The complete mitochondrial genome of a parthenogenetic ant \textit{Monomorium triviale} (Hymenoptera: Formicidae)

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\section*{ABSTRACT}
\textit{Monomorium} is one of the most species-rich yet taxonomically problematic ant genus. An East Asian species, \textit{M. triviale} Wheeler, W.M., 1906, is reproduced by obligate thelytokous parthenogenesis and performs strict reproductive division of labor. We sequenced the \textit{M. triviale} mitogenome using next-generation sequencing methods. The circular mitogenome of \textit{M. triviale} was 16,290 bp in length, consisting of 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNAs, and a single non-coding region of 568 bp. The base composition was AT-biased (82\%). Gene order rearrangements were detected and likely to be unique to the genus \textit{Monomorium}. We announce the \textit{M. triviale} mitogenome as additional genomic resources for elucidating phylogenetic and taxonomic problems of \textit{Monomorium} and comparative genomics of parthenogenetic ant species.
the two Monomorium species had two gene rearrangements: an inversion between trnPa and ND1 (Myrmicinae, ND6-CYTB-trnS; Monomorium, trnS-CYTB-ND6; underlines indicate inverted genes) and translocations between ND3 and trnF (Myrmicinae common, trnA-trnR-trnN-trnS-trnE; Monomorium, trnR-trnE-trnA-trnN-trnS). This feature was different from the common gene order of the subfamily Myrmicinae and likely unique to Monomorium ants (Babbucci et al. 2014; Park 2020). This may help identify the genus Monomorium sensu stricto, in addition to nucleotide substitutions.

We inferred the phylogenetic relationships of 25 ant species using the concatenated nucleotide sequences of all 13 PCGs, with the honeybee Apis mellifera as an outgroup. Sequence alignment was constructed using ClustalW (Thompson et al. 2003) implemented in MEGA-X (Kumar et al. 2018). The GTR + I + G model was determined as a best-fit model by ModelTest-NG v0.1.6 (Darriba et al. 2020). Both a maximum-likelihood tree made by RAxML-NG v1.0.0 (Kozlov et al. 2019) and Bayesian inference tree made by MrBayes v3.2.7 (Ronquist et al. 2012) consistently support the current phylogenetic placement of Monomorium in the subfamily Myrmicinae (Figure 1).

In conclusion, the newly sequenced complete mitochondrial genome of M. triviale provides additional resources for further phylogenetic characterization of the taxonomically problematic genus Monomorium and comparative genomics of parthenogenetic ant species.

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

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Data availability statement
The genome sequence data that support the findings of this study are openly available in DDBJ/GenBank at https://www.ddbj.nig.ac.jp under the accession no. LC605004. The associated BioProject, SRA, and BioSample numbers are PRJDB12079, DRX301164, and SAMD00394597, respectively.
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