

Title: Phylogenetic relationships between Turdus species: Mitochondrial cytochrome b gene analysis

Author(s): [Pan, Qiao-Wa](mailto:panqiaow1980@yahoo.com.cn) (panqiaow1980@yahoo.com.cn); [Lei, Fu-Min](mailto:leifm@ioz.ac.cn) (leifm@ioz.ac.cn); [Yin, Zuo-Hua](mailto:kristin@savzv.sk); [Kristin, Anton](mailto:kristin@savzv.sk) (kristin@savzv.sk); [Kanuch, Peter](mailto:kanuch@peter.com)

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Abstract: The phylogeny of the widespread Turdus genus (Passeriformes, Muscicapidae, Turdinae) still remain controversial. We investigated phylogenetic relationships within the Turdus assemblage using the mitochondrial cytochrome b gene, with an emphasis of the taxonomic status of T. mupinensis. Nineteen species from Turdus were analyzed as ingroups, and Myiophonus caeruleus and Monticola cinclorhynchus were selected as outgroups. Altogether 991 bp gene fragments from these species were obtained, in which 368 variable sites and 278 parsimony informative sites were identified. Phylogenetic analyses indicated that the genus Turdus is paraphyletic and that it forms a well supported clade including three mostly monotypic genera (Cichlherminia, Platycichla and Nesocichla). Three types of phylogenetic tree (MP, ML and Bayesian) support two steady clades (Europe-Asia clade and South America clade) in Turdus. Species from the Europe-Asia clade include T. rubrocanus, T. pallidus, T. obscurus, T. naumanni, T. torquatus, T. boulboul and T. cardis, while species from the South America clade include P. leucops, N. eremita, T. chiguanco, T. fuscater, T. rufiventris and T. grayi. Applying a substitution rate of 2% per million years, the divergence of the Europe-Asia clade was estimated to have occurred approximately 0.95-3.30 Mya, the South America clade divergence occurring at around 1.2-3.7 Mya. Our results also revealed that T. mupinensis was located at the base of all three phylogenetic trees, which suggested that T. mupinensis might be the most primitive taxon among all ingroup clades. The divergent time between T. mupinensis and other Turdus species was estimated at occurring 3.6-5.7 Mya. The high divergence in mtDNA and obvious differences in morphology suggest that T. mupinensis may be considered as a species in a distinctive genus from Turdus.

Address: Lei, Fu-Min ; Chinese Acad Sci, Inst Zool, Beijing 100080, Peoples R **China**

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