The mitochondrial genome of a rare Chinese stag beetle \textit{Kirchnerius guangxii} (Coleoptera: Lucanidae)

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**ABSTRACT**

We sequenced the mitochondrial genome of a rare Chinese stag beetle \textit{Kirchnerius guangxii} using the next-generation sequencing. The mitochondrial genome is 14,562 bp in length, containing 13 protein-coding genes (PCGs), 2 ribosomal RNA genes (rRNAs) and 22 transfer RNA genes (tRNAs). The phylogenetic analyses showed that \textit{K. guangxii} was sister to the clade of \textit{Epidorcos gracilis} and \textit{Serrognathus platymelus}, and had a relatively low genomic affinity to \textit{Prosopocoilus}. Thus, \textit{K. guangxii} had a more close relationship with \textit{Epidorcos}, \textit{Serrognathus} and \textit{Dorcus} than \textit{Prosopocoilus}, which was different from previous morphological study. Our result can provide more available mitogenomic data for discussing the phylogeny of \textit{Kirchnerius} and facilitate the phylogenomic research of the family Lucanidae.

Stag beetles (The family Lucanidae Latreille) are one of the most popular insects due to their large size and decorative mandibles in males that resemble the antlers of stags, which has long received focus from taxonomists and collectors in terms of their fascinating appearance and interesting male–male fighting behavior (Tournant et al. 2012; Kim and Farrell 2015). So far, about 1800 species and subspecies within more than 100 genera are known worldwide (Krajcik 2001; Fujita 2010). The genus \textit{Kirchnerius} was originally described by Schenk (2009), inferring from the type species \textit{Kirchnerius guangxii} due to its unique mandible trait in large male. So far, this species is rarely noticed in the field distributed around the region of Mt. Damingshan in Guangxi. However, there were some different opinions about the systematic position of \textit{Kirchnerius} because the diagnosed characters of \textit{K. guangxii} at generic level partly overlapped with those in \textit{Prosopocoilus} (Huang and Chen 2011, 2013; Schenk 2012). The genetic data, as different datasets, could provide new point of view to deeply understand the systematics and future conservation of this stag beetle (Lin et al. 2017; Chen et al. 2018).

In this study, we sequenced a male specimen of \textit{K. guangxii} collected from Daming Mountain, Guangxi, China (108°2’E, 23°2’N), in July 2011. The sample was stored in 99% ethanol at ~20°C. Total genomic DNA was extracted using Blood and Tissue Kit (Qiagen, Germany) and then sequenced using Illumina HiSeq 2500 platform (GenBank accession number. MK134567). The voucher specimen (D10) was stored in the Museum of Anhui University, Hefei, Anhui, China. High-quality reads were de novo assembled using IDBA-UD (Peng et al. 2012). Preliminary annotations were done under MITOS Web Server (Bernt et al. 2013). The mitochondrial sequence of \textit{K. guangxii} is 14,562 bp in length, containing 13 protein-coding genes (PCGs), 2 ribosomal RNA genes (rRNAs), 22 transfer RNA genes (tRNAs), and partial control region. All 13 PCGs composition of the \textit{K. guangxii} is 38.28% T, 16.71% C, 31.45% A, and 13.56% G, with a strong bias toward A + T (69.73%). Similar situation occurs in the tRNAs and rRNAs, their A + T content were more than 70%. Among 13 PCGs, 12 used ATN (N represents A, C, G, T) as initiation codons, whereas the initiation codon of COX1 was AAC. Nine PCGs terminated with the stop codon TAA or TAG, whereas COX2, NAD5 and NAD4 ended with T; COX3 with TA.

Phylogenetic analysis was carried out using Bayesian inference (BI) method (Ronquist et al. 2012). The ingroup includes 16 lucanid species with the available mitogenomic data from the Genbank. Three scarab beetles (\textit{Cheirotorus jansoni}, \textit{Protaetia brevitarsis} and \textit{Rhopaea magnicornis}) were used as outgroups. The topology showed that \textit{K. guangxii} was a separated branch that was sister to the two species of \textit{Epidorcos gracilis} and \textit{Serrognathus platymelus}, and had a relatively low genomic affinity to those species of \textit{Prosopocoilus} (Figure 1). The phylogenetic analysis supported the original placement of \textit{Kirchnerius}, and determined the relationship with part of stag beetle species, which also suggested that mitogenomic data could provide useful signal for the phylogenetic study as they found in other beetle groups (Breeschoten et al. 2016; Timmermans et al. 2016; Nie et al. 2018, 2020). Furthermore, a large available mitogenomic data could be good molecular marker for resolving the phylogenetic
argument about the placements of other species in *Kirchnerius* and the phylogenetic framework of the family Lucanidae.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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