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Microsatellites applicable for determination of genetic diversity in Sea eagle population from Sachalin

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Introduction

No microsatellite markers have been described for Sea eagle (Haliaeetus pelagicus). Application of such markers is essential to the management and conservation of this species. From this reason we used 16 microsatellite markers developed for Spanish imperial eagle (Martinez-Cruz et al. 2002) and 3 microsatellite markers developed for aquila and haliaeetus eagles (Busch et al. 2005) to assess the individual identification, parentage analysis and genetic variability of Sea eagle population from Sachalin.

Material and Methods

The investigated population consisted of 32 animals from Sachalin. The genetic variability of 19 eagle microsatellite markers was studied and analysed by two multiplex PCR reactions – I. Multiplex: 16 MS (Aa02, Aa04, Aa11, Aa15, Aa26, Aa27, Aa35, Aa36, Aa39, Aa43, Aa49, Aa50, Aa51, Aa53, Aa56, Aa57) and II. Multiplex: 3 MS (IEAAAG04, IEAAAG05, IEAAAG12). Fragment analyses were performed on ABI PRISM 310 Genetic Analyser (Figure 1 and 2).

Results and Conclusion

Results are summarized in Table 1-2. MS were tested in three other eagle species: the white-tailed eagle (Haliaeetus albicilla), the golden eagle (Aquila chrysaetos) and the imperial eagle (Aquila heliaca). Cross-species amplification showed, that these markers were also polymorphic in these species.

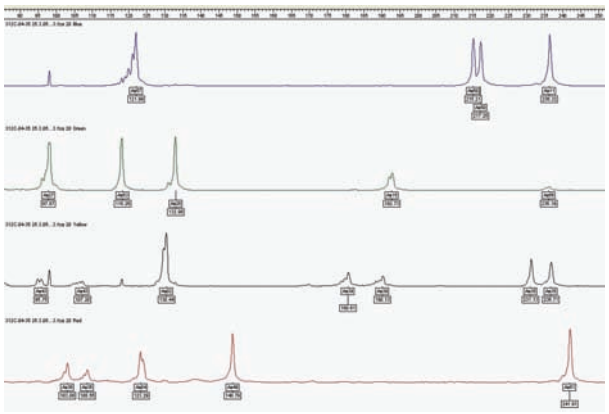
Tab. 1. Number of founded alleles (NA), their sizes, frequencies, real heterozygosity (H), theoretical heterozygosity (tH), polymorphism information content (PIC) and exclusion probabilities (PEs) in Sea eagles.

MS	NA	Size (bp)	Allele frequency	H	tH	PIC	PE1	PE2	PE3
Aa02	1	130	1.000	0.000	0.000	0.000	0.000	0.000	0.000
Aa04	1	123	1.000	0.000	0.000	0.000	0.000	0.000	0.000
Aa11	1	236	1.000	0.000	0.000	0.000	0.000	0.000	0.000
Aa15	2	192	0.825	0.343	0.288	0.246	0.123	0.041	0.202
		196	0.175						
Aa26	1	132	1.000	0.000	0.000	0.000	0.000	0.000	0.000
Aa27	2	98	0.810	0.312	0.308	0.260	0.130	0.047	0.211
		104	0.190						
Aa35	2	230	0.031	0.062	0.060	0.058	0.029	0.001	0.056
		236	0.969						
Aa36	2	103	0.790	0.281	0.331	0.276	0.138	0.054	0.221
		109	0.210						
Aa39	5	178	0.203	0.750	0.782	0.748	0.570	0.390	0.750
		180	0.156						
		188	0.219						
		190	0.297						
		192	0.125						
Aa43	1	95	1.000	0.000	0.000	0.000	0.000	0.000	0.000
Aa49	1	148	1.000	0.000	0.000	0.000	0.000	0.000	0.000
Aa50	2	215	0.047	0.093	0.089	0.085	0.042	0.004	0.079
		217	0.953						
Aa51	1	242	1.000	0.000	0.000	0.000	0.000	0.000	0.000
Aa53	1	118	1.000	0.000	0.000	0.000	0.000	0.000	0.000
Aa56	1	236	1.000	0.000	0.000	0.000	0.000	0.000	0.000
Aa57	4	116	0.266	0.625	0.653	0.585	0.371	0.219	0.528
		118	0.266						
		122	0.453						
		124	0.016						
IEAAAG04	4	214	0.161	0.281	0.497	0.456	0.279	0.129	0.441
		218	0.677						
		226	0.129						
		238	0.032						
IEAAAG05	1	126	1.000	0.000	0.000	0.000	0.000	0.000	0.000
IEAAAG12	3	104	0.156	0.468	0.404	0.366	0.209	0.081	0.342
		108	0.750						
		112	0.094						

Tab. 2. Average theoretical heterozygosity (tH), average polymorphism information content (PIC), combined exclusion probability of CEP1: paternity exclusion, CEP2: one parental genotype unavailable, CEP3: parentage exclusion.

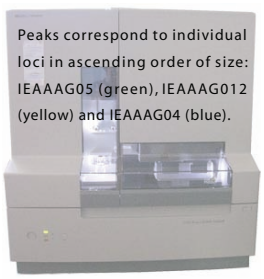
Panel of 19 MS Sea eagle (*Haliaeetus pelagicus*)	
tH	0.1797
PIC	0.1623
CEP1	0.9061
CEP2	0.6737
CEP3	0.9815

Figure 1. Electropherogram of multiplex I analyzed data

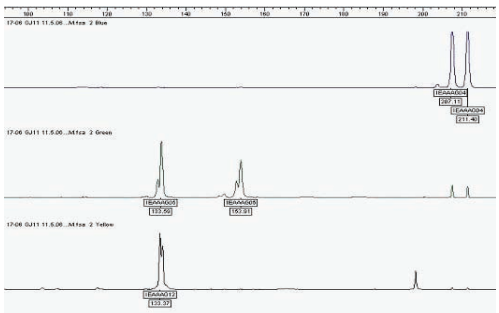


Peaks correspond to individual loci in ascending order of size: Aa43 (yellow), Aa27 (green), Aa36 (red), Aa53 (green), Aa57 (blue), Aa04 (red), Aa02 (yellow), Aa26 (green), Aa49 (red), Aa39 (yellow), Aa15 (green), Aa50 (blue), Aa35 (yellow), Aa56 (green), Aa11 (blue) and Aa51 (red)

Figure 2. Electropherogram of multiplex II analyzed data



Peaks correspond to individual loci in ascending order of size: IEAAAG05 (green), IEAAAG012 (yellow) and IEAAAG04 (blue).



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