

## The importance of voucher specimens: misidentification or previously unknown mtDNA diversity in *Phalacrocorax capillatus* (Aves: Phalacrocoracidae)?

George Sangster<sup>a</sup>  and Jolanda A. Luksenburg<sup>b,c</sup> 

<sup>a</sup>Naturalis Biodiversity Center, Leiden, The Netherlands; <sup>b</sup>Institute of Environmental Sciences, Leiden University, Leiden, The Netherlands; <sup>c</sup>Department of Environmental Science and Policy, George Mason University, Fairfax, VA, USA

### ABSTRACT

A recently published complete mitochondrial genome of Japanese or Temminck's cormorant (*Phalacrocorax capillatus*) was the first of this species (GenBank accession number LC714913). Comparison of COI sequences shows that this mitogenome clustered with great cormorant (*Phalacrocorax carbo*) rather than with its sister taxon *P. capillatus*. This suggests that the mitogenome was either a misidentified *P. carbo* or represents previously unknown intraspecific diversity in *P. capillatus* overlapping with that of *P. carbo*. Unfortunately, no voucher specimen was retained so it remains impossible to distinguish between these alternatives. We suggest that great restraint should be exercised using this mitogenome as a reference for *P. capillatus*. We reiterate previous pleas to retain voucher specimens for mitogenome sequences to enable re-analysis of the identity of the material.

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Cormorants; incorrect identification; mitogenome

### Introduction

Japanese or Temminck's Cormorant (*Phalacrocorax capillatus*) (Temminck & Schlegel, 1850) is a coastal waterbird breeding along northeast Asian coasts, from southeast Russia including Sakhalin, south Kuril Islands, Hokkaido to Kyushu, Japan, the Korean Peninsula and northeast China. In most parts of its range, including Japan, it co-exists with Great Cormorant *P. carbo* (Lethaby and Moores 1999; Squires et al. 2022). The two species are closely related (Kennedy and Spencer 2014; Kennedy et al. 2023). *P. capillatus* and *P. carbo* are very similar in morphology but can be distinguished by subtle differences in shape, structure, and the coloration of the plumage and bare parts (Lethaby and Moores 1999).

The first complete mitochondrial genome sequence (hereafter mitogenome) of *P. capillatus* was published by Honda et al. (2022). This sequence was derived from a blood sample taken from an individual rescued in Aomori City, northern Honshu, Japan, which died a few days later in captivity (GenBank accession number LC714913). Honda et al. (2022) included a phylogram based on complete mitogenomes which, as expected, placed LC714913 sister to a mitogenome of *P. carbo* (KR215630). However, the two sequences showed almost zero divergence suggesting that the two sequences may belong to the same species.

### Materials and methods

We verified the identity of LC714913 by comparing 696 bp of the cytochrome c oxidase subunit I of the mitogenome to reference sequences of *P. capillatus* ( $n = 3$ ) and *P. carbo* ( $n = 28$ ,

including several from Japan). A maximum-likelihood phylogeny was obtained using MEGA7 with 1000 bootstrap replicates (Kumar et al. 2016). Model testing was performed in MEGA7. The appropriate substitution model, GTR + G + I, was selected based on the Akaike information criterion. Sequence divergence was calculated as uncorrected  $p$  values with complete deletion of nucleotide positions with missing data.

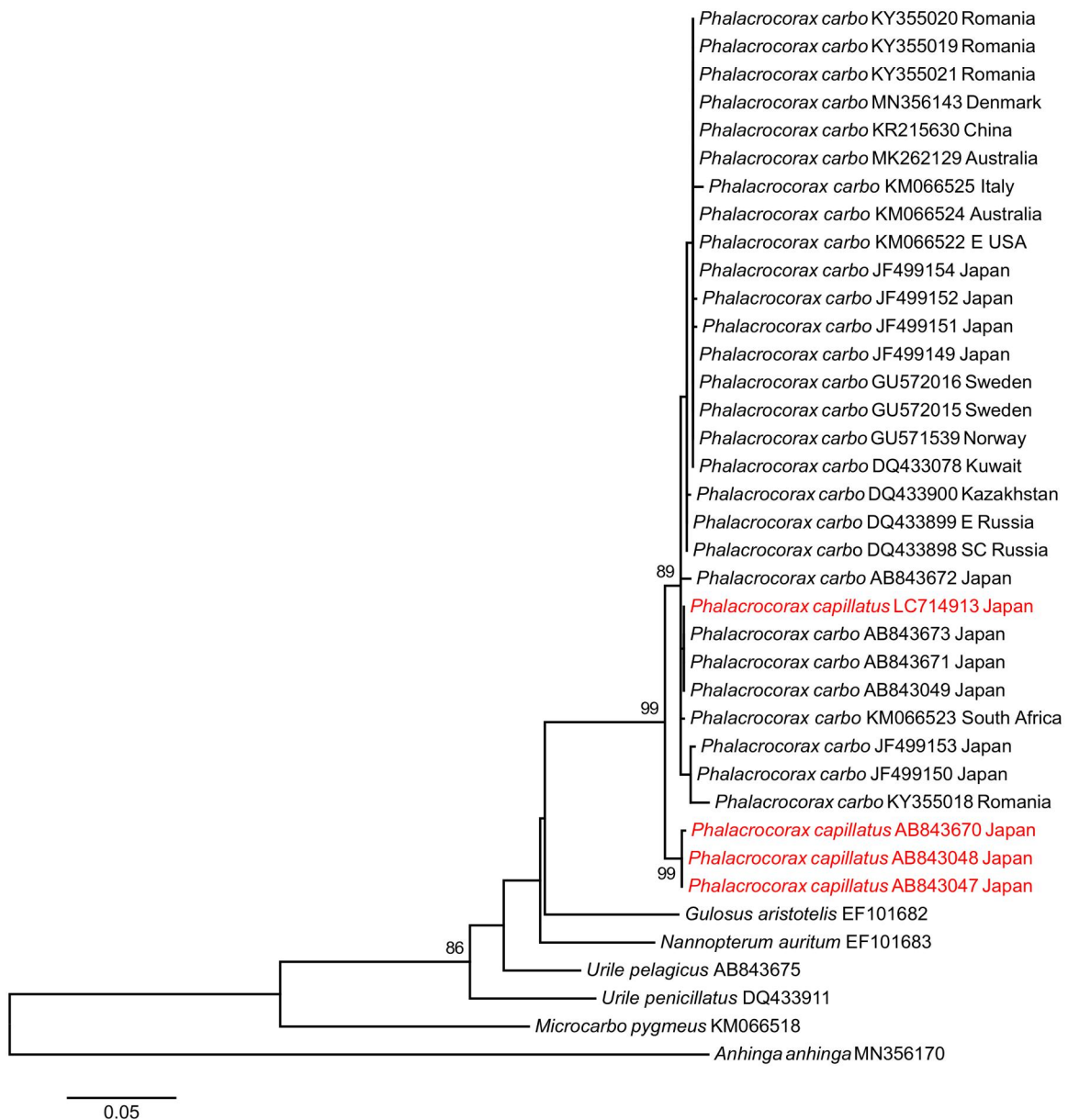
### Results

In the COI phylogeny (Figure 1), *P. carbo* and *P. capillatus* formed well-supported reciprocally monophyletic groups. However, LC714913 was placed within the *P. carbo* clade with strong support (bootstrap support 89%). Mean sequence divergence of *P. carbo* and *P. capillatus* was 1.3%. In both species, mean intraspecific sequence divergence was 0.1%. Mean divergence between LC714913 and *P. carbo* was 0.2%, whereas mean divergence between LC714913 and *P. capillatus* was 1.4%.

### Discussion

Based on current knowledge of sequence variation in *P. carbo* and *P. capillatus*, the phylogenetic position of LC714913 among *P. carbo* and its low sequence divergence with *P. carbo* (similar to mean intraspecific sequence divergence of *P. carbo*) suggest that LC714913 is a misidentified *P. carbo* rather than *P. capillatus*.

Sequence variation in *P. capillatus* is known from only three *bona fide* sequences from a single study (Saitoh et al.



**Figure 1.** ML phylogeny of cormorants (Phalacrocoraciformes) based on COI sequences (696 bp). Numbers along branches represent bootstrap support values (>70%) based on 1000 pseudoreplications. Note the position of LC714913 among *P. carbo* rather than *P. capillatus*.

2015). Thus, it is possible that sequence variation in *P. capillatus* is greater than presently known and perhaps overlaps with that of *P. carbo*. If this is the case, LC714913 could be a valid sequence of *P. capillatus*. It is known that some valid species of birds are reciprocally non-monophyletic in mitochondrial sequences (e.g. Joseph et al. 2009; Kerr et al. 2009; Techow et al. 2010).

A voucher specimen is necessary to distinguish between these two possibilities. Unfortunately, no voucher specimen of LC714913 was preserved (Honda et al. 2022). Without a voucher specimen, the specific identity of LC714913 may long remain uncertain, diminishing its value for population genetic, conservation genetic, and phylogenetic studies. The species identity of the sample used to generate LC714913 may be inferred from nuclear DNA genotyping, but this requires nuclear DNA sequences of *P. capillatus* that are not currently available. Unless and until the species identity of

this sample is ascertained, we suggest that great restraint should be exercised using mitogenome LC714913 as a reference for *P. capillatus*.

Given that most of the recently published mitogenomes are intended to serve as the reference sequence for population genetic, conservation genetic, and phylogenetic studies, it is important that the identity of mitogenomes is established beyond doubt and can be verified after the publication of the sequence. Recent studies have unveiled many misidentified or otherwise problematic mitogenomes, showing that the identity of published mitogenomes cannot be taken at face value (Botero-Castro et al. 2016; Oleinik et al. 2019; Sangster and Luksenburg 2020, 2021a, 2021b, 2021c). The present case shows that DNA identification is sometimes insufficient to establish the identity of a sequence. In such cases, it is necessary to revisit the original specimen. The importance of voucher specimens has been pointed out before in systematics

(Peterson et al. 2007; Pleijel et al. 2008), DNA barcoding (Collins and Cruickshank 2013) and mitogenomics (Strohm et al. 2016). Irrespective of the availability of a voucher specimen, we argue that all mitogenome announcements should include a statement about how the sample was identified, including any diagnostic character states of the relevant animal. As pointed out by Sangster and Luksenburg (2021a), such information can easily be included in the main text or in the online supporting materials. If no specimen could be preserved, photographs of the sampled individual should be included illustrating the diagnostic character states for the relevant taxon.

A third possibility is that the similarity of mitogenome LC714913 to *P. carbo* rather than to *P. capillatus* is due to introgression from *P. carbo* into *P. capillatus*. In this scenario, the phenotype of the bird would have been similar or identical to *P. capillatus* but the nuclear genome would be mixture of both species. Analysis of nuclear DNA would be able to verify this scenario but, again, this requires sequences that are not currently available for *P. capillatus*.

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## Author contributions

George Sangster: conceptualization, methodology, formal analysis, investigation, and writing – original draft. Jolanda A. Luksenburg: writing – review and editing. Both authors agreed to be accountable for all aspects of the work and approved the final draft to be published.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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## ORCID

George Sangster  <http://orcid.org/0000-0002-2475-7468>

Jolanda A. Luksenburg  <http://orcid.org/0000-0003-4424-4368>

## Data availability statement

The sequence data that support the findings of this study were published previously and are openly available on GenBank at <https://www.ncbi.nlm.nih.gov/nucleotide>. All sequences used in this study are referenced in Figure 1 and can be retrieved by typing in the relevant GenBank accession number(s) in the search panel on the aforementioned webpage. The mitochondrial genome of *Phalacrocorax capillatus* (LC714913) is available at <https://www.ncbi.nlm.nih.gov/nuccore/LC714913>.

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