

# Bird specimens - an invaluable resource for genetical studies and conservation

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In recent years phylogenetic investigations at different evolutionary levels based on molecular biology have become very popular in ornithology (Christidis & Norman, 2003). Because fresh material from wild birds with known data is often difficult to obtain or even unavailable, tissues with 'ancient DNA' from museum specimens play a very important role in genetic studies. The advantage of this old material is that it is often easy to obtain and that a large number of samples can be gathered in relatively short time. The main disadvantage is that the percentage of workable samples is lower than in fresh tissue and that DNA sequences obtained are shorter.

In 1999, the bird department at the Naturhistorisches Museum Wien (NMW) initiated close cooperation with the newly established laboratory for molecular biology. Several projects, which focused on phylogeny and taxonomy of different bird groups (mainly birds of prey, especially buzzards, honey-buzzards, hawk-eagles and large falcons) are already finished (Haring et al., 1999; Haring et al., 2001; Riesing et al., 2003; Gamauf & Haring, 2004; Kruckenhauser et al., 2004; Nittinger, 2004) or are in progress (eagles, woodpeckers and corvids). Most analyses were based on mitochondrial DNA (ND6, cytochrome *b*, control region, pseudo-control region). Questions regarding species concepts in connection with conservation strategies have been considered too. The concept that the "species" is the most important "evolutionary significant unit" as expressed by conservationists has in some cases led to the upgrading of subspecies to species because only species status would sufficiently promote their conservation: a bad compromise without scientific basis.

Until recently, taxonomy has focused mainly on morphological features and plumage patterns, even though convergent evolution and morphological adaptations make it sometimes difficult to fix a taxon to its correct systematic position. Using mtDNA our team examined the validity of the classification of SE Asian *Spizaetus* hawk-eagles. We could prove that the genetic distance between two taxa of the Philippine Hawk-eagle (*S. philippensis*), one of which we had described as *S. philippensis pinskeri* Preleuthner & Gamauf, 1998, was of such a scale that the latter taxon was best upgraded to species level, Pinsker's Hawk-eagle *S. pinskeri*. In contrast, the genetic distances between the various island taxa of the Changeable Hawk-eagle *S. cirrhatus* are within a range that can be expected at the intraspecific level. These results may have a negative impact on the conservation policy of *S. cirrhatus* (Gamauf et al., 2005).

Another example of the use of DNA from bird skins is our research on the phylogenetic relationships of the Okinawa Woodpecker *Sapheopipo noguchii* (Seebohm, 1887), possibly the rarest of all woodpeckers and considered "Critically Endangered" by BirdLife

International (2000). Based on morphology, this monotypic genus was usually considered to be a representative of an old lineage of woodpeckers that led to the Eurasian genera *Picus* and to the *Blythipicus-Gecinulus* group. Testing this hypothesis with mtDNA, the cytochrome *b* data showed that the Okinawa Woodpecker belongs to the genus *Dendrocopos*, with White-backed Woodpecker *D. leucotos* (Bechstein, 1803) and Great Spotted Woodpecker *D. major* (Linnaeus, 1758) as closest relatives. The genetic results are supported by colour patterns and these indicate a closer relationship with the White-backed Woodpecker. Consequently, the correct taxonomic designation of the Okinawa Woodpecker would be *Dendrocopos noguchii*. The downgrading of this taxon from a separate genus to a species within the large genus *Dendrocopos* should have no consequences for the efforts to protect it (Winkler et al., 2005).

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