



Testing the utility of mitochondrial *cytochrome oxidase subunit 1* sequences for phylogenetic estimates of relationships between crane (*Grus*) species

D.B. Yu*, R. Chen*, H.A. Kaleri, B.C. Jiang, H.X. Xu and W.-X. Du

Department of Animal Science and Technology,
Nanjing Agricultural University, Nanjing, China

*These authors contributed equally to this study.
Corresponding author: W.-X. Du
E-mail: duwenxing@njau.edu.cn

Genet. Mol. Res. 10 (4): 4048-4062 (2011)

Received November 1, 2011

Accepted December 19, 2011

Published December 21, 2011

DOI <http://dx.doi.org/10.4238/2011.December.21.7>

ABSTRACT. Morphology and biogeography are widely used in animal taxonomy. Recent study has suggested that a DNA-based identification system, using a 648-bp portion of the mitochondrial gene *cytochrome oxidase subunit 1* (*COI*), also known as the barcoding gene, can aid in the resolution of inferences concerning phylogenetic relationships and for identification of species. However, the effectiveness of DNA barcoding for identifying crane species is unknown. We amplified and sequenced 894-bp DNA fragments of *COI* from *Grus japonensis* (Japanese crane), *G. grus* (Eurasian crane), *G. monacha* (hooded crane), *G. canadensis* (sandhill crane), *G. leucogeranus* (Siberian crane), and *Balearica pavonina* (crowned crane), along with those of 15 species obtained from GenBank and DNA barcoding, to construct four algorithms using *Tringa stagnatilis*, *Scolopax rusticola*, and *T. erythropus* as outgroups. The four phylum profiles showed good resolution of the major taxonomic groups. We concluded that reconstruction of the molecular phylogenetic tree can be helpful for classification and that

COI sequences are suitable for studying the molecular evolution of cranes. Although support for several deeper branches was limited, *COI* data gave remarkably good separations, especially considering that our analysis was based on just a fragment of the gene and that *COI* has generally been viewed as useful only for resolving shallow divergences.

Key words: Molecular phylogeny; Mitochondrial DNA; Cytochrome C oxidase 1