

Complete mitochondrial genome of *Minla ignotincta* (Passeriformes: Timaliidae)

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ABSTRACT

We sequenced the complete mitochondrial genome from *Minla ignotincta*. The genome sequence was 17 868 bp in length, and the gene arrangement and contents were identical to those of previously reported Timaliidae mitochondrial genomes. The overall base composition of the mitogenome is biased toward A + T content at 54.04%. All protein-coding genes (PCGs) began with ATG. Nine of the 13 PCGs used complete (TAA) or incomplete (TA or T) stop codon, while *ND1* and *ND5* ended with AGA, *COI* ended with AGG and *ND6* with TAG. All the genes in *M. ignotincta* were distributed on the H-strand, except for the *ND6* subunit gene and eight tRNA genes which were encoded on the L-strand.

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The Timaliidae, generally known as the babblers, was a diverse family of oscine passerine birds that traditionally includes about 275 species in 50 genera (Dickinson & Christidis 2003). Most molecular phylogenetic work have focused on subsets

of the Timaliidae (Pasquet et al. 2006; Zhang et al. 2007; Yeung et al. 2011). Till now, there was little information about the complete mitochondrial genomes of *M. ignotincta* in GenBank. In our study, the complete mitogenome of

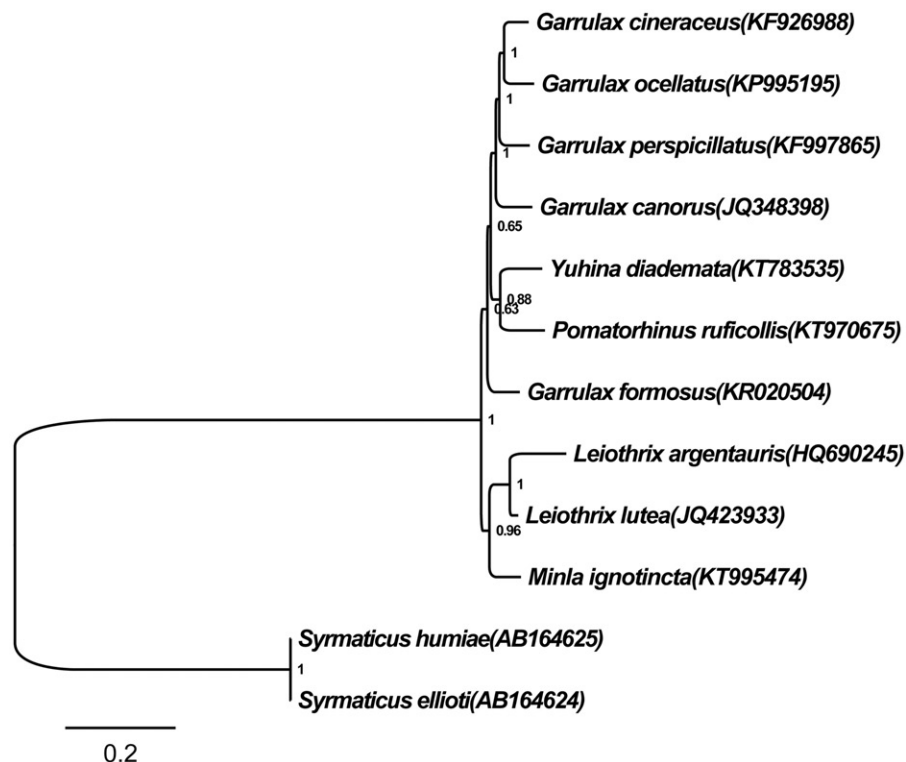


Figure 1. Bayesian tree based on combining 13 protein-coding gene sequences of ten Timaliidae and two *Syrmaticus* birds. The Bayesian tree was reconstructed with general-time-reversible (GTR) model, and the Markov chains for 1 000 000 generations. Numbers at node of the tree branches represent posterior probability. Two *Syrmaticus* birds were used as the outgroup.

M.ignotincta was determined, which might provide some molecular data for the research on the relationships of some babblers.

Minla ignotincta (specimen voucher B43) was obtained from Ya'an, Sichuan province of China (N29.98°, E103.01°) and identified by its morphological characteristics. The complete mitochondrial genome sequence of *M. ignotincta* was amplified and sequenced by 18 pairs of primers with normal LA-PCR and PCR methods. The mitogenome of *M. ignotincta* has been deposited in Genbank (accession no. KT995474). We constructed the phylogeny by Bayesian inference (BI) using Mrbayes 3.1.1 (Huelsenbeck & Ronquist 2001).

Similar to other Timaliidae mitogenomes, the complete mtDNA sequence of *M. ignotincta* (17868 bp in length) had 13 typical protein-coding genes (PCGs), 22 tRNA genes, two rRNA genes (12S rRNA and 16SrRNA) and two control region (*D-loop1* and *D-loop2*) (Zhang et al. 2014; Zhou et al. 2015). The base composition of mtDNA is 30.05% A, 23.99% T, 31.76% C and 14.20% G, so the percentage of A + T (54.04%) was slightly higher than G + C. In 13 PCGs, the shortest one was *ATP8* gene (168 bp) and the longest one was the *ND5* gene (1818 bp). All PCGs began with ATG. Of the 13 PCGs, nine of PCGs used complete (TAA) or incomplete (TA or T) stop codon, while *ND1* and *ND5* ended with AGA, *COI* ended with AGG and *ND6* with TAG. The *12S rRNA* (982 bp) and *16S rRNA* (1600 bp) genes were located between the *tRNA^{phe}* and *tRNA^{Leu(UUR)}* genes, which was separated by the *tRNA^{Val}* gene. The inferred secondary structures of 21 tRNAs (excluding *tRNA^{Ser(AGY)}*) of *M. ignotincta* were all conformed to the common structural features of mitochondrial tRNAs. *D-loop1* and *D-loop2* were located in two different locations of mitogenome. There was eight tRNA genes (*tRNA^{Gln}*, *tRNA^{Ala}*, *tRNA^{Asn}*, *tRNA^{Cys}*, *tRNA^{Tyr}*, *tRNA^{Ser(UCN)}*, *tRNA^{Pro}* and *tRNA^{Glu}*) and one PCG (*ND6*) encoded on the L-strand, other PCGs encoded on the H-strand.

As shown in Figure 1, 10 Timaliidae species clustered into two groups. A separate *M. ignotincta* was the sister lineage to the clade formed by the species of genus *Leiothrix* with more

than 96% of posterior probability, which was consistent with BI analysis results of Gelang et al. (2009) and Moyle et al. (2012). Therefore, we hold that the genomic data of *M. ignotincta* was trustworthy.

Disclosure statement

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