

The Condor
Volume 104, Number 4
November 2002 C.E.
Abstracts

FEATURE ARTICLES

PHYLOGENETIC RELATIONSHIPS OF THE WRENTIT BASED ON MITOCHONDRIAL CYTOCHROME *b* SEQUENCES

DINO N. BARHOUM AND KEVIN J. BURNS¹

Department of Biology, San Diego State University, San Diego, CA 92182-4614

Manuscript received 5 February 2002; accepted 23 July 2002.

¹Corresponding author. E-mail: kburns@sunstroke.sdsu.edu

Abstract. The phylogenetic relationship of the Wrentit (*Chamaea fasciata*) to other passerine birds is understood poorly. A variety of taxa have been proposed as closely related to the Wrentit, but in general this species is placed in a monotypic taxon to emphasize its morphological distinctiveness and lack of clear relationship to other groups of birds. We used the mitochondrial cytochrome *b* gene to infer the relationship of this monotypic genus to other avian groups including representatives of Sylvioidea, Muscicapoidea, and Passeroidea. Results of this study corroborate in part earlier proposals based on DNA-DNA hybridization. Maximum parsimony, maximum likelihood, and Bayesian phylogenetic analyses support the Wrentit, *Sylvia*, and babblers (*Garrulax*, *Illadopsis*, *Leiothrix*, *Pomatorhinus*, *Stachyris*, and *Yuhina*) as a clade, with the Wrentit sharing a more recent common ancestor with *Sylvia* than with babblers. A *Sylvia* and Wrentit association is further supported by similarities in morphology and ecology. In addition to findings on Wrentit relationships, our study in general agrees with the major groups of oscine passerines identified by earlier DNA hybridization studies.

Key words: *babbler*, *Chamaea fasciata*, *mitochondrial DNA*, *phylogeny*, *Sylvia*, *Wrentit*.