MITOCOHNDRIAL DNA PART B
2019, VOL. 4, NO. 1, 614–615
https://doi.org/10.1080/23802359.2018.1561231

MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of Cryptopone sauteri Wheeler, W.M., 1906 (Hymenoptera: Formicidae)

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\textbf{ABSTRACT}

Cryptopone sauteri Wheeler, W.M., 1906, which is one of the common ant species in Ponerine, is found in forest floors of the Korean peninsula. We have determined the mitochondrial genome of \textit{C. sauteri}. The circular mitogenome of \textit{C. sauteri} is 15,367 bp including 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNAs, and a single large non-coding region of 448 bp. The base composition was AT-biased (82.0%). Gene order of \textit{C. sauteri} is almost same to that of Cardiocondyla obscurior even though the two species are in different subfamilies. Phylogenetic tree agrees with the current phylogenetic placement of Cryptopone outside of all other ant mitochondrial genomes and in its own Poneroid clade. \textit{C. sauteri} mitochondrial genome will be a useful resource for further analyses.

The Poneroid clade is a major ant taxon made up of 1,532 species belonging to six subfamilies (Bolton 2018). This clade has been studied with two major topics: i) the evolutionary history due to phylogenetic importance (Borowiec et al. 2017) and ii) evolution of social structures due to their primitive society (Schmidt and Shattuck 2014). Despite of these interesting research topics, genomic resources are not enough: there are two whole genome sequences (Bonasio et al. 2010; Patalano et al. 2015), while there is no mitochondrial genome in this clade.

\textit{Cryptopone sauteri} belonging to subfamily Ponerinae is commonly found in Korean peninsula. It has clear characteristics easily identified from other Korean Ponerine ants: its orange body color and setae on the outer surfaces of middle tibiae. \textit{Cryptopone sauteri} is a hypogenic hunter species of the forest floor feeding on small invertebrates such as beetle and fly larvae (Group and Imai 2003). Its nests and founder queens are mostly found in rotting wood and leaf litter.

As a first step to understand genomic characteristics of Ponerine ants, we completed mitochondrial genome of \textit{C. sauteri} isolated from Jeju Island, Republic of Korea. Genomic DNA was extracted from worker ants and sequenced by HiSeq4000 (Macrogen Inc, Seoul, Korea). Raw sequences were filtered by Trimmomatic 0.33 (Bolger et al. 2014) and \textit{de novo} assembled by Velvet 1.2.10 (Zerbino and Birney 2008). Gaps were filled by SOAPGapCloser 1.12 (Zhao et al. 2008) and confirmed with BWA 0.7.17 and SAMtools 1.9 (Li et al. 2009; Li 2013). Geneious R11 11.1.5 (Biomatters Ltd, Auckland, New Zealand) was used to annotate its genome based on that of \textit{Cardiocondyla obscurior} (KX951753). ARWEN (Laslett and Canb\textsuperscript{a} 2008) was used to annotate tRNAs. DNA sample of these ants was deposited in InfoBoss Cyber Herbarium (IN; Republic of Korea; J. Park, KFDS00047).

\textit{Cryptopone sauteri} mitochondrial genome length (Genbank accession is MK138572) is 15,367 bp. The nucleotide composition is AT-biased (82.0%). The mitogenome contains 13 protein-coding genes (PCGs), two rRNAs, and 22 tRNAs. The tRNAs size ranges from 56 to 78 bp, are similar to other ants (circa 54–90 bp). Gene order of \textit{C. sauteri} is almost identical to \textit{C. obscurior} except the position of tRNA-Val, even though both species are in different subfamilies. The control region presumably corresponds to the single largest non-coding AT-rich region (448 bp, A+T 86.4%).

We inferred the phylogenetic relationship of seven ants including \textit{C. sauteri} and one outgroup species using concatenated nucleotide sequences of all PCGs. Multiple sequence alignment was conducted by ClustalW (Thompson et al. 2003). Neighbour-joining tree was constructed using MEGA X with 10,000 bootstrap replicates (Kumar et al. 2018) presenting the phylogenetic position of \textit{C. sauteri} based on mitochondrial genomes (Figure 1). Results agree with current phylogenetic placement with Cryptopone placed sister to all Formicoid ants (Figure 1). As the first species of which mitochondrial genomes are available in the subfamily Ponerinae, \textit{C. sauteri} mitochondrial genome will be used for understanding molecular phylogenetic relationship of Poneroid clade together with already sequenced mitochondrial genomes of ants in Formicoid clade including Dolichoderus sibiricus (Park et al., doi:10.1080/23802359.2018.1551091).

\textbf{Disclosure statement}

No potential conflict of interest was reported by the authors.

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This study was supported by InfoBoss Research Grant [IBG-0017].

**Funding**

This study was supported by InfoBoss Research Grant [IBG-0017].

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**Figure 1.** Phylogenetic tree of Cryptopone sauteri (This study; MK138572), as well as representative species of all available ant subfamilies: Ooceraea biori (CM010870), Dolichoderus sibiricus (MH719017), Camponotus atrox (NC_029357), Formica fusca (NC_026132), Solenopsis invicta (NC_014672), Pristomyrmex punctatus (NC_015075), and a honey bee, Apis mellifera ligustica (NC_001566) as an outgroup. The numbers above branches indicate bootstrap support values.