


The complete mitochondrial genome of *Aphaenogaster famelica* (Smith, 1874) (Hymenoptera: Formicidae)

Jonghyun Park^{a,b}, Hong Xi^{a,b} and Jongsun Park^{a,b} 

^aInfoBoss Co., Ltd., Seoul, Republic of Korea; ^bInfoBoss Research Center, Seoul, Republic of Korea

ABSTRACT

Aphaenogaster famelica (Smith, 1874) is a slender ant found in Korea. We have completed the mitochondrial genome of *A. famelica* of which length is 19,464 bp, the third longest ant mitogenome so far. It was AT-biased (GC ratio is 18.0%) and includes 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNA genes, and a control region. The extra bases of *A. famelica* are placed in intergenic regions each between *trnV-trnM* and *trnI-trnQ*. Gene order of *A. famelica* is identical to other Myrmicinae ants. Phylogenetic trees show that tribe Stenammini and tribe Myrmicini are closely related.

ARTICLE HISTORY

Received 17 November 2019
Accepted 23 November 2019

KEYWORDS

Aphaenogaster famelica;
mitochondrial genome;
Myrmicinae;
Formicidae; Korea

Aphaenogaster Mayr, 1853 is a group of ants with slender body structures occurring in all bioregions except South America and sub-Saharan Africa (Radchenko and Perkovsky 2016). *Aphaenogaster famelica* (Smith, 1874) is a conspicuous species found in coastal forests of Korea. They hunt insects, sugar sources, and large seeds, contributing to the dispersal of seeds (Takahashi and Itino 2015). To compensate the small internal liquid storages, *A. famelica* and other *Aphaenogaster* species have developed a tool-using behavior of dropping surrounding materials on liquidous food and retrieving the soaked debris. This tactic allows the ants to carry up to 3.5 times of its body weights, giving the ants an upper hand over other ants (Lőrinczi 2014; Tanaka and Ono 1978). To secure their genomic resources, we determined the mitochondrial genome of *A. famelica* as the first mitogenome of both genus *Aphaenogaster* and tribe Stenammini.

Total DNA of *A. famelica* was extracted from a virgin female collected in Haeundae-gu, Busan, Republic of Korea (35°10'26.3"N, 129°08'09.1"E), using DNeasy Blood and Tissue Kit (QIAGEN, Hilden, Germany). Raw sequences obtained from HiSeqX at Macrogen Inc., Korea were filtered using Trimmomatic 0.33 (Bolger et al. 2014). *de novo* assembly and confirmation were conducted using Velvet 1.2.10 (Zerbino and Birney 2008), SOAPGapCloser 1.12 (Zhao et al. 2011), BWA 0.7.17 (Li et al. 2009), and SAMtools 1.9 (Li 2013). Geneious R11 11.1.5 (Biomatters Ltd, Auckland, New Zealand) and ARWEN (Laslett and Canbäck 2008) were used for anno-

tations relaying on mitogenomes of other ants. DNA sample and specimen (95% ethanol) were deposited in InfoBoss Cyber Herbarium (IN; J. Park, KFDS00166).

The mitochondrial genome of *A. famelica* (Genbank accession is MK801109) is 19,464 bp long consisting of 13 protein-coding genes (PCGs), two rRNAs, 22 tRNAs, and a control region. Its GC ratio is 18.0%. It is the third longest ant mitogenome, which is only shorter than two *Atta* species: *Atta sexdens*: 19,748 bp and *Atta texana*: 19,709 bp and longer than *Atta opaciceps*: 19,257 bp (Barbosa et al. 2019). While *Atta* mitogenomes are extended across intergenic regions (Barbosa et al. 2019), *A. famelica* mitogenome is elongated by the two long noncoding regions, each between *trnV-trnM* and *trnI-trnQ*, indicating independent events of mitogenome expansion. Gene order of *A. famelica* shares common feature of Myrmicinae ants where *trnV* is located after 12S rRNA (Babbucci et al. 2014).

Thirteen PCGs and two rRNA genes from 28 ants including all available Myrmimicine and an outgroup species were aligned using MAFFT 7.450 (Kato and Standley 2013) and concatenated. Bootstrapped maximum likelihood, neighbor joining, and Bayesian inference trees were constructed using MEGA X (Kumar et al. 2018) and Mr. Bayes 3.2.6 (Huelsenbeck and Ronquist 2001). Crematogastrini and Attini are polyphyletic in with low support values, which disagrees with the prior study (Figure 1; Ward et al. 2015). Stenammini and Myrmicini are grouped in three trees (Figure 1), which is also

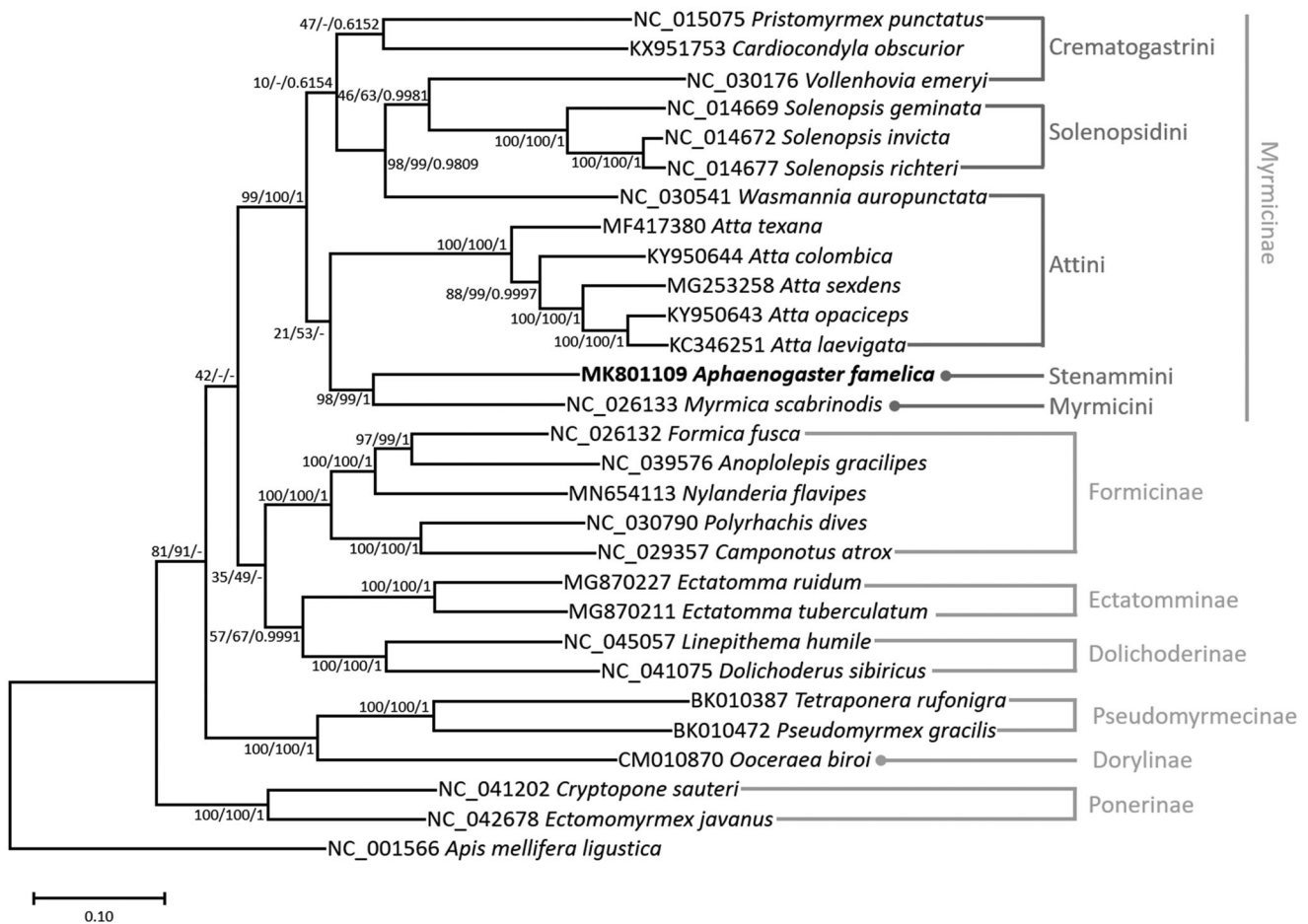


Figure 1. Maximum likelihood (bootstrap repeat is 1,000), neighbor joining (bootstrap repeat is 10,000), and Bayesian inference (1,000,000 generations) phylogenetic trees of all available Myrmicinae ant mitochondrial genomes: *Aphaenogaster famelica* (MK801109 in this study), *Myrmica scabrinodis* (NC_026133), *Pristomyrmex punctatus* (NC_015075), *Cardiocondyla obscurior* (KX951753), *Vollenhovia emeryi* (NC_030176), *Solenopsis geminata* (NC_014669), *Solenopsis invicta* (NC_014672), *Solenopsis richteri* (NC_014677), *Wasmannia auropunctata* (NC_030541), *Atta texana* (MF417380), *Atta colombica* (KY950644), *Atta sexdens* (MG253258), *Atta opaciceps* (KY950643), *Atta laevigata* (KC346251), as well as 14 ants from other subfamilies: *Formica fusca* (NC_026132), *Anoplolepis gracilipes* (NC_039576), *Nylanderia flavipes* (MN654113), *Polyrhachis dives* (NC_030790), *Camponotus atrox* (NC_029357), *Ectatomma ruidum* (MG870227), *Ectatomma tuberculatum* (MG870211), *Linepithema humile* (NC_045057), *Dolichoderus sibiricus* (NC_041075), *Tetraponera rufonigra* (BK010387), *Pseudomyrmex gracilis* (BK010472), *Ooceraea biroi* (CM010870), *Cryptopone sauteri* (NC_041202), *Ectomomyrmex javanus* (NC_042678), and a honey bee: *Apis mellifera ligustica* (NC_001566) as an outgroup. Phylogenetic tree was drawn based on maximum likelihood tree. The numbers above branches indicate bootstrap support values of maximum likelihood and neighbor joining trees and posterior probability of Bayesian inference tree, respectively.

incongruent with ant taxonomy and may be caused by high similarity between two mitogenomes in Stenammini and Myrmicini. *Aphaenogaster famelica* mitogenome will aid our understanding of mitochondrial evolutions of ants.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by both InfoBoss Research Grant [IBG-0017] and "Cooperative Research Program for Agriculture Science & Technology Development [Project No. PJ013389052019]" Rural Development Administration, Republic of Korea.

ORCID

Jongsun Park  <http://orcid.org/0000-0003-0786-4701>

References

- Babbucci M, Basso A, Scupola A, Patarnello T, Negrisola E. 2014. Is it an ant or a butterfly? Convergent evolution in the mitochondrial gene order of Hymenoptera and Lepidoptera. *Genome Biol Evol.* 6(12): 3326–3343.
- Barbosa JT, Barbosa MS, Morais S, Santana AE, Almeida C. 2019. [PROVISIONAL] Mitochondrial genomes of genus *Atta* (Formicidae: Myrmicinae) reveal high gene organization and giant intergenic spacers. *Genet Mol Biol.* 1415–4757.
- Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics.* 30(15):2114–2120.
- Huelsenbeck JP, Ronquist F. 2001. MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics.* 17(8):754–755.
- Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol. Biol. Evol.* 30(4):772–780.
- Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. *Mol Biol Evol.* 35(6):1547–1549.
- Laslett D, Canbäck B. 2008. ARWEN: a program to detect tRNA genes in metazoan mitochondrial nucleotide sequences. *Bioinformatics.* 24(2): 172–175.

- Li H, 1000 Genome Project Data Processing Subgroup, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R. 2009. The sequence alignment/map format and SAMtools. *Bioinformatics*. 25(16):2078–2079.
- Li H. 2013. Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. arXiv preprint arXiv:13033997.
- Lőrinczi G. 2014. Some notes on the tool-using behaviour of the ant, *Aphaenogaster subterranea* (Hymenoptera: Formicidae). *Tiscia* (Szeged). 40:17–24.
- Radchenko A, Perkovsky E. 2016. The ant *Aphaenogaster dluskyana* sp. nov. (Hymenoptera, Formicidae) from the Sakhalin amber—the earliest described species of an extant genus of Myrmicinae. *Paleontol J*. 50(9):936–946.
- Takahashi S, Itino T. 2015. Larger seeds are dispersed farther: the long-distance seed disperser ant *Aphaenogaster famelica* prefers larger seeds. *Sociobiology*. 59(4):1401–1411.
- Tanaka T, Ono Y. 1978. The tool use by foragers of *Aphaenogaster famelica*. *Jpn J Ecol*. 28(1):49–58.
- Ward PS, Brady SG, Fisher BL, Schultz TR. 2015. The evolution of myrmicine ants: phylogeny and biogeography of a hyperdiverse ant clade (Hymenoptera: Formicidae). *Syst Entomol*. 40(1):61–81.
- Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. *Genome Res*. 18(5):821–829.
- Zhao QY, Wang Y, Kong YM, Luo D, Li X, Hao P. 2011. Optimizing *de novo* transcriptome assembly from short-read RNA-Seq data: a comparative study. *BMC Bioinformatics*. 12(Suppl 14):S2.