The mitochondrial genome of the multicolored Asian lady beetle Harmonia axyridis (Pallas) and a phylogenetic analysis of the Polyphaga (Insecta: Coleoptera)

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MITOGENOME ANNOUNCEMENT

The mitochondrial genome of the multicolored Asian lady beetle *Harmonia axyridis* (Pallas) and a phylogenetic analysis of the Polyphaga (Insecta: Coleoptera)

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Abstract

Here, we report the mitochondrial genome sequence of the multicolored Asian lady beetle *Harmonia axyridis* (Pallas, 1773) (Coleoptera: Coccinellidae) (GenBank accession No. KR108208). This is the first species with sequenced mitochondrial genome from the genus *Harmonia*. The current length with partitial A + T-rich region of this mitochondrial genome is 16,387 bp. All the typical genes were sequenced except the *trnI* and *trnQ*. As in most other sequenced mitochondrial genomes of Coleoptera, there is no re-arrangement in the sequenced region compared with the pupative ancestral arrangement of insects. All protein-coding genes start with ATN codons. Five, five and three protein-coding genes stop with termination codon TAA, TA and T, respectively. Phylogenetic analysis using Bayesian method based on the first and second codon positions of the protein-coding genes supported that the Scirtidae is a basal lineage of Polyphaga. The *Harmonia* and the *Coccinella* form a sister lineage. The monophyly of Staphyliniformia, Scarabaeiformia and Cucujiformia was supported. The Buprestidae was found to be a sister group to the Bostrichiformia.

Keywords

Coleoptera, *Harmonia axyridis*, ladybird, phylogeny

History

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The multicolored Asian lady beetle *Harmonia axyridis* (Pallas, 1773) (Coleoptera: Coccinellidae) has been extensively studied in biology, ecology and genetics as both a biological agent and an invasive pest (Koch, 2003; Lombaert et al., 2014; Wang et al., 2015), since its spreading from Asia to four additional continents in the last century (Brown et al., 2011). Here, we sequenced most part of the mitochondrial genome of the *H. axyridis* (GenBank accession No. KR108208), representing the first mitochondrial genome from the genus *Harmonia*. The source DNA sample was kept in the Laboratory of Integrated Pest Management at Beijing, Beijing Academy of Agriculture and Forestry Sciences. The sequenced length of this genome is 16,387 bp, containing 13 protein-coding, 2 rRNA and 20 tRNA genes and a partial A + T-rich region. Part of the A + T-rich region and two tRNA genes of *trnI* and *trnQ* in the upstream of *trnM* were failed to sequence. The predicted length of the A + T-rich region is about 2500 bp. There is no re-arrangement in the sequenced region compared with the pupative ancestral arrangement of insects (Clary & Wolstenholme, 1985). There are totally 67 bp intergenic nucleotides in 6 locations and the length of intergenic spacer is 1–34 bp. Eighteen pairs of genes overlaped each other with a length ranging from 1 to 7 bp. Twelve pairs of genes were directly adjacent.

All protein-coding genes start with ATN codons. Five, five and three protein-coding genes stop with termination codon TAA, TA and T, respectively. The lowest A + T content is 70.5% in the *cox1*, while the highest is 85.6% in *atp8* among all the protein-coding genes. The *rrnL* is 1305 bp long with an A + T content of 82.76%, while the *rrnS* is 779 bp long with an A + T content of 80.23%.

Phylogenetic relationships among the suborder polyphaga of Coleoptera was re-constructed (Figure 1). The phylogenetic tree was re-constructed using the Mrbayes v3.2.2 (Ronquist et al., 2012) based on the first and second codon positions of the protein-coding genes. The sequences were aligned using the MAFFT v7.205 (Katoh & Standley, 2013). The GTR + I + G model ($nst = 6$, rates = invgamma), selected by the PartitionFinder (Lanfear et al., 2012), was used for each partition. Four independent Markov chains were run for 200 million Metropolis-coupled generations, with tree sampling occurring every 20,000 generations and a burn-in of 25% trees. The result supported that *Cyphon* from the Scirtidae is a basal lineage of Polyphaga, as revealed in Kundrata et al. (2014). Within the Coccinellidae, the *Harmonia* and the *Coccinella* form a sister lineage and then sister to the remain *Henosepilachna*. The lineage of the Coccinellidae has a relatively long branch than others in the inferred tree. The monophyly of Staphyliniformia, Scarabaeiformia and Cucujiformia were supported. However, the Buprestidae, traditionally considered as a lineage of Elateriformia (Bocakova et al., 2007), was found to be a sister group to the Bostrichiformia.

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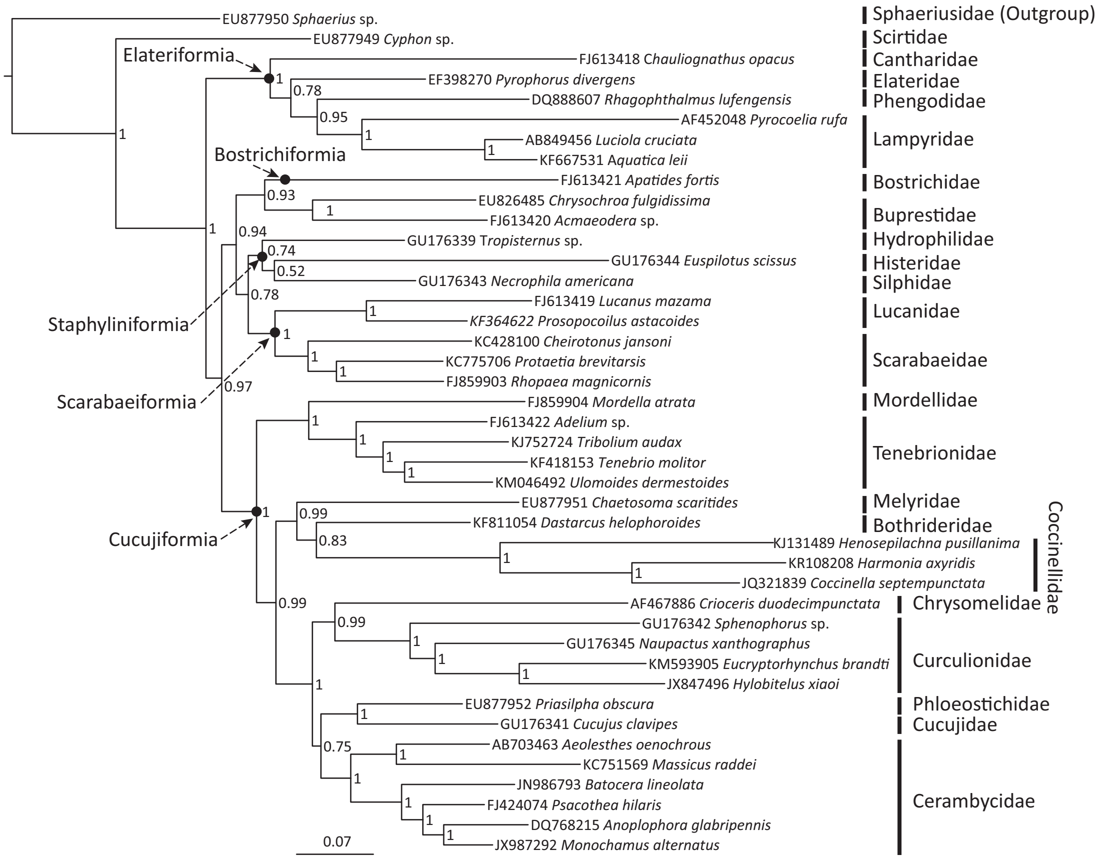

Figure 1. Bayesian phylogenetic tree of the Polyphaga of Coleoptera based on the mitochondrial genome sequences. The *Sphaerius* from the suborder Myxophaga was used as the outgroup (Sheffield et al., 2008). Totally 41 species from the Polyphaga were included in our analysis (Arnoldi et al., 2007; Bae et al., 2004; Behere et al., 2014; Cameron et al., 2009; Chiu et al., 2014; Hong et al., 2009; Kim et al., 2009, 2012, 2014, 2015; Li et al., 2007; Liu & Wang, 2014; Nan et al., 2014; Ou et al., 2014; Shao et al., 2014; Sheffield et al., 2008, 2009; Song et al., 2010; Stewart & Beckenbach, 2003; Wang et al., 2013, 2014a, b; Zhang et al., 2015). Posterior probabilities are indicated near each node.

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Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper. This study was funded by the National Basic Research Program of China (2013CB127600) and the National Science Foundation of China (No. 31472025).

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