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The complete mitochondrial genome of the smallest known free-living insect *Scydosella musawasensis*

Artem Nedoluzhko[a], Fedor Sharko[b], Eugenia Boulygina[a], Svetlana Tsygankova[a], Alexey Sokolov[b], Alexander Mazur[b], Alexey Polilov[c], Egor Prokhortchouk[b,c] and Konstantin Skryabin[a,b,c]

[a]Genome Analysis Laboratory, National Research Centre "Kurchatov Institute", Moscow, Russia; [b]Institute of Bioengineering, Research Center of Biotechnology of the Russian Academy of Sciences, Moscow, Russia; [c]Faculty of Biology, Lomonosov Moscow State University, Moscow, Russia

ABSTRACT

The mitochondrial genome of the smallest known free-living insect *Scydosella musawasensis* (Polilov, 2015) is published in this paper. The mitochondrial DNA (mtDNA) is 14 719 base pairs (bp) in length and contained 13 protein-coding genes, 2 rRNA genes and 21 tRNA genes. The overall base composition of the genome in descending order was 40.59% – A, 13.85% – C, 36.82% – T and 8.73% – G, with a significant AT bias of 77.41%.

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Scydosella musawasensis individuals were collected in Chicaque National Park, Colombia, 10 km west of Bogotá, 2200 m above sea level, on the fungus *Steccherinum* sp. (Meruliaceae). Specimens were deposited in the entomological collection of the Zoological Museum of Lomonosov Moscow State University (ZMMU I-P-00844-854). DNA was extracted using NucleoSpin Tissue XS kit (Macherey-Nagel, Germany). DNA-libraries were constructed using Ovation Ultralow Systems V2 kit (NuGEN, San Carlos, CA). Mitochondrial genome was sequenced used Illumina Hiseq 1500 (Illumina, USA) with 100 bp pared-end reads.

Totally 226 571 628 Illumina paired-end reads were generated. Reads were merged (up to 60%) using Pear software (Zhang et al. 2014). After PCR-duplicate trimming, we used MITObim software (Hahn et al. 2013) and mitogenome of the American carrion beetle *Necrophila americana* (Coleoptera: Silphidae) as reference sequence for reconstructing the mitochondrial genome of *S. musawasensis*.

Surprisingly, we did not find *trnI* gene in our assembly. SPAdes software was used for *de novo* assembly (Bankevich et al. 2012) as proof that *trnI* is absent in *S. musawasensis* mitogenome. Totally 249 988 contigs were assembled (N50 = 1314 bp), but contigs mapping on the MITObim assembly did not yield a *trnI* gene in mitogenome.

As a result, the mitogenome of *S. musawasensis* consists of 14 719 bp (GenBank accession number: KU302777), including 13 protein-coding genes (PCGs), 2 rRNA genes and 21 tRNA genes. Despite that arthropod mitochondrial DNA typically contain the 22 tRNAs (Boore 1999), our data showed that *S. musawasensis* have lost *trnI* gene.

Six of the 13 PCGs (*COX1*, *NAD5*, *NAD4L*, *NAD6*, *COB*, *NAD1*) used ATT as a start codon, and other three (*NAD2*, *COX2*, *NAD4*) used ATA, *ATP6* started with ATG codon, *ATP8 and NAD3* with ATC, and *COX3* with CAC. Three genes (*ATP8*, *COX2*, *NAD3*) ended with a TGA stop codon, *NAD1*, *NAD5* and *NAD4L* ended with ATT, *NAD2* and *NAD4* ended with AAA, *COX1* gene ended with a TTA codon, *ATP6* with TCT, *COX3* with AGT, *NAD6* with CGA, and *COB* with ATT. The *rrnL* and *rrnS* genes were located between *trnL1*(tag) and *trnQ*(ttg) genes, with 631 and 739 bp in length, respectively.

The phylogenetic analysis was performed for the *Staphylinoidea* superfamily and other Coleoptera species (*Phacomorphus fratyi* (KT780668.1); *Sciodrepoides watsoni* (KT780675.1); *Tetartopeus terminatus* (NC_028613.1); *Sepedophilus bipunctatus* (NC_028611.1); *Scaphidium quadrimaculatum* (NC_028609.1); *Pselaphinae sp.* 5 EF-2015 (KT780684.1); *Pselaphinae sp.* 4 EF-2015 (KT780682.1); *Aleocharinae sp.* 6 EF-2015 (KT780687.1); *Aleocharinae sp.* 5 EF-2015 (KT780685.1); *Oxypoda acuminata* (NC_028606.1); *Rugilus geniculatus* (NC_028608.1); *Olophrum piceum* (NC_028605.1); *Myrmecocephalus concinnus* (NC_028604.1); *Liogluta microptera* (NC_028602.1); *Gabronthus thermarum* (NC_028601.1); *Euryusa optabilis* (NC_028600.1); *Dacrila fallax* (NC_028599.1); *Callicerus obscurus* (NC_028598.1); *Atrecus affinis* (NC_028597.1); *Thinonoma atra* (KT780699.1); *Necrophila americana* (NC_018352.1); *Euspilotus scissus* (NC_018353.1); *Margarinotus*

CONTACT Artem Nedoluzhko nedoluzhko@gmail.com; Genome Analysis Laboratory, National Research Centre "Kurchatov Institute", Moscow, Russia; Egor Prokhortchouk prokhortchouk@gmail.com Genome Analysis Laboratory, National Research Centre "Kurchatov Institute", Moscow, Russia

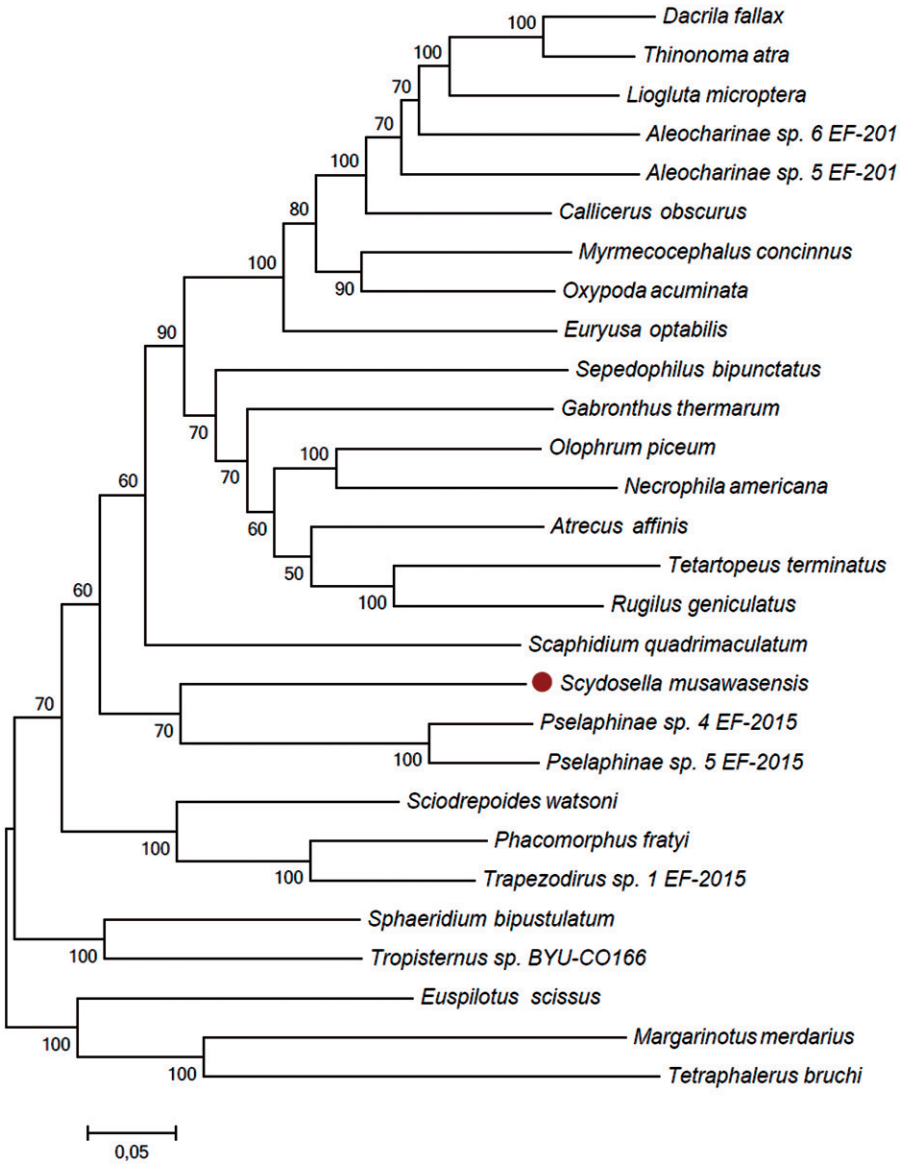

Figure. 1. Neighbor-Joining tree for *Scydosella musawasensis*, Staphylinoidea superfamily and other Coleoptera species and primitive beetle *Tetraphalerus bruchi* as outgroup based on sequence of 9 protein-coding genes (COX3, ATP6, COX2, COX1, NAD5, NAD4, NAD4L, NAD6, and COB) and 9 transfer RNAs.

merdarius (NC_028603.1); *Sphaeridium bipustulatum* (NC_028612.1); *Tropisternus sp.* BYU-CO166 (NC_018349.1) and *Tetraphalerus bruchi* (NC_011328.1) (Figure 1). For phylogenetic analysis, 9 protein-coding genes (*COX3*, *ATP6*, *COX2*, *COX1*, *NAD5*, *NAD4*, *NAD4L*, *NAD6*, *and COB*) and 9 transfer RNAs were used as marker genes. The phylogenetic tree was constructed by neighbor-Joining method, using the MEGA5.0 (Tamura et al. 2011).

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article.

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