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The complete mitochondrial genome of *Tringa ochropus* (Charadriiformes, Scolopacidae)

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ABSTRACT

The green sandpiper *Tringa ochropus* (Charadriiformes, Scolopacidae) is completely migratory with an extremely large distribution range. However, its habitat ecology, and disease spreading are relatively understudied, and the molecular genetics is relatively unclear. In this study, we report the complete mitochondrial genome of *T. ochropus*, which is a circular molecule of 16,906 bp in length and the A + T content of overall base of the composition of H-strand is 54.88% (A: 31.62%, T: 25.53%, C: 29.47%, G: 13.38%). This study strongly supports the monophyly of Charadriiformes, and division of the order into three major clades, including Lari, Scolopaci, and Charadrii.

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The green sandpiper *Tringa ochropus* (Charadriiformes, Scolopacidae) is completely migratory with an extremely large distribution range, which have brown wings with little light dots and a delicate but contrasting neck and chest pattern. Recent studies of *T. ochropus* have paid more attention on habitat ecology, environmental disruption, and disease spreading (Gresíková et al. 1975; Smith et al. 1992; Malekian & Hosseinpour-Mohamadabadi 2015). However, the basic genetics data of *T. ochropus* are relatively unclear. In this study, we sequenced the complete mitogenome of *T. ochropus* to better understand the mitogenomic characteristics and its phylogenetic relationships within Charadriiformes.

The muscle specimen of *T. ochropus* was collected from the Lukou Country, Nanjing, International Airport, Jiangsu Province, China (31°43'47" N, 118°52'26" E). The voucher specimen was preserved in absolute ethanol at Nanjing Normal University (NJNU: Toc-2015017), Nanjing, China. Total DNA was extracted with standard phenol–chloroform methods according to Sambrook and Russell (1989). The complete mitochondrial genome was amplified and sequenced by 13 pairs of primers. Annotations were confirmed by comparing other Charadriiformes species with MITOS-generated annotations (Bernt et al. 2013).

The circular mitogenome of *T. ochropus* is 16,906 bp in length with 13 protein-coding genes, 2 ribosomal RNAs (12S rRNA and 16S rRNA), 22 transfer RNA genes, and a non-coding region. The mitogenome size is well within the range found in Charadriiformes, from 16,357 (*Sternula albifrons*, GenBank No. KT350612) to 17,135 bp (*Vanellus cinereus*, KM873665). The overall nucleotide composition was A: 31.62%, T: 25.53%, C: 29.47%, G: 13.38%. The annotated mitogenome of *T. ochropus* is available online in NCBI (KX668223).

We performed a phylogenetic analysis based on 13 protein-coding genes (PCGs) of the available mitogenome sequences of 19 Charadriiformes and two other species, using maximum Bayesian (BI), likelihood (ML) and neighbour-joining (NJ) methods. These sequences were aligned with Clustal X 1.81 (Thompson et al. 1997) with default parameters. Total of 14,120 bp were used for phylogenetic analyses. There were 8447 (59.82%) conserved sites, 4294 (30.41%) parsim-info sites, and 1379 (9.77%) singleton sites. Models of molecular evolution were assessed using MrModeltest 2.3 (Nylander 2004), and $GTR + I + G$ model was selected. BI were performed using MrBayes 3.1.2 (Ronquist et al. 2012). Four Markov Chains Monte Carlo (MCMC) chains were run for 1.0×10^6 generations. Two independent runs were performed to allow additional confirmation of the convergence of MCMC runs. ML and NJ phylogenetic analyses were performed using PAUP v4.0b10 (Swofford 2002), and the relative support of internal nodes was assessed by bootstrap analyses with 1000 replications.

The phylogenetic analysis (Figure 1) resolved a well-supported clade of Charadriiformes, in which *Tringa* appears to be sister group of *Scolopax*. This result indicates that there is great mitochondrial divergence within the Charadriiformes. Relationships of the order Charadriiformes strongly support the monophyly of Charadriiformes, and division of the order into three major clades including Lari (Laridae, Stercorariidae and Alcidae) and its sister Scolopaci (Scolopacidae and Jacanidae), which is in turn sister to the suborder Charadrii (Charadriidae, Haematopodidae, and Recurvirostridae).

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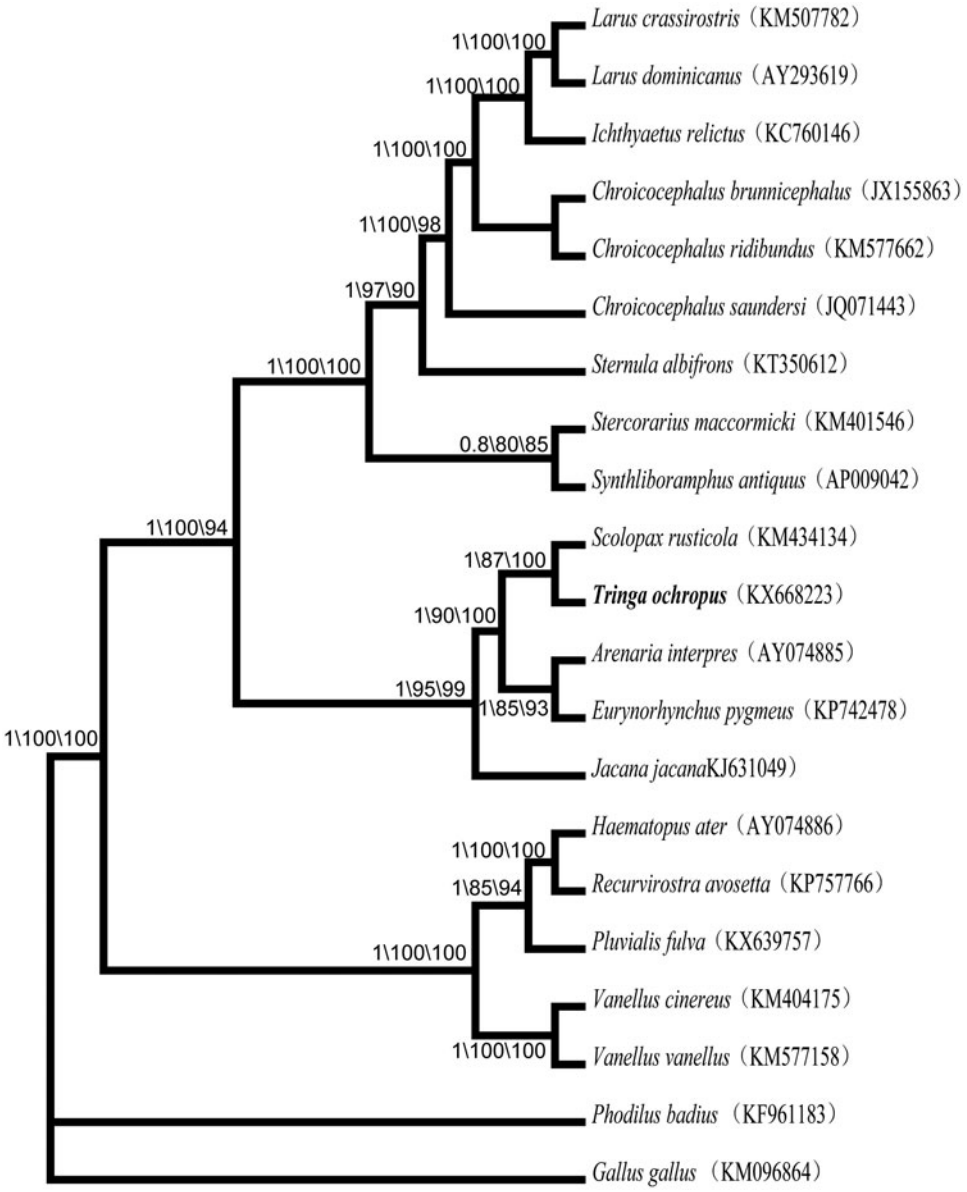

Figure 1. Phylogeny of *T. ochropus* and closely related 18 mitochondrial sequences constructed using the BI, ML and NJ methods by analyzing 13 protein-coding genes (PCGs). Numbers above each branches are the posterior probabilities, ML and NJ bootstrap support. GenBank accession numbers of each species are shown in parentheses.

Disclosure statement

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

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