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The mitochondrial genome of Iberobaenia (Coleoptera: Iberobaeniidae): first rearrangement of protein-coding genes in the beetles

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ABSTRACT
The complete mitochondrial genome of the recently discovered beetle family Iberobaeniidae is described and compared with known coleopteran mitogenomes. The mitochondrial sequence was obtained by shotgun metagenomic sequencing using the Illumina Miseq technology and resulted in an average coverage of 130 × and a minimum coverage of 35 ×. The mitochondrial genome of Iberobaeniidae includes 13 protein-coding genes, 2 rRNAs, 22 tRNAs genes, and 1 putative control region, and showed a unique rearrangement of protein-coding genes. This is the first rearrangement affecting the relative position of protein-coding and ribosomal genes reported for the order Coleoptera.

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16391 bp (Accession no. KT825140) including 13 protein-coding, 2 rRNAs, and 22 tRNAs genes. The overall base composition was 46.9% for A, 14.1% for C, 7.5% for G, and 31.5% for T. All protein-coding genes were encoded on the H-strand with exception of \textit{nad1}, \textit{nad4}, \textit{nad4l}, and \textit{nad5}. All tRNA genes were encoded on the H-strand with the exception of \textit{tRNA-Cys}, \textit{tRNA-Phe}, \textit{tRNA-His}, \textit{tRNA-Val}, \textit{tRNA-Gln}, \textit{tRNA-Pro}, and \textit{tRNA-Leu2}. Our predictive annotation resulted in the canonical ATN start codon (isoleucine) for all genes (ATA: \textit{nad2}, \textit{cox1}, \textit{cob}, \textit{atp6}, \textit{atp8}, and \textit{nad3}; ATG: \textit{cox2} and \textit{cox3}; ATT: \textit{nad5}, \textit{nad4}, and \textit{nad4l}; ATC: \textit{nad6}) but \textit{nad1}, where a TTG start codon was identified as previously reported in other Coleoptera (Sheffield et al. 2008). With regard to the 3' end, \textit{nad2} was predicted with an incomplete stop codon ''T'', three genes showed the stop codon TAG (\textit{nad5}, \textit{nad1}, and \textit{cob}) and all other genes were inferred with the stop codon TAA. The longest gene was \textit{nad5} (1647 bp) and the shortest gene was \textit{atp8} (150 bp). A maximum-likelihood phylogenetic tree was obtained in RaxML (Stamatakis 2006) including some of the closest relatives to Iberobaniidae according to Bocak et al. (2015) (Figure 1). The best tree was selected over 100 alternative runs and node support was calculated with 10 000 bootstrap replicates.

The structure of the mitogenome of \textit{Iberobaenia} showed a unique gene rearrangement with regard to the constant pattern found in all other mitochondrial genomes for the order Coleoptera (Timmermans & Vogler 2012). The rearrangement affected the protein-coding, ribosomal, and tRNAs genes. The gene order for the mitogenome of \textit{Iberobaenia} sp., including tRNAs, is I, M, \textit{nad2}, W,C, Y, \textit{cox1}, L1, \textit{cox2}, K, D, \textit{atp8}, \textit{atp6}, \textit{cox3}, \textit{nad3}, N, R, A, E, F, G, S, \textit{nad5}, H, \textit{nad4l}, \textit{nad1}, control region, Q, \textit{nad4}, T, P, \textit{nad6}, \textit{cob}, S2, L2, \textit{rml}V, \textit{rms}5. The high-sequencing read coverage (average: 130 \times; max: 213 \times; min: 35 \times) provides high reliability to the obtained sequence. This is the first mitochondrial gene rearrangement reported in the order Coleoptera excluding those affecting only to tRNAs (Timmermans & Vogler 2012). This finding adds to the unique features of the enigmatic beetle family Iberobaeniidae recently described from the Iberian Peninsula.

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Figure 1. Maximum-likelihood phylogenetic tree including some of the closest relatives to Iberobaniidae according to Bocak et al. (2015). Numbers on nodes represent bootstrap support. Right: schematic representation of \textit{Iberobaenia} sp. male specimen.


