## Genetic variability of the Bracco Italiano dog breed based on microsatellite polimorphysm

R. Ciampolini<sup>1</sup>, F. Cecchi<sup>1</sup>, A. Bramante<sup>1</sup>, F. Casetti<sup>2</sup>, S. Presciuttini<sup>1</sup>

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<sup>1</sup>Centro Interuniversitario di Ricerca e di Consulenza sulla Genetica del Cane, Facoltà di Medicina Veterinaria, Università di Pisa; <sup>2</sup>Società Amatori Bracco Italiano (SABI).





The Bracco Italiano is one of the oldest pointing dog breed, used for hunting ever since the Renaissance time. Today it has increasing importance as to be the winner of the "Eukanuba World Challenge 2009", one of the most prestigious events of dog shows in USA. In this work we illustrate an assessment of the genetic variability for 21 STRs typed in a sample of 72 unrelated Italian hounds ("Bracchi" - BI) and a sample of 43 dogs from other 23 different breeds ("Other dogs" - OD). The aim of the present study was to estimate the genetic variability of the BI dog breed using microsatellite markers, in order to provide information useful in conservation purposes. Three multiplexes were worked out, which allowed analyzing 21 STR markers from the panels recommended for the 2006 and 2008 ISAG canine comparison test. Allele size in bp was determined using the comparison-test reference samples as anchor values. Number of alleles, allele frequencies, deviations from Hardy-Weinberg proportions, linkage disequilibrium among loci, genetic similarity, genetic distances and molecular coancestry-based parameters were calculated.

INTRODUCTION and MATERIALS AND METHODS

Table 1. Details on microsatellite marked used, number of alleles and polymorphism information content for Bracco Italiano and for Other Doas.

	Bracco Italiano				Other Dogs					
	38.4		Heterozigosity			-		Heterozigosity		
Microsatellite Marker	No of alleles	PIC	Observed	Expected	P.	No of alleles	PIC	Observed	Expected	P.
AHT121	7	0.675	0.649	0.719	0.198	Ш	0.869	0.605	0.891	0.000
AHT137	8	0.602	0.740	0.643	0.274	10	0.835	0.698	0.862	0.001
AHTH130	6	0.602	0.597	0.668	0.033	11	0.810	0.605	0.841	0.000
AHTh171	9	0.693	0.675	0.743	0.133	п	0.827	0.791	0.854	0.026
AHTH260	7	0.418	0.364	0.444	0.000	10	0.812	0.674	0.840	0.036
AHTk211	5	0.449	0.597	0.528	0.816	6	0.739	0.698	0.784	0.231
AHTK253	6	0.527	0.481	0.574	0.244	6	0.631	0.488	0.674	0.011
CXX279	6	0.627	0.597	0.665	0.008	9	0.769	0.744	0.805	0.036
FH2054	8	0.690	0.714	0.740	0.112	9	0.825	0.791	0.853	0.184
FH2848	8	0.574	0.597	0.601	0.715	8	0.813	0.535	0.844	0.000
INRA21	7	0.728	0.792	0.768	0.359	6	0.715	0.605	0.760	0.131
INU005	6	0.576	0.571	0.642	0.085	8	0.703	0.465	0.747	0.000
INU030	3	0.467	0.506	0.532	0.866	9	0.732	0.605	0.775	0.006
INU055	5	0.408	0.442	0.472	0.676	7	0.778	0.721	0.813	0.174
REN105L03	5	0.513	0.338	0.560	0.000	10	0.802	0.628	0.832	0.000
REN162C04	5	0.591	0.675	0.665	0.009	9	0.736	0.512	0.778	0.002
REN169018	6	0.773	0.727	0.807	0.204	8	0.779	0.628	0.804	0.053
REN169D01	8	0.676	0.675	0.708	0.113	8	0.764	0.674	0.815	0.004
REN247M23	8	0.651	0.675	0.686	0.168	7	0.645	0,465	0.704	0.002
REN54P11	7	0.626	0.532	0.664	0.000	7	0.761	0.558	0.802	0.005
REN64E19	5	0.509	0.519	0.597	0.072	9	0.822	0.558	0.851	0.000

## RESULTS

Table 2. Genetic Similarities, self molecular coancestry, inbreeding, average molecular coancestry and kinship distance.

	Bracco Italiano	Other dogs
Genetic similarities	0.455	0.285
Self molecular coancestry (s)	0.703	0.689
Inbreeding	0.406	0.379
Mean Molecular Coancestry coancestry (fij)	0.337	0.203
Kinship distance (Dk)	0.336	0.486
F <sub>is</sub>	0.060	0.220

In BI the genetic similarity within the whole population was high  $(0.455\pm0.018)$ ; this parameter reveals the great homogeneity of the sampled animals as confirmed also by the small kinship distance (0.336) and by the high values of the self molecular coancestry (0.703) and of the inbreeding coefficient (0.406).

The number of different alleles ranged 3 to 9 (mean 6.43) in the BI, compared with 6-11 (mean 8.52) in the OD, whereas the expected heterozygosity ranged 0.44-0.81 (mean 0.64) compared with 0.51-0.89 (mean 0.81).



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Viale delle Piagge 2, 56124 Pisa, Italy; Phone +390502216877; Fax +390502216901

<sup>1</sup> Università di Pisa







CONCLUSIONS

Our findings highlight that the Bracco Italiano dog has quite a low genetic variability, as shown by the allele number, heterozygosity level, genetic similarities and molecular coancestry-based parameters suggesting the need for a careful genetic management of the population in order to avoid the risk of an excessive increase in the inbreeding level which would result in significant inbreeding depression and in significant loss of genetic variation.