GENETIC VARIABILITY IN PEREGRINE FALCON POPULATIONS OF THE WESTERN PALEARCTIC REGION

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We analysed variation in ten polymorphic microsatellites and a portion of cytochrome b mitochondrial DNA in 4 populations of peregrine falcon (*Falco peregrinus*), living in northern and southern Italy, Spain and Czech Republic to assess species diversity in the poorly investigated Western Palearctic region. The Spanish population lives in the contact zone between *F. peregrinus peregrinus* and *F. p. brookei*, both the northern Italian and the Czech populations live within the range of *F. p. peregrinus* and the southern Italian is within the *F. p. brookei*. We added to our cytochrome b sequence dataset comprising 81 samples, previously published mitochondrial DNA sequences (n = 31) of English *F. p. peregrinus*, Spanish *F. p. brookei* and 8 peregrine falcon subspecies to outline genetic variation in the region on a worldwide basis. Genetic differentiation in nuclear STR loci was almost absent and it is not possible to distinguish geographical groupings. Regarding mtDNA we identified 17 haplotypes from the 112 peregrine falcon samples, of which 11 were unique and 6 were shared among two or more subspecies. The 68% of sample belonged to 2 shared haplotypes. Overwintering of *F. p. calidus* in Italy was confirmed on a genetic basis. The Spanish and Sicilian *brookei* peregrines split up among haplotypes, but the 35% of Sicilian falcon shared a new haplotype unique for the island. There was neither concordance between cytochrome b variation and taxonomic designation at the subspecies level, nor any phylogeographic pattern in the genetic data. Our analysis, regarding the investigated European region, supported that historical and recent dispersal, combined with rapid morphological evolution, may have originated such a lack of concordance between genetic variation (cytochrome b mtDNA sequences and nuclear STR loci) and phylogeography in peregrine falcon.