



Supplementary Material

Characterization and Phylogenetic Analysis of the Mitochondrial Genome of *Clangula hyemalis* (Linnaeus, 1758)

Hengjiu Tian¹, Yan Liu², Rigude Bu³, Yaqian Fan⁴, Lin Li⁴, Shumiao Zhang⁵, Xiangnan Sun¹, Muhammad Younis Laghari⁶ and Meng Meng^{7,8*}

¹Beijing Wildlife Rescue and Rehabilitation Center, Beijing, 100029, China

²Beijing Key Laboratory of Captive Wildlife Technologies, Beijing Zoo, Beijing, 100044, China

³Academy of Inventory and Planning, National Forestry and Grassland Administration, Beijing, 100714, China

⁴Beijing Songshan National Nature Reserve, Beijing, 102115, China

⁵Beijing Milu Ecological Research Center, Beijing, 100076, China

⁶Department of Freshwater Biology and Fisheries, University of Sindh Jamshoro 76080-Pakistan

⁷China Wildlife Conservation Association, Beijing, 100029, China

⁸College of Wildlife and Protected Area, Northeast Forestry University, Harbin, 150040, China

Table 1. Primers used for amplification of *Clangula hyemalis* mitogenome.

Primers name	Sequence
<i>col</i>	F= AATGTAATCGTCACCGCCCA R= TACAGGATTGGGTCTCCCCC
<i>cytb</i>	F= ATCCTGACAGGTCTCCTGCT R= TACGAGGAGGTTGGCCACTA
<i>dloop</i>	F= GCTCCTACTCATACTACCCTGC R= CAGTGTC AAGGTGATTCCCCA
<i>nd2</i>	F= CGCATTGGGCACAACAATCA R= ATAGTGAGGCGAGGATTGCG
<i>nd3-nd4</i>	F= CCCCCGTACGAATGTGGATT R= GGAGGCAGATTGAGCTGGTT

Table continued on next colum.....

Primers name	Sequence
<i>nd1-3</i>	F= AATCTGTGAAAGGAACCTCGGC R= ATCATAGGATTGAGTAGACGGC
<i>16S</i>	F= GTGATAGCTGGTT(A/G)CC(C/T)G R= AAG(C/T)TCCACAGGGTCTTCTCG
<i>CO3</i>	F= ATGGCCACCAAGCACACTC R= CAATATCAGGCTGCTGCTTC
<i>ND3</i>	F= AAACCT(A/C/G)TCCCC(A/G/C/T)TACGAATG R= ATTCTGCTCATTCTAGGC
<i>ND4</i>	F= TAGCAAGCCAAAACACCT R= GATCAGTGGGTTTGGATTAT
1	F= CAAAGTGGCATCTGTGGAAT R= CTGGCACAAGATTTACCGAC
2	F= AAAGAGCCCATTCGACC(C/T)TC R= GTTGGGTGGTTGAGCTGTGT
3	F= GACTCATCATCCAAGAGCTA R= GGATATACGGTTCAGCCTGT
4	F= AAACCTCCCGCACTCTCACA R= GACAACATCCCGTCATCATT
5	F= GATTCCACGGACTCCACGTA R= GGTTCAAGGCGAGGGTTAGTA
6	F= AGA(A/G)CCAAACCCCTCATTC R= AAAATAGCGCTAGTTCTGTG
7	F= CGCTCAATCCCAAACAACT R= ATGGTATGTCCGCTTGTAT

* Corresponding author: mengmaoxian@163.com
0030-9923/2026/0002-0989 \$ 9.00/0



Copyright 2026 by the authors. Licensee Zoological Society of Pakistan.

This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

Table II. Genetic diversity of *Clangula hyemalis* mitogenome from China and American.

SNP/ InDel	No.	Gene name	Type
INDEL	1	Control region	34bp
SNP	4	Control region	C/T, C/T, G/A, T/C
SNP	2	Control region	A/G
SNP	1	<i>ND1</i>	G/A
SNP	1	<i>tRNA-Cys</i>	T/A
SNP	1	<i>COXI</i>	A/G
INDEL	1	<i>COXI</i>	C
SNP	1	<i>tRNA-Arg</i>	A/R
SNP	3	<i>ND4L</i>	T/C, T/C, A/G
SNP	1	<i>ND6</i>	A/G