

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, Red-naped 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 ALFexpress DNA sequencer, AMV 3.0 (Pharmacia).

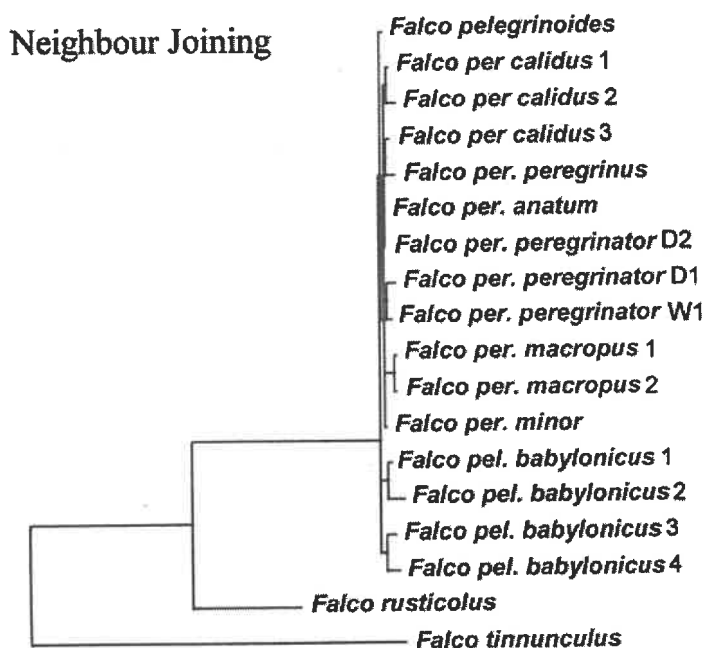
Sequences (1250 nt) were aligned and analyzed with PAUP*, employing Maximum Parsimony (MP), Neighbour Joining (NJ), and Maximum Likelihood (MLE) to reconstruct phylogenetic trees. More details on the methodology can be found in Wink (1998, 1999), Heidrich *et al.*, (1998), Leisler *et al.* (1997).

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).

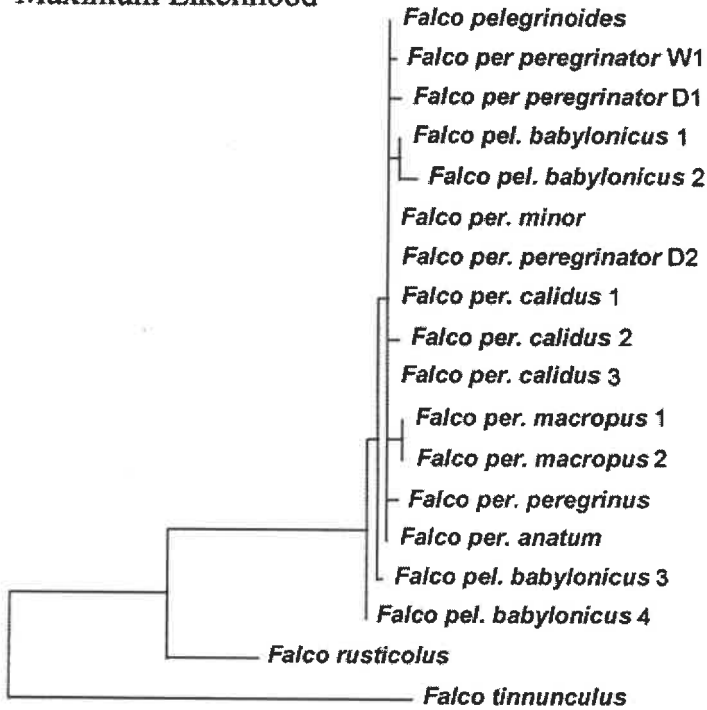
Figure 1: Molecular phylogeny of Black and Red-naped Shaheens and allies.

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

Maximum Likelihood



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
<i>F. p. pelegrinoides</i>	captivity (D. Schmidl)
<i>F. p. babylonicus</i>	captivity (D. Schmidl)
<i>F. p. peregrinus</i>	Scotland
<i>F. p. anatum</i>	North America
<i>F. p. calidus</i>	Siberia
<i>F. p. minor</i>	South Africa
<i>F. p. peregrinator</i>	Sri Lanka

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