A colony of dog guides: analysis of the genetic variability assessed by pedigree data

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ABSTRACT - The study presents the analysis of the genetic variability in a colony of dog guides. Three breeds, Labrador (L), Golden Retriever (GR), and German Shepherd (GS), were evaluated. Pedigrees data on 370 L, 260 GR, and 85 GS dogs bred for guide by the National Guide Dog School (SNCG) of Scandicci (Florence, Italy) were used. Data were available beginning from 1994. The average coefficient of coancestry and the mean F were 0.8% and 0.45% in GR, 0.7% and 0.38% in L, 1.0% and 0.49% in GS, respectively. The rate of increase in inbreeding was lower in L population (0.17) than in GR population (0.54), while in GS only the dogs with 5 e 7 traced generations resulted inbred. The results of this research point out that the genetic management of the dogs seems to be carefully and rationally monitored. Nevertheless, the population that may require a greater attention seems to be the GR, where a higher increase of the coefficient of inbreeding per generation is observed; therefore, the importation of germplasm from other working dogs is desirable in order to avoid in future an excessive increase of the inbreeding that could lead to adverse consequences for dogs health and fertility.

Key words: Dog guide, Pedigree data, Genetic variability.

Introduction - The National Guide Dog School (SNCG) of Scandicci (Florence, Italy) was born for initiative of the Italian Union of the Blind; since April, 1st 1979 (D.P.R. 616/1977), the Regional Administration of Tuscany has been appointed as responsible for the management of the School. The employment of few reproducers may determine an excessive increase of the inbreeding and the mortality of puppies can significantly increase (Van der Beek *et al.*, 1999); in fact, a positive correlation was shown between the frequency of some genetic diseases and the average coefficient of inbreeding (Ubbink *et al.*, 1992). Moreover, purebred dogs often have to deal with genetic diseases and more than 400 genetic diseases are registered in this species (Nielen *et al.,* 2001). For these reasons, the aim of the present work was to estimate genetic variability of a colony of dogs bred at the SNCG.

Material and methods - Data were provided by the National Guide Dog School (SNCG) of Scandicci (FI) which breeds and trains dogs to be guides for blind people. Data were available beginning from 1994. The data included pedigrees of 370 L, 260 GR, and 85 GS dogs, although not all these animals had completed the training and worked as guides. For each breed, after being entered into an electronic database, genealogical information was used to determine several demographic and genetic parameters, including the whole population inbreeding level and inbreeding for the two males and females populations, inbreeding for each traced generation, average coancestry coefficient, and generation intervals. Calculations were performed using the program ENDOG v4.5 (Gutiérrez and Goyache, 2008) and CFC (Sargolzaei *et al.*, 2006). The rate of inbreeding is estimated by $\Delta F = (lxb)/\{1-[F_{last}-(lxb)]\}$ where *l* is the average generation interval, *b* is the

average annual increase in inbreeding coefficient, estimated by regressing F on birth year and F_{last} is the inbreeding coefficient in the last year studied (Gutiérrez *et al.*, 2003).

Results and conclusions - The most complete genealogies were observed for the L population, where the 68.65% of the dogs had both parents known *vs.* 66.54% of GR and 56.47% of GS. Estimates of f_e, f_a, and f_t for each breed are reported in Table 1. As expected, the number of ancestors (f_a) for all populations was lower than the effective population size of founders (f_e). The ratio f_e/f_t was similar in GR and L and was higher than that observed in GS (0.71 and 0.70 *vs.* 0.42). The comparison between the effective number of founders (f_e) and the effective number of ancestors (f_a) allows to reveal the decrease in genetic variation of populations that have passed through a bottleneck. This decrease was found to be rather important in GR, where the lowest value of the ratio f_a/f_e (0.35) was observed. The expected contributions of founders and/or ancestors were even more unbalanced in the GR breed than in the L breed, as some founders have contributed very little or, in some cases, not at all.

The total number of sires was 111, 85, and 33 for L, GR, and GS respectively, while the total number of dams was 131, 91, and 44 for L, GR, and GS respectively, with a dams-sires ratio of 1.18, 1.07, and 1.33 for L, GR, and GS respectively. Several dams and sires in each breed had just one litter, and no dam produced more than 7 offspring in GS (data not shown). In the L breed, 3 sires and 3 dams produced more than 17 offspring (maximum values: 32 for one sire and 27 for one dam), while in GR one sire produced 45 offspring and 4 dams produced more than 10 offspring each (maximum value: 32). In the L breed, 25 full-sib groups were identified (5.48, average family size; 11, maximum value; 2, minimum value); in the GR breed, 12 full-sib groups were identified (7.25, average family size; 19, maximum value; 2, minimum value), while in GS only 2 full-sib groups were identified (6, average family size; 7, maximum value; 5, minimum value). Overall generation intervals were 2.63±0.26 years for GR, 2.17±0.42 for GS, and 2.08±0.31 for L.

Number and percentage of inbred animals and mean inbreeding coefficients (F) in the three breeds are reported in Table 1. Mean inbreeding was less than 0.50% in all breeds, even if the lowest value was observed in the L population (0.38% *vs.* 0.45% for GR and 0.49% for GS). Inbred animals represented 5.77% of the GR population, 10.59% of the GS population, and 13.78% of the L population. Inbreeding value was higher in females than in males for the GR e L breeds.

Analyzing the inbreeding for each traced generation (Table 2), we observed that L subjects have rather contained inbreeding coefficients, except for the subjects with 4 and 5 traced generations (2.05 and 2.63% respectively).

Also for the GR animals, the mean inbreeding coefficient for each traced generation resulted rather contained, except for the 28 subjects with 7 generation traced, for which the mean F was higher than 3.125%, i.e. the value resulting from the mating of two animals sharing a single grandparent.

In the GS population, only the dogs with 5 e 7 traced generations resulted inbred (100% of the animals, with mean values of 3.91 e 4.69%, respectively).

In GR and GS, the average coefficient of inbreeding was substantially lower than the average coefficient of coancestry of the parents: the average ratio between the offspring inbreeding value and the average parental coancestry coefficient ranged from 0.32 in the GS population to 0.45 in the GR population. In the L population, the average ratio was equal to 1.05.

The rate of increase in the inbreeding values was lower in the L population (0.17) than in the GR population (0.54).

The results of this research point out that the genetic management of the dogs of the School seems to be carefully and rationally monitored. Nevertheless, the population that may require a greater attention seems to be the GR, where an higher increase of the coefficient of inbreeding for generation is observed; therefore, the importation of germplasm from other working dogs is desirable in order to avoid in future an excessive increase of the inbreeding that could lead to adverse consequences for dogs health and fertility.

Table 1.   Mean genealogical parameters, number of inbred animals and F coefficients by population.

Breed	*f_t	f_e	f_a	f_e/f_t	f_a/f_e	N° dogs	N° inbred	N° founders	** NDBKP	Mean F (%)	Average F for inbred (%)	*** ACC (%)
GR	88	62.11	22	0.71	0.35	260	15	90	173	0.45	8.0	0.80
males						127	7	41	85	0.40	7.2	0.85
females						133	8	43	88	0.53	8.7	0.75
L	127	88.57	37	0.70	0.42	370	51	111	254	0.38	2.7	0.70
males						175	26	47	122	0.30	1.9	0.80
females						195	25	52	132	0.49	3.6	0.70
GS	85	35.53	20	0.42	0.56	85	9	35	48	0.49	4.5	1.00
males						42	6	14	26	0.66	4.4	1.20
females						43	3	19	22	0.34	4.7	0.80

*f_t: Base population; f_e: Effective population size of founders; f_a: Effective n° of ancestor for the reference population; **NDBKP=N° dogs with both known parents; ***ACC=Average Coancestry Coefficient.

Table 2.   Mean inbreeding for maximum generation by population.

Traced Generation	N° dogs			Mean F (%)			% Inbred			Average Coancestry (%)		
	L	GR	GS	L	GR	GS	L	GR	GS	L	GR	GS
0	118	87	37									
1	92	57	20	0.00	0.00	0.00	0.00	0.00	0.00	0.93	1.13	2.10
2	27	22	9	0.00	0.57	0.00	0.00	4.55	0.00	0.83	1.28	2.83
3	22	14	5	1.14	0.45	0.00	4.55	7.14	0.00	1.08	1.83	3.34
4	15	8	4	2.50	0.00	0.00	13.33	0.00	0.00	1.29	2.27	3.90
5	11	40	2	2.63	0.23	3.91	27.27	7.50	100	1.76	4.40	3.95
6	35	4	1	0.13	1.95	0.00	31.43	25.00	0.00	2.02	2.41	5.11
7	49	28	7	0.25	3.25	4.69	34.69	39.29	100	2.57	3.24	5.67
8	1			1.03			100			2.85		

REFERENCES - **Gutiérrez,** J.P., Altarriba, J., Diaz, C., Quintanilla, R., Cañon, J., Piedrafita, J., 2003. Pedigree analysis of eight Spanish beef cattle breeds. Genet. Sel. Evol. 35:43-63. **Gutiérrez**, J.P., Goyache, F., 2008. ENDOG v4.5 - A computer program for monitoring genetic variability of populations using pedigree information. **Nielen**, A.L., Van der Beek, S., Ubbink, G.J., Knol, B.W., 2001. Population parameters to compare dog breeds: differences between five Dutch purebred populations. Vet. Q. 23:43-49. **Sargolzaei**, M., Iwaisaki, H., Colleau, J.J., 2006. CFC (Contribution, Inbreeding (F), Coancestry, Release 1.0. A software package for pedigree analysis and monitoring genetic diversity. **Ubbink**, G.J., Knol, B.W., Bouw, J., 1992. The kinship between homozigosity and the occurrence of specific disease in Boubier Belge des Flandes dogs in the Netherlands. Vet. Q. 14:137-140. **Van der Beek**, S., Nielen, A.L., Schukken, Y.H., Brascamps, E.W., 1999. Evaluation of genetic, common litter, and within-litter effects on preweaning mortality in a birth cohort of puppies. Am. Vet. Res. 60:1106-1110.