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Аннотация: В сборнике представлены тезисы работ участников 9-ой Московской конференции по вычислительной молекулярной биологии MCCMB'19. Работы посвящены актуальным вопросам анализа аминокислотных и нуклеотидных последовательностей, структур биополимеров, молекулярной эволюции, методов высокопроизводительного секвенирования, системной биологии и биоалгоритмов.

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## **The genome of new Echinophthiridae Enderlein species *Antarctophthirus nevelskoy*.**

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Sucking lice (Anoplura, formerly known as Siphunculata) is a suborder of small obligate ectoparasite of Lice (Phthiraptera) order. Sucking lice oral organs are adapted to pierce host's skin and to suck the blood in [2]. The level of morphofunctional organization of sucking lice is so high that every sucking lice species is only able to parasitize in one or several similar host species [3; 5; 1]. The Echinophthiridae Enderlein family (1904), which consists of 13 species combined into 5 genera [3; 6], demonstrates the most sophisticated adaptation form – it adapts to the aquatic environment, which evolved with the same adaptation of their homeothermic hosts - earless seal (*Plocidae* Gray, 1821), eared seal (*Otariidae* Gray, 1825), walruses (*Odobenidae* Allen, 1880), weasels (*Mustelidae* Fischer-waldheim, 1817) [3: 7]. Although every Echinophthiridae species prefer to parasitize on a specific host's body area, they don't have the possibility to occupy all pelage surface of pinnipeds in the cold waters of Arctic and Antarctic regions, thus they migrate to nasal cavity threshold [3].

Let us consider some characteristics of *Antarctophthirus* genus from Anoplura suborder [8] in the case of *A. callorhini*, particularly widespread in the Far East, as this species is the most relative to the new unstudied Echinophthiridae species, described further in our study. Specifically, *A. callorhini* is not impacted by the change of such factors as illuminance and humidity, the optimal temperature for biological processes is 25-31 ° C. Females lay 8 – 10 eggs daily. The life cycle includes egg stage, 3 nymph stages and adult stage. Every nymph stage lasts about 3-4 days until molting, the life cycle from egg lay till last molting lasts about 18 – 20 days, with the temperature of the host animal being 31 ° C. At the moment it is unknown which factors influence the slow and delayed development of *A. callorhini*. Possibly, that may be circadian

rhythm, hormonal and physical activity changes in pinniped host, but additional research is needed for theory confirmation [4].

The genome of *Antarctophthirus nevelskoy* was assembled from 1290603 non-paired reads acquired through whole-genome sequencing using Ion Torrent S5. Adapter removal from reads was performed with Trimmomatic-0.33. Further, genome assembly was performed by SPAdes-3.13.0. 43999 contigs were obtained. After that, using DIAMOND, most homological protein sequences to the sequenced *A. nevelskoy* protein sequences were identified. As a result, following proportions were acquired:

	Mammals	Insects	Bacteria	Archaea
Species count	70	270	1030	35

The genome of *Antarctophthirus microchir* was taken for comparison. It was assembled with SPAdes-3.13.0 from SRA archive SRX2405454.

Usually, bilateral animals mitochondrial genome consists of one circular chromosome, 16 kb in size, which includes 37 genes. However, it was shown on the examples of *Pediculus humanus* and *Pediculus capitis* species that mitochondrial genome of lice consists of 20 minichromosomes, each chromosome being 3 - 4 kb in size and including 1-3 genes. Also, a study was published in 2012 [10], in which authors have shown that heteroplasmy level in mitochondrial gene *cox1* in *Pediculus humanus* and *Pediculus capitis* species is significantly higher than in humans and other animals. It was suggested that high level of heteroplasmy in lice could be associated with mtDNA fragmentation, possibly, due to recombinational activity increase between minichromosomes [9].

All studied sucking lice mitochondrial genomes are fragmented, unlike most other organisms mitochondrial genomes. Those genomes are organised in circular minichromosomes, their count might be as many as 20, which strongly differs from one circular mitochondrial DNA.

4 minichromosomes were assembled in the genome of *A. nevelskoy*, and more than 10 minichromosomes were identified, a part of them might include pseudogenes.

The highest similarity in mitochondrial sequences was identified between 49 contig's sequence *A. nevelskoy* genome assembly and a part of gene of 1st subunit of cytochrome oxidase (COI) of *Echinophthirius horridus*, the similarity being 100% for 95 amino acids.

The nearest neighbours of *A. nevelskoy* at mt DNA tree are *Hoplopleura acanthopus*, *Haematopinus apri* and *Columbicola macrourae*, taxonomically far distant species.

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