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Genetic variability of falcon microsatellite DNA markers

L. Putnová[1], J. Pokorádi[2], K. Civáňová[1], T. Urban[1], I. Křížanová[1], A. Kúbek[2], J. Dvořák[1]

[1]Mendel University of Agriculture and Forestry Brno, Department of Genetics, Brno, Czech Republic, putnova@mendelu.cz
[2]Slovak Agriculture University, Department of Genetics and Breeding Biology, Nitra, Slovakia

Introduction:

The variability based on microsatellite DNA markers is using for the identification of species, populations, individuals and parent-offspring relationships. All species of Falco family (*Falconidae* sp.) are protected by CITES and EU laws. Consequently we want to contribute to the legal breeding of endangered species, wildlife protection, crime suppression and also to determination of populations in Slovakia and the Czech Republic.

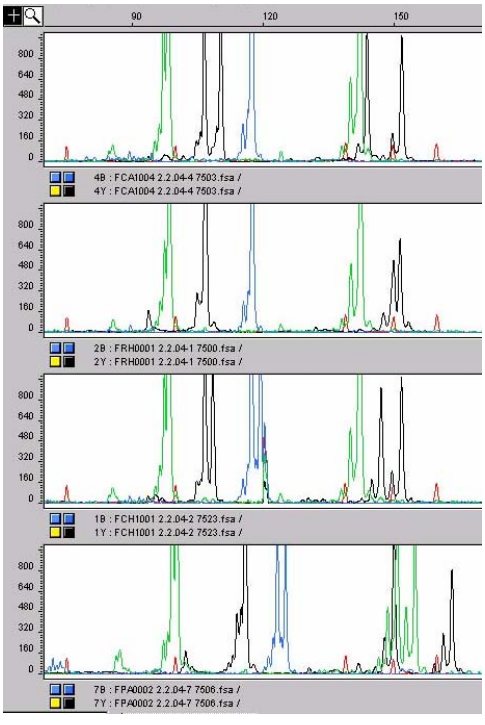
Material and methods:

We studied the genetic variability of five falcon microsatellite markers (***NVHfp13***, ***NVHfp31***, ***NVHfp79-4***, ***NVHfp92-1*** and ***NVHfp89***) analysed by multiplex PCR reaction and fragment analysis (ABI 310). The investigated population consisted of 20 animals: *Falco biarmicus* (n=3), *Falco cherrurg* (n=5), *Falco peregrinus* (n=5), *Falco tinnunculus* (n=1) and their interspecific hybrids: *Falco cherrug x Falco rusticolus* (n=1), *Falco peregrinus x Falco cherrug* (n=1), *Falco rusticolus x Falco cherrug* (n=3) and *Falco rusticolus x Falco peregrinus* (n=1).

Tab. Number of founded alleles (NA) and their real heterozygosity (H), polymorphism information content (PIC), exclusion probabilities (EP) and combined exclusion probabilities (CEPs) in falcons

Microsatellite	NA	PIC	H	EP1	EP2	EP3	CEP1	CEP2	CEP3
NVHfp89	7	0.5475	0.5750	0.3734	0.1947	0.5741	***0.9820***		
NVHfp13	4	0.4033	0.4563	0.2334	0.1064	0.3710			
NVHfp31	10	0.7435	0.7650	0.5877	0.4045	0.7906		***0.9092***	
NVHfp79-4	16	0.8832	0.8925	0.8038	0.6718	0.9388			
NVHfp92-1	7	0.7097	0.7413	0.5366	0.3545	0.7336			***0.9991***

Fig. Electropherogram of analyzed data



NVHfp13 / NVHfp92-1 / *NVHfp89* / *NVHfp31* / NVHfp79-4

Results:

All microsatellites show polymorphic variability across the study samples. A total number of 44 alleles was obtained. The number of alleles at individual loci ranged from 4 (*NVHfp13*) to 16 (*NVHfp79-4*). The highest heterozygosity and polymorphism information content (over 70%) was observed for locus *NVHfp79-4*, *NVHfp31* and *NVHfp92-1*. The probabilities of paternity exclusion/one parental genotype unavailable/and parentage exclusion were for this panel 98.20%/90.92%/99.91%, respectively.

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