

## Complete mitochondrial genome sequence of *Jianmen-guan phasianus colchicus* (Aves, Galliformes, phasianidae) and its phylogenetic analysis

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### ABSTRACT

*Jianmen-guan phasianus colchicus* are one of the most important and be cherished uncultivated animals, although, origins of the most *J. phasianus colchicus* remain unknown. Therefore, the complete mitochondrial genome of the *J. phasianus colchicus* (also named seven-colours *J. phasianus colchicus*, one of the oldest wild birds in China known for their preciousness) was obtained for the first time, the mitogenome is 166,786 bp in length, and it harbours 2rRNA genes, 13 protein-coding genes, 22tRNA genes, and a D-loop region. According to the phylogenetic tree, we can assume that *Jianmen-guan* and *Xianju* are within the same lineage, and *J. phasianus colchicus* is a different group with Red Jungle.

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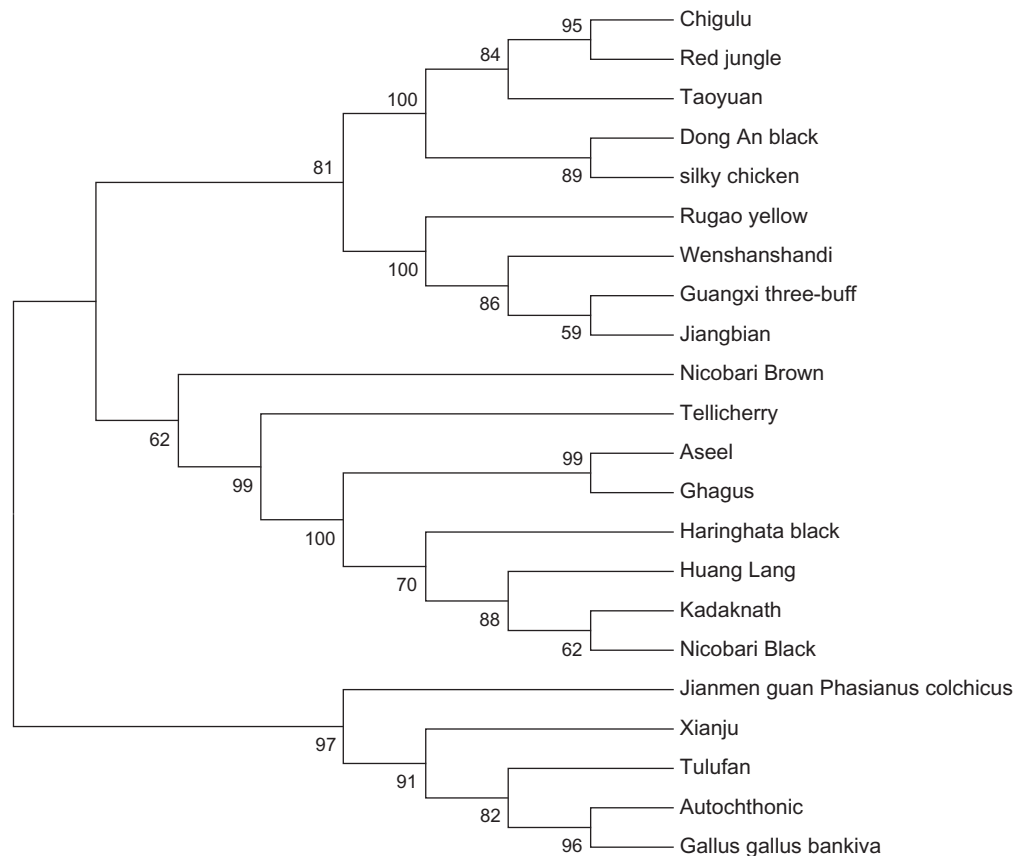
China has the maximum genetic resources of *Jianmen-guan phasianus colchicus*, a phasianidae bird, in the world (Bao et al. 2008). The *J. phasianus colchicus* is mainly spread through southwest China, which named seven-colours *J. phasianus colchicus*. *Jianmen-guan phasianus colchicus* is among the most popular and widely cherished wild animal species, although it was reported that the rare birds originates from nine mtDNA lineages (A-I), and very little information is known about the origins of majority indigenous *J. phasianus colchicus* breeds (Liu et al. 2006). In order to enrich the mtDNA data of *J. phasianus colchicus* family and discuss the phylogenetic relationship of this species, we sequenced the mitogenome of *J. phasianus colchicus*.

In this study, the *J. phasianus colchicus* was obtained from Guangyuan County, Sichuan Province, China. Samples of *J. phasianus colchicus* were recorded by the Ministry of Agriculture of the People's Republic of China (announcement No. 2437). We reported the complete mitogenome sequence of *J. phasianus colchicus* (GenBank NO. KX512321). We use common phenol/chloroform methods to extract the total genomic DNA from its blood, and amplified by 16 pairs of primers. We then downloaded 19 other Gallus domesticus and pheasants mitochondrial DNA sequences from the GenBank (Figure 1). A neighbour-joining phylogenetic tree

was structured based on 13 protein-coding genes using the MEGA 5.0.

In our study, the assembled mtDNA sequence was up to 16,785 bp in length, similar to other 19 *J. phasianus colchicus* and local rare birds downloaded from GenBank. This includes 2rRNA, 13 PCGs, 22tRNAs, and a D-loop region. The nucleotide composition of the mtDNA of *J. phasianus colchicus* is A = 30.26%, T = 23.70%, G = 13.51%, C = 32.52%. Most PCGs started with the ATG codon, except *ND6* started with TTA, and *COX1* initiated with GTG. However, they are terminated with six types of stop codons, incorporating TAA (*ND1*, *COX2*, *ATP8*, *ATP6*, *ND3*, *NADH*, *ND5*, *Cytb*), AGG (*COX1*), CTT (*COX3*), TAT (*ND4*), CAT (*ND6*). The mitochondrial genome contains 22 tRNA genes, which range in size from 64 to 77 nucleotides (Lowe & Eddy 1997). The 12s rRNA is 975 bp in length and the 16s rRNA is 1622 bp in length, respectively.

As shown in Figure 1, the *J. phasianus colchicus* and the *Xianju* form the monophyletic clade, with *J. phasianus colchicus* having the fastest distance with *Nicobari Brown*; and *J. phasianus colchicus* is different group with *Red Jungle*; the *J. phasianus colchicus*, *Xianju* and *Nicobari Brown* belong to the *black-bone rare bird* group. This result was consistent with a research which genetic diversity of Chinese *black-bone rare bird* is not rich and the special chickens may overwhelmingly originate from three subspecies of *Red Jungle* fowl (Zhu et al. 2014).



**Figure 1.** Phylogenetic analysis of the *Jianmen-guan phasianus colchicus*. The complete mitogenome is downloaded from GenBank and the phylogenetic tree is constructed by a maximum-likelihood method with 500 bootstrap replicates by MEGA 5.1. The gene's accession number for tree construction is listed as follows: *Aseel* (NC\_KP211418.1), *Autochthonic* (NC\_GU261687.1), *Bankiva* (NC\_AP003323.1), *Chigulu* (NC\_GU261684.1), *Dong An blank* (NC\_KM886936.1), *Ghagus* (NC\_KP211419.1), *Guangxi three-buff* (NC\_KP681581.1), *Haringhata black* (NC\_KP211420.1), *Huang Lang* (NC\_KF954727.1), *Jiangbian* (NC\_GU261714.1), *Kadaknath* (NC\_KP211425.1), *Nicobari Black* (NC\_KP211421.1), *Red jungle* (NC\_GU261695.1), *Rugao yellow* (NC\_KP742951.1), *Silky chicken* (NC\_AB086102.1), *Taoyuan* (NC\_KF981434.1), *Tellicherry* (NC\_KP211424.1), *Tulufan* (NC\_GU261683.1), *Wenshanshandi* (NC\_GU261699.1), *Xianju* (NC\_GU261677.1).

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## Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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