The complete mitochondrial genome of the Ferruginous Duck (Aythya nyroca) from Ningxia, China

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ABSTRACT
The Ferruginous Duck (Aythya nyroca) is a diving duck that is widely distributed in Asia, Africa, and Europe. We determined the complete mitogenome of the Ferruginous Duck gathered at Ningxia, China. The total length of the complete mitogenome is 16,623 bp and it consists of 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and 1 control region (CR). Only one overlap among the 13 protein-coding genes was found: ND4L/ND4. The CR is 1068 bp in length. The nucleotide composition is 29.66% A, 22.28% T, 15.35% G, and 32.71% C. The result of phylogenetic analysis showed that there is close genetic relationship among Aythya nyroca and three ducks in the Genus Aythya.

The Ferruginous Duck (Aythya nyroca), also named white-eyed pochard, is a partial migrant, medium-sized diving bird with a range spanning Europe, Asia, and Africa (Robinson and Hughes 2006). The Duck prefers shallow fresh waterbodies with rich submerged and floating vegetation with dense stands of emergent vegetation on the margins (Snow and Perrins 1998). According to the Red List of Threatened Species, this species is listed as Near Threatened, and destruction of the duck’s favored habitats across its range is thought to be the primary cause for its disjunct distribution and declining numbers (BirdLife International 2019). Also, the introduction of non-native species and climate change may pose a threat to the duck.

The complete mitochondrial genome of the Ferruginous Duck was sequenced using muscle tissue collected from Ningxia, China (105°57'E, 37°44'N), and the specimen was deposited in College of Wildlife and Protected Area, Northeast Forestry University (No.BYQY201004). DNA library was constructed using MGIEasy DNA Library Prep Kit (MGI, China) and sequenced by MGI MGISEQ-2000 with 150 paired-ends. The annotation and phylogenetic tree of the mitogenome sequence were conducted by MITOS (Bernt et al. 2013) and MEGA7 (Kumar et al. 2016). The bootstrap consensus tree inferred from 1000 replicates is taken to represent the evolutionary history of the taxa analyzed (Felsenstein 1985) (Figure 1). The phylogenetic tree indicated that the phylogenetic relationship of Ferruginous Duck is very close to the three species in the Genus Aythya: Aythya ferina, Aythya americana and Aythya fuligula.
Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/) under the accession no. MW287344. The associated SRA number is PRJNA685540.

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