

Evolution and biogeography of suboscine birds analysed by DNA sequence data – a research program at the Swedish Museum of Natural History

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The suboscine passerines comprise about 1100 species traditionally divided into three groups. The Old World suboscines (pittas, broadbills and asities) consist of only about 50 species, distributed from tropical Africa to Melanesia. The New World suboscines, consisting of Furnariida (e.g. ovenbirds, woodcreepers, typical antbirds, ground antbirds, gnateaters and tapaculos) and Tyrannida (e.g. tyrant flycatchers, cotingas and manakins) are far more species-rich and diverse with about 500 species each. They constitute an important part of the land bird fauna in every type of habitat in the Neotropics, and only a few genera of tyrant flycatchers reach North America.

A research team at the Swedish Museum of Natural History currently investigates the evolution and biogeography of the suboscines. The long-term objective of our project is a) to produce robust estimates of the phylogenetic relationships among suboscine birds, and b) to describe their morphological and behavioural evolution. This is achieved by analysing DNA-sequence data from multiple nuclear as well as mitochondrial genes. Our research strategy is to first outline the major evolutionary units (Irestedt et al., 2001, 2002; Johansson et al., 2002; Ericson et al., 2002), after which we proceed to studies of smaller, monophyletic groups that can be more densely taxonomically sampled (Irestedt et al., 2004).

We strongly believe in building research networks that include researchers at other museums and institutions, not least because blood and tissue samples are a limited resource in this kind of projects. Our foremost collaborator is Prof. Jon Fjeldså at the Zoological Museum, University of Copenhagen, but we also collaborate with colleagues in, for example, USA, Australia, Vietnam, Germany, Switzerland and France. Several of the studies are conducted as part of a Masters or Ph.D. program. Until now, two Ph.D. dissertations, two Ph.Lic. dissertations and five Masters degrees are based on data obtained within the project. As of May 2004, the research group has submitted 800+ sequences to GenBank (corresponding to ca 725,000 basepairs) and published 16 peer-reviewed papers since 2000 (three papers are currently in review with another six in an advanced stage of preparation).

The results so far largely support the traditional (morphological) division of the suboscines into an Old World group and a New World group, respectively, and the further division of the New World taxa into a furnariid and a tyrannoid assemblage (see Ericson et al., 2003 for a review of the major results). The only exception is the Broad-billed Sapayoa (*Sapayoa aenigma* Hartert, 1903) that, despite being a New World taxon,

is closest related to the Old World suboscines (Fjeldså et al., 2003). Our work has also shown that many traditional views of the higher-level relationships within the group (i.e. between genera and families) are dubious at best. We foresee that future DNA-based research will provide an increasingly better understanding of these relationships. This, in turn, will enable us to outline the evolution and biogeography of the suboscines at a finer scale.

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