

Spatial genetic structure in the Eurasian otter (*Lutra lutra*) meta-population from its core range in Italy

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Supplementary material

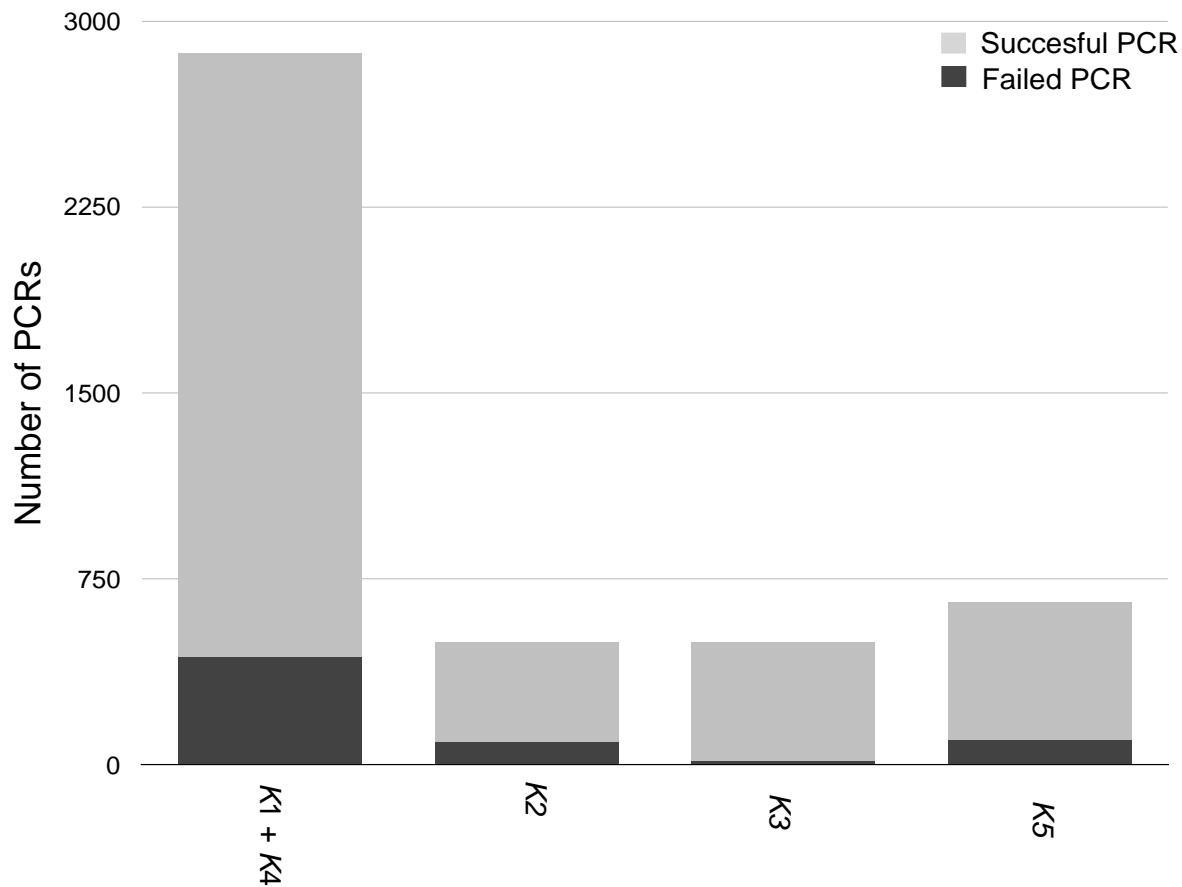


FIGURE S1 Distribution pattern of the number of successful and failed PCRs within populations (K) inferred by STRUCTURE using 11 microsatellite loci on 137 samples.

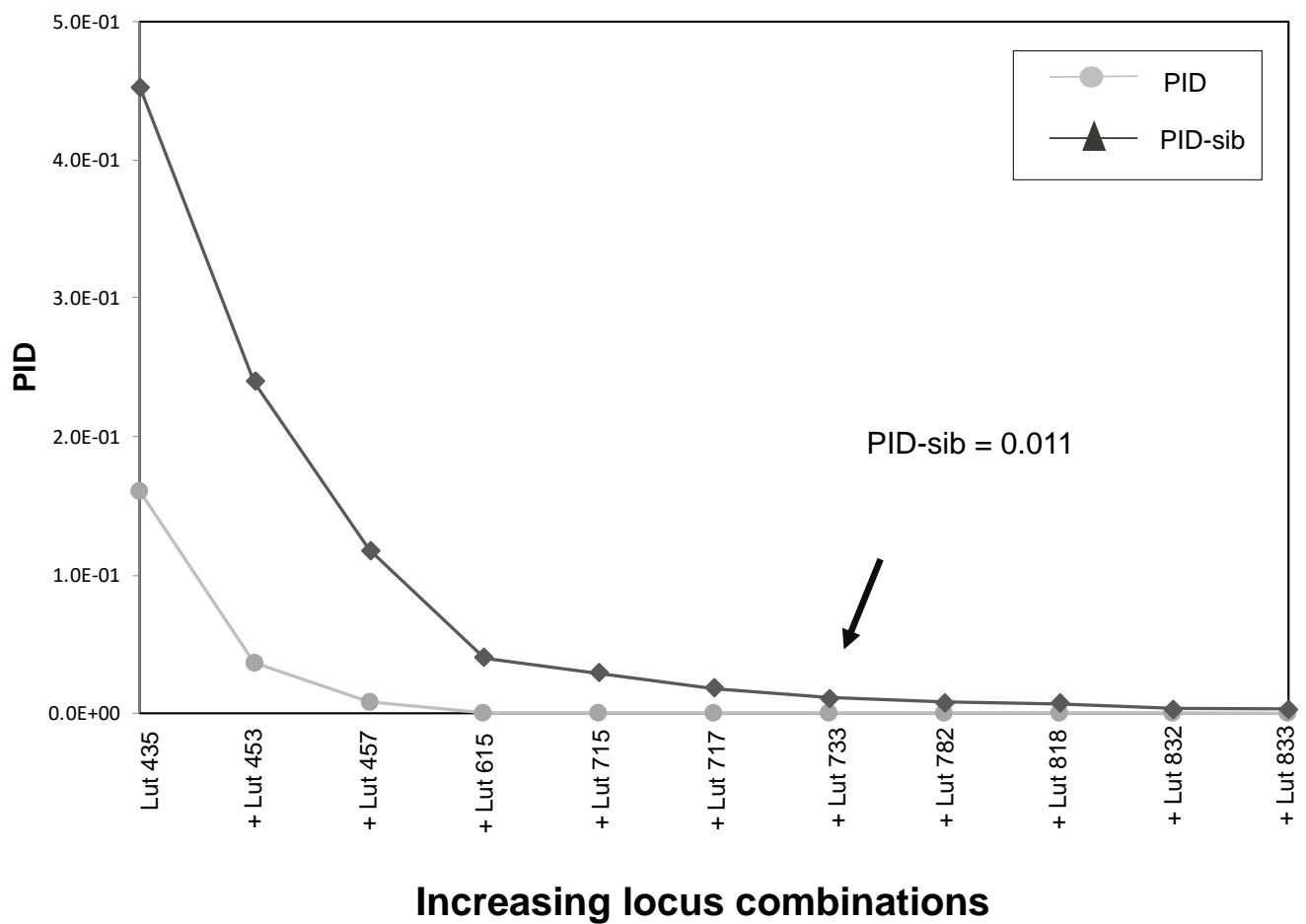


FIGURE S2 Multilocus probabilities of identity (PID) and sibling (PID-sibs) for 11 microsatellite loci estimated with all the identified individuals ($N = 136$) with software GenALEX v.6.51b2 (Peakall & Smouse, 2012). The arrow indicates the PID-sib value obtained using 7 loci.

TABLE S1 Number of alleles (N) and allelic richness (AR) for 11 microsatellite loci and calculation of deviation from Hardy-Weinberg Equilibrium (HWE) over genotypes of the sub-populations inferred according to their geographical positions on the six river basins. *P*, level of significance for the probability of deviation from Hardy Weinberg equilibrium through heterozygote deficit (HWE).

	N	AR					HWE	
		Cilento	Agri	Sinni	Lao	Basento	Abatemarco	<i>P</i>
Lut 435	4	1.98	2.83	2.11	1.95	2.00	2.00	1.000
Lut 453	10	3.56	2.74	2.58	2.86	1.00	2.00	0.102
Lut 457	6	1.98	3.18	2.65	2.23	2.00	2.00	1.000
Lut 615	9	3.42	4.48	3.99	4.08	2.75	3.00	0.000
Lut 715	2	2.33	2.61	1.70	1.98	1.96	2.00	0.001
Lut 717	3	2.23	1.90	2.12	2.15	2.71	2.00	1.000
Lut 733	5	2.44	2.52	2.53	2.73	1.00	2.00	0.000
Lut 782	2	2.78	2.21	2.35	1.90	2.00	3.00	1.000
Lut 818	3	1.64	2.08	1.32	1.22	1.00	1.00	1.000
Lut 832	5	2.25	2.40	3.01	2.50	2.00	2.00	1.000
Lut 833	3	1.56	1.90	1.08	1.06	1.00	1.00	1.000

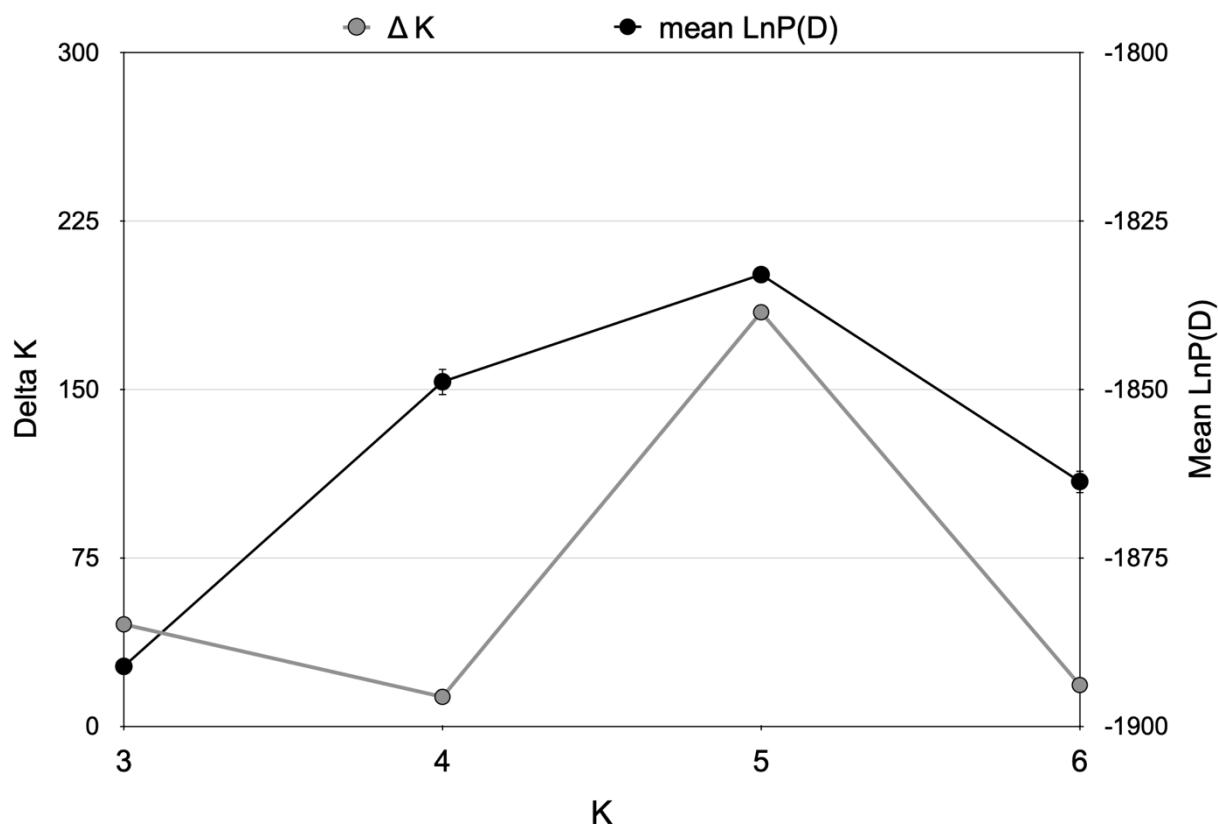


FIGURE S3 Estimated probability of the data at a given K (Mean $\text{LnP}(D)$) and rate of change in the log probability of data between successive K values (ΔK) in STRUCTURE analysis. In grey, mean log-likelihood ($\text{LnP}(D)$); in black, ΔK values for 3 independent runs of each value of K (from $K = 3$ to $K = 6$) with their corresponding standard deviation.

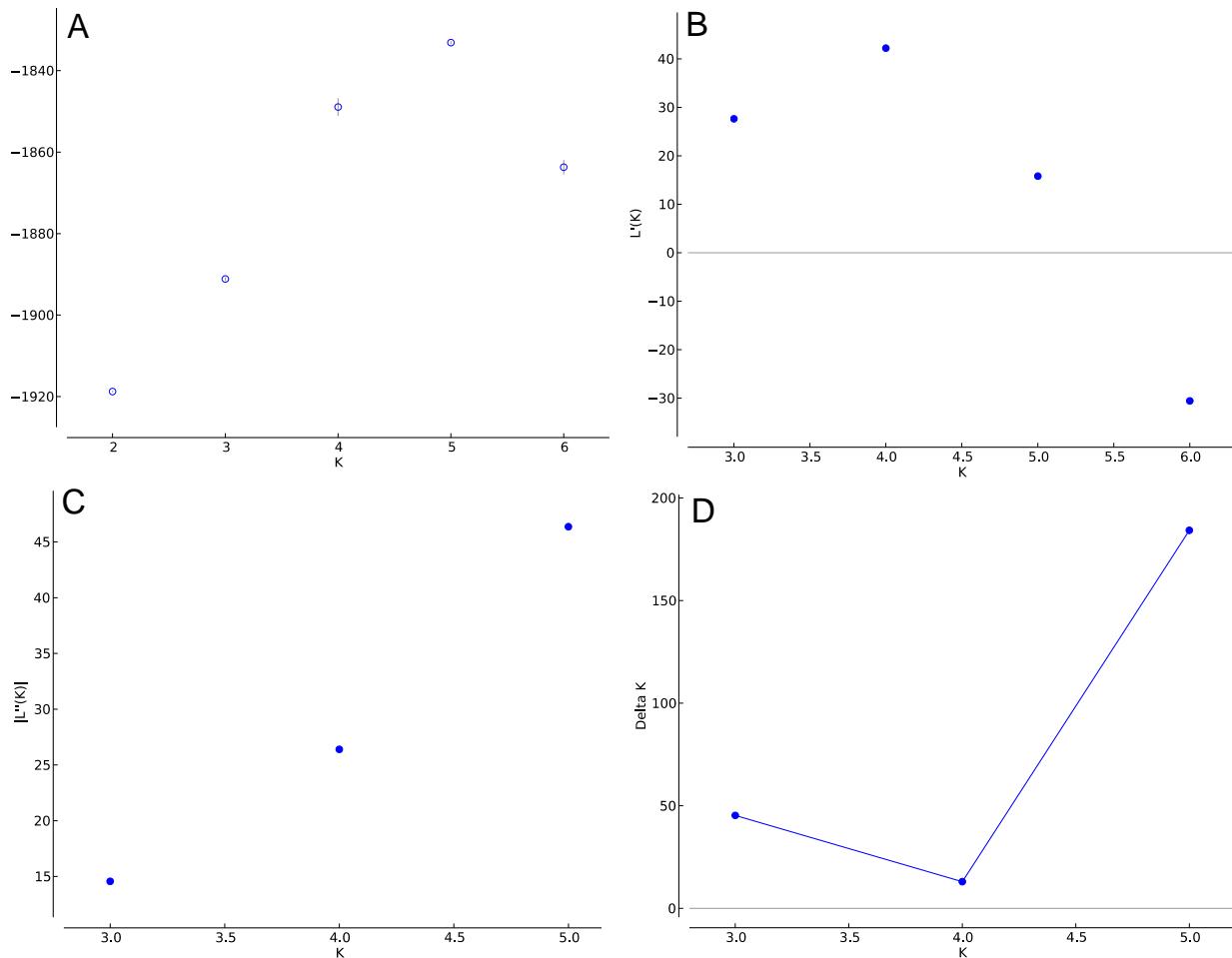


FIGURE S4 Estimation of the most likely value describing populations' clusterization according to the Evanno method (Evanno et al., 2005) produced with STRUCTURE Harvester software (Earl & von Holdt, 2012), see also supplementary tables S2 and S3 for details.

A) $L(K)$ (mean \mp standard deviation (SD); B) Rate of change of the likelihood distribution (mean); C) Absolute value of the second order rate of change of the likelihood distribution (mean); D) ΔK according to mean ($|L''(K)|$) / sd ($L(K)$) formula.

TABLE S2 STRUCTURE Harvester (Earl, 2012) output and implementing the Evanno method (Evanno et al., 2005).

#K	Reps	Mean LnP(K)	Stdev LnP(K)	Ln'(K)	Ln''(K)	ΔK
2	3	-1918.7667	0.0577	-	-	-
3	3	-1891.1333	0.3215	27.633333	14.566667	45.314789
4	3	-1848.9333	2.0257	42.200000	26.400000	13.032734
5	3	-1833.1333	0.2517	15.800000	46.366667	184.24245
6	3	-1863.7000	1.6703	-30.566667	-	-

TABLE S3 Details of the STRUCTURE Harvester (Earl, 2012) output and implementing the Evanno method (Evanno et al., 2005).

File name	#Run	K	Est. Ln probability of data	Mean value of Ln likelihood	Variance of Ln likelihood
Results_run_1_f	1	2	-1918.8	-1888.7	60.30
Results_run_2_f	2	2	-1918.8	-1888.7	60.20
Results_run_3_f	3	2	-1918.7	-1888.7	60.20
Results_run_4_f	4	3	-1890.9	-1819.4	143.0
Results_run_5_f	5	3	-1891.5	-1819.1	144.7
Results_run_6_f	6	3	-1891.0	-1819.1	143.8
Results_run_7_f	7	4	-1847.3	-1755.5	183.7
Results_run_8_f	8	4	-1851.2	-1755.5	191.4
Results_run_9_f	9	4	-1848.3	-1755.6	185.2
Results_run_10_f	10	5	-1833.1	-1715.7	234.9
Results_run_11_f	11	5	-1833.4	-1715.5	235.8
Results_run_12_f	12	5	-1832.9	-1715.7	234.4
Results_run_13_f	13	6	-1862.2	-1706.0	312.3
Results_run_14_f	14	6	-1865.5	-1706.7	317.5
Results_run_15_f	15	6	-1863.4	-1706.9	312.9

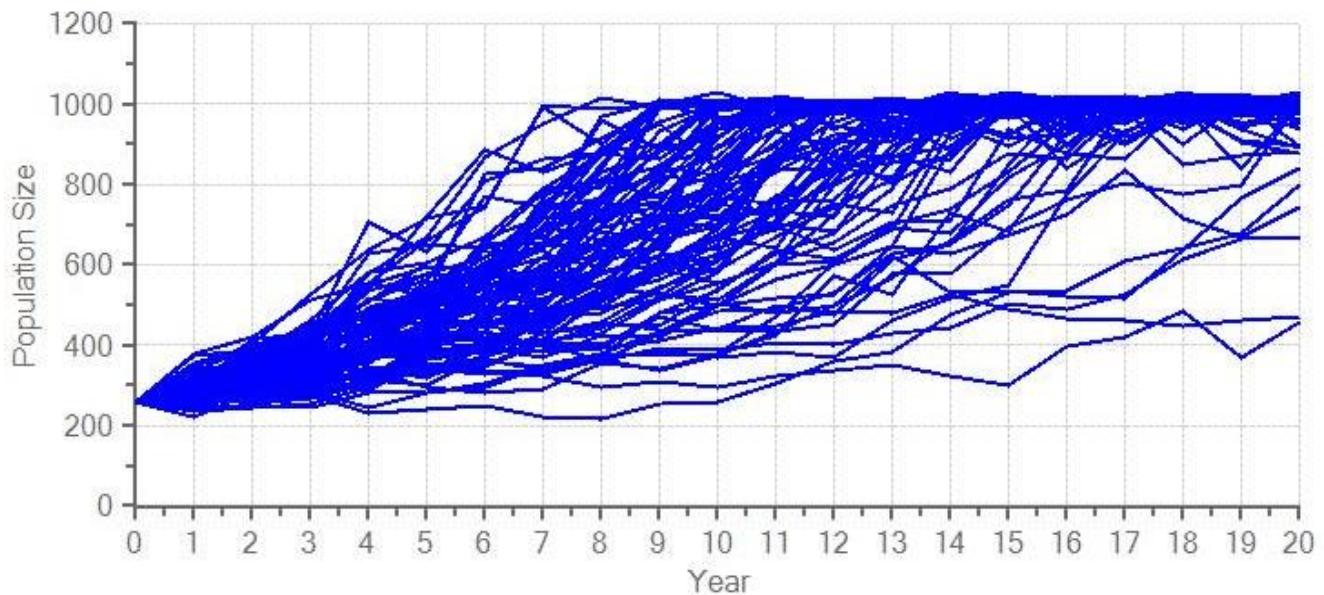


FIGURE S5 Plot of the individual iterations of the baseline VORTEX (Lacy & Pollak, 2015; Lacy et al., 2015) model of the simulated otter population dynamics in the past 20 years. The lines represent the 100 run iterations.

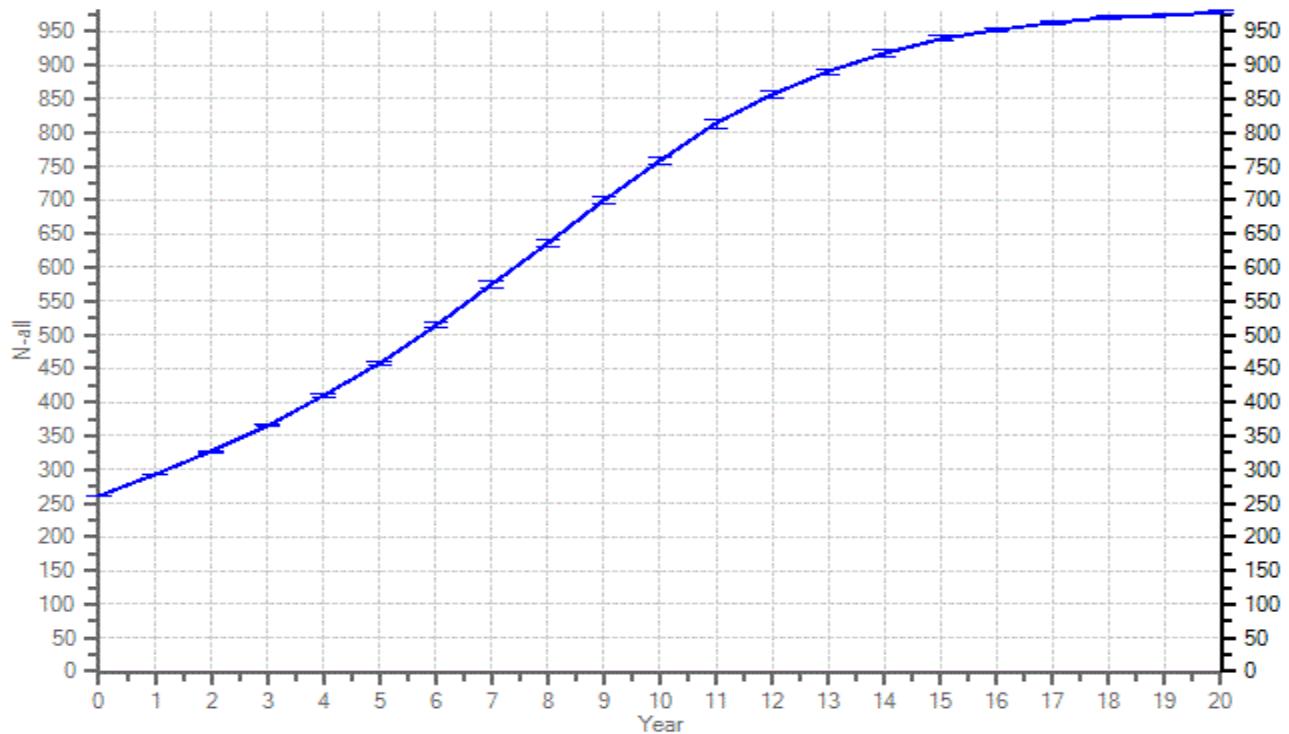


FIGURE S6 Plot of the individual iterations of the baseline VORTEX (Lacy & Pollak, 2015; Lacy et al., 2015) model of the simulated otter population dynamics in the past 20 years. The line is the average of the 100 independent runs of the simulation.

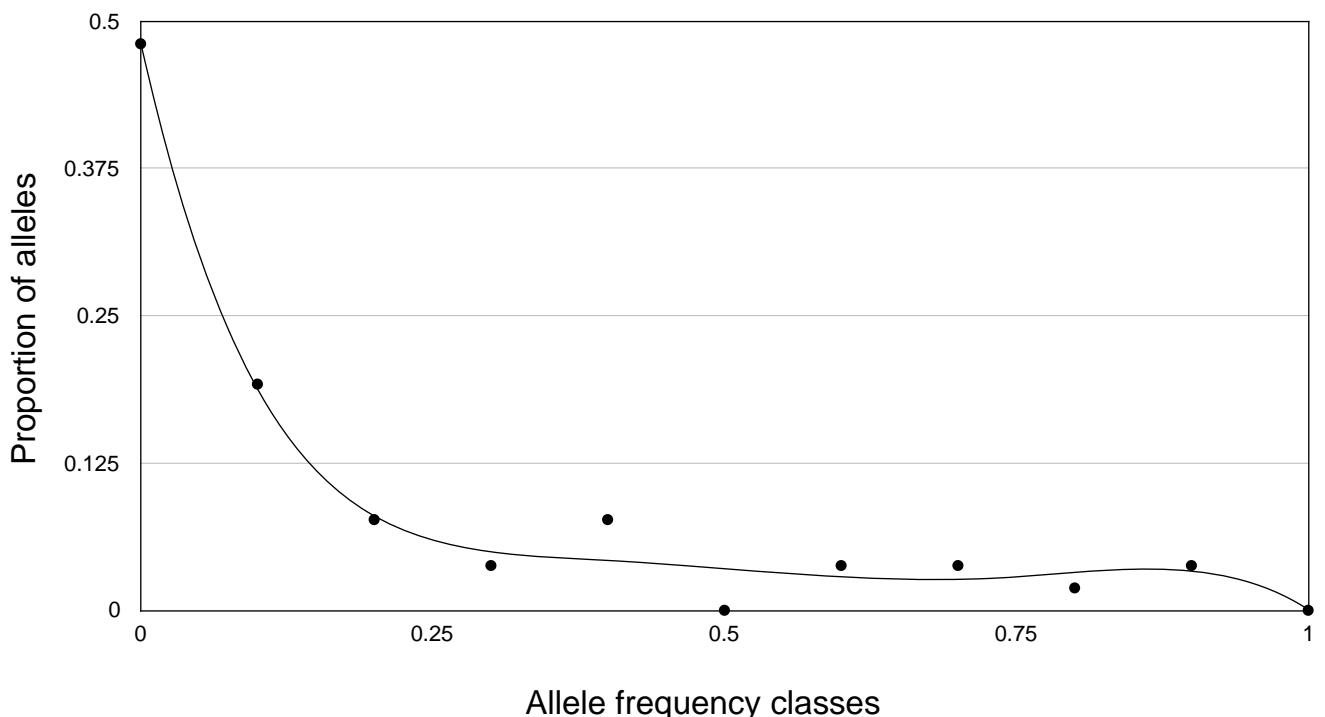


FIGURE S7 Normal L-shaped curve of the distribution of the proportion of alleles in different allelic frequency classes performed with BOTTLENECK software v.1.2.02 (Cornuet & Luikart, 1996; <http://www.montpellier.inra.fr/URLB/bottleneck/bottleneck.html>), assuming both infinite allele model (IAM), stepwise mutation model (SMM) and two phase model (TPM, with 50% of SMM and TPM, with 90% of SMM). This graphical representation is expected for a population that has not experienced a recent bottleneck that affected genetic variability (Cornuet & Luikart, 1996), suggesting that there is not a recent decline in the Italian meta-population.