

Complete mitochondrial genome of *Urocissa erythroryncha* (Passeriformes: Corvidae)

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ABSTRACT

The complete mitochondrial genome of *Urocissa erythroryncha* is 16930 bp in length. It was predicted to contain 13 PCGs, 22 *tRNA* genes, and 2 *rRNA* genes, and a putative control region. All of the PCGs initiated with ATG, except for *MT-COX1* which began with GTG and *MT-ND3* began with ATA, while stopped by three types of stop codons. Phylogenetic analysis showed that *Urocissa erythroryncha* and the other species of Corvidae were monophyletic group in this study. And the monophyly of the genus *Pyrrhocorax* was strongly supported. Moreover, our results also support a sister-group relationship between Corvidae and Muscicapidae.

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Passeriformes is the largest order of Aves (Clements et al. 2016). The birds generally known as corvids is a widespread family named Corvidae (Aves: Passeriformes) (Gill and Donsker 2018). In our study, an adult *Urocissa erythroryncha* specimen was caught from Wuhu (geographic coordinate: 31.33°N, 118.38°E), Anhui Province, southeastern of China. The specimen was preserved in ethanol and stored to Anhui Normal University, under the voucher number Kan-K0024. Through the standard phenol/chloroform methods, the total genomic DNA of the *Urocissa erythroryncha* (code Kan-K0024) was extracted from the muscle tissue. The fourteen PCR and sequencing primers specific to *U. erythroryncha* mitochondrial genome were designed, and two long overlapping fragments were amplified to avoid the possibility of nuclear copies of mitochondrial genes (Kan et al. 2010; Zhang L et al. 2012; Zhang Q et al. 2017).

We obtained the complete mitochondrial genome of *U. erythroryncha* (GenBank Accession NC_020426) in this study. We described 16930 bp of *U. erythroryncha* mitochondrial genome DNA, including 13 protein-coding genes (PCGs), 22 transfer RNA (*tRNA*) genes, 2 ribosomal RNA (*rRNA*) genes, and 1 putative control region. All *tRNA* genes can fold into a typical cloverleaf second structure. All of the PCGs initiated with ATG, except for *MT-COX1* which began with GTG. And meanwhile three types of termination codons were identified. AGG for *MT-COX1*; TAA for *MT-ND2*, *MT-COX2*, *MT-ATP6*, *MT-ATP8*, *MT-ND3*, *MT-ND4L*, *MT-ND6*, and *MT-CYTB*; AGA for *MT-ND1* and *MT-ND5*; and incomplete stop codon T- for *MT-ND2*, *MT-COX3*, and *MT-ND4*. We can detect one single control region (D-loop) between *tRNA^{Glu}* and *tRNA^{Phe}*. The D-loop region is 1346 bp in length.

The overall base composition of the mitochondrial genome is as follows: A (30.92%), T (24.66%), G (14.32%), C (30.10%), with the A + T content of 55.58%. Nucleotide composition was calculated by MEGA v6.06 (Tamura et al. 2013). AT and GC skews were calculated by using the formulas $(A - T)/(A + T)$ and $(G - C)/(G + C)$ (Perna and Kocher 1995; Kan et al. 2016), respectively. The *MT-ND6* gene of *U. erythroryncha* mitogenome has strong skews of T versus A (−0.41), and a strong skew of C versus G (0.52). The other 12 protein-coding genes of the *U. erythroryncha* mitochondrial genome have a slight skew of A vs T (0 to 0.20), and a strong skew of C versus G (GC skew = −0.75 to −0.30).

The phylogenetic position of *U. erythroryncha* was estimated from a concatenated dataset based on 13 PCGs. Maximum likelihood (ML) analyses were performed with Raxml GUI v 1.3.1 (Silvestro and Michalak 2012; Zhang et al. 2012; Jiang et al. 2015). The complete mitochondrial DNA sequences have been used successfully to estimate phylogenetic relationships among Passeriformes. The results showed that *U. erythroryncha* and the other species of Corvidae were monophyletic group in this study. Furthermore, other genera of Corvidae (*Garrulus*, *Corvus*, *Pyrrhocorax*, *Nucifraga*, *Podoces*, *Pica*, *Cyanopica*) were basal to the balance of the Corvidae. Moreover, our results also support a sister-group relationship between Corvidae and Muscicapidae. They all appear 100% bootstrap value in ML analyses which is strongly supported. We speculate that there is still a complex phylogenetic relationship between finch and other families that is not known to us. This study will contribute to the phylogenetic analyses in Passeriformes.

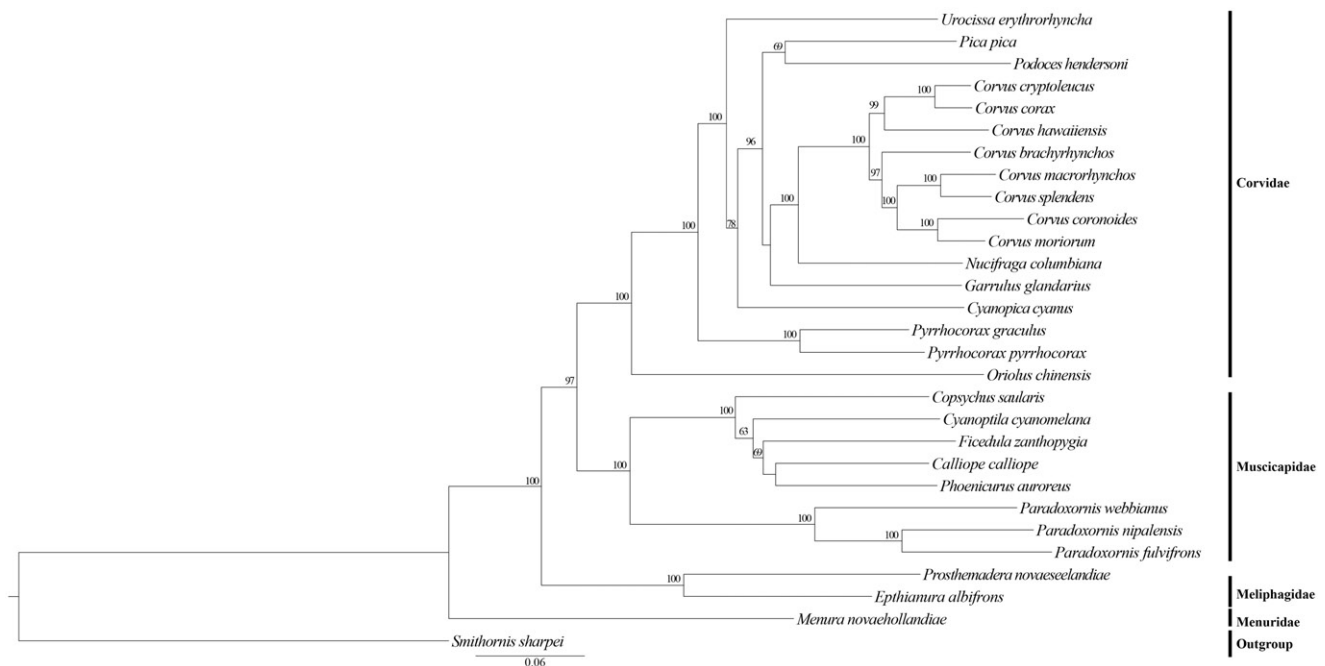


Figure 1. Phylogenetic tree of the relationships among Passeriformes based on the nucleotide dataset of the 13 PCGs. *Smithornis sharpei* was chosen as outgroup. ML analyses were implemented in ML + rapid bootstrap for 1000 replicates under GTRGAMMA, Branch lengths and topologies came from the ML analysis. All 29 species' accession numbers are listed as below: *Corvus brachyrhynchos* NC_026461, *C. corax* NC_034838, *C. cryptoleucus* NC_034839, *C. coronoides* NC_035877, *C. hawaiiensis* NC_026783, *C. macrorhynchos* NC_027173, *C. moriorum* NC_031518, *C. splendens* NC_024607, *Cyanopica cyanus* NC_015824, *Garrulus glandarius* NC_015810, *Nucifraga columbiana* NC_022839, *Oriolus chinensis* NC_020424, *Pica pica* NC_015200, *Podoces hendersoni* NC_014879, *Pyrrhocorax graculus* NC_025927, *P. pyrrhocorax* NC_025926, *Urocissa erythrorhyncha* NC_020426, *Epthianura albifrons* NC_019664, *Prosthemadera novaeseelandiae* NC_029144, *Menura novaehollandiae* NC_007883, *Calliope calliope* NC_015074, *Copsychus saularis* NC_030603, *C. cyanomelana* NC_015232, *Ficedula zanthopygia* NC_015802, *Paradoxornis nipalensis* NC_028437, *P. webbianus* NC_024539, *Phoenicurus aureus* NC_026066, *Smithornis sharpei* NC_000879.

Disclosure statement

No potential conflict of interest was reported by the authors.

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