

# The use of museum specimens as source of DNA

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The availability of fresh tissue samples in studies of molecular phylogeny is often restricted, especially when species are difficult to access or threatened. Collecting fresh material is even impossible when a species is extinct. In such cases, museum collections are the only place where specimens suitable for DNA extraction are available. These specimens are usually preserved as bones or skins or are stored in fluid. The recent improvement of molecular techniques has allowed the use of increasingly older museum specimens as source of DNA. However, difficulties are still numerous, as older material suffers from more or less severe degradation of DNA or the occurrence of PCR contaminants. Another serious problem is the caused damage to museum specimens in order to extract DNA, though new techniques allow the collecting of tiny amounts of tissue, restricting visible deterioration of the specimen. The use of DNA taken from museum specimens of extinct taxa can be divided into three categories:

The first category is formed by research on the identification or delimitation of a single taxon. For instance, bone remains of an extinct Hawaiian raptor identified it as a sea eagle (genus *Haliaeetus*) using molecular characters (Fleischer et al., 2000), and a study of the extinct moa's Dinornithidae from New Zealand revealed that several taxa described previously were in fact males and females of a single taxon (Huynen et al., 2003).

In the second research category, DNA from museum specimens is used to infer the closest living relative of an extinct taxon. For instance, the extinct Dodo *Raphus cucullatus* (Linnaeus, 1758) and Solitaire *Pezophaps solitarius* (Sélys-Longchamps, 1848) from Mauritius and Rodriguez appeared genetically closest to the living Nicobar Pigeon *Caloenas nicobarica* (Linnaeus, 1758) (Shapiro et al., 2002), and the Great Auk *Pinguinus impennis* (Linnaeus, 1758) was found to be a sister species of the Razorbill *Alca torda* Linnaeus, 1758 (Moum et al., 2002).

In the third research category, extinct taxa can be extremely useful for time calibration in branching events, avoiding the assumption of the hypothesis of a steady molecular clock. See, for instance, the study of ratite diversification which includes moa sequences (Cooper et al., 2001).

In our study abstracted here (Cibois et al., 2004), we focused on a passerine genus endemic to eastern Polynesia, *Pomarea* (monarchs, Monarchidae), restricted to some high volcanic islands of the Cook, Society, and Marquesas archipelagos. Recent extinctions of these birds have been documented for several islands, and most of the remaining forms are rare and liable to become extinct soon due to the introduction of rats and habitat loss (BirdLife International, 2000). With mitochondrial DNA obtained from specimens lodged at the American Museum of Natural History and collected during the Whitney South Sea Expedition in the 1920s, we developed a phylogeny of the entire genus *Pomarea*,

including extinct taxa. This phylogeny was compared to geological data of the eastern Polynesian islands, with emphasis on the Marquesas archipelago where *Pomarea* has undergone its most extensive diversification. The phylogeny of *Pomarea* monarchs is consistent with the sequential apparition of the Marquesas islands. The age of the lineages are approximated using two analyses: the first is based on a molecular clock to infer lineages dating, the second is based on Bayesian methods that include geological data (see Cibois et al., 2004 for further explanations). Both analyses show differences between the age of the islands and the age of the nodes, from 1 to 2 million years for most islands. We suggest that these differences are due to a latent period during which the islands had emerged but were not yet successfully colonized by *Pomarea*. Phylogenetic hypotheses suggest also that several species traditionally recognized within *Pomarea* on phenotypical characters are polyphyletic. These results have consequences on the classification of the genus as well as implications for the evolution of sexual dimorphism in monarchs.

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