

Phylogeny of Old World Perninae (Accipitridae) based on mitochondrial DNA sequences

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Because of some morphological characteristics the honey-buzzards (genus *Pernis*) always had a special position within the Accipitridae. Since birds of prey were considered to have evolved from less predatory birds, which subsisted largely on insects, Peters (1931) placed the genus *Pernis*, together with the genera *Aviceda*, *Henicopernis*, *Lepidotod*, *Chondrohierax* and *Elanoides*, in the subfamily Perninae which lack the os supraorbitale, a bony shield projecting above the eye that is present in hawks. The Perninae are assumed to have branched off early within the Accipitridae (Brown, 1976).

The genus *Henicopernis* is supposed to be the closest relative of *Pernis*. Both genera comprise only a few species: since Stresemann (1940) the genus *Pernis* consists of three species subdivided into ten subspecies (Vaurie & Amadon, 1962), whereas *Henicopernis* consists of only two species. Species within the genus *Pernis* are difficult to classify because of morphometric variation, plumage polymorphism (colour and pattern) and the presence or absence of a crest. Nevertheless, systematics of this genus is based mainly on these characters, which have been interpreted controversially in previous studies.

To investigate geographical differentiation and speciation of the honey-buzzards a molecular study was undertaken using a partial sequence of the cytochrome *b* gene (382 bp). We analysed 35 specimens, mostly study skins, of the genus *Pernis* representing all ten valid taxa and representatives of the other Old World Perninae, the long-tailed honey-buzzards *Henicopernis* and the cuckoo-hawk *Aviceda*. Sequences of presumed relatives, the Bearded Vulture *Gypaetus barbatus* (Linnaeus, 1758) and the Egyptian Vulture *Neophron percnopterus* (Linnaeus, 1758) (Seibold & Helbig, 1995) as well as the Common Buzzard *Buteo buteo* (Linnaeus, 1758) were used as outgroups. Interestingly, the distances found between *H. longicauda* (Garnot, 1828) and the sequences of the taxa representing the genera *Gypaetus*, *Neophron*, *Aviceda* and *Pernis* are considerably high (11.2-13.0%), similar to those between *B. buteo* and the ingroup taxa ranging from 11.2-14.2% and those between *H. longicauda* and *B. buteo* (13%). In the phylogeny derived from the sequence data *Aviceda* appears as the sister group of a cluster composed of all *Pernis* sequences, whereas the genera *Pernis*, *Henicopernis* and the Old World vultures *Gypaetus* and *Neophron* are only distantly related. A sister group relationship between *Pernis* and *Henicopernis* can be excluded. Within *Pernis*, *P. apivorus* (Linnaeus, 1758) stands basal (clade 1, Fig. 1) followed by a clade (2) representing specimens of *P. celebensis* Wallace, 1868 (taxa *steerei* Sclater, 1919, and *winkleri* Gamauf & Preleuthner, 1998). The sequences of nominate *P. c. celebensis* are found in a separate clade (3). Thus, *P. celebensis* appears paraphyletic in our trees, but the relationships among the clades remain ambiguous as

indicated by poor bootstrap support. Clade 3 is the sister group to the *P. ptilorhynchus* (Temminck, 1821) clade which is further divided into two distinct groups: one containing the subspecies *orientalis* Taczanowski, 1891, *philippensis* Mayr, 1939, and *ruficollis* Lesson, 1830 (clade 4), the other consisting of the subspecies *ptilorhynchus*, *torquatus* Lesson, 1830, and *palawanensis* Stresemann, 1940 (clade 5).

Moreover, *Henicopernis* does not cluster with *Gypaetus* and *Neophron*, but seems to belong to an old endemic Australasiatic lineage standing somewhere between the *Gypaetus/Neophron* lineage and *Buteo*. Morphological similarities may be explained by convergent evolution of specific characters in adaptation to similar functions under similar environmental conditions. Among the Old World genera of the subfamily Perninae *Aviceda* seems to be the closest relative to *Pernis*, as already proposed on the basis of osteological analysis (Jollie, 1976-1977). Characteristic display behaviour and vocalisation of *Aviceda* which resembles that of *Pernis*, but is quite different from that of *Henicopernis*, supports this relationship.

P. apivorus and *P. ptilorhynchus* represent clearly separated, monophyletic groups, thus confirming their species status. On the other hand, for *P. celebensis* we propose a split into the species *P. celebensis* (Sulawesi) and *P. steerei* (Philippines).

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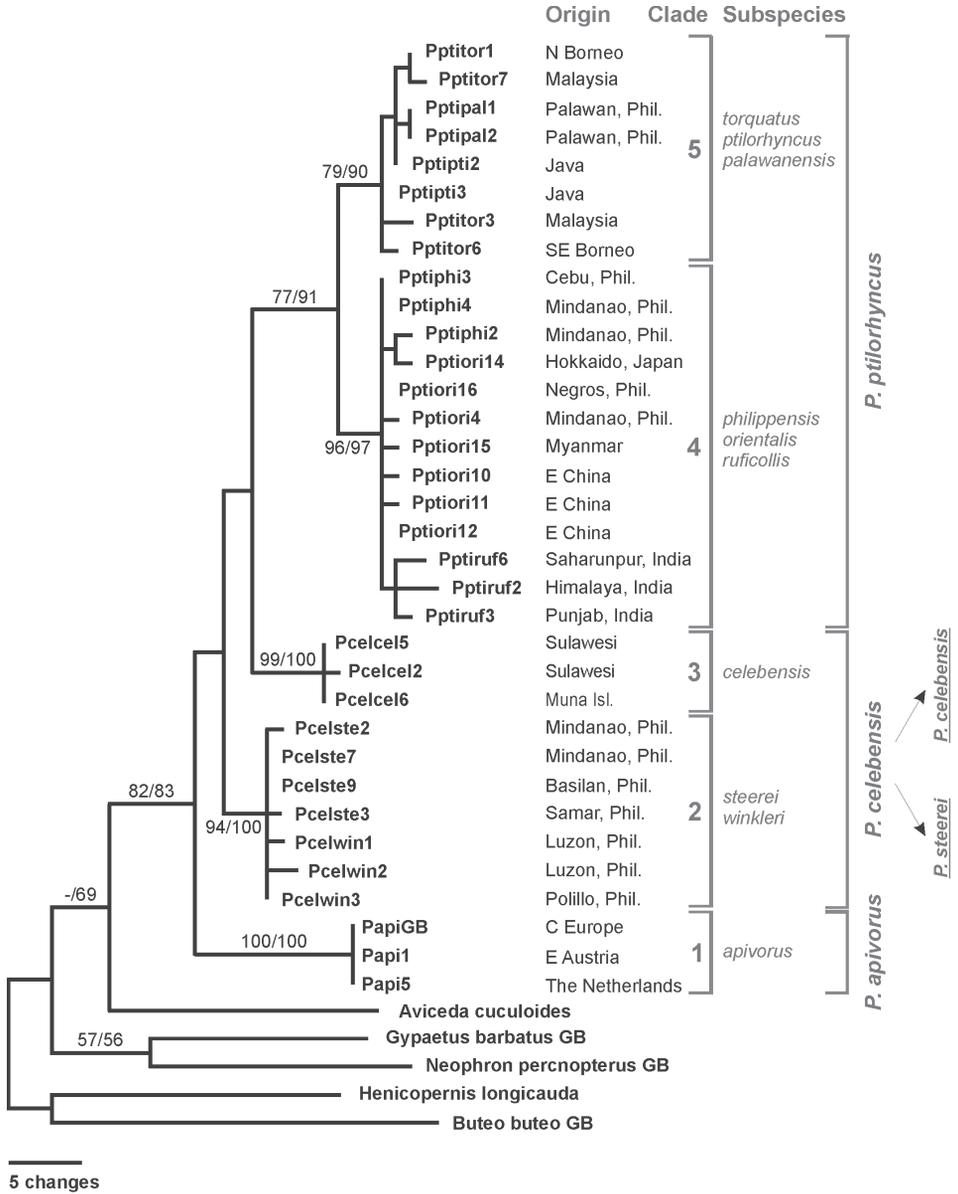


Fig. 1. Molecular phylogeny of Old World Perninae (after Gamauf & Haring, 2004). Maximum Parsimony (MP) tree based on a partial *cyt b* sequence, which is congruent with a Neighbour Joining (NJ) tree (outgroup taxa: *Henicopernis longicauda*, *Buteo buteo*). Clades 1 - 5 are described in the text. Bootstrap values (1000 replicates) >50 % are given at the nodes (left: MP, right: NJ).

