



Complete mitochondrial genome of the Chinese Hwamei *Garrulax canorus* (Aves: Passeriformes): the first representative of the Leiothrichidae family with a duplicated control region

D.S. Chen^{1*}, C.J. Qian^{1*}, Q.Q. Ren^{1,2}, P. Wang¹, J. Yuan¹, L. Jiang¹, D. Bi¹, Q. Zhang¹, Y. Wang¹ and X.Z. Kan^{1,2}

¹Provincial Key Laboratory of the Conservation and Exploitation Research of Biological Resources in Anhui, College of Life Sciences, Anhui Normal University, Wuhu, China

²The Institute of Bioinformatics, College of Life Sciences, Anhui Normal University, Wuhu, China

*These authors contributed equally to this study.

Corresponding author: X.Z. Kan

E-mail: xianzhao@ahnu.edu.cn

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ABSTRACT. The Chinese Hwamei *Garrulax canorus*, a member of the family Leiothrichidae, is commonly found in central and southern China, northern Indochina, and on Hainan Island. In this study, we sequenced the complete mitochondrial genome of *G. canorus*. The circular mitochondrial genome is 17,785 bp in length and includes 13 protein-coding genes, 22 transfer RNA (tRNA) genes, and two ribosomal RNA genes. In addition, two copies of highly

similar putative control regions were observed in the mitochondrial genome. As found in other vertebrates, most of the genes are coded on the H-strand, except for one protein-coding gene (*nad6*; NADH dehydrogenase subunit 6) and eight tRNA genes (*tRNA^{Gln}*, *tRNA^{Ala}*, *tRNA^{Asn}*, *tRNA^{Cys}*, *tRNA^{Tyr}*, *tRNA^{Ser(UCN)}*, *tRNA^{Pro}*, and *tRNA^{Glu}*). All the protein-coding genes start with ATG, with the exception of *cox1* (cytochrome oxidase subunit 1), which starts with GTG. All tRNA genes have the potential to fold into the typical clover-leaf structure. Conserved sequences in three domains were observed in the two putative control regions. These results provide basic information for future phylogenetic analyses among species of the order Passeriformes.

Key words: Chinese Hwamei; *Garrulax canorus*; Passeriformes; Mitochondrial genome; Leiothrichidae