


## The complete mitochondrial genome of *Nylanderia flavipes* (Smith, 1874) (Hymenoptera: Formicidae)

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### ABSTRACT

*Nylanderia flavipes* (Smith, 1874) is a Formicine ant found in East Asia. We have completed mitochondrial genome of *N. flavipes* of which length is 16,687 bp including 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNAs, and a control region. The base composition was AT-biased (GC ratio is 18.9%). Gene order of *N. flavipes* presents a unique inversion of *trnP* in comparison to *Camponotus* species. Our phylogenetic trees together with phylogenomic analysis suggest that the gene order rearrangements occurred independently in *Camponotus* and *N. flavipes*.

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The genus *Nylanderia* is an ecologically significant group of ants found all around the world, especially in warmer environments. They are mainly generalist foragers, highly efficient in locating resources, and recruiting nestmates, often resulting as the most abundant ants (LaPolla et al. 2011). *Nylanderia flavipes* is an Asian *Nylanderia* species, which was introduced to northern Europe and the United States, replacing some native species (Wetterer 2011). They are often the dominant species in their natural habitats of Korea where colonies are usually found queenless due to their unique polydomous colony structure (Ichinose 1986). They are also common in urban areas, sometimes even indoors utilizing their excellent foraging techniques for leftovers. We completed the mitogenome of *N. flavipes* as the first mitogenome of both the genus *Nylanderia* and tribe Lasiini.

Total DNA of *N. flavipes* was extracted from females collected in Namyangju-si, Gyeonggi-do, Republic of Korea (37°34'13.2''N, 127°18'08.8''E) using DNeasy Blood & Tissue Kit (QIAGEN, Hilden, Germany). Raw sequences obtained from HiSeqX at Macrogen Inc., Korea, were filtered by Trimmomatic 0.33 (Bolger et al. 2014). *De novo* assembly and confirmation were conducted by 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 annotation based on alignments with other ant mitogenomes. DNA sample and specimen (95% ethanol) were deposited in InfoBoss Cyber Herbarium (IN; Korea; J. Park, KFDS00153).

The mitochondrial genome of *N. flavipes* (Genbank accession is MN654113) is 16,687 bp long and its GC ratio is 18.9%. It contains 13 protein-coding genes (PCGs), 2 rRNAs, 22 tRNAs, and a control region. All PCGs start with either ATG or ATT and end with TAA except *ND2* containing TAG as a stop codon. Gene order (GO) of *N. flavipes* is identical to that of *Camponotus* (Kim et al. 2016), where GO of tRNA is rearranged from *trnM-trnI-trnQ* to *trnI-trnM-trnQ* compared to other Formicine ants (*Anoplolepis*, *Formica*, and *Polyrhachis*; Babbucci et al. 2014; Liu et al. 2017; Lee et al. 2018). *N. flavipes* also presents *trnP* gene with forward strand, which is unique among all ant mitogenomes. Additional mitogenomes are required to confirm whether this uniqueness is common in the genus or the tribe or not.

Thirteen PCGs and two rRNA genes from 23 ants including all available Formicine species and an outgroup species were aligned by MAFFT 7.450 (Kato and Standley 2013). 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). Our tree constructed based on mitogenome is congruent with that of the previous study from 959 ultra-conserved elements except for position of tribe Camponotini (Figure 1; Ward et al. 2016). Both trees suggest that the same GO of *Nylanderia* and *Camponotus* was formed by independent rearrangements events during evolution. *N. flavipes* mitogenome will contribute to understanding mitochondrial structures of ants with upcoming ant mitogenomes.

