

Morphological, Vocal, and Genetic Characterization of *Motacilla flava* – *tschutschensis* Allopecies Complex in Sri Lanka

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Abstract

Yellow wagtail complex was long considered a single species (*Motacilla flava*). Recent phylogenetic studies however, split this species into two; the Western Yellow Wagtail (*Motacilla flava*) and the Eastern Yellow Wagtail (*Motacilla tschutschensis*). Until 2020, there were no records of the Eastern Yellow Wagtail in Sri Lanka. Nonetheless, using several vocal, plumage, and a single genetic marker, a study in 2021 indicated that the Eastern Yellow Wagtail is wintering in Sri Lanka. In the present study, the yellow wagtail complex in Sri Lanka was critically evaluated using an assortment of phenotypic and genetic characteristics obtained from live-caught birds. The phylogenetic affinities of yellow wagtails wintering in Sri Lanka were constructed using Maximum likelihood inference and Bayesian inference using the mitochondrial ND2 gene region as the genetic marker. The morphological and vocal variations between Eastern (n = 15) and Western (n = 11) yellow wagtails were analyzed through the ANOVA test and the principal component analysis (PCA). The molecular phylogenetic trees and the number of peaks at the downstroke of the first flight call ($p = 0.00015$) of the yellow wagtail reveal that both Eastern and Western yellow wagtails are wintering in Sri Lanka. However, the morphological characteristics failed to separate the two species into two distinct clusters ($F_{n=26} = 3.9816$, $p = 0.0147$). Our study revealed the migratory occurrence of both the Western Yellow and the Eastern Yellow wagtails in Sri Lanka. The studied Eastern Yellow Wagtails clustered to the North Asian *tschutschensis* clade.

Keywords: *Molecular markers, ND2, Eastern yellow wagtail, Western yellow wagtail, Phylogeny, Integrative systematics*