

Preliminary genetic status of the spotted seal *Phoca largha* in Liaodong Bay (China) based on microsatellite and mitochondrial DNA analyses

Xiang Li,¹ Athanasia C. Tzika,^{2,3} Yingying Liu,⁴ Karine Van Doninck,¹ Qian Zhu,^{4,5} Michel C. Milinkovitch²

¹Evolutionary Ecology and Genetics, URBO, Department of Biology, University of Namur (FUNDP), Namur, Belgium;

²Laboratory of Artificial and Natural Evolution (LANE), Dept. of Genetics and Evolution, Sciences III, Genève 4, Switzerland;

³Evolutionary Biology and Ecology, Université Libre de Bruxelles, Brussels, Belgium;

⁴Ocean College, Shandong University at Weihai, Weihai, PR China;

⁵Third Institute of Oceanography, State Oceanic Administration, PR China

Supplementary files

Supplementary Table 1. Molecular genetic diversity indices computed from microsatellite and mitochondrial control region data.

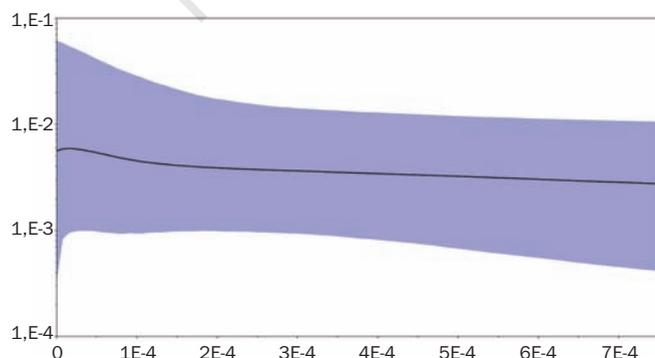
	LB (LB1+LB2)	LB1	LB2	Japan
Microsatellites				
No. of samples		25	176	
Mean No. of alleles		7.9	2.73	
H _O		0.74	0.55	
H _E		0.76	0.51	
Reference		This study	Han <i>et al.</i> (2010) ⁸	
mtDNA CR				
No. of samples	71	25	46	66
No. of haplotypes	15	10	14	57
H	0.8241±0.0371	0.8733±0.0412	0.7942±0.0560	0.9953±0.0036
π	0.0033±0.0022	0.0033±0.0022	0.0033±0.0022	0.0165±0.0085
Reference	This study & Han <i>et al.</i> (2007) ¹¹	This study	Han <i>et al.</i> (2007) ¹¹	Mizuno <i>et al.</i> (2003) ¹⁰

Number of samples, mean number of alleles per locus, observed (H_O) and expected (H_E) heterozygosities are given for the Liaodong Bay *Phoca largha* population using species-specific (LB1, our study) and non-species-specific (LB2)⁸ microsatellite loci. For mtDNA control region (CR), number of samples and of haplotypes, as well as haplotype (H) and nucleotide (π) diversities are given for the spotted seals from Liaodong Bay population (LB1, our study; LB2:¹¹ LB: combined LB1 and LB2 data) and the Japanese population (Japan).¹⁰

Supplementary Table 2. Mitochondrial genetic differentiation (control region) in terms of pairwise F-statistics (above diagonal, Φ_{st} values; below diagonal, F_{st} values) among spotted seal samples from Liaodong Bay population (LB1, our study; LB2¹¹; LB: combined LB1 and LB2 data) and Japanese population (Japan).¹⁰

A			B	
	LB1	LB2	LB	Japan
LB1		-0.004 ^{ns}	0.328 ^{***}	
LB2	0.006 ^{ns}		0.370 ^{***}	
Japan	0.062 ^{***}	0.103 ^{***}		0.338 ^{***}

***, P<0.001; **, P<0.01; *, P<0.05; ns, P>0.05



Supplementary Figure 1. Bayesian skyline plots (BSPs) of effective population size of the Liaodong Bay population. The black line represents the median posterior effective population size through time. The blue area shows the 95% highest posterior densities' (HPD) limits for effective population size. Time is measured in units of mutations per site on the X-axis, and the population size is presented as $N_e\mu$ on the Y-axis, where N_e is the effective population size and μ is the rate of mutation per generation.

Correspondence: Karine Van Doninck, Evolutionary Ecology and Genetics, URBO, Department of Biology, University of Namur (FUNDP), Rue de Bruxelles 61, 5000 Namur, Belgium.

E-mail: karine.vandoninck@fundp.ac.be

Qian Zhu Third Institute of Oceanography, State Oceanic Administration, Daxue Road 178, Xiamen 361005, PR China; Ocean College, Shandong University at Weihai, Weihai 264209, PR China. E-mail: qianzhu@sdu.edu.cn

Key words: spotted seal, *Phoca largha*, population genetics, conservation genetics, China, Liaodong Bay.

Contributions: the work presented here was carried out in collaboration among all authors. XL, QZ, MCM conceived the study; XL, ACT, MCM designed the methods and experiments; XL carried out most of the laboratory experiments; YYL participated in the mtDNA experiments; XL, KVD, ACT, MCM analyzed the data and interpreted the results; XL drafted, and KVD, ACT, MCM revised the manuscript. All authors have approved the manuscript.

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