Phylogenetic relationships between Black Shaheen Falco peregrinus peregrinator, Red-naped Shaheen F. pelegrinoides babylonicus and Peregrines F. peregrinus

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ABSTRACT

Nucleotide sequences of the mitochondrial cytochrome b gene from the Black Shaheen F. p. peregrinator from the Sri Lanka population, the Red-naped Shaheen Falco pelegrinoides babylonicus and from several subspecies of the Peregrine peregrinus, calidus, anatum, minor, macropus were used to reconstruct underlying phylogenetic relationships. Genetic variation is quite low (< 0.6% sequence divergence) in the peregrinus/pelegrinoides group, indicating that both taxa form a young species complex. Systematic consequences would be either to treat all subspecies of F. peregrinus and F. pelegrinoides as subspecies of F. peregrinus or to give species rank to all of them.

INTRODUCTION

The Peregrine Falcon Falco peregrinus shows cosmopolitan distribution and 19 geographic subspecies have been distinguished (Cade & Digby, 1987; del Hoyo et al., 1994; Weick 1980). The Barbary Falcon with 2 subspecies Falco pelegrinoides pelegrinoides and F. p. babylonicus which occurs from North Africa to south and central Asia, has been either treated as a distinct species (Vaurie, 1965; Cramp 1980) or as a subspecies of F. peregrinus (del Hoyo et al., 1994; Sibley & Monroe, 1990).

Some of the Peregrine subspecies show very characteristic plumage patterns and morphometric differences. Falconers from India, Pakistan or Arabia distinguished between Peregrine Falcons, Rednaped Shaheen and the Black Shaheen (Ratcliffe, 1871) and their different qualities in falconry. In a cladistic analysis performed on morphological data Kemp and Crowe (1993) showed that Falco pelegrinoides, Falco peregrinus peregrinator and F.p. minor are morphometrically very close and separated from Falco peregrinus pealei.

We have employed sequence data of the mitochondrial cytochrome b gene in order to analyse the phylogenetic relationships in the *peregrinus-pelegrinoides* complex and present first results in this communication.

MATERIAL AND METHODS

DNA was isolated from blood, muscle tissue or feathers and stored in EDTA buffer (Heidrich et al. 1998). The mitochondrial cytochrome b gene was amplified by PCR (ca 1250 base pairs). The PCR product was directly sequenced by "Cycle sequencing" using two internal overlapping fluorescent primers. A Thermo Sequenase labelled primer kit with 7-deaza-dGTP (Amersham LIFE SCIENCE) was employed, according to a protocol provided by the manufacturer. Sequencing was performed on an ALF express DNA sequencer, AMV 3.0 (Pharmacia).

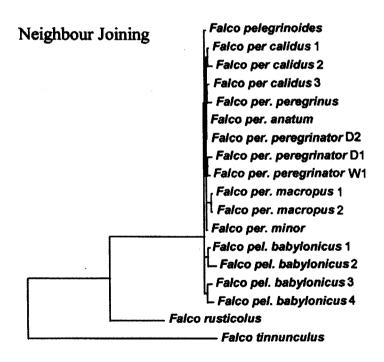
Sequences (1250 nt) were aligned and analyzed with PAUP*, employing Maximum Parsimony (MP), Neighbour Joining (NJ), and Maximum Likelihood (MLE) to reconstruct phylogenetic trees. More details on the methodology can be found in Wink (1998, 1999), Heidrich et al., (1998), Leisler et al. (1997).

RESULTS AND DISCUSSION

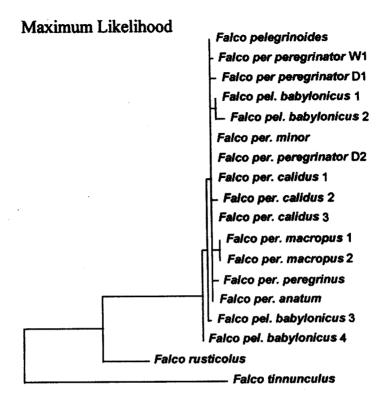
Phylogenetic relationships were reconstructed using *Falco tinnunculus* as a distant outgroup and *F. rusticolus* as an ingroup; however, other ingroups or outgroups do not change tree topologies. Results are illustrated as NJ and MLE trees (Fig. 1).

Figure 1: Molecular phylogeny of Black and Red-naped Shaheens and allies.

A. NJ phylogram (p distance as distance algorithm)



B. MLE settings: Assumed nucleotide frequencies: A=0.301, C=0.334, G=0.122,T=0.243; all sites were assumed to evolve at same rate; transition/transversion ratio was set to 2; score of the best tree found= 2456



Branch lengths are proportional to evolutionary distances

In order to study the phylogenetic relationships of the *peregrinus/pelegrinoides* complex in more detail cytochrome b sequences were studied from 16 different specimens representing 6 subspecies of *F. peregrinus* and the 2 described subspecies of *F. pelegrinoides* (Table 1).

Falco peregrinus, and its subspecies peregrinus, calidus, anatum, minor, macropus, peregrinator and F. pelegrinoides, F. pel. babylonicus are closely related and share common ancestry. They represent

Table 1. Origins of the falcons studied

Taxon	Origin
F. p. pelegrinoides	captivity (D. Schmidl)
F. p. babylonicus	captivity (D. Schmidl)
F. p. peregrinus	Scotland
F. p. anatum	North America
F. p. calidus	Siberia
F. p. minor	South Africa
F. p. peregrinator	Sri Lanka

a sister group to the monophyletic Hierofalco complex (Wink & Sauer-Gürth, 1999). Genetic distances (expressed as % pairwise nucleotide substitutions) were below 0.6%, a level typical for intraspecific differentiation in falcons (Table 2).

Table 2. Illustration of variable nucleotide positions in the cytochrome b data setDiagnostic substitutions are printed in bold.

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	111111
	113555678991111112
	053667343671666780
Taxon	0 2 3 3 5 2 0 6 0 5 4 0 0 5 8 0 4 5
Falco p.calidus 1	ATA???AAACCCCCTGAG
Falco p.calidus 2	ATAAACAAACCCGCTGAG
Falco p.calidus 3	ATA???AAACCCCCTGAG
Falco p.anatum	ATAAAAAACCCCCTGAG
Falco p.peregrinus	ATAGAAAGACCCCCTGAG
Falco p.macropus 1	ATGAAAAACCCCCCGAG
Falco p.macropus 2	ATGAAAAACCCC??????
Falco p.minor	ATAAAAAACCCCCTGAG
Falco p.peregrinator D1	ATAAAAAACCCCSTAAA
Falco p.peregrinator D2	ATAAAAAACCCCCTGAG
Falco p.peregrinator W1	ATAAAAAACCACCTGA?
Falco pelegrinoides	? ? AAAAAACCCCCTGAG
Falco p.babylonicus 1	? CAAAAGAGCCCCCTGAG
Falco p.babylonicus	ATAAAAGAGCCCCGTGCG
Falco p.babylonicus	CTAAAAAATCCCCTGAG
Falco p.babylonicus	CCAAAAAATTCCCTGCG

F. pelegrinoides hardly differs from F. p. peregrinus, F.p. anatum, and F.p. peregrinator (no character was parsimony informative), indicating the close ancestry between peregrinus and pelegrinoides. Within the babylonicus group, two haplotypes were detected (Fig. 1 A,B). Whether these haplotypes reflect different geographic origins or are the result of distant hybridisations needs to be analyzed in future studies.

Within the peregrinus group, unambiguous relationships could not be resolved. F. p. macropus from Australia and F. per. calidus from Siberia form distinct haplotypes and differ by 0.2 to 0.4% nucleotide substitutions from F. p. peregrinus indicating a low level of phylogeographic differentiation. The DNA sequence of Black Shaheen is almost identical with F. p. peregrinus, F. p. calidus, F.p. minor and F. pelegrinoides which would confirm findings of a morphometric analysis by Kemp and Crowe (1993).

Distances between pelegrinoides and peregrinus are below 0.6-0.7% nucleotide substitutions indicating a rather recent divergence of both groups. Distances found in "good" species within the Falconidae and Accipitridae are usually higher than 1.5% (Seibold et al., 1996). As a consequence, both falcon taxa could be either treated as a single species F. peregrinus with pelegrinoides and babylonicus as a subspecies or the other subspecies of peregrinus would deserve species rank.

ACKNOWLEDGEMENTS

We would like to thank W. Bednarek, N. Fox, C. Eastham, D. Schmidl, and N. Mooney for providing blood or feather samples, and the Elmar-Schlögl-Stiftung and the Department of Wildlife Conservation Sri Lanka for their support.

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