

The complete mitochondrial genome of *Anas penelope* (Anatidae: Anas)

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ABSTRACT

The complete mitochondrial DNA genome of the Eurasian Wigeon, *Anas penelope*, was mapped by the next-generation sequencing and Mega 7.0. The circular mitogenome (16,596 bp in length) contains 13 protein-coding genes, 2 rRNA genes (12S ribosomal RNA and 16S ribosomal RNA), 22 tRNA genes and a control region. The content of four base pairs of the complete mitochondrial DNA is 28.9% of A, 22.3% of T, 32.7% of C and 16.1% of G. To validate the phylogenetic relationship, 25 published complete mitochondrial genomes of Anseriformes along with the genome of Terek sandpiper were used to construct the phylogenetic tree.

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The Eurasian Wigeon (*Anas penelope*) is a widespread duck-species estimated to number 2,800,000–3,300,000 individuals (IUCN 2016). The overall population trend of *A. penelope* is decreasing due to recreational impacts, dams, water management, and prion-induced diseases (Lei et al. 2008). Except for some behavioral and habitat research, *A. penelope* is less well studied in literature (Guillemain et al. 2002; Mayhew and Houston 2008). Mitochondrial DNA (mtDNA) is regarded as a useful tool in population conservation, phylogeographic, and phylogenetic studies. The mitochondrial DNA control region of *A. penelope* was examined to assess the genetic differentiation (Kulikova & Zhuravlev 2010). Hence, it is necessary to obtain the complete mitochondrial DNA by the next-generation sequencing. The muscle specimen of *A. penelope* was collected from the coast of Rudong Country, Jiangsu Province, China (32°32'43.42" N, 121°06'09.02" E). A voucher specimen was stored in Nanjing Normal University (NJNU: ANPE20191005), Nanjing, China. The complete genome sequence was aligned by Mega 7.0 and deposited in GenBank (Accession Number: MT304825).

The complete mitochondrial genome of *A. penelope* is circular molecular and 16,596 bp in length. The genome contains 37 genes, including 13 protein-coding genes, 2 ribosomal RNAs, 22 tRNA genes, and a control region (D-loop). Most of the genes were encoded on the H-strand, while ND6 and 8tRNA were encoded on the L-strand. For the 13 PCGs, the most common start codon is ATG, followed

by GTG. The termination codon (TAA) is most common and two protein-coding genes (COIII and ND4) use single T as their stop codons, which were presumably completed as TAA by post transcriptional polyadenylation. The base composition of mtDNA is A(28.9%), G(16.1%), C(32.7%) and T(22.3%), and thus the percentage of G and C (48.8%) was slightly lower than A and T (51.2%).

To confirm the phylogenetic position of *A. penelope* among Anseriformes species, a Bayesian analysis was conducted on the complete mitogenome. It is shown that the phylogenetic relationship of *A. penelope* is very close to the *A. falcata* in the family Anatidae (Figure 1). We hope this study will provide more information for the phylogenetic analyses of Anseriformes in future research.

Disclosure statement

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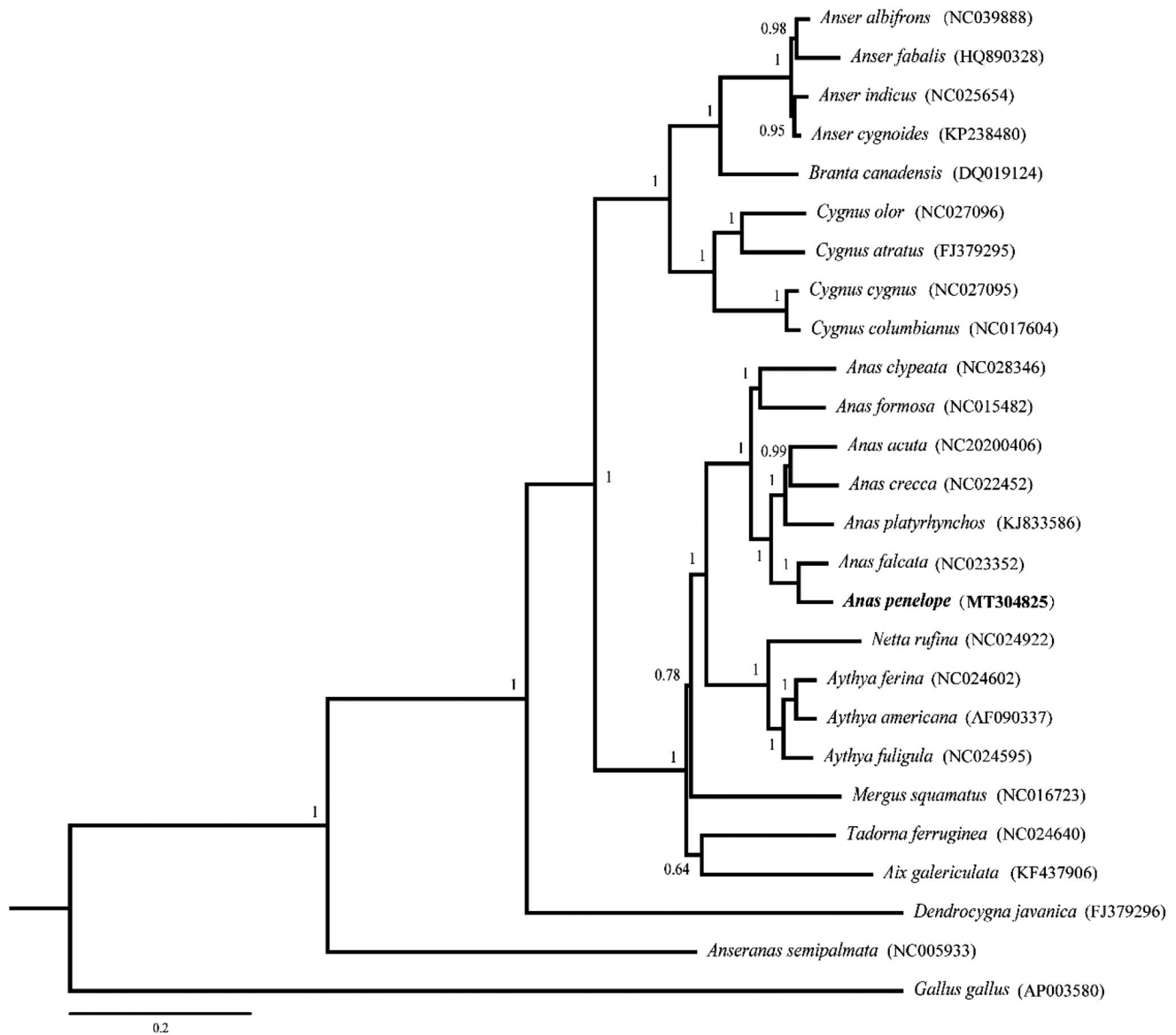


Figure 1. Phylogenetic relationship of *Anas peneope* and the other 25 species based on the Bayesian method. The bootstrap values are shown at the nodes.

Data availability statement

The data that support the findings of this study are openly available in NCBI at www.ncbi.nlm.nih.gov, reference number (MT304825).

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