



Effect of adult weight and CT-based selection on the performances of growing rabbits

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Genetic analysis reveals Roe deer (*Capreolus capreolus*) population structure in North-Eastern Italian Alps

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ABSTRACT - This preliminary study described the genetic variability and analysed the population structure of 119 roe deer (*Capreolus capreolus*) sampled over the provinces of Belluno and Trento, in the north-eastern Italian Alps, using 11 microsatellite markers. The panel of microsatellites was highly informative, and the whole population was subdivided into 2 distinct sub populations. The observed ecological population sub-units did not coincide with the administrative subdivision (the provinces borders) that are now in use for management. The results of this work confirm that molecular genetic approaches may provide useful indication for roe deer management in that area.

Key words: Roe deer, Molecular genetic, Microsatellite.

Introduction - Roe deer (*Capreolus capreolus*) is the most widely distributed cervid in Europe. Information on population sub-units is essential for a correct management, and approaches of molecular genetics may be very useful to this purpose (Zannèse *et al.*, 2006). Aim of this preliminary work is to verify whether: a) the roe deer population in the provinces of Trento and Belluno (north-eastern Italian Alps) is genetically structured in sub-populations, and b) the spatial distribution of sub-populations is consistent with the administrative subdivision of the provinces.

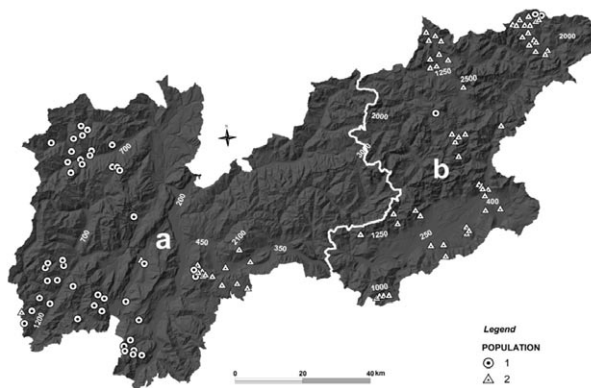
Material and methods - A total of 119 roe deer (*Capreolus capreolus*) of different ages and sex, shot in the hunting season 2007-2008 in the provinces of Trento (61 deer) and Belluno (58 deer) were sampled. Hunting management of roe deer is based on hunting districts coordinated within, provinces. Each deer was georeferenced with the geographic coordinates of the centroid of the hunting district of shooting. Genomic DNA was extracted from ear punches using a modified PURGENE DNA tissue kit (Gentra System INC) protocol. Eleven microsatellite markers (Bonnet *et al.*, 2002; Galan *et al.*, 2003; Vial *et al.*, 2003) were amplified in singleplex “touch-down PCR” (Vial *et al.*, 2003). Fragments were analyzed with Beckman Coulter CEQ 8000 automated sequencer and scored with

Table 1. Number of alleles per locus (N_a), overall expected (H_e) and observed (H_o) heterozygosity, F_{IS} values and P-value (P) in roe deer (*Capreolus capreolus*) shot in North-Eastern Italian Alps.

Locus	N_a	N_a Trento	N_a Belluno	H_e	H_o	F_{IS}	P
BL4	10	8	8	0.591	0.433	0.257	<0.001
BM1706	8	7	7	0.804	0.758	0.044	0.1548
BM757	10	9	8	0.718	0.477	0.333	<0.001
BM848	10	10	9	0.794	0.679	0.149	<0.001
BMC1009	7	7	6	0.750	0.576	0.233	<0.001
CSSM39	7	6	7	0.737	0.611	0.173	0.0092
CSSM41	6	5	5	0.501	0.470	-0.036	0.1564
CSSM43	6	6	5	0.580	0.628	-0.095	0.8703
HUJ1177	10	8	9	0.766	0.710	0.070	0.2012
IDVGA8	6	6	4	0.486	0.400	0.179	0.1737
OARFCB304	13	12	9	0.861	0.710	0.167	<0.001
Mean \pm s.d.	8.45 \pm 2.30	-	-	0.689 \pm 0.128	0.586 \pm 0.124	0.134	-

the Fragment Analysis software (Genetic Analysis System v.9, Beckman Coulter). Summary statistics were calculated using Genepop v.4.0 (Raymond and Rousset, 1995), MSA (Microsatellite analyzer) v.4.05 (Dieringer *et al.*, 2003), F-stat v.2.9.3 (Goudet *et al.*, 2001) and Genetix v.4.01 (Belkir *et al.*, 1998). Population structure was assessed using STRUCTURE version 2.2 (Pritchard *et al.*, 2000), with an admixture model. The true number of K clusters was detected by using the ΔK criteria of proposed by Evanno *et al.* (2005), testing a range from 1 to 6 populations.

Figure 1. Distribution of deer within the two populations identified across the Trento (a) and Belluno (b) provinces.



Results and conclusions - A total of 93 alleles were obtained in the whole population, ranging from 6 to 13 with an average of 8.45 alleles per locus (table 1). There was no significant linkage disequilibrium between pairs of loci using Bonferoni adjustments for multiple tests. F_{IS} was low (0.13) but significantly different from zero; six loci showed a significant heterozygosity deficit. The roe deer population was not in Hardy Weinberg equilibrium (HWE), in agreement with Coulon *et al.* (2004) and Targhetta (2006).

The total population was struc-

tured in 2 sub-populations, one distributed in the hunting districts of the western part of the Trento province (Sub-1), and the other in those of the eastern part of the province and in the Belluno province (Sub-2) (figure 1). The border between Sub-1 and Sub-2 coincides with a motorway and a highly urbanised area in the “Valle dell’Adige”, and the observed ecological population sub-units do not coincide with the administrative subdivisions that are now in use for management. Sub-1 showed a higher genetic variability than Sub-2 ($H_o=0.596$ and 0.577 and $H_e=0.711$ and 0.640 , respectively). The F_{IS} estimates were 0.163 for Sub-1 and 0.114 for Sub-2. In conclusion, the results of this work provide useful indication for roe deer management in the provinces of Trento and Belluno, and confirm that molecular genetic approaches may give essential indications for wildlife management.

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