mato Grosso, Brazil*
[37]*Departamento de Fitopatologia, Universidade Federal de Viçosa, Viçosa, MG, 36570-900, Brazil*
[38]*Senckenberg Biodiversity and Climate Research Centre, Senckenberganalge 25, 60325 Frankfurt am Main, Germany; Goethe University, Department of Biological Sciences, Institute of Ecology, Evolution and Diversity, Max-von-Laue-Str. 13, 60348 Frankfurt am Main, Germany; LOEWE Centre for Translational Biodiversity Genomics, Georg-Voigt-Str. 14-16, 60325 Frankfurt am Main, Germany*
[39]*State Scientific Institution V.F. Kuprevich Institute of Experimental Botany / 27 Akademichnaya St., Minsk BY-220072, Republic of Belarus*
[40]*Department of Biological Sciences, College of Science, University of Santo Tomas, Manila, Philippines*
[41]*UST Collection of Microbial Strains, Research Center for the Natural and Applied Sciences, University of Santo Tomas, Manila, Philippines*
[42]*Laboratório de Micologia and Programa de Pós-Graduação em Biologia da Relação Parasito-Hospedeiro, Instituto de Patologia Tropical e Saúde Pública, Universidade Federal de Goiás. Rua 235, s/n, 74605–050, Goiânia, Goiás, Brazil*
[43]*Department of Agronomy, State University of Santa Cruz, Ilhéus, Brazil*
[44]*Biology Division, Vishnugupta Vishwavidyapeetam, Ashoke, Gokarna 581326, India*
[45]*Dto. de Biología, Bioquímica y Farmacia. Universidad Nacional del Sur (UNS), Centro de Recursos Naturales Renovables de la Zona Semiárida (CERZOS-UNS-CONICET), Bahía Blanca, Argentina*
[46]*Department of Environmental Management, West Pomeranian University of Technology in Szczecin, Szczecin 71434, Poland*
[47]*College of Science, King Saud University, Riyadh 11451, Saudi Arabia*
[48]*Department of Plant Soil and Microbial Sciences, Michigan State University, East Lansing MI, 48824, United States of America*
[49]*National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), 111 Thailand Science Park, Phahonyothin Road, Khlong Nueng, Khlong Luang, Pathum Thani 12120, Thailand*
[50]*Dipartimento Territorio e Sistemi Agro-Forestali, Università degli Studi di Padova, Viale dell'Università 16, 35020 Legnaro, Italy*
[51]*Manaaki Whenua – Landcare Research, Private Bag 92170, Auckland 1142, New Zealand*
[52]*Univ Brest, INRAE, Laboratoire Universitaire de Biodiversité et Écologie Microbienne, F-29280 Plouzané, France*
[53]*Harry Butler Institute, 90 South St, Murdoch, WA 6150, Australia*

[54]*Herbier de mycologie, Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles CP 39, 57 rue Cuvier, 75005 Paris, France*
[55]*Department of Botany and Zoology, University of Guadalajara, Apdo. postal 1-139, Zapopan, Jal., 45147, Mexico*
[56]*Departamento de Biociências, Universidade Federal de Sergipe, Av. Vereador Olimpio Grande, s/n, Bairro Centro, CEP 49500-000, Itabaiana, Sergipe, Brazil*
[57]*Guizhou Provincial Institute of Tea, Guiyang 550006, People's Republic of China*
[58]*State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China*
[59]*State Key Laboratory of Biocontrol, School of Ecology, Sun Yat-Sen University, Shenzhen 518107, China*
[60]*Division of Biological Sciences, College of Arts and Sciences, University of the Philippines Visayas, Miagao, Iloilo, 5023, Philippines*
[61]*Mycokosmos – Mycology and Scientific Communication, Rua JP 11 Quadra 18 Lote 13, Jd. Primavera 1ª etapa, Anápolis, GO, 75090-260, Brazil*
[62]*Laboratório de Pesquisa em Ensino de Ciências – LabPEC, Centro de Pesquisas e Educação Científica, Universidade Estadual de Goiás, Campus Central (CEPEC/UEG), Anápolis, GO, 75132-903, Brazil*
[63]*Organización Juvenil, Hongos Perú, Av. Ejército B-12, Cusco, Perú*
[64]*Centro de Investigación y Producción de Hongos Alimenticios y Medicinales, Universidad Nacional de San Antonio Abad del Cusco, Av. De la Cultura 733, Cusco, Perú*
[65]*Laboratorio de Biología y Fisiología Vegetal, Universidad Nacional Intercultural de Quillabamba, El Arenal S/N, Quillabamba, Perú*
[66]*Departamento de Agronomia, Universidade Federal Rural de Pernambuco, Recife, 52171-900, Brazil*
[67]*Mycology and Environmental Microbiology Unit, Faculty of Medicine, University Rovira i Virgili, 43201 Reus, Spain*
[68]*Postgraduate Program in Earth and Environmental Sciences Modeling, Feira de Santana State University, Ave. Transnordestina, Feira de Santana, Bahia 44036900, Brazil*
[69]*State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, P.R. China*
[70]*Departamento Ciencias de la Vida, Facultad de Biología, Universidad de Alcala, 28805, Alcala de Henares, Madrid, Spain*
[71]*Life and Health Sciences Research Institute (ICVS), School of Medicine, University of Minho, 4710-057 Braga, Portugal*
[72]*Instituto de Investigaciones de Sanidad Vegetal, Calle 110 No. 514, Playa, La Habana 11600, Cuba*
[73]*Mycology and Nematology Genetic Diversity and Biology Laboratory, US Department of Agriculture, Agricultural Research Service, Beltsville, MD 20705, USA*
[74]*Instituto Criptogámico, Sección Micología - Área Botánica - Fundación Miguel Lillo, Miguel Lillo 251- (T4000JFE) San Miguel de Tucumán, Tucumán, Argentina*
[75]*Departamento de Botânica, Universidade Federal de Pernambuco, Recife, Pernambuco, Brazil*
[76]*Ecology Research Group of Abitibi RCM, Forest Research Institute, Université du Québec en Abitibi-Témiscamingue, Amos, QC J9T 2L8, Canada*
[77]*Centre for Forest Research, Université du Québec à Montréal, P.O. Box 8888, Stn. Centre-ville, Montréal, QC H3C 3P8, Canada*
[79]*Institute of Microbiology, Technische Universität Braunschweig, Spielmannstraße 7, 38106 Braunschweig, Germany*
[80]*Office of Research Administration, Chiang Mai University, Chiang Mai 50200, Thailand*
[81]*Department of Botany, Scottish Church College (affiliated to University of Calcutta), Kolkata, West Bengal, Pin-700006, India*
[82]*Department of Natural Sciences, Bowie State University, Bowie, Maryland, U.S.A. 20715*
[83]*School of Biology and Natural Products Research Centre (CIPRONA), University of Costa Rica, San Pedro, San José, Costa Rica*
[84]*Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50200, Thailand*
[85]*Department of Plant Pathology, National Chung Hsing University, Taichung 402202, Taiwan*
[86]*Biodiversity Research Center, Academia Sinica, Taipei, 115, Taiwan*
[87]*State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, No. 1 Beichen West Road, Chaoyang District, Beijing 10010, China*
[88]*Center for Mycomedicine Research, Basic Medical School, Guizhou University of Traditional Chinese Medicine, Guiyang 550025, Guizhou, P. R. China*
[89]*School of Life Science and Technology, Center for Informational Biology, University of Electronic Science and Technology of China, Chengdu 611731, China*
[90]*Department of Ecological and Biological Sciences, University of Tuscia, Viterbo 01100, Italy*
[91]*Departamento de Microbiologia, Universidade Federal de Viçosa, 36570–900, Viçosa, Minas Gerais, Brazil*
[92]*Center of Biotechnology and Genetics, Department of Biological Sciences, Universidade Estadual de Santa Cruz, Rodovia Jorge Amado km 16, Ilhéus 45662-900, Brazil*
[93]*Laboratorio de Biología y Genética Molecular, Universidad Nacional de San Martín, Jr.*
Amorarca N° 315, Morales, Peru
[94]*Departamento de Ciências Biológicas, Programa de Pós-graduação em Botânica, Universidade Estadual de Feira de Santana, Av. Transnordestina s/n, Novo Horizonte, Feira de Santana, Bahia 44036-900, Brazil*

[95]Laboratoire de Génie civil et Géo-environnement (LGCgE) – ER4. LSVF, Faculté de Pharmacie, UFR3S – Université de Lille. 3, rue du Professeur Laguesse, 59000 Lille, France
[96]Foreign Disease/Weed Science Research Unit, United States Department of Agriculture, Agricultural Research Service, Fort Detrick, Maryland, U.S.A.
[97]Westerdijk Fungal Biodiversity Institute, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands
[98]Institute of Microbiology, School of Ecology and Nature Conservation, Beijing Forestry University, Beijing 100083, China
[99]Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, Yunnan, China
[100]Yunnan Key Laboratory for Fungal Diversity and Green Development, Kunming 650201, Yunnan, China
[101]Department of Life and Environmental Sciences, University of California, Merced, Merced, California 95343, United States of America
[102] IUCN SSC Aquatic Fungi Specialist Group, 1196 Gland, Switzerland
[103]Senckenberg Museum of Natural History Görlitz, PF 300 154, 02806 Görlitz, Germany
[104]W. Szafer Institute of Botany, Polish Academy of Sciences, Lubicz 46, PL-31-512 Kraków, Poland
[105]Department of Plant Protection, Faculty of Agriculture, Ferdowsi University of Mashhad, Iran
[106]Central National Herbarium, Botanical Survey of India, P.O. - Botanic Garden, Howrah 711103, India
[107]College of Agriculture and Life Sciences, Kyungpook National University, Daegu 41566, South Korea
[108]Royal Botanic Gardens Victoria, South Yarra, VIC 3141, Australia
[109]Altai State University, Lenin Ave. 61, Barnaul, 656049, Russia
[110Denchev]Postgraduate Institute of Agriculture, Old Galaha Road, 20400, Sri Lanka
[111]Mycothèque de l'Université catholique de Louvain, Croix du Sud 2 bte L7.05.06, 1348 Louvain-la-Neuve, Belgoque
[112]Research Group Mycology, Department of Biology, Ghent University, K.L. Ledeganckstraat 35 9000 Ghent, Belgium
[113]Research Institute for Nature and Forest (INBO), Havenlaan 88 box 73, 1000 Brussels, Belgium
[114]Conservatoire et Jardin botaniques de Genève, Chemin de l'Impératrice 1, 1292 Chambésy-Genève, Switzerland
[115]University of Illinois at Urbana-Champaign, Illinois Natural History Survey, Champaign, IL 61820, USA
[116]Eurofins Built Environment Houston, 6110 W. 34th St., Houston, TX 77092, USA
[117]Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, 2 Gagarin St., 1113 Sofia, Bulgaria
[118]Research Center of Microbial Diversity and Sustainable Utilization, Chiang Mai University, Chiang Mai 50200, Thailand
[119]Nucleus of Applied Biology - Embrapa Milho e Sorgo, Sete Lagoas, Minas Gerais 35702-098, Brazil
[120]Natural History Museum of Utah; School of Biological Sciences, University of Utah, Salt Lake City, UT, USA.
[121]Microbial Type Culture Collection and Gene Bank (MTCC), CSIR-Institute of Microbial Technology, Chandigarh, 160036, India
[122]Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, 201002, India
[123]Institute of Biological Sciences, Mycological Collection, Universidade de Brasília, 70910-900 Brasília, DF, Brazil
[124]Department of Plant Anatomy, Institute of Biology, Eötvös Loránd University, Pázmány Péter sétány 1/C, H-1117 Budapest, Hungary
[125]Engineering and Research Center for Southwest Bio-Pharmaceutical Resources of National Education, Ministry of China, Guizhou University, Guiyang 550025, China
[126]Department of Biology, Faculty of Science, Selcuk University, Konya, Türkiye
[127]Innovative Institute for Plant Health/ Key Laboratory of Green Prevention and Control on Fruits and Vegetables in South China, Ministry of Agriculture and Rural Affairs, Zhongkai University of Agriculture and Engineering, Guangzhou, 510225, China
[128]Department of Biology, Hakim Sabzevari University, Sabzevar, Iran
[129]College of Agronomy, Jiangxi Agricultural University, Nanchang 330045, China
[130]Department of Plant Sciences, University of Colombo, Colombo 00300, Sri Lanka
[131]Departamento de Biociências, Universidade Federal de Sergipe, CEP 49500-000, Itabaiana, Sergipe, Brazil
[132]MIND.Funga/MICOLAB, Botany Department, Universidade Federal de Santa Catarina, Florianópolis, Brazil
[133]Department of Biotechnology, University Center for Research & Development (UCRD), Chandigarh University, Mohali, Punjab 140413, India
[134]Molecular and Applied Mycology Laboratory, Department of Botany, Gauhati University, Gopinath Bordoloi Nagar, Jalukbari, Guwahati 781014, Assam, India
[135]Hawkesbury Institute for the Environment, Locked Bag 1797 Penrith New South Wales, 2751, Australia
[136]Ecosystem Management, School of Environmental and Rural Science, University of New England, Armidale, NSW 2351, Australia
[137]Department of Microbiology and Molecular Genetics Oklahoma State University, Stillwater, OK, USA
[138]Department of Landscape Architects, Faculty of Agriculture, Kırşehir Ahi Evran University, Kırşehir, 40200, Turkey
[139]Navarro Villoslada 16, 3º dcha, 31003 Pamplona, Navarra, Spain
[140]CABI, UK Centre Egham, Surrey TW20 9TY, UK
[141]The Key Laboratory for Silviculture and Conservation of the Ministry of Education, Beijing Forestry University, Beijing 100083, China

[142]*Hainan Key Laboratory for R&D of Tropical Herbs, School of Pharmacy, Hainan Medical University, Haikou, 571199, China*
[143]*Laboratory of Systematics and Geography of Fungi, Komarov Botanical Institute, Russian Academy of Sciences, Prof. Popov Street 2, St. Petersburg, 197022, Russia*
[144]*Rosenstiel School of Marine and Atmospheric Science, University of Miami, 4600 Rickenbacker Causeway, Key Biscayne, Fl. 33149*
[145]*Centre of Molecular and Environmental Biology (CBMA), Department of Biology, University of Minho, 4710-057 Braga, Portugal*
[146]*Institute of Science and Innovation for Bio-Sustainability (IB-S), University of Minho, 4710-057 Braga, Portugal*
[147]*Universidade Federal de Uberlândia, campus Monte Carmelo, Centro de Ciências Agrárias, 38500-000, Monte Carmelo, Minas Gerais, Brazil*
[148]*Universidade Federal do Rio Grande do Norte, Centro de Biociências, Av. Senador Salgado Filho, 3000, Lagoa Nova, Natal-RN, Brazil*
[149]*Internationally Cooperative Research Center of China for New Germplasm Breeding of Edible Mushroom, Jilin Agricultural University, Changchun 130118, China*
[150]*Laboratory of Microbiology and Enzymology-LEMA, Universidade Federal do Agreste de Pernambuco, 55292-270, Garanhuns, Pernambuco, Brazil*
[151]*Department of Biotechnology and Biomedicine, Technical University of Denmark, Soltofts Plads B 221, 2800 Kongens Lyngby, Denmark*
[152]*College of Science and Engineering, Flinders University, G.P.O. Box 2100, Adelaide SA 5001, Australia*
[153]*Barcelona Supercomputing Centre (BSC-CNS). Plaça Eusebi Güell, 1-3 08034 Barcelona, Spain*
[154]*Institute for Research in Biomedicine (IRB Barcelona), The Barcelona Institute of Science and Technology, Baldiri Reixac, 10, 08028 Barcelona, Spain*
[155]*Catalan Institution for Research and Advanced Studies (ICREA), Barcelona, Spain*
[156]*CIBER de Enfermedades Infecciosas, Instituto de Salud Carlos III, Madrid, Spain*
[157]*All-Russian Institute of Plant Protection, Saint Petersburg, 196608, Russia*
[158]*The Institute of Environmental and Agricultural Biology (X-BIO), University of Tyumen, Tyumen, 625003, Russia*
[159]*Universitat Rovira i Virgili, Facultat de Medicina i Ciències de la Salut and IURESCAT, Unitat de Micologia i Microbiologia Ambiental, 43201, Reus, Catalonia, Spain*
[160]*Facultad de Ciencias, Universidad Nacional Autónoma de México*
[161]*Av Universidad 3000, CP 04510, CDMX, México*
[162]*Germplasm Bank of Wild Species, Yunnan Key Laboratory for Fungal Diversity and Green Development, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China*
[163]*Molecular Ecology Group (MEG), Water Research Institute (IRSA), National Research Council (CNR), Largo Tonolli 50, 28922 Verbania (VB), Italy*
[164]*Patanjali Herbal Research Department, Patanjali Research Institute, Haridwar-249405, Uttarakhand, India*
[165]*International Fungal Research and Development Centre, Institute of Highland Forest Science, Chinese Academy of Forestry, Kunming 650224, China*
[166]*Universitat Rovira i Virgili, Facultat de Medicina i Ciències de la Salut and IURESCAT, Unitat de Micologia i Microbiologia Ambiental, 43201, Reus, Catalonia, Spain*
[167]*Department of Biotechnology, Iranian Research Organization for Science and Technology (IROST), P. O. Box 3353-5111, Tehran 3353136846, Iran*
[168]*Department of Microbiology, Federal University of Santa Catarina, Florianópolis, 88040-970, Brazil*
[169]*Institute of Biological Sciences, Federal University of Minas Gerais, Belo Horizonte, 31270-901, Brazil*
[170]*Department of Biology, University of Oxford, Oxford OX1 3SZ, United Kingdom*
[171]*Department of Botany and Plant Physiology, Plant-DNA Biobank, University of Salamanca. Salamanca 37007, Spain*
[172]*Departamento de Botânica e Zoologia, Universidade Federal do Rio Grande do Norte, Campus Universitário, Natal 59078–900, Brazil*
[173]*Escuela de Agronomía, Estación Experimental Fabio Baudrit and Centro de Investigaciones en Estructuras Microscópicas, Universidad de Costa Rica, San Pedro, San José 11801, Costa Rica*
[174]*Department of Life Sciences, Cledwyn Building, Aberystwyth University, Aberystwyth, Ceredigion WALES SY23 3DD, UK*
[175]*Department of Plankton and Microbial Ecology, Leibniz Institute of Freshwater Ecology and Inland Fisheries, Zur Alten Fischerhuette 2, D-16775 Stechlin, Germany*
[176]*Institute of Biochemistry and Biology, Potsdam University, Maulbeerallee 2, D-14469 Potsdam, Germany*
[177]*CSIRO - National Facilities and Collections, National Research Collections Australia, Australian National Herbarium, GPO Box 1700, Canberra ACT 2601, Australia*
[178]*Department of Bioresources for Bioeconomy and Health, Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures, Inhoffenstrasse 7B, 38124 Braunschweig, Germany*
[179]*Department of Biological Sciences, State University of Feira de Santana, 44036-900, Feira de Santana, BA, Brazil*
[180]*Centro de Estudios Parasitológicos y de Vectores (CEPAVE), Consejo Nacional de Investigaciones Científicas (CONICET), Universidad Nacional de La Plata (UNLP), La Plata 1900, Buenos Aires, Argentina*
[181]*Unidad Académica de Biotecnología y Agroindustrial, Universidad Politécnica de Huatusco, Huatusco 94116, Mexico*

[182]*Faculty of Science, University of South Bohemia, 370 05 České Budějovice, Czech Republic*
[183]*Biology Centre of the Czech Academy of Sciences, Institute of Entomology, 370 05 Česke Budějovice, Czech Republic*
[184]*Institute of Systematic Botany, The New York Botanical Garden, Bronx, New York 10458, USA*
[185]*Denver Botanic Gardens, 909 York St., Denver, CO 80206, USA*
[186]*Institute of Fungus Resources, College of Life Science, Guizhou University, Guiyang 550025, P. R. China*
[187]*College of Biodiversity Conservation, Southwest Forestry University, Kunming 650224, P.R China*
[188]*University of Copenhagen, Dep. of Biology, Sect. of Terrestrial Ecology, 2100 København Ø, DK-Denmark*
[189]*Department of Plant Pathology, Entomology and Microbiology, Iowa State University, Ames, Iowa 50011, USA*
[190]*Forestry and Forest Products Research Institute, Matsunosato 1, Tsukuba, Ibaraki, Japan*
[191]*The R&D Center, Novozymes China, 14 Xin Xi Lu, Shangdi, Haidian District, Beijing 100085, P.R. China*
[192]*Department of Plant Pathology, University of Florida, Gainesville, Florida 32611, USA*
[193]*Instituto de Ecología A.C., Laboratorio de micromicetos, Xalapa, Veracruz, 91073, Mexico*
[194]*Plant Pathology Herbarium, School of Integrative Plant Science, Cornell University, Ithaca, New York 14850, USA*
[195]*Laboratorio de Micologia Aplicada, Centro de Investigación y Producción de Hongos Alimenticios y Medicinales - CIPHAM, Facultad de Ciencias Biológicas, Universidad, Nacional de San Antonio Abad del Cusco, Av. De la Cultura 733, Cusco, Perú*
[196]*Sociedad Botanica del Cusco, Universidad Nacional de San Antonio Abad del Cusco, Av. De la Cultura 733, Cusco, Perú*
[197]*Organización de Mujeres en Ciencia para el mundo en Desarrollo -OWSD, Capítulo Perú*
[198]*Research Center of Microbial Diversity and Sustainable Utilization, Faculty of Sciences, Chiang Mai University, Chiang Mai 50200, Thailand*
[199]*Shenzhen Key Laboratory of Microbial Genetic Engineering, College of Life Sciences and Oceanography, Shenzhen University, Shenzhen 518060, China*
[200]*Eidgenössische Technische Hochschule (ETH) Zürich, , CH-8092 Zürich, Switzerland*
[201]*Schlossfeld 17, A-6002 Innsbruck, Austria*
[202]*National Museum of Nature and Science, 4-1-1 Amakubo, Tsukuba, Ibaraki Pref. 305-0005, Japan*
[203]*School of Resources and Environment, Zunyi Normal University, Zuny, 563006, China*
[204]*Korean Lichen Research institute, Sunchon National University, Suncheon 57922, Korea*
[205]*Northwest Missouri State University, 800 University Drive, Maryville, Missouri 64468 USA*
[206]*Department of Life, Health and Environmental Sciences (MeSVA), University of L'Aquila, via Vetoio, Coppito 1, 67100 L'Aquila, Italy*
[207]*Department of Botany, Section of Mycology, National Institute of Plant Protection, Tehran, Iran*
[208]*School of Food Science and Engineering, Yangzhou University, Yangzhou 225127, China*
[209]*Department of Natural Resources, Faculty of Applied Sciences, Sabaragamuwa University of Sri Lanka, Belihuloya 70140, Sri Lanka*
[210]*Center for Yunnan Plateau Biological Resources Protection and Utilization, Qujing Normal University, Qujing City, Yunnan Province, P.R. China*
[211]*Kyung Hee University, 26 Kyungheedae-ro, Dongdaemun-gu, Seoul 02447, South Korea*
[212]*Department of Health Sciences, Faculty of Medicine and Health Sciences, University of Mauritius, Réduit, Moka, Mauritius*
[213]*Department of Zoology, College of Science, King Saud University, P.O. Box 2455, Riyadh, 11451, Saudi Arabia*
[214]*College of Plant Health and Medicine, Qingdao Agricultural University, Qingdao, Shandong, 266109, China*
[215]*Department of Plant Protection Bu-ali Sina University. Hamedan, Iran*
[216]*33B St Edwards Road, Southsea, Hants, PO53DH UK*
[217]*Shandong Provincial Key Laboratory of Water and Soil Conservation and Environmental Protection, College of Resources and Environment, Linyi University, West Side of North Section of Industrial Avenue, Linyi, Shandong 276000, China*
[218]*New Brunswick Museum, Saint John, New Brunswick, E2K 1E5, Canada*
[219]*New York State Museum, 3140 Cultural Education Center, Albany, NY, 12230, USA*
[220]*University of Tsukuba, Tsukuba, Ibaraki 305-8572, Japan*
[221]*Mycology Working Group, Biologicum, Goethe University of Frankfurt, Max-von-Laue-Str. 13, 60438 Frankfurt am Main, Germany*
[222]*School of Agriculture and Forestry Engineering and Planning, Tongren University, Tongren 554300, China*
[223]*Guizhou Key Laboratory of Biodiversity Conservation and Utilization in the Fanjing Mountain Region, Tongren University, Tongren 554300, China*
[224]*Engineering and Research Center for Southwest Bio-Pharmaceutical Resources of National Education Ministry of China, Guizhou University, Guiyang 550025 China*
[225]*Zoological Institute RAS, Universitetskaya emb. 1St Petersburg, 199034. Russian Federation*
[227]*National Institute of Fundamental Studies (NIFS), Hantana Road, Kandy 20000, Sri Lanka*
[228]*ZHAW School of Life Sciences and Facility Management, Institute of Natural Resource Sciences, Einsiedlerstrasse 29, 8820 Wädenswil, Switzerland*
[229]*Organismic Botany and Mycology, University of Hamburg, Ohnhorststr. 18, 22609 Hamburg, Germany*

[230]*Department of Microbiology, University Innsbruck, Technikerstr. 25, 6020 Innsbruck, Austria*
[231]*Department of Ecological and Biological Sciences, University of Tuscia, Largo dell'Università snc, 01100 Viterbo, Italy*
[232]*Laboratório de Estudos de Biodiversidade, Campus Pantanal de Aquidauana, Universidade Federal de Mato Grosso do Sul, Rua Oscar Trindade de Barros, 740, Bairro Serraria, CEP 79200-000, Aquidauana, Mato Grosso do Sul, Brazil*
[233]*Department of Biological Oceanography, Leibniz Institute for Baltic Sea Research Warnemünde (IOW), Seestr. 15, 18119 Rostock, Germany*
[234]*Institute of Microbiology, Czech Academy of Sciences, Videnska 1083, Praha 4, 14220, Czech Republic*
[235]*Centro de Investigación en Ciencias Biológicas, Universidad Autónoma de Tlaxcala, San Felipe Ixtacuixtla, Tlaxcala, 90120, Mexico*
[236]*Instituto Multidisciplinario de Biología Vegetal (CONICET), FCEFyN, Universidad Nacional de Córdoba, Córdoba, Argentina*
[237]*Department of Plant Taxonomy and Nature Conservation, Faculty of Biology, University of Gdańsk, Wita Stwosza 59, PL-80-308 Gdańsk, Poland*
[238]*Forest Pathology Department, KSCSTE-Kerala Forest Research Institute, Peechi, Thrissur, Kerala 680653, India*
[239]*Laboratory for Biological Diversity, Ruđer Bošković Institute, Bijenička cesta 54, HR-10000 Zagreb, Croatia*
[240]*Real Jardín Botánico, CSIC. Plaza de Murillo 2, 28014 Madrid, Spain*
[241]*Natural History Museum, University of Oslo, P.O. Box 1172 Blindern, 0318 Oslo, Norway*
[242]*Gothenburg Global Biodoversity Centre, P.O. Box 463, 405 30 Göteborg, Sweden*
[243]*Department of Botany, University of Calicut, Kerala, 673 635, India*
[244]*Department of Botany, H.S. Skovoroda Kharkiv National Pedagogical University, Kharkiv, Ukraine*
[245]*Institute of Botany and Landscape Ecology, University of Greifswald, Greifswald, Germany*
[246]*Research Organization for Life Sciences, National Research and Innovation Agency (BRIN), Cibinong 16911, Bogor, Indonesia*
[247]*The Connecticut Agricultural Experiment Station Valley Laboratory, Windsor, CT 06095, USA*
[248]*Medical school of Kunming University of Science and Technology, Kunming 650500, China, 727 Jingming South Road, Chenggong University Town, Kunming, Yunnan Province, China*
[249]*School of Food and Pharmaceutical Engineering, Guizhou Institute of Technology, Guiyang 550003, P.R. China*
[250]*State Key Laboratory of Functions and Applications of Medicinal Plants, Guizhou Medical University, Guiyang 550004, P.R. China*
[251]*Urban Water Systems Engineering, Technical University of Munich, Am Coulombwall 3, 85748 Garching, Germany*
[252]*School of Pharmaceutical Engineering, Guizhou Institute of Technology, Guiyang, Guizhou 550003, China*
[253]*Department of Agricultural Biological Chemistry, College of Agriculture & Life Sciences, Chonnam National University, Gwangju 61186, Republic of Korea*
[254]*Tropical Microbiology Research Foundation, 96/N/10, Meemanagoda Road, 10230 Pannipitiya, Sri Lanka*
[255]*School of Biological Sciences and Institute of Microbiology, Seoul National University, Seoul 08826, Korea*
[256]*School of Life Sciences, Guizhou Normal University, Guiyang, 550025, China*
[257]*Division of Ecology & Evolution, Research School of Biology, ANU College of Science. Australian National University, Canberra ACT 2600, Australia*
[258]*School of Food and Pharmaceutical Engineering, Guizhou Institute of Technology, Guiyang 550003, China*
[259]*Centre for Mountain Futures, Kunming Institute of Botany, Kunming 650201, Yunnan, P.R. China*
[260]*College of Life Sciences, Shandong Normal University, Jinan 250358, China*
[261]*Department of Microbiology, College of Life Science, Nankai University, 94 Weijin Road, Nankai District, Tianjin 300071, P.R. China*
[262]*National Biobank of Thailand, National Science and Technology Development Agency (NSTDA), Thailand Science Park, Khlong Luang, Pathum Thani 12120, Thailand*
[263]*Collections, Conservation and Research Division, Field Museum of Natural History, 1400 S DuSable Lake Shore Drive, Chicago, IL 60605, USA*
[264]*Center of Excellence in Microbial Diversity and Sustainable Utilization, Chiang Mai University, Chiang Mai 50200, Thailand*
[265]*The Academy of Science, Royal Society of Thailand, Bangkok10300, Thailand*
[266]*Department of Plant Biology and Pathology, Rutgers University, New Brunswick, New Jersey, USA*
[267]*Ministry of Education Key Laboratory for Ecology of Tropical Islands, Key Laboratory of Tropical Animal and Plant Ecology of Hainan Province, College of Life Sciences, Hainan Normal University, Haikou 571158 China*
[268]*Departamento de Tecnología Médica, Facultad de Ciencias de la Salud, Universidad de Tarapacá, Sede Iquique, Av. Luis Emilio Recabarren 2477, Iquique, Chile*
[269]*Institute of Biology, Biotechnology and Environmental Protection, Faculty of Natural Sciences, University of Silesia in Katowice, Katowice 40032, Poland*
[270]*National Center for Public Health and Pharmacy, Budapest 1097, Hungary*
[271]*Graduate School of Environmental and Life Sciences, Okayama University, Okayama 7008530, Japan*
[272]*Plant Pathology Division, Tea Research Institute of Sri Lanka, Talawakelle 22100, Sri Lanka*
[273]*Department of Biosystems Technological Studies, Faculty of Technological Studies, Uva Wellassa University, Badulla, Sri Lanka*

[274]Key Laboratory of Integrated Management on Crops in Northwestern Oasis, Ministry of Agriculture and Rural Affairs, Institute of Plant Protection, Xinjiang Academy of Agricultural Sciences, Urumqi, Xinjiang 830091, China
[275]Department of Botany, Faculty of Applied Sciences, University of Sri Jayewardenepura, Sri Soratha Mawatha, Nugegoda, Sri Lanka, 10250
[276]Departamento de Sistemática e Ecologia, Universidade Federal da Paraíba, João Pessoa, Paraíba, Brazil
[277]Escuela de Biología and Herbario Luis Fournier Origgi, Centro de Investigación en Biodiversidad y Ecología Tropical (CIBET), Universidad de Costa Rica, San Pedro de Montes de Oca, 11501- 2060, San José, Costa Rica
[278]Department of Microbial Drugs, Helmholtz Centre for Infection Research (HZI) and German Centre for Infection Research (DZIF), Partner Site Hannover/Braunschweig, Inhoffenstrasse 7, 38124 Braunschweig, Germany
[279]Department of Biology and Geology, Physics and Inorganic Chemistry, Rey Juan Carlos University, C/Tulipán s/n, 28933 Móstoles, Madrid, Spain
[280]Plankton and Microbial Ecology, Leibniz Institute for Freshwater Ecology and Inland Fisheries (IGB), Neuglobsow, Germany
[281]Royal Botanic Gardens Victoria, Birdwood Avenue, Melbourne, Victoria 3004, Australia
[282]CAS Key Laboratory of Forest Ecology and Management, Institute of Applied Ecology, Chinese Academy of Sciences, Shenyang 110164, P. R. China
[283]Laboratory of In Vitro Plant Cultures, Faculty of Sciences and Philosophy, Peruvian University Cayetano Heredia, Av. Honorio Delgado 430, Urb Ingeniería, Lima, Peru
[284]School of Public Health, Zunyi Medical University, Guizhou 563000, China
[285]Department of Forest Mycology and Plant Pathology, Swedish University of Agricultural Sciences, Box 7026, 75007 Uppsala, Sweden
[286]IFungiLab, Departamento de Ciências e Matemática (DCM), Instituto Federal de Educação Ciência e Tecnologia de São Paulo (IFSP), São Paulo, SP, 01109-010, Brazil
[288]CIPHAM Research Center, National University of San Antonio Abad of Cusco. Av. La Cultura N° 733. Cusco, Perú
[289]Department of Botany, University of Wyoming, Laramie, Wyoming 82071, USA
[290]Licenciatura en Biología, Universidad Distrital Francisco José de Caldas, Cra. 4 No. 26B-54, Torre de Laboratorios, Herbario, Bogotá, Colombia
[291]Botanischer Garten, Königin-Luise-Straße 6-8, 14195 Berlin, Germany
[292]Department of Ecology and Evolutionary Biology, University of Toronto, 25 Willcocks Street, Toronto, ON M5S 3B2, Canada
[293]Department of Natural History, Royal Ontario Museum, 100 Queens Park, Toronto, ON M5S 2C6, Canada
[294]Coordenação de Botânica, Museu Paraense Emílio Goeldi, Av. Perimetral 1901, 66077-830 Belém, PA, Brazil
[295]Instituto Tecnológico Vale, Rua Boaventura da Silva, 955, Nazaré, 66055-090, Belém, PA, Brazil
[296]Botany Department, Postgraduate Program in Fungi, Algae and Plants Universidade Federal de Santa Catarina, Florianópolis, Brazil
[297]División de Ciencias Naturales y Exactas, Universidad de Guanajuato, Noria Alta s/n, Col. Noria Alta, Guanajuato, Gto. CP 36050, México
[298]EA 4489 LGCgE (Laboratoire de Génie Civil et Géo-Environnement), Univ Lille, F-59000 Lille, France
[299]Negaunee Institute for Plant Conservation and Action, Chicago Botanic Garden, Glencoe, Illinois 60022, USA
[300]Institute for Biochemistry, Biological Research Centre Szeged, Szeged 6726, Hungary
[301]Plant Diseases Research Department, Iranian Research Institute of Plant Protection, P.O. Box 1985813111, Agricultural Research, Education and Extension Organization (AREEO), Tehran, Iran
[302]Instituto Federal de Educação, Ciência e Tecnologia do Piauí, Piripiri, Pi, 64260-000, Brazil
[303]School of Civil Engineering and Architecture, Anhui University of Technology, Ma'anshan 243002, China
[304]Federal University of Santa Catarina, Graduate Program in Biology of Fungi, Algae and Plants, Florianópoli, Brazil
[305]Natural Science Department, College of Arts and Sciences, Iloilo Science and Technology University, La Paz, Iloilo City 5000, Philippines
[306]Gothenburg Global Biodiversity Centre, Department of Biological and Environmental Sciences, University of Gothenburg, Box 463, 405 30 Göteborg, Sweden
[307]Botany Unit, Finnish Museum of Natural History, P.O. Box 7, 00014 University of Helsinki, Helsinki, Finland
[308]Instituto de Botánica del Nordeste (UNNE - CONICET). Facultad de Ciencias Exactas y Naturales y Agrimensura. Universidad Nacional del Nordeste. Sgto Cabral 2131, CC. 209, CP 3400. Corrientes, Argentina
[309]Naturalis Biodiversity Centre; P.O. Box 9517; 2300 RA; Leiden; The Netherlands; private address Ronsseweg 726, 2803wz Gouda, The Netherlands.
[310]Laboratorio de Geología de Llanuras (CICYTTP-FCYT), Centro de Investigación Científica y de Transferencia Tecnológica a la Producción (Consejo Nacional de Investigaciones Científicas y Técnicas - Gobierno de la Provincia de Entre Ríos - Universidad Autónoma de Entre Ríos), España 149, Diamante, Entre Ríos, Argentina
[311]Division of Ecology & Evolution, Research School of Biology, Australian National University, Canberra ACT, 2612, Australia
[312]Competence Division for Plants and Plant Products, Müller-Thurgau-Strasse 29, CH-8820 Wädenswil, Switzerland
[313]Department of Biology and Geology, Physics and Inorganic Chemistry, Rey Juan Carlos University, C/Tulipán s/n, 28933 Móstoles, Madrid, Spain

[314]*Instituto de Botánica del Nordeste, Laboratorio de Micología, Sargento Cabral 2131, CC 209 - CP 3400, Corrientes, Argentina*
[315]*Institute of Marine Biology and Center of Excellence for the Oceans, National Taiwan Ocean University, 2 Pei-Ning Road, Keelung 202301, Taiwan*
[316]*Department of Botany, Hungarian University of Agriculture and Life Sciences, Villányi út 29-43, H-1118 Budapest, Hungary*
[317]*Institute of Evolutionary Biology, Faculty of Biology, University of Warsaw, ul. Żwirki i Wigury 101, 02-089 Warsaw, Poland*
[318]*Departamento de Fitopatologia, Universidade Federal de Viçosa, 36570-900, Viçosa, MG, Brazil*
[319]*School of Biological Sciences and Institute of Microbiology, Seoul National University, Seoul, 08826, Republic of Korea*
[320]*Colegio de Postgraduados, Campus Montecillo, Edafologia, Texcoco 56230, Mexico*
[321]*Department of Mycology, Real Jardín Botánico (CSIC), Claudio Moyano 1, 28014, Madrid, Spain*
[322]*National Collection of Agricultural and Industrial Microorganisms, Institute of Food Science and Technology, Hungarian University of Agriculture and Life Sciences, H-1118, Budapest, Hungary*
[323]*BioISI – Biosystems and Integrative Sciences Institute, Faculdade de Ciências, Universidade de Lisboa, 1749-016 Lisbon, Portugal*
[324]*Instituto de Pesquisas Ambientais, Secretaria de Meio Ambiente, Infraestrutura e Logística, São Paulo, Brazil*
[325]*Department of Integrative Biology, Oregon State University, Corvallis, Oregon 97331, USA*
[326]*Department of Biology and Geology, Physics and Inorganic Chemistry, Rey Juan Carlos University, C/Tulipán s/n, 28933 Móstoles, Madrid, Spain*
[327]*Department of Ecology and Evolutionary Biology, University of Colorado Boulder, Boulder, CO 80309, USA*
[328]*Freie Universität Berlin, Institute of Biology, Evolutionary Biology, Königin-Luise-Str. 1-3, 14195 Berlin, Germany*
[329]*Department of Plant Protection, Mycology Lab, Faculty of Plant Production, Gorgan university of Agricultural Sciences & Natural Resources, Golestan-Gorgan, Iran*
[330]*Department of Botany, Mahatma Gandhi Government Arts College, Mahe, Union Territory of Pondicherry, 673 311, India*
[331]*National Fungal Culture Collection of India (NFCCI), Biodiversity and Palaeobiology (Fungi) Group, MACS Agharkar Research Institute, Pune 411 004, Maharashtra, India*
[332]*Norwegian College of Fishery Science, UiT The Arctic University of Norway, Tromsø, Norway*
[333]*University of Bayreuth, Dept. of Mycology, Universitätsstraße 30, 95440 Bayreuth, Germany*
[334]*International Training Centre for Environmental Research (ITCER), Ng'iya, Kogelo Rd., PO Box 300, 40600 Siaya, Kenya*
[335]*Universiteì Savoie Mont Blanc, INRAE, CARRTEL, 74200 Thonon les Bains, France*
[336]*School of Pharmacy, Guiyang Healthcare Vocational University, Guiyang 550081, China*
[337]*Guizhou Provincial Engineering Research Center of Medical Resourceful Healthcare Products, Guiyang Healthcare Vocational University, Guiyang 550081, China*
[338]*Universidad Nacional de Córdoba, Facultad de Ciencias Agropecuarias, CONICET, Córdoba Argentina*
[339]*Instituto de Ecología, Universidad Mayor de San Andrés, La Paz, Bolivia*
[340]*Systematic Biology program, Department of Organismal Biology, Uppsala University, Norbyvägen 18 D, 752 36 Uppsala*
[341]*Institute of Biological Sciences, University of Oslo, Norway, P.B. 1066 Blindern, N-0316 Oslo, Norway*
[342]*Fundación Miguel Lillo, Instituto Criptogámico-Sección Micología, Miguel Lillo 251, (4000) San Miguel de Tucumán, Argentina*
[343]*Postgraduate Department of Geology, RTM Nagpur University, Nagpur, 440001, MH, India*
[344]*Estación Experimental del Zaidín (CSIC), Profesor Albareda 1, 18008 Granada, Spain*
[345]*Department of Forest Mycology and Plant Pathology, Swedish University of Agricultural Sciences, Box 7026, 750 07, Uppsala, Sweden*
[346]*Fungal Biotechnology Lab, Department of Biotechnology, Pondicherry University, Kalapet, Pondicherry-605014, India*
[347]*Institute of Ecology and Earth Sciences, University of Tartu, J. Liivi 2, 50409, Tartu, Estonia*
[348]*Department of Biological Sciences, Butler University, Indianapolis, IN 46208, USA*
[349]*Birbal Sahni Institute of Palaeosciences, 53 University Road, Lucknow–226007, India*
[350]*State Museum of Natural History Karlsruhe, Erbprinzenstr. 13, D-76133 Germany*
[351]*Italian Antarctic National Museum (MNA), Mycological Section, Genoa, Italy*
[352]*Kırsehir Ahi Evran University, Sciences and Arts Faculty, Department of Molecular Biology and Genetics, 40200, Kırsehir, Turkiye*
[353]*Innovative Institute for Plant Health/Key Laboratory of Green Prevention and Control on Fruits and Vegetables in South China, Ministry of Agriculture and Rural Affairs, Zhongkai University of Agriculture and Engineering, Haizhu District, Guangzhou 510225, China*
[354]*Master Program for Plant Medicine, National Taiwan University, Taiwan*
[355]Department of Botany and Plant Pathology, Purdue University, West Lafayette, Indiana 47907, USA
[356]*Centre of Advanced Study (CAS) in Botany, Institute of Science, Banaras Hindu University, Varanasi 221005, India*

[357]*Instituto de Bioprospeccíon y Fisiología Vegetal-INBIOFIV (CONICET-UNT), San Lorenzo 1469, San Miguel de Tucumán 4000, Tucumán, Argentina*
[358]*Department of Respiratory and Critical Care Medicine, Affiliated Hospital of Guangdong Medical University, Zhanjiang, China*
[359]*University of Cologne, Faculty of Medicine and University Hospital of Cologne, Department I of Internal Medicine, Center for Integrated Oncology Aachen Bonn Cologne Duesseldorf (CIO ABCD), European Diamond Excellence Center for Medical Mycology (ECMM), Kerpener Strasse 62, 50937 Cologne, Germany*
[360]*Cologne Excellence Cluster on Cellular Stress Responses in Aging-Associated Diseases (CECAD), University of Cologne, Herderstrasse 52, 50931 Cologne, Germany*
[361]*German Centre for Infection Research (DZIF), partner site Bonn - Cologne, Herderstrasse 52, 50931 Cologne, Germany*
[362]*Department of Biological Sciences, University of Arkansas, Fayetteville, Arkansas 72701, USA*
[363]*Leibniz Institute of Freshwater Ecology and Inland Fisheries, Evolutionary and Integrative Ecology, Müggelseedamm 301, 12587 Berlin, Germany*
[364]*Institute of Laboratory Animal Sciences, Chinese Academy of Medical Sciences (CAMS) & Comparative Medicine Center, Peking Union Medical College (PUMC), Beijing, 100021, China*
[365]*National Biobank of Thailand, National Center for Genetic Engineering and Biotechnology (BIOTEC), 113 Thailand Science Park, Phahonyothin Road, Khlong Nueng, Khlong Luang, Pathum Thani, 12120, Thailand*
[366]*Department of Plant Pathology, College of Agriculture, Guizhou University, Guiyang 550025, People's Republic of China*
[367]*Department of Organismal Biology, Uppsala University, Norbyvägen 18D, 75236 Uppsala, Sweden*
[368]*Gothenburg Global Biodiversity Centre, P.O. Box 461, 405 30 Göteborg, Sweden*
[369]*Faculty of Bioresources, Mie University, 1577 Kurima-Machiya, Tsu 514-8507, Japan*
[370]*Faculty of Agriculture and Life Science, Hirosaki University, Bunkyo-cho3, Hirosaki, Aomori 035-8561, Japan*
[371]*School of Continuing Education, The Hong Kong Baptist University, Hongkong, P.R. China*
[372]*Engineering and Research Center for Southwest Biopharmaceutical Resource of National Education Ministry of China, Guizhou University, Guiyang, 550025, Guizhou Province, People's Republic of China*
[373]*Pacific Forestry Centre, Canadian Forest Service, Natural Resources Canada, 506 Burnside Road West, Victoria, BC V8Z 1M5, Canada*
[374]*Royal Botanic Garden Edinburgh, 20A Inverleith Row, Edinburgh EH3 5LR, United Kingdom*
[375]*Faculty of Science, The University of Melbourne, Victoria, Australia 3010*
[376]*Mycology and Microbiology Center, University of Tartu, 40409 Tartu, Estonia*
[377]*Institute of Eastern-Himalaya Biodiversity Research, Dali University, Dali, Yunnan 671003, China*
[378]*Guizhou Key Labratory of Agricultural Biotechnology, Guizhou Academy of Agricultural Sciences, Guiyang 550006, People's Republic of China*
[379]*Centre for Mountain Futures (CMF), CAS Key Laboratory for Plant Biodiversity and Biogeography of East Asia (KLPB), Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China*
[380]*Department of Organismal Biology, Evolutionary Biology Centre, Uppsala University, Norbyvägen 18D, 75236 Uppsala, Sweden*
[381]*Department of Forest Protection and Wildlife Management, Faculty of Forestry and Wood Technology, Mendel University in Brno, Zemědělská 1, CZ-61300, Czechia*
[382]*Plant Health and Environment Laboratory, Ministry for Primary Industries, Auckland 1072, New Zealand*
[383]*Federal Scientific Center of East Asian Terrestrial Biodiversity of the Far Eastern Branch of the Russian Academy of Sciences, 100th anniversary of Vladivostok Avenue, 159, Vladivostok, 690022, Russia*
[384]*Yunnan Key Laboratory for Fungal Diversity and Green Development, Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, Yunnan 650201, China*
[385]*Department of Biology, Francisk Skorina Gomel State University, Sovetskaja str. 104, 246028 Gomel, Belarus*
[386]*Department of General and Bioorganic Chemistry, Gomel State Medical University, Lange str. 5, 246000 Gomel, Belarus*
[387]*Department of Biology, Brandon University, Brandon, MB, Canada*
[388]*Sofia University "St Kliment Ohridski", Faculty of Biology, Department of Botany, 8 Dragan Zankov, Blvd., BG-1164, Sofia, Bulgaria*
[389]*Dept. of Animal and Plant Biology and Ecology. Autonomous University of Barcelona, 08193, Spain*
[390]*Department of Biology, University of Turku, Vesilinnantie 5, 20014 Turku, Finland*
[391]*Ascomycete.org, 13 chemin du Bois Ponard, 69160 Tassin-la-Demi-Lune, France*
[392]*Departamento de Botánica, Instituto de Biología, Universidad Nacional Autónoma de México, Mexico City, Mexico*
[393]*Department of Plant Pathology, Punjab Agricultural University Ludhiana, 141004, India*
[394]*Universidade de Brasília, Departamento de Fitopatologia, Brasília, 70910-900, Distrito Federal, Brazil*
[395]*Department of Life Sciences and Systems Biology, University of Torino, Viale Pier Andrea Mattioli 25 - 10125 Torino, Italy*
[396]*Department of Biology, Acadia University, Wolfville, NS, Canada*
[397]*Department of Biological Sciences, Faculty of Applied Sciences, Rajarata University of Sri Lanka, Sri Lanka, 50300, Sri Lanka*

[398]*Laboratory no. 14, Department of Botany, University of Rajasthan, Jaipur - 302004, Rajasthan, India*
[399]*Department of Microbiology, College of Life Science, Nankai University. Tianjin 300071, China*
[400]*National Institute of Fundamental Studies, Hantane Road, Kandy, Sri Lanka*
[401]*College of Advanced Agriculture and Ecological Environment, Heilongjiang University, Harbin, Heilongjiang Province 150080, China*

Hyde KD, Abdel-Wahab MA, Abdollahzadeh J, Abeywickrama PD, Absalan S, Afshari N, Ainsworth AM, Akulov OY, Aleoshin VV, Al-Sadi AM, Alvarado P, Alves A, Alves-Silva G, Amalfi M, Amira Y, Amuhenage TB, Anderson J, Antonín V, Aouali S, Aptroot A, Apurillo CCS, Araújo JPM, Ariyawansa HA, Armand A, Arumugam E, Asghari R, Assis DMA, Atienza V, Avasthi S, Azevedo E, Bahkali AH, Bakhshi M, Banihashemi Z, Bao DF, Baral HO, Barata M, Barbosa F, Barbosa RN, Barreto RW, Baschien C, Belamesiatseva DB, Bennett Reuel M, Bera I, Bezerra JDP, Bezerra JL, Bhat DJ, Bhunjun CS, Bianchinotti MV, Błaszkowski J, Blondelle A, Boekhout T, Bonito G, Boonmee S, Boonyuen N, Bregant C, Buchanan P, Bundhun D, Burgaud G, Burgess T, Buyck B, Cabarroi-Hernández M, Cáceres MES, Caeiro MF, Cai L, Cai MF, Calabon MS, Calaça FJS, Callalli M, Camara MPS, Cano-Lira JF, Cantillo T, Cao B, Carlavilla JR, Carvalho A, Castañeda-Ruiz RF, Castlebury L, Castro-Jauregui O, Catania MDV, Cavalcanti LH, Cazabonne J, Cedeño-Sanchez ML, 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Kirchmair M, Kirk PM, Kitaura MJ, Klawonn I, Kolarik M, Kong A, Kuhar F, Kukwa M, Kumar S, Kušan I, Lado C, Larsson KH, Latha KPD, Lee HB, Leonardi M, Leontyev DL, Lestari AS, Li CJY, Li DW, Li H, Li HY, Li L, Li QR, Li WL, Li Y, Li YC, Liao CF, Liimatainen K, Lim YW, Lin CG, Linaldeddu BT, Linde CC, Linn MM, Liu F, Liu JK, Liu NG, Liu S, Liu SL, Liu XF, Liu XY, Liu XZ, Liu ZB, Lu L, Lu YZ, Luangharn T, Luangsa-ard JJ, Lumbsch HT, Lumyong S, Luo L, Luo M, Luo ZL, Ma J, Machado AR, Madagammana AD, Madrid H, Magurno F, Magyar D, Mahadevan N, Maharachchikumbura SSN, Maimaiti Y, Malosso E, Manamgoda DS, Manawasinghe IS, Mapook A, Marasinghe DS, Mardones M, Marin-Felix Y, Márquez R, Masigol H, Matočec N, May T, McKenzie EHC, Meiras-Ottoni A, Melo RFR, Mendes ARL, Mendieta S, Meng QF, Menkis A, Menolli N Jr, Mešić A, Meza Calvo JG, Mikhailov KV, Miller SL, Moncada B, Moncalvo JM, Monteiro JS, Monteiro M, Mora-Montes HM, Moreau PA, Mueller GM, Mukhopadyay S, Murugadoss R, Nagy LG, Najafiniya M, Nanayakkara CM, Nascimento CC, Nei Y, Neves MA, Neuhauser S, Niego AGT, Nilsson RH, Niskanen T, Niveiro N, Noorabadi MT, Noordeloos ME, Norphanphoun C, Nuñez Otaño NB, O'Donnell RP, Oehl F, Olariaga I, Orlando FP, Pang KL, Papp V, Pawłowska J, Peintner U, Pem D, Pereira OL, Perera RH, Perez-Moreno J, Perez-Ortega S, Péter G, Phillips AJL, Phonemany M, Phukhamsakda, Phutthacharoen K, Piepenbring M, Pires-Zottarelli CLA, Poinar G, Pošta A, Prieto M, Promputtha I, Quandt CA, Radek R, Rahnama K, Raj KNA, Rajeshkumar KC, Rämä T, Rambold G, Ramírez-Cruz V, Rasconi S, Rathnayaka AR, Raza M, Ren GC, Robledo GL, Rodriguez-Flakus P, Ronikier A, Rossi W, Ryberg M, Ryvarden LR, Salvador-Montoya CA, Samant B, Samarakoon BC, Samarakoon MC, Sánchez-Castro I, Sánchez-García M, Sandoval-Denis M, Santiago ALCMA, Santamaria B, Santos ACS, Sarma VV, Savchenko A, Savchenko K, Saxena RK, Scholler M, Schoutteten N, Seifollahi E, Selbmann L, Selcuk F, Senanayake IC, Shabashova TG, Shen HW, Shen YM, Silva-Filho AGS, Simmons DR, Singh R, Sir EB, Song Chang-Ge, Souza-Motta CM Sruthi OP, Stadler M, Stchigel AM, Stemler J, Stephenson SL, Strassert JFH, Su HL Su L, Suetrong S, Sulistyo B, Sun YF, Sun YR, Svantesson Sten' Sysouphanthong P, Takamatsu S, Tan TH, Tanaka K, Tang AMC, Tang X, Tanney JB, Tavakol NM, Taylor JE, Taylor PWJ, Tedersoo L, Tennakoon DS, Thamodini GK, Thines M, Thiyagaraja V, Thongklang N, Tiago PV, Tian Q, Tian WH, Tibell L, Tibell S, Tibpromma S, Tkalčec Z, Tomšovský M, Toome-Heller M, Torruella G, Tsurykau A, Udayanga D, Ulukapi M, Untereiner WA, Uzunov BA, Valle LG, Van Caenegem W, Van den Wyngaert S, Van Vooren N, Velez P, Verma RK, Vieira LC, Vieira WAS, Vizzini A, Walker A, Walker AK, Wanasinghe DN, Wang CG, Wang K, Wang SX, Wang XY, Wang Y, Wannasawang N, Wartchow F, Wei DP, Wei XL, White JF, Wijayawardene NN, Wijesinghe SN, Wijesundara DSA, Wisitrassameewong K, Worthy FR, Wu F, Wu G, Wu HX, Wu N, Wu WP, Wurzbacher C, Xiao YP, Xiong YR, Xu LJ, Xu R, Xu RF, Xu RJ, Xu TM, Yakovchenko L, Yan JY, Yang H, Yang J, Yang ZL, Yang YH,Yapa N, Yasanthika E, Youssef NH, Yu FM, Yu Q, fD, Yu YX, Yu ZF, Yuan HS, Yuan Y, Yurkov A, Zafari D, Zamora JC, Zare R, Zeng M, Zeng NK, Zeng XY, Zhang F, Zhang H, Zhang JF, Zhang JY, Zhang QY, Zhang SN, Zhang W, Zhang Y, Zhang YX, Zhao CL, Zhao H, Zhao Q, Zhao RL, Zhou LW, Zhou M, Zhurbenko MP, Zin HH, Zucconi L 2023 – Global consortium for the classification of fungi and fungus-like taxa. 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Abstract

The Global Consortium for the Classification of Fungi and fungus-like taxa is an international initiative of more than 550 mycologists to develop an electronic structure for the classification of these organisms. The members of the Consortium originate from 55 countries/regions worldwide, from a wide range of disciplines, and include senior, mid-career and early-career mycologists and plant pathologists. The Consortium will publish a biannual update of the *Outline of Fungi and fungus-like taxa*, to act as an international scheme for other scientists. Notes on all newly published taxa at or above the level of species will be prepared and published online on the *Outline of Fungi* website (https://www.outlineoffungi.org/), and these will be finally published in the biannual edition of the *Outline of Fungi and fungus-like taxa*. Comments on recent important taxonomic opinions on controversial topics will be included in the biannual outline. For example, ‘to promote a more stable taxonomy in *Fusarium* given the divergences over its generic delimitation’, or ‘are there too many genera in the *Boletales*?’ and even more importantly, ‘what should be done with the tremendously diverse ‘dark fungal taxa?’ There are undeniable differences in mycologists’ perceptions and opinions regarding species classification as well as the establishment of new species. Given the pluralistic nature of fungal taxonomy and its implications for species concepts and the nature of species, this consortium aims to provide a platform to better refine and stabilise fungal classification, taking into consideration views from different parties. In the future, a confidential voting system will be set up to gauge the opinions of all mycologists in the Consortium on important topics. The results of such surveys will be presented to the International Commission on the Taxonomy of Fungi (ICTF) and the Nomenclature Committee for Fungi (NCF) with opinions and percentages of votes for and against. Criticisms based on scientific evidence with regards to nomenclature, classifications, and taxonomic concepts will be welcomed, and any recommendations on specific taxonomic issues will also be encouraged; however, we will encourage professionally and ethically responsible criticisms of others' work. This biannual ongoing project will provide an outlet for advances in various topics of fungal classification, nomenclature, and taxonomic concepts and lead to a community-agreed classification scheme for the fungi and fungus-like taxa. Interested parties should contact the lead author if they would like to be involved in future outlines.

Keywords – classification – nomenclature – scientific criticism – taxonomy

Introduction

The series *Outline of Fungi and fungus-like taxa* (including fossil fungi) commenced with its first publication in 2020, has garnered over 450 citations to date, and is proving to be a very important publication in fungal classification. Since the inaugural outline by Wijayawardene et al. (2020a), we have strived to improve the effectiveness and accuracy of the outline, and this resulted in an updated 2022 outline (Wijayawardene et al. 2022a) featuring contributions from 57 authors. Nevertheless, worldwide participation was not sufficient to overcome arguments that the outline was not representative of most mycologists. Therefore, in 2022, we launched the Global Consortium for the Classification of Fungi and fungus-like taxa and its associated webpage, outlineoffungi.org, and invited numerous interested parties from around the world to form an internationally representative consortium. In this paper, we have more than 550 members representing 55 countries with a range of disciplines, providing a balanced participation in the Global Consortium for the Classification of Fungi and fungus-like taxa. As the project progresses, we will publish the *Outline of Fungi and fungus-like taxa* biannually, with notes on new taxa at or above the level of species. Along with the updated classification scheme for fungi and fungus-like taxa, any notes, critiques, or remarks on controversial topics, especially those pertaining to taxonomy and the establishment of novel taxa, will also be included. Where possible, we will provide appropriate parties with opposing arguments or any clarifications on these topics. Given the dynamic nature of fungal taxonomy as a field of study, it undergoes frequent updates and revisions as new data is acquired from various disciplines such as biochemistry, ecology, evolution, genomics, genetics, morphology, metabolomics, transcriptomics, phylogenetics, physiology, and proteomics. These advancements contribute to the modification of classification and taxonomic concepts at different taxonomic hierarchy. Therefore, it is essential to publish an *Outline of Fungi and fungus-like taxa* biannually to stay up-to-date on the changes and provide a universal platform to discuss controversial topics.

Values and numbers of fungi

The estimation of fungal species ranges from 1 to 11 million, depending on the criteria employed by various researchers (Hyde et al. 2020a). Among these estimates, Hawksworth & Lücking (2017) have proposed a potentially more accurate range of 2.3 to 3.8 million species. In 2022, the journal *Fungal Diversity* published a special issue on the numbers of fungi with nine papers dealing with different taxonomic groups (e.g., *Ascomycota*, *Basidiomycota* – He et al. 2022a, Wijayawardene et al. 2022b, Yeasts – Boekhout et al. 2022). High-throughput sequencing approaches yielded the highest estimates (OTUs; Baldrian et al. 2022). In the editorial of that special issue, Hyde (2022) had planned to provide a more accurate estimate following these various reviews; however, in the end, this editorial was only able to propose prospective research needed to accomplish better estimates of total fungal numbers.

While the discussion of fungal species numbers is still ongoing, the value of fungi is, however, indisputable with both beneficial and negative impacts. In terms of forest health, Niego et al. (2023a) showed how important and undervalued fungi are. They placed the value of fungi at USD 54.61 trillion annually and reported numerous benefits that fungi provide (e.g., food, industrial products, and novel drug discovery) (Niego et al. 2023b). Although any such appraisal has yet to be perfected, the data of Niego et al. (2023b) serves as an important baseline. The cumulative negative roles of fungi for humans, agriculture, and the environment have not been fully considered by Niego et al. (2023b). However, various studies show that human fungal infections are a global concern, causing ~1.7 million deaths annually. Growers worldwide experience losses of 10% to 23% of their crops due to fungal infections each year, with an additional 10-20% lost during post-harvest (Stukenbrock & Gurr 2023). Though having great monetary value despite difficulties in quantitatively estimating fungal populations, the framework of the Fungi and fungus-like taxa will give scientists a much-needed categorization model to work from.

History of fungal classification

The history of fungal classification systems dates back to the late 18th and the first third of the 19th century and connects with the writings of Persoon (1794, 1801, 1822–1828), Nees von Esenbeck (1817), Fries (1821–1832, 1825, 1835, 1836–1838, 1849), and Link (1833). Those systems were based on the external characters and morphology of the fruit-bodies, characters of hymenophore, and the place and mode of spore formation. By the mid-19th century, the knowledge pertaining to the classification and hierarchy of taxa in the field of mycology was not uniformly established and exhibited discrepancies between different authors. However, throughout this period, significant progress had been made in identifying and categorizing major fungal groupings, including hymenomycetes, discomycetes, pyrenomycetes, and gasteromycetes. The most important books of those times that made significant contributions to fungal classification include '*Synopsis methodica fungorum*' (Persoon 1801), '*Systema mycologicum*' with additional '*Index*' and '*Elenchus fungorum*' (Fries 1821–1832), not only because they were a base for subsequent fungal classifications and systems (e.g., Bonorden 1851, Gillet 1879–1887), as well as regional checklists (e.g., Berkeley 1860, Fuckel 1860, Crouan & Crouan 1867, Cooke 1871, Bernard 1882, Karsten 1871–1879, Quélet 1886, Phillips 1887), but also because of their influence on contemporary nomenclature of fungi. For a considerable period, they served as a starting point for fungal nomenclature up to the Shenzhen Code (Turland et al. 2018) and are now treated as sanctioning works (Turland et al. 2018).

The next major step in fungal classification was a series of twenty-five volumes, the '*Sylloge Fungorum*', led by P.A. Saccardo (1882-1931). Among these publications, the significance of Saccardo & Sydow's work in 1899 lies in their use of distinct terminology regarding conidial fungi, i.e., deuteromycetes, along with other ranks for fungi and fungus-like taxa. Meanwhile, novel systematics based on minutious microscopical observations were proposed for hymenomycetes by Fayod (1889) and Patouillard (1900), and for discomycetes by Boudier (1907). Subsequent studies by Ainsworth (1966) and Moore (1971) introduced, respectively, *Deuteromycotina* and *Deuteromycota* to accommodate conidial fungi.

Ainsworth (1966) made some of the most important compilations on the classification of fungi. The subsequent series *Systema Ascomycetum* (Eriksson 1982, Eriksson & Hawksworth 1998), which was conceived by Eriksson & Hawksworth (1998), can be considered as the foundation of compilations of fungal names, particularly when it comes to genera of *Ascomycota*. In addition to this series, several issues were published exclusively on the classification of ascomycetous taxa (i.e., Eriksson & Hawksworth 1998). Since 1997, *Myconet* has been published as hard copies and online (http://archive.fieldmuseum.org/myconet/printed.asp) (Lumbsch & Huhndorf 2007). Nonetheless, all these efforts have focused on sexually typified genera and their classification, i.e., prior to the use of DNA sequences for fungal taxonomy and classification based on phylogenetic reconstructions.

Hyde et al. (2011) were the first to attempt to list all asexually typified genera in a natural classification. However, Kirk et al. (2008) (i.e., *The Dictionary of Fungi*) also provided higher-level classifications of asexually typified genera, but in their classification, they listed them alphabetically. Subsequent publications by Wijayawardene et al. (2012, 2017) provided the current classification of asexually typified genera, and Wijayawardene et al. (2021) compiled the classification of asexually typified genera with notes on pleomorphic genera.

Since the paper of White et al. (1990), molecular biology techniques have widely been used in mycology, and thus, taxonomists have started to use DNA sequences in taxonomy and classification (Chethana et al. 2021). With these implementations, the dual nomenclature (e.g., Saccardo 1904) was abandoned and the 'one fungus, one name' concept for pleomorphic taxa was implemented (McNeill et al. 2011). Thus, maintaining separate classification systems for asexually typified genera was redundant, and all genera were incorporated into a natural classification. Wijayawardene et al.

(2020a) compiled both sexually typified and asexually typified genera into one classification. At the same time, the authors recognized the importance and necessity of developing and maintaining a continuously updated webpage based on new publications and new concepts or ideas. Hence, Wijayawardene et al. (2020a) introduced '*outlineoffungi.org*', which provides the classification of the kingdom *Fungi*. The website is currently being updated based on new studies and publications.

Operation of Outline of Fungi and fungus-like taxa

With the advent of molecular techniques, fungal taxonomy and classification have undergone a revolution (Ullah et al. 2022). Thus, the availability and accessibility of data to the end user are critical (Durkin et al. 2020). In the past decade, numerous databases have been established that provide easy access to fungal data (Jayasiri et al. 2015, Prakash et al. 2017, Nilsson et al. 2019, Põlme et al. 2020, Zanne et al. 2020, Ullah et al. 2022, Zhou & May 2022). Some databases are restricted to molecular, morphological, or ecological data (Nilsson et al. 2019, Ullah et al. 2022, Zhou & May 2022), while others are designed for specific fungal groups. They also mainly deal with taxonomy, such as https://marinefungi.org/ (Jones et al. 2019), www.freshwaterfungi.org (Calabon et al. 2020), https://gmsmicrofungi.org (deals with microfungi from the Greater Mekong Subregion; Chaiwan et al. 2021), theyeasts.org (yeasts), https://eumycetozoa.com (fungus-like taxa such as *Myxomycetes*, *Dictyosteliomycetes* and *Protosteliomycetes*; Lado 2005–2023), https://invertebratefungi.org/ (invertebrate-associated fungi and fungus-like taxa; Wei et al. 2022), https://botryosphaeriales.org (Wu et al. 2021) and https://www.fusarium.org/ (commonly referred to as FUSARIOID ID database that deals with *Fusarium* and fusarium-like genera, primarily for DNA-based identification and taxonomy). The classification of fungi is constantly and inevitably changing due to the discovery of new taxa, the use of novel DNA based techniques to better understand relationships, and the incorporation of more DNA sequences from multigenes and increasingly whole genome datasets to reanalyse existing classification schemes. Sometimes databases may also become obsolete over time (Prakash et al. 2017) often due to a lack of curation. Many taxonomic studies tend to overlook important features, such as ecology, which are crucial sources of information for fungal identification and biological conservation (Durkin et al. 2020). Where possible, this type of information should be made available.

The registration of new taxa, combinations, and typifications in one of the three taxonomic repositories, Index Fungorum, MycoBank (Crous et al. 2004), and Fungal Names (https://nmdc.cn/fungalnames) is a condition of validity of these operations (May 2017, May et al. 2019, art. 5.F) and as they are linked to the other repositories, they are constantly being updated. Subsequently, the *Outline of Fungi and fungus-like taxa* database will provide a biannual update on new information, which will be curated by members of the consortium. The cross-database communications will help to identify and fill gaps, increase the discovery of, and improve the focus on genetic, ecological, and evolutionary information (Zanne et al. 2020). Thus, we expect to derive a stable classification of the Fungi and fungus-like taxa over time (Lado & Eliasson 2022).

Notes on problems with classifications, nomenclature and taxonomic concepts

The *Outline of Fungi* online database presented here will provide updated information on taxonomic changes in the notes part. Newly introduced taxa will be assigned to curators by the head curators. A note for newly introduced genera and higher-level taxa will be provided, which includes the current classification, synonyms, morphological characters, habitat, host, lifestyle, molecular evidence, phylogenetic placement, and current issues in the classification and nomenclature, including controversial topics. The curators will write notes on their expertise, which will be corrected and edited by the head curator. The author(s) of the original paper, where the genera or higher-level taxa were introduced, will not usually write the entry to avoid partiality.

The notes will be linked to the repositories Index Fungorum, MycoBank, and Fungal Names. Furthermore, the fungal names will be linked to relevant databases such as coelomycetes (https://www.coelomycetes.org; Huanraluek et al. 2021), *Dothideomycetes* (https://dothideomycetes.org/, Pem et al. 2019), Faces of Fungi (http://www.facesoffungi.org;

Jayasiri et al. 2015), Freshwater fungi (http://fungi.life.illinois.edu/; Calabon et al. 2020), Genera of Fungi (https://fungalgenera.org/), Lichenicolous fungi (http://www.lichenicolous.net/), Macrofungi (https://nmdc.cn/macrofungi/; He et al. 2022b), Marine fungi (https://marinefungi.org/; Jones et al. 2019), One stop shop to genera of phytopathogens (https://onestopshopfungi.org/; Jayawardena et al. 2019), fungus-like taxa (https://eumycetozoa.com/; Lado 2005–2023), *Sordariomycetes* (https://sordariomycetes.org/, Bundhun et al. 2020), theyeasts.org and UNITE (https://unite.ut.ee/; Nilsson et al. 2019). The online preprint of notes will be sent to the corresponding curator for final approval before the notes are posted on the outline webpage periodically as new taxa are published. All the notes and the new classification will be published biannually in the '*Outline of Fungi and fungus-like taxa*' towards the end of the following year.

While new genera and higher-level taxa introduced in the preceding year are easy to determine and include in the biannual outline, it is difficult to trace changes in the classifications that are published in papers that do not include new taxa. This problem has also been encountered on other webpages, such as Index Fungorum (P. Kirk, personal communication). It can be reduced by the participation of more than 500 curators who are experts on various groups of fungi and can provide an updated classification of their expert group. However, it is unlikely that even with more than 500 curators, the whole spectrum of fungi can be curated adequately. Therefore, alongside the *Outline*, a database *Fungalpedia* (Hyde et al. in press) will, over time, provide up-to-date notes on all genera of fungi so that the classification can also be updated. If there is a major disagreement in any classification, both sides of the disagreement will be encouraged to present entries in the outline justifying their opinion. The links to the entries in *Fungalpedia* will be added to the entry in the master file of the outline. Thus, this database will act as a user-friendly and informative platform that directs and allows users to browse and retrieve all the relevant updated information.

Use of molecular and evolutionary data to improve fungal classification

The classification of fungal species has historically relied heavily on the study of morphology (Taylor et al. 2000, Hyde et al. 2010). In fact, the initial investigations into fungal diversity were primarily conducted through field observations of macro- and micro-morphological characteristics (Truong et al. 2017, Cazabonne et al. 2022), establishing morphology as a fundamental aspect of early fungal diversity studies. However, morphology alone can lead to misidentifications due to overlapping structural characters shown by fungi (Hyde et al. 2009, Marin-Felix et al. 2020, Bhunjun et al. 2021b, Senanayake et al. 2022). Several studies have demonstrated that morphological crypsis masks the true diversity of taxa, whereas circumscriptions based on molecular data often reveal the presence of distinct lineages (Hyde et al. 2009, Manamgoda et al. 2014, Haelewaters et al. 2022, Leontyev et al. 2023a). On the other hand, one particular phylogenetically circumscribed species can also exhibit phenotypic plasticity which ultimately can result in categorizing taxon below species level (Van Caenegem et al. 2023). Accurate species identification is crucial to more accurately estimate the number of species, considering that the kingdom *Fungi* comprises, perhaps, 2.3–3.8 million species, but only about 156,000 of these have been properly named and classified (Hawksworth & Lücking 2017, Hyde et al. 2020a, Bhunjun et al. 2022, 2023, Phukhamsakda et al. 2022). Accurate species identification is also important to take necessary actions for effective plant disease control, quarantine measures, medical and veterinary mycology treatment (Opathy & Gabaldón 2019, Bhunjun et al. 2021a, Jayawardena et al. 2021a, b), biotech industry and patenting, agro-food industries (both in terms of spoilage and technological fungi), product authorisation (EFSA 2021), as well as for species conservation. Accurate species identification is a fundamental requirement for the comprehensive assessment of various aspects pertaining to specific fungal species, such as their geographic distribution, population dynamics, habitat preferences, and ecological interactions. These crucial criteria are employed to further evaluate the potential threats faced by these species and determine their conservation status. However, the process of identifying fungal species and individuals is often impeded by various challenges, thereby hindering the accurate evaluation of these aforementioned factors (Dahlberg & Mueller 2011, Mueller et al. 2022).

Molecular studies have enhanced the way in which fungal species are defined and identified, clarifying inter- and intra-species phylogenetic relationships and correcting taxonomical errors arising from the phenotypic classification and identification methods used in the past. For this reason, the long-held convention of fungal species having two or more valid names for their teleomorph (sexual) and anamorph (asexual) states was abandoned in 2013 (Hawksworth et al. 2011). Moreover, advances in DNA based techniques and analyses revealed extensive genetic variation within species, leading to the description of new species (Kidd et al. 2023). The ITS region is often considered to include the whole ITS1-5.8S-ITS2 fragment of the ribosomal DNA and is the universal barcode marker for fungi, and it is commonly used to identify taxa to genus level in the case of speciose genera (Schoch et al. 2012, Bhunjun et al. 2021b); however, this is not the case with, e.g., within some groups of rust fungi (*Pucciniales*) (Ebinghaus et al. 2022, 2023a,b) or fungus-like protists (Leontyev & Schnittler 2022). For some fungal groupings, high levels of intragenomic variation compromise the utility of ITS. However, the introduction of the full ribosomal operon as extended fungal barcode alleviated some of these problems (Wurzbacher et al. 2019). Thus, accurate species-level identification now mainly relies on multi-gene analyses, and it is recommended to use a polyphasic approach based on multiple species recognition criteria (Simões et al. 2013, Jeewon & Hyde 2016, Bhunjun et al. 2020, Phukhamsakda et al. 2020, Chethana et al. 2021, Gannibal 2022, Haelewaters et al. 2022). Phylogenetic analyses are also the most commonly used method to infer the evolutionary relationships of fungal species based on molecular data (Laurence et al. 2014, Naranjo-Ortiz & Gabaldón 2019, Bhunjun et al. 2021b, Chethana et al. 2021, Strassert et al. 2021,, Ebinghaus et al. 2022, Su et al. 2022 García-Martín et al. 2023).

Divergence time estimates (based on molecular clocks/dating) is also increasingly being used to unravel evolutionary relationships, origin and divergence of species. These analyses have also provided evidence to support the ranking of taxa (Zhao et al. 2016a, 2017, Hyde et al. 2017, Liu et al. 2017a, Guterres et al. 2018, Zhang et al. 2018b, He et al. 2019). Several studies have used divergence time estimates as additional evidence to introduce new families (Mapook et al. 2016, Phukhamsakda et al. 2016, Bhunjun et al. 2021c) and to support the ranking of taxa at higher levels (Pérez-Ortega et al. 2016, Samarakoon et al. 2016, Hyde et al. 2017, Zhao et al. 2017, Haelewaters et al. 2019). An ultrametric tree derived from divergence time estimates is also needed for analyses such as the general mixed Yule coalescent method and ancestral character state analysis (Parnmen et al. 2012, Zhao et al. 2016b, Thiyagaraja et al. 2020, Bhunjun et al. 2021b, Samarakoon et al. 2022). Coalescence methods play an important role in demarcating species as they provide a solution for incongruence among gene trees (Fujisawa & Barraclough 2013). These methods are becoming increasingly important in resolving cryptic species (Fujita et al. 2012, Fujisawa & Barraclough 2013, Sánchez-Ramírez et al. 2015, Bhunjun et al. 2021b).

The use of whole genome data for classification

Fungi, being one of the most diverse and speciose kingdoms, is estimated to have 2.3–3.8 million species, among which less than 10% have been identified (Blackwell 2011, Hawksworth & Lücking 2017, Baldrian et al. 2022). Several studies proposed the use of genome-wide phylogenies for species delimitation, as genome data can limit the impact caused by individual genes and produce a phylogeny that gives a snapshot of the entire genome (Fitzpatrick et al. 2006, Sobel et al. 2010, Steele & Pires 2011, Bobay & Ochman 2017, Hibbett et al. 2017, Zhao et al. 2017, Matute & Sepúlveda 2019, Xu 2020, Chethana et al. 2021, Chen et al. 2023). As this technique becomes widely used and prices become more acceptable, dedicated pipelines to facilitate genome-wide phylogenetic analyses of fungi are beginning to emerge (Kim et al. 2023). Molecular data have shown whether taxonomic groups that have been classified and named based on common morphological or phenotypic characters share a single common ancestor (i.e., monophyletic) or whether they have mixed ancestry (i.e., polyphyletic). In the case of polyphyletic genera, transferring the species that do not share a common ancestry into a more appropriate genus is clearly justified (Kidd et al. 2023). Molecular techniques, specifically multi-gene phylogenetic analyses, have become common approaches in most research studies, improving fungal taxonomy (Hibbett et al. 2007). However, research has shown that phylogenetic analyses using multi-genes may lead to erroneous phylogenetic interpretationsdue to insufficient information, gene-specific noises, the availability of sequences from only a few markers (mostly for ribosomal genes only), and incongruent phylogenies generated from different individual gene trees. The latter two issues cause poor resolution in the deep internal branches and poorly supported clades (Ebersberger et al. 2012, Xu 2016, 2020, Matute & Sepúlveda 2019, Chethana et al. 2021, García-Cunchillos et al. 2022, Liimatainen et al. 2022). In addition, whole genomes provide sufficient data to resolve internal nodes deeper in phylogenomic trees, and relationships evolved in short divergence times (James et al. 2020, Chen et al. 2023, Han et al. 2023). For example, there are many controversies around the class *Sordariomycetes* due to the introduction of numerous families and other higher ranks based mainly on a few markers, resulting in a grouping of phylogenetically unrelated taxa (Hyde et al. 2020b, Maharachchikumbura et al. 2022), low-resolution phylogenies and phylogenetic inconsistencies among different studies (Senanayake et al. 2018, Voglmayr et al. 2018, Hyde et al. 2020b, Samarakoon et al. 2022, Sun et al. 2022). Chen et al. (2023) conducted a phylogenomics analysis with 1,224 conserved protein sequences, covering 625 species across 50 families, 17 orders, and five subclasses. Their phylogenomic analyses demonstrated well-supported higher-level ranks, species-level phylogenies, and a strengthened backbone for *Sordariomycetes*, providing confirmative phylogenomic evidence to resolve some long-term debates in the mycological community. In addition to phylogenomics, comparative genomics establishes a robust evolutionary framework for fungal classification by decoding the genomic content responsible for functional and morphological similarities and divergences among closely related taxa (Floudas et al. 2012, Shen et al. 2018, Chethana et al. 2021, Wibberg et al. 2021, Díaz-Escandón et al. 2022).

Among different phylogenomic approaches, the two most commonly used are i) the concatenated approach, which mainly infers relationships at deeper internal nodes, and ii) the coalescence approach, which resolves relationships at shallow nodes of the fungal tree (Matute & Sepúlveda 2019, James et al. 2020, Chen et al. 2023). Some studies employ both (Shen et al. 2018, Davis et al. 2019, Li et al. 2021, Strassert & Monaghan 2022), whereas some employ only one (Shen et al. 2016). Both nucleotides and amino acids (protein sequences) have been used for phylogenomics (Li et al. 2021, Wibberg et al. 2021, Strassert & Monaghan 2022, Chen et al. 2023). A previous study suggested that protein-level phylogeny reflects evolutionary divergence better as it directly correlates with the morphology and function of fungi (Chowdhury & Garai 2017). Furthermore, protein sequences evolve more slowly, as slight “silent” changes at the nucleotide level do not necessarily alter the protein sequences. Regier et al. (2008) showed that relatively slow-evolving genes produce higher congruence in their respective gene trees compared to those of fast-evolving ones, and the exclusion of the latter resulted in improved node support (Philippe et al. 2000, Nozaki et al. 2007). Similarly, Wibberg et al. (2021) demonstrated that the use of protein sequences facilitated a more robust inference of relationships between fungal families and higher ranks.

Li et al. (2021) established a robust phylogenetic framework to assess fungal evolution and resolve conflict-prone and poorly supported major lineages in the fungal kingdom. They also established those that are sisters and the degree to which current taxonomy reflects their evolutionary relationships using 1,707 publicly available genomes of 1,679 taxa, representing every known major lineage across fungi and 28 taxa representing the outgroup. This study provided evidence that the relative evolutionary divergence (RED) of the current taxonomic ranks is consistent with their relative divergence times, resulting from the relaxed molecular clock approach, supporting the use of divergence times as a ranking criterion in fungal classification as suggested by previous studies (Avise & Johns 1999, Zhao et al. 2016a, 2017, Tedersoo et al. 2018). Using a smaller taxon-reduced but more balanced dataset, which allowed for computationally intensive analyses using best-fitting evolutionary models, Strassert & Monaghan (2022) resolved several contested deep nodes in the fungal tree of life, such as a sister relationship of *Chytridiomyceta* to all other non-*Opisthosporidia* fungi (with *Chytridiomycota* being sister to *Monoblepharomycota* + *Neocallimastigomycota*), a branching of *Blastocladiomycota* + *Sanchytriomycota* after *Chytridiomyceta* but before other non-*Opisthosporidia* fungi, and a branching of *Glomeromycota* as sister to the *Dikarya*. Recently, Groenewald et al. (2023) used the RED approach to reclassify the subphylum *Saccharomycotina* to make it consistent with high level classifications of another *Ascomycota*. Since the 2010s, several phylogenomic studies have been conducted separately for diverse *Fungi* and fungus-like taxonomic groups for species delineations, such as *Aspergillaceae* (Steenwyk et al. 2019), *Cortinariaceae* (Liimatainen et al. 2022), *Glomeromycota* (Montoliu-Nerin et al. 2021), *Hypoxylaceae* (Wibberg et al. 2021), *Peronosporomycetes* (McCarthy & Fitzpatrick 2017), *Parmeliaceae* (Pizarro et al. 2018), *Peltigera* (Magain et al. 2017), *Rhizopus* (Gryganskyi et al. 2018), *Sordariomycetes* (Chen et al. 2023), *Trichoderma* (Druzhinina et al. 2018) and *Tilletia* (Nguyen et al. 2019), as well as to establish higher level classifications (Fitzpatrick et al. 2006, Spatafora et al. 2016, Shen et al. 2018, 2020, Johnston et al. 2019, Haridas et al. 2020, Li et al. 2021, Montoliu-Nerin et al. 2021). Based on the ability of the genomic data to eliminate inconsistencies in multi-gene phylogeny and to integrate diverse criteria in fungal taxonomy, Xu (2020) proposed a new genome sequence-based fungal recognition criterion, the genomic species recognition.

Comparative genomics approaches such as percentage of conserved proteins (POCP), average nucleotide identities (ANI), average amino acid identities (AAI), and shared and individual genes and gene families between taxa facilitate the establishment of relationships and taxonomic hierarchies as well as possible lifestyles (Wibberg et al. 2021). Changes to genomic content can occur because of selection pressure or other evolutionary forces like gene flow and bottleneck effects, hence reflecting evolution way better than sequence data. Whiston & Taylor (2016) suggested that gene family expansions and contractions influenced by adaptive radiation led to species or generic-level adaptations. Therefore, changes in genome content are often more suitable to distinguish species than those in nucleotide sequences of the selected markers. Wibberg et al. (2021) successfully used these genomic comparisons to differentiate *Hypoxylaceae* species. Though this approach has been applied previously to other organisms (Nobrega & Pennacchio 2004), this is the first study to apply genomic comparisons to deduce taxonomic hierarchies in fungi.

Since these are all sequence-based classification approaches, the accuracy of the completeness and whole genome sequences, their annotation and the associated metadata must be ensured for effective and efficient phylogenomic analyses. Furthermore, sequencing errors and misassemblies can strongly influence protein-level phylogenomic reconstructions. Therefore, prior to analysis, it is important to establish that the target genomes are of high quality (Zhou 2023). Collectively, these studies demonstrate the success achieved using genomic data via phylogenomic reconstructions and comparative genomic approaches to re-evaluate current taxonomic concepts.

Morphology in the molecular era of fungal classification

Morphological characterization of newly described fungal taxa is still needed in the molecular era of fungal classification (Hyde et al. 2010). The written parts of a description should focus on the shapes, colours and typical dimensions (length, width, breadth) of the fungal elements (usually hyphae or yeast cells, mature spores, and sporogenesis), focusing on those with a distinctive diagnostic value over similar taxa. The shape descriptions (if possible) should be made with examination in the living state (Baral 1992, Dominguez de Toledo 1994), following the recommendations given in the Dictionary of Fungi (Kirk et al. 2008). Image analysis is a novel, high-throughput method that allows the automated recording and evaluation of microscopic images (Posch et al. 2012). Colony colours can be determined by the 'RGB profiling' procedure (Puchkov 2016). Line drawings and microphotographs (preferably both) are essential elements of a useful description. Authors should consider which illustration technique is most relevant to show key characteristics (Fawcett 1987). Details hardly visible on photographs should be illustrated with line drawings, SEM, or different focus /illumination settings of a light microscope. High quality descriptions should show more than one spore, all of them rotated in the same orientation, which will facilitate visual recognition (Harman et al. 1999). The appearance of the colony on the host, natural, and/or artificial substrate is also required in some taxa. Scale bars should be used instead of an indication of magnification. Figure legends should contain the full *genus* and *species* names and the techniques (e.g., staining) used to produce the figure.

The use of ecology to improve fungal classification

Fungi are often considered a hidden component of the ecosystem and play crucial roles as decomposers, antagonistic or mutualistic symbionts of animals, plants, and other organisms. Fungi are essential for the recycling of nutrients in all habitats and interact in various ways with themselves, with representatives of other phylogenetic groups, and with organic and inorganic substrates (Dilly & Munch 2001, Dilly et al. 2004, Osono 2017, Jeewon et al. 2018, Zhang et al. 2018a, Gkoutselis et al. 2021, Chen et al. 2022a). Pieces of evidence also tend to suggest that aquatic fungi may be important promoters of nutrient and energy transfer in aquatic ecosystems (Danger et al. 2016). In addition, fungi exist in almost every conceivable habitat where organic carbon is available (e.g., freshwater, marine water, soil, rock surfaces, plants and animals, microplastic), which causes a vast range of variation in their morphology, reproduction, life cycles and modes of dispersal (Tsui et al. 2016, Grossart et al. 2019, Hyde et al. 2020a, Chen et al. 2022b). Ecological information, together with fungal identification, is important to achieve the predicted fungal diversity and ultimately fungal classification (Hyde et al. 2020b). However, although only some 156,000 species of fungi have been formally described and are accepted in the fungal kingdom so far, the ecological strategies they have evolved have been very successful even in adverse (Cantrell et al. 2011) or special environmental conditions, e.g., plant trichomes (Pereira-Carvalho et al. 2009). Giant diverse ecosystems such as those present in the African savannas are unexplored, while Neotropical vegetation is also underexplored (Dianese et al. 2022).

In recent years, an enormous number of unidentified molecular operational taxonomic units (OTUs) or amplified sequence variants (ASVs) were discovered because of ecological studies of fungal diversity (e.g., fungal succession) using high-throughput sequencing techniques (O'Brien et al. 2005, Porter et al. 2008, Ge et al. 2017, Li et al. 2017, Pietsch et al. 2019, Gui et al. 2020, Purahong et al. 2022). These sequences show the high diversity of fungal resources; however, the naming of taxa is required for fungal classification under the International Code of Nomenclature for Algae, Fungi and Plants. Numerous deposited sequences, however, lack taxonomic assignment, resulting in a great amount of 'uncultured fungus' unvouchered sequences (Hofstetter et al. 2019) unlikely to be integrated into any fungal classification. Numerous mycologists have suggested that an integrated naming system is needed to facilitate unambiguous communication (Hibbett et al. 2011, Hawksworth et al. 2018, Ryberg & Nilsson 2018, Nilsson et al. 2023). Mycologists have debated the inclusion of molecular operational taxonomic units in taxonomy (Zamora et al. 2018), and the subject is still being discussed. Hongsanan et al. (2018) provided case studies on some genera (*Botryosphaeria*, *Colletotrichum*, *Penicillium*, and *Xylaria*) and illustrated that it is inappropriate to use DNA as holotypes in assigning names to fungal species due to the shorter fragments of internal transcribed spacer (ITS) obtained from environmental sequencing. In the meantime, Wu et al. (2019) proposed that attempts to obtain cultures of specimens as physical types should be the priority, the complete genome sequence of fungi (single-cell genome) as a DNA type is the second choice, and fungal sequence data generated from environmental genomic DNA can be a temporary digital type. Thus, these ecology-based studies have remarkable significance for revealing unknown fungal taxa and supporting fungal classification. As shown by Nilsson et al. (2023) "species discovery through environmental sequencing vastly outpaces traditional, Sanger sequencing-based efforts, in a strongly increasing trend over the last five years".

Fungal ecology-related aspects of fungal classification provide many merits, but there are also some misconceptions. One is that most historical fungal identifications were made based on cyanobacterial, algal, plant, or animal host associations (Jeewon et al. 2004, Dayarathne et al. 2016, Liu et al. 2017). This approach is quite error-prone and has resulted in species with few character differences and egregious misidentifications. For instance, according to assessments of *Pestalotiopsis* species by Jeewon et al. (2004) and Maharachchikumbura et al. (2014), numerous species that have been described based on host association (without phylogenetic data) are probably not valid species. An assumed very narrow natural host range of a fungus may potentially be much wider, as shown in an experimental setup with a carabidicolous *Laboulbenia* species (De Kesel 1996). On the other hand, a single host can support different species belonging to the same genus. For example, Jeewon et al.

(2004) revealed two species of the endophytic genus *Pestalotiopsis* (*P. sydowiana* (Bres.) B. Sutton and *P. theae* (Sawada) Steyaert) from *Protea mellifera* Thunb., and neither species appears to be closely related. Liu et al. (2017) introduced eight *Pestalotiopsis* species and three *Pseudopestalotiopsis* species from a single host. Thus, host-based fungal species nomenclature reflects multiple misleading points and needs molecular approaches for better resolution for identification and ultimately fungal classification. New host records are also extremely important (Hyde et al. 2020c) because they can reveal the diversity of adaptations and evolutionary traits of a species.

The use of chemical profiles to improve fungal classification

Fungi are diverse in terms of their morphology, ecology, and chemical profiles (Naranjo-Ortiz & Gabaldón 2019). There are 845 publications and 26,288 citations on the Web of Science website using the keywords ‘fungi’, ‘natural product’ and ‘classification’ and 259 publications with 4,662 citations with the words ‘fungi’ and ‘chemotaxonomy’ from 2010 to 2022. Many publications highlight the advantages of involving chemical profiles in fungal classifications (Frisvad et al. 2008, Raja et al. 2017, Reich & Labes 2017, Guo et al. 2021, Maharachchikumbura et al. 2021). Morphological characters in speciose groups can be misleading due to cryptic speciation, hybridization, and convergent evolution (Raja et al. 2017, Sun et al. 2019, Boekhout et al. 2022); therefore, the application of chemotaxonomy has often been used to increase the efficiency of identifying, exploring and exploiting fungi (Frisvad 2015). However, studies have suggested that the secondary metabolite, also referred to as specialized metabolite profiles in fungi can be strain-specific, species-specific, or common to all species. This could be because fungal extracts include secondary as well as primary metabolites. In yeasts, growth patterns have been used for decades, as well as biochemical tests, i.e., chemotaxonomy (Kurtzman et al. 2011). Also, it is crucial to note that even minor changes in cultivation conditions can lead to a profound shift in the fungal metabolomic profile, underscoring the importance of maximizing the number of culture media and conditions to comprehensively assess the fungal metabolome (Rédou et al. 2016)

Chemotaxonomy is commonly used to classify and identify filamentous fungi using their chemical diversity for taxonomic purposes. This commonly consists of compounds produced on different media and includes toxins, antibiotics and other compounds defined very broadly, such as fatty acids, proteins, carbohydrates, or secondary metabolites, (Frisvad et al. 2008). However, not all compounds can be used for chemotaxonomy as the profile is based only on compounds with differentiation ability (Frisvad et al. 2008). Most fungi are fast-growing and have a high reproductive capacity; thus, metabolite profiles are generally unique in an individual group (Walker & White 2017). Different fungal species can produce one or more common secondary metabolites. For example, cytochalasin D has been reported as being produced by several fungal species in phylogenetically different groups, such as *Basidiomycota* (*Coriolus vernicipes* (Berk.) Murrill) and *Ascomycota* (*Hypoxylon terricola* J.H. Mill., *Metarhizium anisopliae* (Metschn.) Sorokīn and *Zygosporium masonii* S. Hughes) (Cole et al. 2003, Vicente et al. 2003). The hypocrealean genus *Pochonia* produces several secondary metabolites such as monordens and other resorcyclic acid lactones, citreoviridin A and aurovertin B, common to *Penicillium* and *Aspergillus* species (Stadler et al. 2003).

Chemotaxonomy is very helpful in delimiting species, especially in the resolution of species complexes that could not have been distinguished based on classical morphology and can be used as chemotaxonomic markers in comparative studies (Saag et al. 2009, Læssøe et al. 2010, Surup et al. 2014, Kuhnert et al. 2017, Dickschat et al. 2018, Rinkel et al. 2018, Lambert et al. 2019, Ekman & Tønsberg 2022). Fatty acids have been used as potential chemotaxonomic markers for identification in *Albugo*, *Cunninghamella*, *Mortierella*, *Mucor*, *Plasmopara*, *Puccinia*, *Pustula*, *Rhizomucor* and *Wilsoniana* species (Blomquist et al. 1992, Weete & Gandhi 1999, Spring & Haas 2002, Spring et al. 2005, Wołczańska et al. 2021). Some hypoxylean taxa, such as *Hypoxylon griseobrunneum* (B.S. Mehrotra) J. Fourn., Kuhnert & M. Stadler, *H. invadens* J. Fourn. and *H. macrocarpum* Pouzar, yielded several new natural volatiles that can be used as chemotaxonomic markers for a comparative volatiles study (Dickschat et al. 2018, Rinkel et al. 2018). In the myxomycete genus *Lycogala*, the presence and structure of crystallic lime in peridial vesicles were shown to be a useful criterion for delimiting species (Leontyev et al. 2022, 2023b).

Use of integrative approaches to improve fungal classification

Concurrent application of multiple characters or integrative approaches has the power to reduce confusion in identifications and help to improve contrasting classifications arising from various species concepts based on phenetics, phylogeny, ecology, evolution, chemistry, and physiology. Using polyphasic approaches based on morphological, molecular, and chemotaxonomic data is recommended and appears to provide a more useful classification tool, and is helpful in delimiting species (Stadler et al. 2014, Cao et al. 2021, Maharachchikumbura et al. 2021). In addition, biosynthesis, physiological, and genotypic information show functional characteristics that can improve the potential industrial production of fungal metabolites (Keller 2019).

The use of physiology to improve fungal classification

Although not so common, physiological tests can be a useful tool for fungal classification. Basidiomycetous yeasts produce urease amongst other enzymes (i.e., see Kurtzman et al. 2011 and theyeasts.org), with quite extensive growth profiles, whereas in ascomycetous yeasts that enzyme is mostly lacking. Splitting of esculin by *Apophysomyces elegans* P.C. Misra, K.J. Srivast. & Lata growing on bile esculin agar is sufficient to separate that species from the rest of the genus (Alvarez et al. 2010). Fermentation and utilisation of compounds have proven useful for circumscription of genera, for example, *Mrakia* (glucose-fermenting basidiomycete), *Ogataea* (methanol assimilation), and *Scheffersomyces* (xylose fermentation).

Professional criticism of mycological scientific work

Mycologists have different opinions, which could be subject to different interpretations, and unlike computers, humans make mistakes. This might involve missing references, poor alignments, ambiguous trees, and incorrectly deposited or missing data, amongst others. Phylogenomic information obtained from multi-gene sequences must be coupled and complemented with morphological characters during taxonomic studies (Hyde et al. 2010). In this context, reference to type specimens should be emphasized to adequately calibrate the morphological definition of species. Efforts should further include obtaining DNA sequences from type specimens of already described species and using these sequences in phylogenetic analyses whenever possible to ensure a direct reference to taxa within the phylogeny (e.g., Forin et al. 2018, Ronikier et al. 2022). The separation of genotype and phenotype criteria increases the frequency of mistakes by mycologists, which can be observed in mycological publications. It is essential that when other scientists encounter these mistakes, they should point them out. This might involve notifying the authors, asking for data that were not deposited, or discussing the work in publications. Most importantly, though, any criticism should be written professionally. It is rare that scientists deliberately publish incorrect research or data, although it is known to happen. However, it is not always possible to pick up every error. An eminent Chinese mycologist once stated that the job of the supervisor "is to find the silly hidden mistakes that students make in papers submitted for comment". Unfortunately, scientists can make mistakes, and professionally worded criticism or helpful advice will be much better received. Unhelpful or spiteful criticism does not help the situation and may discourage new scientists from continuing in their careers. The number of mycologists has been declining rapidly in Western countries; meanwhile, there have been an increasing number of mycologists being trained in other countries, such as Brazil, Thailand, and China. Members of the community should engage in encouraging and helping all who are interested in continuing their careers (Hyde et al. 2010).

Therefore, in the *Outline of Fungi and fungus-like taxa* and other related publications, we will follow our ethics of professional criticism of mycological scientific work. We hope that these ethics will be adopted throughout the mycological literature.

Voting for opinions on problems of classification, nomenclature and taxonomic concepts

In cases where there are major differences in opinion regarding classification, nomenclature, and taxonomic concepts, we will encourage authors with opposing views to write arguments supporting their approaches and publish these in the outline. In some cases, we may need to follow one approach and also list a different one in the notes or outline. We may also send arguments, disseminated through electronic emails, to the consortium and ask them to vote on their preference, including a comment on their point of view, in a confidential online vote. The results of the vote can then be presented to the International Commission on the Taxonomy of Fungi and the Nomenclature Committee for Fungi with opinions and percentages of votes for and against each view. The members of the consortium are listed in Table 1 with their expertise and country.

Table 1 List of mycologist names, expertise, and countries.

Name	Expertise	Country/Region
Abdel-Wahab Mohamed A	Marine fungi	Egypt
Abdollahzadeh Jafar	*Dothideomycetes*, phytopathogens	Iran
Abeywickrama Pranami D.	*Dothideomycetes*, phytopathogens	China
Absalan Sahar	*Eurotiomycetes*	Thailand
Afshari Naghmeh	*Ascomycota*	Thailand
Ainsworth A. Martyn	Poroid and corticioid *Basidiomycota*, *Hygrocybe* s.l. and stipitate hydnoids	UK
Akulov Olexander Yu	*Ascomycota*, fungicolous and plant-associated fungi	Ukraine
Aleoshin VV	Eukaryotes (in general), *Holomycota*	Russia
Al-Sadi Abdullah Mohammed	Phytopathogens	Oman
Alvarado Pablo	*Pezizales*	Spain
Alves Artur	*Botryosphaeriales*, phytopathogens, marine fungi	Portugal
Alves-Silva Genivaldo	Polypores (*Polyporales / Hymenochaetales*)	Brazil
Amalfi Mario	Polypores / wood decay fungi / (*Polyporales / Hymenochaetales / Cantharellales / Boletales / Russulales*)	Belgium
Amira Yacoub	*Leotiomycetes*	Brazil
Amuhenage Tharindu Bhagya	Aquatic fungi	Thailand
Anderson Jennifer	Aquatic fungi	Sweden
Antonín Vladimír	*Basidiomycota* (macrofungi)	Czechia
Aouali Souhila	Macrofungi and forest tree pathogenic fungi	Algeria
Aptroot Andre	*Dothideomycetes*, lichenized fungi	Netherlands
Apurillo Carlo Chris S	Mangrove fungi, marine fungi	Philippines
Araújo João PM	Insect-associated hypocrealean fungi	Brazil
Ariyawansa Hiran A.	*Dothideomycetes*, phytopathogens	Taiwan
Armand Alireza	*Sordariomycetes*, phytopathogens	Iran, Thailand
Arumugum Elangovan	*Hymenochaetaceae*	India
Asghari Raheleh	Marine fungi	Iran, Thailand
Assis Daniele Magna Azevedo	*Glomeromycota*	Brazil
Atienza Violeta	Lichenized fungi, lichenicolous fungi	Spain
Avasthi S	Phytopathogens	India
Azevedo Egídia	Marine fungi	Portugal
Bai Fengyan	Asco- and basidiomycetous yeasts	China
Bakhshi Mounes	*Hyphomycetes*, *Dothideomycetes*, *Mycosphaerellales*, phytopathogens	Iran
Banihashemi Zia	Fungus-like organisms, *Phytophthora* and *Pythium* spp.	Iran

Table 1 Continued.

Name	Expertise	Country/Region
Bao Danfeng	Freshwater fungi, *Dothideomycetes*	China
Baral Hans-Otto	*Leotiomycetes*, *Orbiliomycetes*	Germany
Barata Margarida	Marine fungi	Portugal
Barbosa Flavia	Freshwater and terrestrial asexual *Ascomycota*	Brazil
Barbosa Renan do Nascimento	*Eurotiales* (*Aspergillaceae*, *Trichocomaceae*, *Thermoascaceae*)	Brazil
Barreto Robert W	*Mycosphaerellaceae*, phytopathogens, fungicolous and endophytic fungi and oomycetes	Brazil
Baschien Christiane	Aquatic fungi	Germany
Belamesiatseva DB	Forest phytopathology, invasive pathogens of forest species	Belarus
Bennett Reuel M	Basal fungi, fungus-like organisms	Philippines
Bera I	*Basidiomycota* (macrofungi)	India, Thailand
Bezerra Jadson Diogo Pereira	*Ascomycota*	Brazil
Bezerra JL	*Ascomycota*	Brazil
Bhat D Jayarama	*Dothideomycetes*, asexual *Ascomycota*	India
Bhunjun Chitrabhanu S.	*Dothideomycetes*, *Eurotiomycetes*, phytopathogens	Thailand
Bianchinotti M Virginia	Fossil fungi, *Ascomycota*	Argentina
Błaszkowski Janusz	*Glomeromycota*	Poland
Blondelle Aimée	*Laboulbeniales*	Belgium
Boekhout Teun	Asco- and basidiomycetous yeasts	Netherlands
Bonito Gregory	*Pezizales*, *Mucorales*, *Endogonales*, *Mortierellales*, truffles	USA
Boonmee Saranyaphat	*Dothideomycetes*	Thailand
Boonyuen Nattawut	*Sordariomycetes*, freshwater fungi	Thailand
Bregant Carlo	*Botryosphaeriales*, *Peronosporales*	Italy
Buchanan Peter	*Basidiomycota* (macrofungi)	New Zealand
Bundhun Digvijayini	*Sordariomycetes*	Thailand
Burgaud Gaëtan	General fungi	France
Burgess Treena	Phytopathogens	Australia
Buyck Bart	*Basidiomycota* (*Russulales*, *Cantharellales*, tropical ECM fungi)	France
Cabarroi-Hernández M.	Polypores / wood decaying fungi / *Polyporales*	Mexico
Caceres Marcela E. da Silva	Lichenized fungi (tropical crustose, foliicolous)	Brazil
Cadež Neža	Ascomycetous yeasts	Slovenia
Caeiro M. F.	*Lulworthiales*, *Halosphaeriaceae*	Portugal
Cai Lei	*Sordariomycetes*	China
Cai M. Feng	*Hypocreales*, halophilic fungi	China
Calabon Mark S	Freshwater fungi, marine fungi	Philippines
Calaça Francisco J. Simões	Dung-inhabiting fungi, *Ascomycota*, *Basidiomycota*	Brazil
Callalli Chancahuaña, Mario	*Basidiomycota*, *Agaricomycetes*	Peru
Camara Marcos Paz Saraiva	Phytopathogens	Brazil
Cano-Lira JF	*Ascomycota*	Spain
Cantillo Taimy	Asexual *Ascomycota*, *Sordariomycetes*	Brazil
Cao Bin	*Basidiomycota*	China
Carlavilla Juan Ramón	General fungi, especially *Pezizales* and *Agaricales*	Spain
Carvalho A	Medically relevant fungi	Portugal
Castañeda-Ruiz Rafael F.	*hyphomycetes*	Cuba
Castlebury Lisa	*Diaporthales*, *Ustilaginales*	USA
Castro-Jauregui Oscar	Macrofungi, myxomycetes	Mexico

Table 1 Continued.

Name	Expertise	Country/Region
Catania Myriam del Valle	*Ascomycota*	Argentina
Cavalcanti Laíse H.	Myxomycetes	Brazil
Cazabonne Jonathan	General macrofungi, *Laboulbeniales*	France, Canada
Cedeño-Sanchez Marjorie Lisset	*Xylariales*	Germany
Chaharmiri-Dokhaharani S	*Polyporales*	Thailand
Chaiwan Napalai	*Ascomycota*	Thailand
Chakraborty Nilanjan	*Geoglossales*	India
Chaverri Priscila	*Ascomycota* with emphasis on *Hypocreales* and *Trichoderma*	Costa Rica, United States
Cheewangkoon R	Phytopathogens	Thailand
Chen Chao	Coelomycetes	China
Chen Chiyu	General fungi	Taiwan
Chen Jie	*Basidiomycota*	Mexico
Chen Kohsuan	*Eurotiomycetes*	Taiwan
Chen Qian	*Dothideomycetes*	China
Chen Wenhao	Insect fungi	China
Chen Yanpeng	*Ascomycota*	China
Chethana K.W. Thilini	*Dothideomycetes*, discomycetes	Thailand
Coleine Claudia	Black fungi, *Dothideomycetes Capnodiales*	Italy
Corazon-Guivin Mike Anderson	*Glomeromycota*	Peru
Cortés-Pérez Alonso	*Agaricales*, *Mycenaceae*, *Psilocybe*	Mexico
Costa-Rezende Diogo Henrique	Polypores (*Polyporales / Hymenochaetales*)	Brazil
Courtecuisse Régis	*Basidiomycota* (mainly gilled) – mainly Europe and the Neotropics	France
Crouch Jo Anne	Phytopathogens (*Calonectria*, *Clarireedia*, *Waitea*, *Colletotrichum*), *Peronosporaceae*	USA
Crous Pedro W	General fungi	Netherlands
Cui Baokai	Polypores, *Hymenochaetales*	China
Cui Yangyang		China
Czachura Paweł	Resinicolus fungi, sooty moulds	Poland
Da Silva Danielle Karla Alves	*Glomeromycota*	Brazil
da Silva Gladstone Alves	*Glomeromycota*, endophytes	Brazil
da Silva Iolanda Ramalho	*Glomeromycota*	Brazil, USA
da Silva Rejane M Ferreira	*Ascomycota*	Brazil
da Silva Santos Ana Carla	*Fusarium*, *Hypocreales*, insect-associated fungi	Brazil
Dai Dongqin	*Dothideomycetes*	China
Dai Yucheng	*Basidiomycota*	China
Dal Forno Manuela	Lichenized fungi	Brazil
Damm Ulrike	*Ascomycota* (*Cadophora*, *Colletotrichum*, *Phaeomoniellales*, *Tympanidaceae*)	Germany
Darmostuk Valerii	Lichenicolous fungi, *Hypocreales*, *Acrospermales*	Poland
Daroodi Zoha	*Xylariomycetidae*	Iran
Das Kallol	Soil fungi	Korea
Das Kanad	*Basidiomycota*	India
Davoodian Naveed	*Boletales*, *Hysterangiales*	Australia, USA
Davydov Evgeny A	Lichenized fungi	Russia
Dayarathne Monika	Freshwater fungi, marine fungi	Sri Lanka
de Groot Michiel	*Laboulbeniomycetes*	Netherlands, Belgium
De Kesel André	*Laboulbeniomycetes*, *Agaricomycetes*	Belgium
De Lange Ruben	*Russulaceae*	Belgium
de Oliveira Neiva Tinti	Phytopathogens	Brazil

Table 1 Continued.

Name	Expertise	Country/Region
de Silva NI	*Ascomycota*	Thailand
de Souza FA	*Glomeromycota*	Brazil
Decock Cony	Polypores, wood decay fungi (*Polyporales, Hymenochaetales, Russulales*), asexual *Ascomycota*	Belgium
dela Cruz Thomas Edison E	Fungal endophytes, endolichenic fungi, myxomycetes	Philippines
Delgado Gregorio	Asexual *Ascomycota*	USA
Denchev Cvetomir M	Smuts	Bulgaria
Denchev Teodor T	Smuts	Bulgaria
Dentinger Bryn	*Agaricales*, *Boletales*	USA
Devadatha B	Marine fungi	India
Dianese Jose C	*Pucciniales*, *Sordariomycetes*	Brazil
Dima Bálint	*Entolomataceae*, *Cortinariaceae*, EcM *Basidiomycota*	Hungary
Diniz Athaline Gonçalves	Fungal entomopathogens	Brazil
Dissanayake Asha J	*Dothideomycetes*	China
Dissanayake Lakmali S	*Sordariomycetes*	China
Doğan Hasan Hüseyin	*Basidiomycota*	Turkey
Doilom Mingkwan	*Ascomycota*	China, Thailand
Dolatabadi S	*Mucorales*	Iran
Dong Wei	Freshwater fungi	China, Thailand
Dong Zhangyong	*Fusarium*, *Trichoderma*	China
Dos Santos LA	Lichenized fungi	Brazil
Drechsler-Santos Elisandro Ricardo	*Hymenochaetaceae* (*Hymenochaetales*), *Ganodermataceae*, *Polyporaceae* (*Polyporales*)	Brazil
Du Tianye	Asexual *Ascomycota*	China
Dubey Manish Kumar	Zoosporic fungi	India
Dutta Arun Kumar	*Basidiomycota*	India
Egidi Eleonora	*Dothideomycetes*	Australia
Elliott Todd F	*Ascomycota*, *Basidiomycota*, truffles, fungal ecology	Australia, USA
Elshahed Mostafa S	*Neocallimastigomycota*	USA
Erdoğdu M	General fungi	Turkey
Ertz Damien	*Arthoniomycetes*, *Dothideomycetes*, *Basidiomycota*, lichenicolous fungi	Belgium
Etayo Javier	Lichenicolous fungi	Spain
Evans Harry Charles	Endophytes, entomogenous, phytopathogens	UK
Fan Xinlei	*Sordariomycetes*	China
Fan Yuguang	*Inocybaceae*, *Agaricales*	China
Fedosova Anna G	*Ascomycota*, *Geoglossomycetes*	Russia
Fell Jack	Basidiomycetous yeasts	USA
Fernandes Isabel	Aquatic asexual *Ascomycota*	Portugal
Firmino André Luiz	Epifoliar fungi, entomogenous, phytopathogens, forest pathology	Brazil
Fiuza Patrícia Oliveira	Freshwater fungi	Brazil
Flakus Adam	Lichenicolous and lichenized fungi (tropical)	Bolivia, Poland
Fragoso de Souza CA	Zygosporic fungi (*Mucoromycota* and *Mortierellomycota*)	Brazil
Frisvad Jens Christian	*Ascomycota*, especially *Apiospora*, *Aspergillus*, *Fusarium*, *Monascus*, *Paecilomyces*, *Penicillium* and *Talaromyces*	Denmark
Fryar Sally C	Freshwater and marine fungi	Australia
Gabaldon Toni	Yeast	Spain
Gábor Péter	*Taphrinales*, ascomycetous yeasts	Hungary
Gajanayake Achala J	Fungicolous fungi	Thailand

Table 1 Continued.

Name	**Expertise**	**Country/Region**
Galindo Luis Javier	Zoosporic fungi and unicellular *Holomycota*	UK
Gannibal Philipp B	*Dothideomycetes*	Russia
Garcia Dania	*Ascomycota*	Spain
Garcia-Sandoval Ricardo	*Gloeophyllales*	Mexico
Garrido-Benavent Isaac	Lichenized fungi and *Basidiomycota* (*Cortinarius*)	Spain
Garzoli Laura	Marine and freshwater *Ascomycota*, freshwater zoosporic parasites	Italy
Gautam Ajay K	Phytopathogens	India
Ge Zaiwei	*Basidiomycota*	China
Gené Díaz Josepa	*Ascomycota*	Spain
Gentekaki Eleni	Basal fungi	Thailand
Ghobad-Nejhad Masoomeh	Corticioid and poroid fungi, wood-inhabiting *Basidiomycota*, *Corticiales*	Iran
Giachini Admir J	*Gomphales*, ECM, agriculture soil fungi	Brazil
Gibertoni Tatiana Baptista	*Agaricomycotina*	Brazil
Góes-Neto Aristóteles	*Basidiomycota*, especially *Hymenochaetales*, *Polyporales*, *Ganodermatales*	Brazil
Gomdola Deecksha	Saprobes and forest pathogens	Thailand
Gorjón Sergio P	Corticioid fungi, polypores	Spain
Goto BT	*Glomeromycota*	Brazil
Granados-Montero María del Milagro	Phytopathogens	Costa Rica
Griffith Gareth W	Anaerobic fungi, grassland *Basidiomycota*, *Hygrophoraceae*, *Microglossum*, *Pterulaceae*	UK
Groenewald Ewald JZ	*Dothideomycetes*	Netherlands
Groenewald Marizeth	Ascomycete yeasts	Netherlands
Grossart Hans-Peter Grube Martin	Aquatic fungi, *Chytridiomycota* lichenized fungi	Germany, Austria
Gueidan Cecile	Lichenized fungi (*Verrucariales*, *Pyrenulales*)	Australia
Gunarathne Anujani	Fungi on basal plants	Thailand
Gunaseelan Sugantha	*Hymenochaetaceae*, *Polyporales*	India
Gusmão Luis F. Pascholati	Asexual *Ascomycota*	Brazil
Gutierrez Alejandra C	Entomopathogenic fungi, *Laboulbeniomycetes*	Argentina
Guzmán-Dávalos Laura	Macrofungi	Mexico
Haelewaters Danny	*Laboulbeniomycetes, Leotiomycetes,* entomopathogenic fungi	Belgium
Halling Roy	*Basidiomycota*	USA
Han Yanfeng	Soil fungi	China
Hapuarachchi Kalani K.	*Ganodermataceae*	China
Harder Christoffer Bugge	*Mycenaceae*	Denmark
Harrington Thomas C	Forest pathogens	USA
Hattori Tsutomu	Polypores	Japan
He Maoqiang	*Basidiomycota*	China
He Shuanghui	Corticioid fungi	China
He Shucheng	Phytopathogens	China
Healy Rosanne	*Pezizales*	USA
Heredia Gabriela	Asexual *Ascomycota*	Mexico
Hernández-Restrepo Margarita	Asexual *Ascomycota*	Netherlands
Hodge Kathie T	Insect pathogenic fungi, *Ascomycota*	USA
Holgado-Rojas Maria Encarnacion	*Agaricales*	Peru
Hongsanan Sinang	Epi-foliar fungi, *Dothideomycetes*, *Sordariomycetes*	China, Thailand

Table 1 Continued.

Name	Expertise	Country/Region
Horak Egon	*Basidiomycota*, *Agaricales* and *Boletales*	Switzerland
Hosoya Tsuyoshi	Discomycetes	Japan
Houbraken Jos	*Eurotiomycetes*, *food and indoor fungi*	Netherlands
Huang Shike	*Sordariomycetes*	China
Huanraluek Naruemon	*Dothideomycetes*	Thailand
Hur Jae Seoun	Lichenized fungi	Korea
Hurdeal Vedprakash G	Basal fungi/*Chytridiomycota/Mucorales*	Thailand
Hustad Vincent P	Discomycetes	USA
Iotti Mirco	Macrofungi (truffles)	Italy
Iturriaga Teresa	*Leotiomycetes*	USA
Janik Paulina	*Myxomycetes*	Poland
Jany Jean-Luc	*Mucoromycota* (*Mucor*), *Ascomycota (Cladosporium, Bisifusarium)*	France
Jayalal Udeni	Lichenized fungi	Sri Lanka
Jayasiri Subashini C	*Dothideomycetes*	Australia
Jayawardena Ruvishika S	Phytopathogens	Thailand
Jeewon Rajesh	Phytopathogens	Mauritius
Jerônimo Gustavo Henrique	Zoosporic eufungi	Brazil
Jesus Ana Lucia	*Zoosporic eufungi*	Brazil
Jin Jing	*Ascomycota*	China
Johnston Peter R.	Discomycetes	New Zealand
Jones E.B. Gareth	*Dothideomycetes*	UK
Joshi Y	Lichenicolous fungi	India
Justo Alfredo	*Basidiomycota*	Canada
Kaishian Patricia	*Laboulbeniomycetes*	USA
Kakishima Makoto	*Pucciniales*	Japan
Kang Gongping	General macrofungi	China
Kang Jichuan	*Amphisphaeriales*	China
Karimi Omid	*Xylariomycetidae*	Thailand
Karpov Sergey A	Basal fungi, *Aphelida*	Russia
Karunarathna Samantha C.	*Basidiomycota* (macrofungi)	China, Sri Lanka
Kaufmann Moritz	Bioinformatics	Switzerland
Kemler Martin	Smuts	Germany
Kezhocuyi Kezo	*Hymenochaetaceae*, *Polyporales*	India
Khyaju S	*Basidiomycota* (macrofungi)	Thailand
Kirchmair Martin	*Agaricomycotina*, asexual *Ascomycota*	Austria
Kirk PM	General fungi	UK
Kitaura Marcos Junji	Cyanolichens, especially *Leptogium*	Brazil
Klawonn Isabell	Marine fungi	Germany
Kolarik Miroslav	*Ascomycota*	Czechia
Kong Alejandro	*Russulaceae*, edible & ectomycorrhizal fungi	Mexico
Kossmann Thiago	*Leotiomycetes*, *Agaricomycotina*	Brazil, USA
Kuhar Francisco	Sequestrate fungi, corticioid, tomentelloid fungi, *Gasteromycetes*	Argentina
Kukwa Martin	Lichenized and lichenicolous fungi	Poland
Kumar Shambhu	Phytopathogenic fungi	India
Kušan Ivana	*Onygenales*, *Mycocaliciales*, *Sclerococcales*, *Geoglossomycetes*, *Ostropales*, *Helotiales*, *Leotiales*, *Marthamycetales*, *Thelebolales*, *Orbiliomycetes*, *Pezizomycetes*	Croatia
Lachance Marc-André	Ascomycetous yeasts	Canada
Lado Carlos	Myxomycetes	Spain
Larsson Karl-Henrik	Corticioid *Agaricomycetes*	Sweden
Latha K.P. Deepna	*Basidiomycota* (macrofungi)	India
Lee Hyang Burm	Basal fungi	Korea
Leonardi Marco	*Laboulbeniales*, macrofungi (tuffles)	Italy

Table 1 Continued.

Name	Expertise	Country/Region
Leontyev Dmytro L	Myxomycetes	Ukraine
Lestari Anis Sri	Discomycetes	Indonesia, Thailand
Li Cuijinyi	Discomycetes	China, Thailand
Li CY	*Basidiomycota*	China
Li Dewei	Asexual fungi, phytopathogens	USA
Li Hua	*Ascomycota*	China
Li Haiyan	Endophytes	China
Li Lu	Microfungi	China
Li Qirui	*Xylariomycetidae*	China
Li Wenli	*Ascomycota*	China
Li Yanchun	Macrofungi	China
Li Yue	*Basidiomycota*	China
Li Yanxia	*Xylariomycetidae*	China
Liao Chunfang	*Ascomycota*	China
Libkind Diego	Asco- and basidiomycetous yeasts	Argentina
Liimatainen Kare	*Basidiomycota* (*Cortinariaceae*, *Inocybaceae*)	UK
Lim YW	*Basidiomycota Ascomycota* (marine fungi)	Korea
Lin Chuangen	Hyphomycetes	China
Linaldeddu Benedetto Teodoro	*Botryosphaeriales* and *Peronosporales*	Italy
Linde Celeste	Orchid mycorrhizal fungi	Australia
Linn Maung Maung	Yeasts	Thailand
Liu Fei	*Basidiomycota*	China
Liu Jiankui	*Dothideomycetes*	China
Liu Ningguo	Hyphomycetes	China
Liu Shiliang	*Basidiomycota*	China
Liu Shun	*Polyporales*	China
Liu Xiangfu	Bat associated fungi	China
Liu Xiaoyong	Zygomycota	China
Liu Xingzhong	Nematode trapping fungi	China
Liu Zhanbo	*Basidiomycota*	China
Lu Yongzhong	*Dothideomycetes*, helicosporous fungi	China
Luangharn Thatsanee	*Basidiomycota*	Thailand
Luangsa-ard Jennifer J	Insect fungi	Thailand
LumbschThorsten	Lichenized fungi	USA
Lumyong Saisamorn	*Basidiomycota*	Thailand
Luo Le	Discomycetes	China
Luo Mei	Endophytes, *Trichoderma*	China
Luo Zonglong	*Dothideomycetes*	China
Ma Jian	*Dothideomycetes*, helicosporous fungi	China
Machado Alexandre Reis	*Botryosphaeriales*, *Mycosphaerellaceae*, *Fusarium*, phytopathogens	Brazil
Madagammana AD	*Dothideomycetes*	Thailand
Madrid Hugo	Coelomycetes, *Eurotiomycetes*, hyphomycetes	Chile
Magurno F	*Glomeromycota*	Poland
Magyar Donat	*Hagnosaceae*; hyphomycetes on pollen grains	Hungary
Mahadevan Niranjan	Phytopathogens	Japan, Sri Lanka
Maharachchikumbura Sajeewa	Phytopathogens, *Sordariomycetes*	China
Maimaiti Y	Biotrophic fungi	China
Malarvizhi Kaliyaperumal	*Hymenochaetales*, *Polyporales*	India
Malosso Elaine	Asexual *Ascomycota*, Ingoldian fungi	Brazil
Manamgoda Dimuthu S.	Phytopathogens	Sri Lanka
Manawasinghe Ishara	Phytopathogens	China
Mapook Ausana	*Dothideomycetes*	Thailand
Marasinghe Diana S.	*Dothideomycetes*, epi-foliar fungi	Sri Lanka

Table 1 Continued.

Name	Expertise	Country/Region
Mardones Melissa	*Phyllachorales*, *Coronophorales*, mainly the genus *Lichenochora*	Costa Rica
Marin-Felix Yasmina	*Sordariales*, *Melanosporales*, helminthosporioid fungi	Germany
Márquez Rodrigo	*Cantharellales*	Spain
Masigol Hossein	*Oomycota*	Iran, Germany
Matočec Neven	*Onygenales*, *Mycocaliciales*, *Sclerococcales*, *Geoglossomycetes*, *Ostropales*, *Helotiales*, *Leotiales*, *Marthamycetales*, *Thelebolales*, *Orbiliomycetes*, *Pezizomycetes*	Croatia
May Tom W	*Basidiomycota*	Australia
McKenzie Eric	Rusts	New Zealand
Meiras-Ottoni A	*Ascomycota*	Brazil
Melo Roger Fagner Ribeiro	Coprophilous *Ascomycota* (*Podospora*, *Saccobolus*, *Sporormiella*)	Brazil
Mendes Alvarenga Renato Lúcio	*Auriculariales*, *Tremellales*, *Dacrymycetes*	Brazil
Mendieta Yañez Stephany	Entomopathogenic fungi	Peru
Meng Qingfeng	Lichenicolous fungi, lichenized fungi	China
Menkis Audrius	Forest Pathology	Sweden
Menolli Nelson Jr.	Agaricoid fungi	Brazil
Mešić Armin	*Agaricomycotina*	Croatia
Meza Calvo Jackeline	Entomopathogenic fungi	Peru
Mikhailov KV	Eukaryotes (in general), *Holomycota*	Russia
Miller Steven L	*Russulaceae*, Sequestrate *Basidiomycota*, ectomycorrhizal *Basidiomycota*	USA
Moncada Bibiana	Lichenized fungi	Colombia, Germany
Moncalvo Jean-Marc	*Agaricales*, *Ganodermataceae*	Canada
Monteiro Josiane Santana	Asexual *Ascomycota*	Brazil
Monteiro, Marcela	*Hymenochaete*, *Hymenochaetaceae* (*Hymenochaetales*)	Brazil
Mora-Montes Héctor M.	Clinical yeasts	Mexico
Moreau Pierre-Arthur	*Agaricales*, *Tricholomataceae* and other white-spored agarics, *Hymenogastraceae*, *Strophariaceae*, *Morchellaceae*	France
Mostert Lizel	*Togniniales*, *Phaeomoniellales*, *Diatrypaceae*, *Botryosphaeriaceae*, *Diaporthe*	South Africa
Mueller Greg M	*Basidiomycota*	USA
Mukhopadyay Samhita	Marine fungi	India, Thailand
Murugadoss Ramesh	*Hymenochaetaceae*	India
Nagy László G.	Coprinoid *Agaricales*	Hungary
Najafiniya Mousa	Phytopathogens	Iran
Nanayakkara Chandrika M	Phytopathogenic and endophytic fungi	Sri Lanka
Nascimento Cristiano Coelho	Agaricoid fungi	Brazil
Nei Yong	Entomophthoroid fungi	China
Neuhauser Sigrid	*Phytomyxea*, plant-associated fungi, zoosporic fungi	Austria
Neves Maria Alice	Ectomycorrhizae, *Agaricales*, *Boletales*	Brazil
Niego Allen Grace	*Basidiomycota*	Philippines
Nilsson Henrik	*Basidiomycota*	Sweden
Niskanen Tuula	*Basidiomycota*	Finland
Niveiro Nicolás	*Agaricales*	Argentina
Nuñez Otaño Noelia B	Fossil fungi	Argentina
O'Donnell Ryan Patric	Orchid mycorrhizal fungi (*Ceratobasidiaceae*)	Australia
Oehl Fritz	*Glomeromycota*	Switzerland

Table 1 Continued.

Name	Expertise	Country/Region
Olariaga Ibai	*Cantharellales* overall, *Ceratellopsis*, *Typhula*, *Macrotyphula*, *Clavariaceae*, *Tricholomopsis*, *Otidea*, *Sclerococcum*	Spain
Pang Kalai	Aquatic fungi	Taiwan
Papp Viktor	Polypores, *Basidiomycota*, phytopathogens	Hungary
Pawłowska Julia	Basal fungi	Poland
Peintner Ursula	*Mucorales*, *Mortierellaceae*, *Agaricales* (*Cortinariaceae*), polyporoid taxa, Endophytes	Austria, Italy
Pem Dhandevi	*Dothideomycetes*	Thailand
Pereira Olinto Liparini	*Ascomycota* (fungicolous and plant-associated fungi), orchid mycorrhizal fungi (*Ceratobasidiaceae*, *Sebacinaceae*, *Tulasnellaceae*)	Brazil
Perera Rekhani Hansika	*Sordariomycetes*	Korea
Pérez-Ortega Sergio	*Collemopsidiales*, *Verrucariaceae* (Marine genera), *Lecanoraceae*, *Ramalina*	Spain
Phillips Alan J. L.	*Dothideomycetes*, phytopathogens	Portugal
Phonemany Monthien	*Basidiomycota*	Laos, Thailand
Phukhamsakda Chayanard	*Dothideomycetes*	Thailand
Phutthacharoen K	Discomycetes	Thailand
Piątek Marcin	Black yeasts, sooty moulds, smut fungi	Poland
Piepenbring M	*Pucciniales*, *Meliolales*, *Ustilaginales* and other smut fungi	Germany
Pires-Zottarelli Carmen L A	Zoosporic eufungi	Brazil
Poinar George	Fossil fungi	USA
Popoff Orlando Fabián	Corticioid fungi, *Polyporales*	Argentina
Pošta Ana	*Agaricomycotina*, *Helotiales*, *Xylariales*	Croatia
Prieto M	*Coniocybomycetes*	Spain
Promputtha Itthayakorn	Endophytic fungi	Thailand
Quandt Alisha	*Leotiomycetes*, *Hypocreales*, *Cryptomycota*, mycoparasites	USA
Radek R	*Nephridiophagales* (*Chytridiomycota*)	Germany
Rahnama Kamran	Fungal endophytes, *Ascomycota Venturiales* & phytopathogen	Iran
Raj K.N. Anil	*Basidiomycota* (macrofungi)	India
Rajeshkumar KC	Asexual *Ascomycota*, *Xenospadicoidales*	India
Rämä Teppo	Aquatic fungi	Norway
Rambold Gerhard	Lichenized fungi	Germany
Ramírez-Cruz Virginia	*Agaricales* (*Basidiomycota*)	Mexico
Rasconi Serena	*Chytrids and zoosporic parasites*	France
Rathnayaka Achala	*Botryosphaeriales*	Sri Lanka, Thailand
Raymundo Tania	*Sarcoscyphaceae*, *Sarcosomataceae*, *Patellariaceae*, *Pyronematceae*, *Mytilinidiales*, *Hysteriaceae*, *Hypoxylaceae* and *Xylariaceae*	Mexico
Raza Mubashar	Phytopathogens	China, Pakistan
Ren Guangcong	*Ascomycota*	China
Robledo Gerardo Lucio	Polypores (*Antrodia* clade, *Ganodermataceae*, *Polyporus s.l.*, *Hymenochaetaceae*, Phlebioid clade)	Argentina
Rodriguez-Flakus P	Lichenized fungi including *Lecidea* s.l.	Bolivia, Poland
Ronikier Anna	Myxomycetes	Poland
Rossi Valter	*Laboulbeniales*	Italy
Ryberg Martin	*Basidiomycota*	Sweden
Ryvarden Leif R	Polypores	Norway
Salvador-Montoya, Carlos A.	Polypores (*Hymenochaetales*, *Polyporales*)	Peru
Samant Bandana	Fossil fungi	India

Table 1 Continued.

Name	Expertise	Country/Region
Samarakoon Binu Chamini	Asexual *Ascomycota*	Thailand
Samarakoon Milan C.	*Sordariomycetes*	Thailand
Sánchez-Castro I	*Glomeromycota*	Spain
Sánchez-García Marisol	*Agaricales*, mainly *Tricholomataceae*	Sweden
Sandoval-Denis Marcelo	*Microascales*, *Hypocreales*, *Fusarium*	Netherlands
Santamaria Brianna	*Laboulbeniales*	Belgium
Santiago, André Luiz C.M.de A	*Mucoromycota, Zoopagomycota*	Brazil
Sarma VV	Marine fungi	India
Savchenko Anton	*Dacrymycetes*, heterobasidiomycetes	Ukraine, Estonia
Savchenko Kyryll	Phytopathogens	Estonia
Saxena RK	Fossil fungi	India
Scholler Markus	*Pucciniales* (rust fungi)	Germany
Schoutteten Nathan	*Corticiaceae*, *Heterobasidiomycetes*, Mycoparasitic fungi	Belgium
Seifollahi Ellaheh	Phytopathogens	Thailand
Selbmann L	*Black fungi, Dothideomycetes Capnodiales*	Italy
Selçuk Faruk	Asexual *Ascomycota*	Turkey
Senanayake I Chinthani	Coelomycetes	China
Shabashova Tatiana G	*Basidiomycota*, myxomycetes	Belarus
Shen Hongwei	*Spathulosporales*	China
Shen Yuanmin	General fungi	Taiwan
Silva-Filho Alexandre G.S.	Agaricoid fungi	Brazil
Simmons D. Rabern	Zoosporic eufungi / basal fungi, *Chytridiomycota*	USA
Singh Raghvendra	Pathogenic fungi, saprobic fungi related to *Ascomycota* and *Basidiomycota* (Rust fungi)	India
Sir Esteban B.	*Xylariales*	Argentina
Song Chang-Ge	*Basidiomycota*	China
Souza-Motta Cristina M	*Ascomycota*	Brazil
Sruthi OP	Asexual *Ascomycota*	India
Stadler Marc	*Sordariomycetes*	Germany
Stchigel Alberto Miguel	*Ascomycota*, coelomycetes, *Mucoromycota*	Spain
Stemler Jannik	Phytopathogens	Germany
Stephenson Steven L	Myxomycetes	USA
Strassert JFH	*Chytridiomycota* (parasites of insects and phytoplankton)	Germany
Stryjak-Bogacka Monika	Endophytic fungi of bryophytes, sooty moulds	Poland
Su Hongli	Discomycetes	China, Thailand
Su Lei	Lichenized fungi, endophytes, phytopathogens, coprophilous fungi (*Anthracina*, *Rupestriomyces*, *Spissiomyces*, *Talaromyces*, *Penicillium*, *Phialemoniopsis*, *Plectosphaerella*, *Lecanicillium*, *Kernia*, *Acaulium*)	China
Suetrong Satinee	*Dothideomycetes*	Thailand
Sulistyo Bobby	*Atheliales*	Belgium, Indonesia
Sun Yaru	Phytopathogens	China
Sun Yifei	*Polyporales, Ganodermataceae*	China
Svantesson Sten	*Atheliales* and *Thelephorales*	Sweden
Sysouphanthong Phongeun	*Basidiomycota*	Laos, Thailand
Takamatsu Susumu	*Erysiphaceae*	Japan
Takashima Masako	Asco- and basidiomycetous yeasts	Japan
Tan Tinghong	Macrofungi	China
Tanaka Kazuaki	*Dothideomycetes*	Japan

Table 1 Continued.

Name	Expertise	Country/Region
Tang Alvin MC	*Xylariales*	Hong Kong
Tang Xia	Forest fungi	China
Tanney Joey B	*Leotiomycetes*, endophytes, forest fungi	Canada
Tavakol Maryam	*Eurotiomycetes*	China
Taylor Joanne	*Ascomycota*	UK
Taylor Paul WJ	Phytopathogens, *Colletotrichum*, *Pythium*	Australia
Tedersoo Leho	Basal fungi, *Sebacinales*	Estonia
Tennakoon Danushka S.	*Dothideomycetes*	Thailand
Thamodini GK	*Ascomycota*	Oman
Thines Marco	*Oomycota*, *Peronosporomycetes*, *Saprolegniomycetes*, *Basidiomycota*, *Bartheletiomycetes*, *Ustilaginomycetes*, *Exobasidiomycetes*	Germany
Thiyagaraja Vinodhini	*Dothideomycetes*, lichenicolous fungi, lichenized fungi, *Eurotiomycetes*	China
Thongklang Naritsada	*Basidiomycota* (macrofungi)	Thailand
Tiago Patricia Vieira	Fungal entomopathogens	Brazil
Tian Qing	*Eurotiomycetes, Melanommataceae*	China
Tian WH	*Ascomycota*	China
Tibell Leif	Lichenized fungi	Sweden
Tibell Sanja	Lichenized fungi	Sweden
Tibpromma Saowaluck	*Dothideomycetes*, endophytic fungi, *Sordariomycetes*	China, Thailand
Tkalčec Zdenko	*Agaricomycotina*)	Croatia
Tomšovský M	*Polyporales*, *Hymenochaetaceae*, *Armillaria*, *Melanoleuca*, phytopathogens	Czechia
Toome-Heller Merje	Phytopathogens	New Zealand
Torruella G	Sister lineages of fungi	Spain
Tsurykau Andrei	*Eurotiomycetes*, lichenized fungi, lichenicolous fungi	Belarus
Turchetti Benedetta	Asco- and basidiomycetous yeasts	Italy
Udayanga Danuska	Phytopathogens	Sri Lanka
Ulukapı Merve	Asexual *Ascomycota*	Turkey
Untereiner Wendy	*Leotiomycetes*	USA
Uzunov Blagoy Angelov	General fungi (incl. lichenized fungi)	Bulgaria
Valenzuela Ricardo	*Polyporales*	Mexico
Valle Laia Guardia	Freshwater fungi	Spain
Van Caenegem Warre	*Laboulbeniomycetes*	Belgium
Van den Wyngaert Silke	Phytoplankton associated zoosporic fungi, *Chytridiomycota*	Finland
Van Vooren Nicolas	*Pezizomycetes*	France
Velez P	*Ascomycota*	Mexico
Verma Rajnish Kumar	Phytopathogens	India
Vieira LC	*Glomeromycota*	Brazil
Vieira Willie Anderson dos Santos	*Colletotrichum*	Brazil
Vizzini Alfredo	*Basidiomycota* and *Ascomycota* (*Pezizales*)	Italy
Walker Allison K		Canada
Walker Arttapon	*Basidiomycota*	Thailand
Wanasinghe Dhanushka N.	*Dothideomycetes*, epi-foliar fungi	China
Wang Chaoge	Macrofungi	China
Wang Ke	Macrofungi	China
Wang SX	*Basidiomycota*	China
Wang Xinyu	Lichenized fungi, *Caliciales*	China
Wang Yong	Phytopathogens	China
Wannasawang Narumon	General fungi	Thailand

Table 1 Continued.

Name	**Expertise**	**Country/Region**
Wartchow Felipe	Agaricoid fungi	Brazil
Wei Deping	Insect pathogens	China
Wei Xinli	Lichenized fungi	China
Westphalen Mauro	*Steccherinaceae*	Brazil
White Jim F	Endophytes, *Ascomycota*	USA
Wijayawardene Nalin N.	Coelomycetes	China, Sri Lanka
Wijesinghe Nuwanthika	*Ascomycota*	Sri Lanka
Wijesundara DSA	Fungal ecology	Sri Lanka
Wisitrassameewong Komsit	*Basidiomycota*	Thailand
Worthy Fiona Ruth	Lichenized fungi	China
Wu Fang	*Auriculariales*, *Tremellales*, jelly fungi	China
Wu Gang	*Boletales*	China
Wu Haixia	Epi-foliar fungi, *Ascomycota*	China
Wu Na	*Ascomycota*	China
Wu Wenping	Asexual fungi, including chaetosphaeriaceous, *Chalara*-like, *Sporidesmium*-like fungi	China
Wurzbacher Christian	*Aquatic fungi*	Germany
Xiao Yuanpin	Insect fungi	China
Xiong Yinru	*Ascomycota*	China
Xu Biao	Phytopathogens	China
Xu Lijian	*Ascomycota*	China
Xu Rongju	*Ascomycota*	China
Xu Rong	*Ascomycota*	China
Xu Ruifang	Rubber associated fungi	China
Xu Taimin	Macrofungi	China
Yakovchenko Lidia	Lichenized fungi	Russia
Yan Jiye	Phytopathogens	China
Yang Hongde	Phytopathogens	China
Yang Yunhui	*Ascomycota*	China
Yang Jing	Asexual *Ascomycota*	China
Yang Zhuliang	*Basidiomycota*	China
Yapa N	*Ascomycota*	Sri Lanka
Yasanthika Erandi	Soil fungi	Thailand
Youssef Noha H	*Neocallimastigomycota*	USA
Yu Fengming	Discomycetes	China
Yu Quan	*Chaetothyriales*	China
Yu R	*Basidiomycota* (macrofungi)	China
Yu Xiandong	*Ascomycota*	China
Yu Yongxiu	*Ascomycota*	China
Yu Zefen	Nematode trapping fungi	China
Yuan Haisheng	*Thelephorales* in *Basidiomycota*, hydnaceous, polyporoid and corticioid *Basidiomycota*	China
Yuan Yuan	*Polyporales*, *Hymenochaetales*	China
Yurkov Andrey	Ascomycetous and basidiomycetous yeasts	Germany
Zafari D	*Ascomycota*, *Hypocreales*	Iran
Zamora Juan Carlos	*Geastrales*, *Dacrymycetes*, *Tremellales*	Spain/Switzerland
Zare Rasoul	Phialidic hyphomycetes (phytopathogens, entomogenous and nematophagous fungi)	Iran
Zeng Ming	Discomycetes	China
Zeng Niankai	*Basidiomycota*	China
Zeng Xiangyu	Phytopathogens, epi-foliar fungi (or epiphytes)	China
Zhangyong Dong	*Ascomycota*	China
Zhang Fa	*Ascomycota*	China
Zhang Huang	Freshwater fungi	China
Zhang Jinfeng	*Ascomycota*	China
Zhang Jingyi	*Ascomycota*	China

Table 1 Continued.

Name	Expertise	Country/Region
Zhang Qiuyue	*Mycenaceae* (*Favolaschia*, *Panellus*)	China
Zhang Shengnan	*Dothideomycetes*	China
Zhang Wei	Phytopathogens	China
Zhang Ying	*Dothideomycetes*	China
Zhang Yunxia	Phytopathogens	China
Zhang Zhiyuan	*Arthrodermataceae*	China
Zhao Changlin	*Basidiomycota*	China
Zhao Heng	*Mucoromycota*	China
Zhao Qi	*Pezizales*	China
Zhao Ruilin	*Basidiomycota*	China
Zhou Liwei	Macrofungi, *Basidiomycota*	China
Zhou Meng	Macrofungi	China
Zhurbenko Mikhail P.	Lichenicolous fungi	Russia
Zin Hnin Htet	*Ascomycota*	Thailand
Zucconi Laura	*Ascomycota*	Italy

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