

## ORIGINAL ARTICLE

**Genetic variability in French dog breeds assessed by pedigree data**G. Leroy<sup>1,2</sup>, X. Rognon<sup>1</sup>, A. Varlet<sup>2</sup>, C. Joffrin<sup>1</sup> & E. Verrier<sup>1</sup>

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**Summary**

Pedigree data of nine French dog breeds, namely Barbet (BAR), Basset fauve de Bretagne (BAF), Beauceron (BEN), Berger des Pyrénées (BRP), Bouledogue Français (BUF), Braque Saint-Germain (BQG), Dogue de Bordeaux (DOB), Epagneul Breton (EPB) and Montagne des Pyrénées (MOP), were analysed. The effective numbers of ancestors of dogs born from 1997 to 2001 were equal to 6.7 (BAR), 40.2 (BAF), 36.5 (BEN), 16.0 (BRP), 37.0 (BUF), 13.1 (BQG), 28.9 (DOB), 33.3 (EPB) and 34.0 (MOP). The expected contributions of the major ancestors were found to be highly unbalanced in the EPB and BRP. The average coefficient of inbreeding of dogs born from 1997 to 2001 with both parents known was equal to 12.4% (BAR), 3.9% (BAF), 5.4% (BEN), 7.2% (BRP), 3.3% (BUF), 6.0% (BQG), 4.1% (DOB), 4.5% (EPB) and 4.0% (MOP). These values were found to be significantly higher than the average coefficient of kinship between the male and the female parents of these animals, except in the BAR and BQG, revealing an usual practice of mating between related animals. The results are discussed in relation with the demographic situation and the use of each breed. The method used to class an endangered breed and the ways to preserve the genetic variability, when necessary, are evoked.

**Introduction**

Genetic variability and structure in domestic breeds largely depend on the breeders' decisions and practices. Selection for specialized types of animals may result in strong bottlenecks within the populations, leading to high rates of inbreeding. Moreover, in dogs, the mating between close relatives is frequently used (e.g. Ubbink 1998). Mortality of puppies significantly increases with inbreeding (Van der Beek *et al.* 1999) and 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 (Patterson 1993, in Nielen *et al.* 2001). For these reasons, the evolution of inbreeding within some dog populations has been studied on the basis of pedigree data (Karjalainen & Ojala 1997; Mäki *et al.* 2001; Nielen *et al.* 2001). From the same data, the computation of the probabilities of gene origin (James 1972) may provide a complementary view of the within-population genetic variability, as illustrated in several studies on livestock breeds (e.g. Moureaux *et al.* 1996; Gutiérrez *et al.* 2003; Huby *et al.* 2003).

The total number of dogs in France is about 8 million. One-and-a-half million of these animals are purebred dogs and approximately a third of them are registered by the *Société Centrale Canine* (SCC),

which is the national federation of French kennel clubs. There are 300 different dog breeds kept in France and, on the basis of historical data, 55 of these breeds are considered to be of French origin by the SCC. In this paper, we investigated the genetic structure of some French dog breeds, using pedigree data and we compared their genetic variability. The results are discussed in relation to two main objectives: (i) to make a diagnosis, which represents the first step to genetic management of such populations and (ii) to provide, on a sample of breeds, original results on genetic variability in French dog breeds, which has never been investigated.

## Materials and methods

### Populations studied and data file

Nine breeds have been chosen among the 55 French breeds, in order to represent a large range of situations according to the morphology of the animals, their use and the demographical parameters of the population (Table 1). The Epagneul Breton (EPB) and the Beauceron (BEN) breeds are the two dog breeds of French origin with the highest population size. These two breeds have large numbers of registered animals. On the contrary, the Barbet (BAR), Braque Saint-Germain (BQG) and Montagne des Pyrénées (MOP) breeds have a small and/or a decreasing population size and they may be considered as endangered. The other four breeds show an intermediate population size, the numbers of Bouledogue Français (BUF) and Dogue de Bordeaux (DOB) dogs have recently strongly increased, the numbers of Basset fauve de Bretagne (BAF) and Berger des Pyrénées (BRP) dogs have recently decreased. The number of breeders having registered at least one litter in 2004 ranged from three in the BAR breed to 529 in the EPB breed.

The national pedigree file of the SCC was used, including all registered dogs from 1975 to 2001. In France, the matings and the litters have to be declared by the breeders, in order for the puppies to be registered. The registry is definitive only when the dog has passed an examination called 'confirmation' but only a third of the owners ask for confirmation. Paternity parentage control is made, on the basis of simple criteria: (i) consistency between dates of mating and birth and gestation lengths, (ii) consistency between colour patterns of offspring and assumed parents. Molecular parentage control is not compulsory.

The animals born from 1997 to 2001, with both parents known, were used to perform some analyses of interest mainly for the current population. This

**Table 1** Some characteristics of the nine dog breeds studied and of their data files

Full name	Abbreviation used in this paper	Uses (other than petdog)	Owner/breeders information in 2004, no. of breeders having registered at least one litter (SCC data)	Populations parameters, evolution of the no. of births from 1994 to 2003	Content of data files	
					Total no. of registered dogs 1975–2001	No. of registered dogs born in 1997–2001 with both parents known: reference population
Barbet	BAR	Waterdog	3	+6%	307	38
Basset fauve de Bretagne	BAF	Scent hound	149	– 10%	10 077	2211
Beauceron	BEN	Watchdog, sheepdog	310	+3%	30 942	5031
Berger des Pyrénées	BRP	Sheepdog	82	– 19%	8687	1092
Bouledogue Français	BUF	–	429	+157%	8812	3306
Braque Saint-Germain	BQG	Pointing dog	5	+31%	980	146
Dogue de Bordeaux	DOB	Watchdog	108	+76%	3355	924
Epagneul Breton	EPB	Pointing dog	529	+5%	51 973	8775
Montagne des Pyrénées	MOP	Livestock protection dog	38	–32%	5565	413

group of animals was called the reference population. The total number of animals in the data file and the number of animals from the reference population are given in Table 1.

## Methods

The analyses were performed for each breed separately, using the PEDIG software (Boichard 2002, <http://www-sgqa.jouy.inra.fr/sgqa/diffusions.htm>). The pedigree completeness level, the demographic parameters and the probabilities of gene origin were analysed for the reference population of animals born from 1997 to 2001. The percentage of known ancestors was computed by simple counting, for each generation of ancestors of the animals born from 1997 to 2001, including those that had unknown parents. The number of equivalent complete generations traced (*EqG*) was computed as the sum over all known ancestors of the terms  $(1/2^t)$ , where  $t$  is the ancestor's generation number, which is equal to one for the parents, two for the grandparents, etc. (Maignel *et al.* 1996). Generation lengths ( $T$ ) were computed in the four pathways as the average age of parents at the birth of their useful offspring (an offspring was considered as useful when itself had registered offspring).

Ancestors without known parents were considered as non-inbred and non-related founder animals. The major ancestors (founders or not) of the reference population were detected using the iterative method by Boichard *et al.* (1997). The expected genetic contribution to the reference population of each founder was computed as the probability ( $p_i$ ) for a gene taken at random within the reference population to come from founder  $i$  ( $\sum_i p_i = 1$ ; James 1972). The expected marginal contribution ( $q_j$ ) of each major ancestor ( $j$ ) was computed as its expected genetic contribution independent of the contributions of the other ancestors ( $\sum_j q_j = 1$ ; see Boichard *et al.* 1997 for details). The effective number of founders ( $f_e$ ) and the effective number of ancestors ( $f_a$ ) are defined as the reciprocal of the probability that two genes drawn at random in the reference population come from the same founder or from the same ancestor respectively. These numbers were computed as follows:

$$f_e = \frac{1}{\sum_i p_i^2} \quad \text{and} \quad f_a = \frac{1}{\sum_j q_j^2}.$$

Individual coefficients of inbreeding were computed for all animals in the data file, using the method by Van Raden (1992). The realized effective size

( $Ne_r$ ) was estimated as follows: First the evolution of the average coefficient of inbreeding per birth year was observed from 1975 to 2001. The annual increase rate of inbreeding was estimated by linear regression over time. Next by combining the annual rate and the average generation length of each breed, the inbreeding between two successive generations ( $\Delta F_t$ ) could be computed by the following equation (Falconer & Mackay 1996)

$$\Delta F_t = \frac{F_{t+1} - F_t}{1 - F_t}.$$

The average rate of inbreeding over the whole period ( $\Delta F$ ) was computed as the mean of the different  $\Delta F_t$ . Then the realized effective size ( $Ne_r$ ) of each population was computed as follows:

$$Ne_r = \frac{1}{2\Delta F}.$$

In order to categorize breeds among class of endangerment (Simon 1999), the maximum value of inbreeding after 50 years of conservation ( $F-50$ ) was computed as follows,  $g$  being the number of generations during 50 years.

$$F - 50 = 1 - (1 - \Delta F)^g$$

The coefficients of kinship (Malécot 1948) between all the male parents and all the female parents of the reference population were computed. This average coefficient of kinship represents the expected average coefficient of inbreeding of the reference population under the hypothesis of random mating. In order to assess the impact of the mating practices, this expected coefficient of inbreeding was compared with the observed average coefficient of inbreeding of the reference population.

## Results

### Pedigree completeness level

Some criteria of the pedigree completeness level of the reference population are given in Table 2 for each breed (percentage of known ancestors for the first and the fifth generation, number of equivalent generations traced). The highest depths of pedigree were observed in the two breeds with the highest population sizes, namely the BEN and the EPB breeds. The number of equivalent generations traced (*EqG*) was found to be around five to six in the other breeds, except in the BAR breed where a much lower value was observed because of a large number of animals registered without or with little knowledge of their pedigree.

**Table 2** Pedigree completeness level for the dogs born from 1997 to 2001

Breed	Proportion (%) of ancestors known		Number of equivalent generations traced ( $E_{QG}$ )
	Parents	Ancestors from the fifth generation	
Barbet	87	31	3.5
Basset fauve de Bretagne	97	83	6.3
Beauceron	100	97	8.1
Berger des Pyrénées	97	81	6.1
Bouledogue Français	98	65	6.0
Braque Saint-Germain	99	80	5.9
Dogue de Bordeaux	98	60	6.2
Epagneul Breton	100	95	8.2
Montagne des Pyrénées	92	57	5.2

### Demographic parameters

Table 3 shows the average generation lengths between parents of the reference population and their useful offspring. Because of the small numbers of animals, the results for the BAR, BQG and MOP breeds should be taken with caution. For the BEN, the EPB and the BUF breeds, the generation lengths were found to be larger for the sire-offspring pathways than for the dam-offspring ones, probably because of the usual longer reproductive life of the males. The highest values of the average generation length over the four pathways were found for the BQG breed. On the contrary, the smallest values were found for the BUF and the DOB breeds.

### Probabilities of gene origin

The results of the analysis of probabilities of gene origin are given in Table 4. The larger the population size of the breed, the larger its total number of founders. The effective number of founders ( $f_e$ ) depends on both the total number of founders and the disequilibrium between their expected contributions to

the gene pool. A substantial disequilibrium has been found in the two largest breeds, the EPB and the BEN breeds, their value of the ratio  $f_e/f$  (0.06 and 0.11 respectively) being much lower than those of the other breed. On the contrary, the very small total number of founders of the BAR and BQG breeds did not let the opportunity for a large disequilibrium between their expected contributions (0.53 and 0.42). For the other breeds, the results were quite similar, with a ratio, which ranged between 0.16 and 0.22.

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 in populations that have passed through a bottleneck (Boichard *et al.* 1997). This decrease was found to be rather important for the BRP breeds, for which the lowest value of the ratio  $f_a/f_e$  (0.31) was observed. In the other breeds, this ratio ranged from 0.44 in the BAF breed to 0.66 in the MOP breed, except in the BAR breed where both effective numbers were almost equal ( $f_a/f_e = 0.97$ ). This similarity between  $f_a$  and  $f_e$  can be partially explained by the low pedigree completeness level of the breed.

The effective number of ancestors as the number of ancestors contributing the most for a cumulated expected contribution of 50% of the genes reveals the narrow genetic basis for all the breeds and especially for the two populations with the lowest population size, the BAR and BQG breeds and of a breed with decreasing population size, the BRP breed.

### Inbreeding and kinship

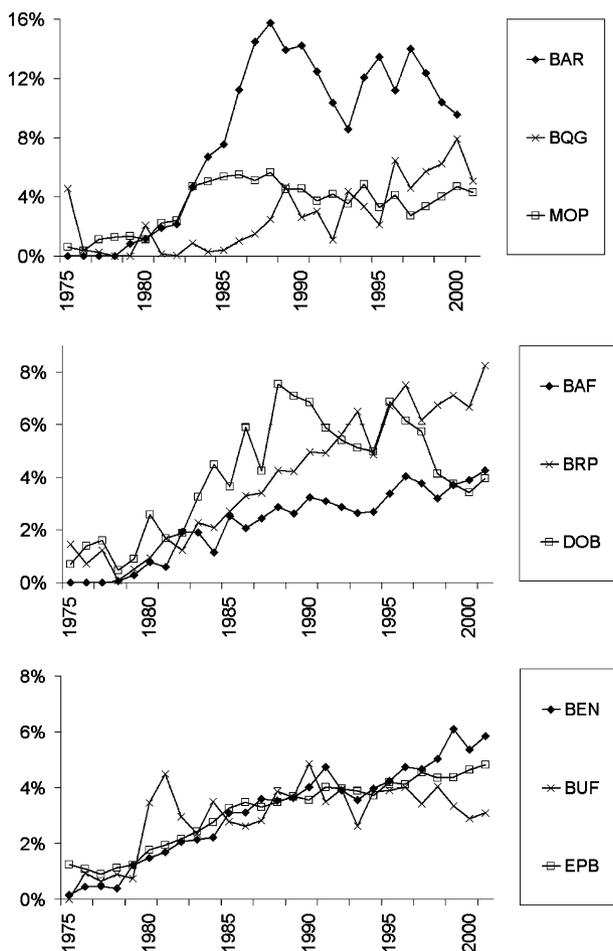
Figure 1 shows the evolution of the average coefficient of inbreeding of dogs according to their birth year. Up to the 1980s, the values were low or almost null, because of the lack of pedigree data. Next, mainly because of smaller numbers of animals on which the means were computed, there were more

**Table 3** Average generation lengths ( $T$ , in years) between useful offspring born from 1997 to 2001 and their parents

Breed (see Table 1)	BAR	BAF	BEN	BRP	BUF	BQG	DOB	EPB	MOP
Total number of useful male offspring used to compute $T$ sires–sires	4	198	303	73	302	13	62	502	25
$T$ sires–sires	4.8	4.0	4.9	4.0	3.7	5.2	3.1	4.9	4.9
Total number of useful male offspring used to compute $T$ dams–sires	4	198	302	73	297	13	58	510	24
$T$ dams–sires	5.0	4.0	4.1	5.2	3.0	5.5	3.0	4.4	4.9
Total number of useful female offspring used to compute $T$ sires–dams	8	304	586	122	742	19	151	962	37
$T$ sires–dams	5.2	3.5	4.7	4.4	3.5	5.9	3.5	4.9	4.9
Total number of useful female offspring used to compute $T$ dams–dams	8	304	584	121	739	19	146	976	36
$T$ dams–dams	3.9	3.8	4.1	5.7	3.2	5.7	3.1	4.4	4.8
Average $T$ over the four pathways	4.7	3.8	4.4	4.9	3.3	5.6	3.2	4.6	4.9

**Table 4** Analysis of the probabilities of gene origin for the dogs born from 1997 to 2001 with both parents known

Breed (see Table 1)	BAR	BAF	BEN	BRP	BUF	BQG	DOB	EPB	MOP
Total no. of founders ( <i>f</i> )	13	417	676	317	370	49	240	1 158	286
Effective no. of founders ( <i>fe</i> )	6.9	91.3	75.9	51.0	67.5	20.7	47.5	70.7	51.4
Effective no. of ancestors ( <i>fa</i> )	6.7	40.2	36.5	16.7	37.0	13.1	28.9	33.3	34.0
No. of ancestors contributing the most for a cumulated expected contribution of 50% of the genes	3	15	13	7	13	5	10	14	14
Ratio <i>felf</i>	0.53	0.22	0.11	0.16	0.18	0.42	0.20	0.06	0.18
Ratio <i>falfe</i>	0.97	0.44	0.48	0.31	0.55	0.63	0.61	0.47	0.66

**Figure 1** Evolution of the average coefficient of inbreeding (*F* in %) of dogs per birth year from 1975 to 2001. Note that the scale on the y-axis can be different between the graphs. For the breed abbreviations see Table 1.

fluctuations in the breeds with the smallest population sizes. In the BAR, DOB, MOP and BUF breeds, the recording of new dogs with no genealogical data, during the second half of the 1980s and early 1990s, led to a decrease or a stabilization of the mean of the computed coefficients of inbreeding. The annual

rate of inbreeding over the whole period (1970–2001) ranged from 0.1% points per year in the BUF breed to 0.5% points per year in the BAR breed (see Table 5).

The realised effective population sizes (Table 5), computed from the annual rate of inbreeding, ranged from 21 for the BAR breed to 152 for the BUF Breed, which was the only breed with a realized effective population size over 100.

The results on inbreeding in the reference population and on kinship between the parents of this reference population are given in Table 6. In all breeds, the average coefficient of inbreeding was higher than 3.125%, i.e. the value resulting from the mating of two animals sharing a single grandparent. The proportion of coefficients higher than 6.25%, i.e. the value resulting from the mating of two animals sharing two grandparents, was generally large. Despite pedigrees known to a substantially lower extent than in other breeds (see Table 2), the BAR breed showed the highest average coefficient of inbreeding and the highest proportion of high coefficients because of its much smaller population size. In all but one breed (the BQG breed), the average coefficient of inbreeding was substantially higher than the average coefficient of kinship of the parents: the ratio of offspring inbreeding over the average parental kinship ranged from 1.7 in the BRP breed to 2.0 in the BEN breed.

## Discussion

The nine breeds considered in this paper show different pictures for several criteria of within-population variability. The population size of the breed and its evolution over time, on the one hand and the management practices, on the other hand, are the main factors explaining the observed differences. Indeed, the higher the population size, the lower the increase of inbreeding over time. When the population size was higher, the disequilibrium between the expected contributions of the founders was higher but, as the total number of founders was much

**Table 5** Annual rate of inbreeding, realized effective population size and status of endangerment according to the FAO and the EAAP methods

Breed	Annual increase rate of inbreeding (%)	Realized effective population size ( $N_{e,t}$ )	Breeding males and females between 1997 and 2001		Status of endangerment according to the FAO method	Assumed maximum value of inbreeding during 50 years (%)	Status of endangerment according to the EAAP method
			Total of sires	Total of dames			
Barbet	0.5	20	13	11	Critical	24	Minimally endangered
Basset fauve de Bretagne	0.14	76	429	755	Endangered	8.4	Not endangered
Beauceron	0.21	53	726	1342	Not at risk	10.3	Potentially endangered
Berger des Pyrénées	0.3	33	225	387	Endangered	14.5	Potentially endangered
Bouledogue Français	0.1	147	471	919	Endangered	5	Not endangered
Braque Saint-Germain	0.22	40	26	36	Critical	10.7	Potentially endangered
Dogue de Bordeaux	0.17	88	175	298	Endangered	8.5	Not endangered
Epagneul Breton	0.15	70	1315	2402	Not at risk	7.5	Not endangered
Montagne des Pyrénées	0.12	82	93	152	Endangered	6	Not endangered

Breed	Average coefficient of kinship between male and female parents of dogs born in 1997–2001	Coefficients of inbreeding in the dogs born in 1997–2001 with both parents known	
		Mean	Proportion (%) of coefficients higher than 6.25% (1/16)
Barbet	9.7	12.4	74
Basset fauve de Bretagne	2.0	3.9	20
Beauceron	2.7	5.4	28
Berger des Pyrénées	4.4	7.2	46
Bouledogue Français	2.0	3.3	14
Braque Saint-Germain	6.9	6.0	29
Dogue de Bordeaux	2.2	4.1	22
Epagneul Breton	2.6	4.5	21
Montagne des Pyrénées	2.1	4.0	27

**Table 6** Coefficients of inbreeding ( $\times 100$ ) in the dogs born from 1997 to 2001 with both parents known and average coefficient of kinship ( $\times 100$ ) between their parents

higher, the effective number of founders was generally higher too. On the contrary, the current average coefficient of inbreeding does not seem to be much dependent of the population size, because of the use of mating between close relatives, which was observed in several breeds. Of course pedigree completeness level explains in some ways some of the results: inbreeding was probably underestimated for the breeds with a low completeness level and the number of founders and ancestors were overestimated for such breeds.

Because of its very small population size, the BAR breed is the most endangered breed of the group but its situation was quite different from the other breed with a very small population size, the BQG breed. These two breeds had a small effective number of ancestors, but pedigree completeness level was quite good for the BQG breed, on the contrary to the BAR breed (see Table 2). For this breed, the average co-

efficient of inbreeding was then underestimated and actually the number of effective ancestors is probably much lower than predicted. However, the BAR breed already has the most important inbreeding rate and the smallest effective number of founders. Moreover, the average coefficient of inbreeding was very high and 74% of the dogs had a coefficient higher than 1/16. Because the difference between the inbreeding of the reference population and kinship of the parents was not significant, it was not possible to know if breeders voluntarily use inbreeding. One may strongly recommend to avoid mating between close relatives within a so endangered breed. In the BAR breed, some crosses with the Poodle and Spanish Water dogs have been made and among the seven most important ancestors of the breed, three are not purely BAR. Crossbreeding with a close breed may be a solution to reintroduce some genetic variation (Denis 1997). For this breed, this

means that even with such crossbreeding, which introduced some variation, the genetic situation of the BAR breed seems critical. Such a lack of variability could be avoided if the breeding would be more rationally organized within the BAR breed. In this study, it was not possible to have complete data from the national pedigree file about the breeders. However, according to the breed club, not more than eight breeders produce litters but none regularly, explaining the fact that only three breeders produced a litter in 2004. This fact and the difficulty of finding owners of few related dogs and convincing them to use it for mating, are the main obstacles to a better management of genetic variability. The situation of the BQG breed seems, in comparison, much better. Population size and effective population size were higher and the coefficient of inbreeding was not as important as in other breeds with a population size much higher (BRP breed). This can be explained by the fact that the breed club is trying to encourage mating between non-related or little related dogs (C. Fauquembert, secretary of the Braque Saint Germain's Club, personal communication).

The BEN breed and the EPB breed have a similar and very good pedigree completeness level. These two breeds share several results: their generation lengths are almost equal, among the nine breeds studied these two breeds showed the most unbalanced paternal progeny sizes and they have suffered from some bottlenecks, as their effective number of ancestors was found to be less than half the effective number of founders. However, the decrease of genetic variation seems to be quite higher for the EPB breed: despite a larger total number of founders, its effective numbers of founders and of ancestors were smaller than those of the BEN breed. This observed difference shows that the expected contributions of founders and/or ancestors were even more unbalanced in the EPB breed than in the BEN breed.

Three breeds showed a decreasing population size, namely the BAF, the BRP and the MOP breeds. Among these three breeds, the BRP breed seems to be the most endangered because of its lower effective number of ancestors and its higher rate of inbreeding.

Two breeds showed a large increase of their population size, the BUF and the DOB breeds, which contributed to the observed moderate rate of inbreeding. These two breeds were found to have a substantially lower average generation length than the other breeds. This could be explained by the fact that the BUF and the DOB breeds are brachycephalic breeds. This kind of breed is known to have some

health problems (e.g. Couille-Beillon 1983). Because of such difficulties, the breeders probably use breeding animals during a few years only.

The probabilities of origin method was little used for analysing dog breeds but a lot of studies have reported inbreeding results on dog breeds. Nielen *et al.* (2001) have found quite similar results on Dutch breeds. The average coefficient of inbreeding ranged from 1.8% in the Golden Retriever breed to 7.0% in the Kooiker dog breed. Such values were quite larger than the average kinship between the parents. In a study on breeds raised in Finland (Mäki *et al.* 2001), the average coefficient of inbreeding of dogs born in 1998 ranged from 2.3% in the German shepherd breed to 5.1% in the Finnish hound breed.

### Implications

Most breeds can be considered as more or less endangered regarding the criteria used by the FAO and EAAP for determining breeds at risk. According to the FAO (2000), the situation of a breed is categorized as critical if there is <100 reproductive females or five reproductive males and endangered if there is less than 1000 reproductive females or 20 reproductive males. In our study, two breeds should be categorized as critical (BAR and BQG breeds) and five breeds as endangered, including the BUF breed, which is, however, the 13th breed in France among 300 considering the annual number of births. The criteria used by the FAO seems then unadapted for the dog species, partially because there is no such numerical disequilibrium between males and females as in other domestic species. The EAAP (Simon 1999) determines a class of endangerment using an assumed maximum value of inbreeding during 50 years of conservation. We could compute an approximation of this rate using an annual increase of inbreeding (see Table 5). Three of the breeds, including the BEN breed (11th breed raised in France), were considered as potentially endangered and the BAR breed was categorized as minimally endangered. The use of inbreeding by the breeders can partially explain these results, because it causes important increases of inbreeding even among breeds with high population size. In such a case, the criteria used to determine endangerment classes cannot take population size into account, which is probably the main parameter in such a process. Therefore, not only one parameter should be taken into account to determine the endangerment status of domestic breeds. From our study, three breeds could be considered as endangered: the BAR and

BQG breeds, because of their small actual and effective population sizes and the BRP breed, because of its decreasing population size and its low genetic variability assessed by probabilities of gene origin results.

To conclude, probabilities of gene origin added to computation of inbreeding gave us a lot of information about genetic structure and differences among breeds. Such results can be used to manage the genetic variability of breeds. For the breeds with a large population size, it is possible to limit the number of litters per male: such a rule is already applied in the German Shepherd dog in Germany (Guyader 1989). Moreover breed clubs could support breeding animals, which are little related to the whole population. Such dogs can be detected for instance by the average relatedness of each individual with the whole population (Goyache *et al.* 2003). For breeds with a small and/or decreasing population size, mating should be made between little related dogs. Indeed, it is quite easy to compute kinship or relatedness, especially within breeds with a small population, like the BAR breed. It could also be possible to split each population into several families of related dogs and to organize matings between dogs from different families. The efficiency of such methods has been theoretically assessed (e.g. Rochambeau & Chevalet 1990) and applied with success in some farm animal breeds, including rare breeds (Huby *et al.* 2003) or large and selected breeds (Palhière *et al.* 2000; Kerdiles & de Rochambeau 2002). The need for such actions to limit the loss of genetic variation seems to be urgent for the breeds with a disturbing situation, the BAR, BQG and BRP breeds. In comparison with other domestic species, purebred dog populations are over dispersed and according to the SCC, a breeder produces on average in France two litters per year. That is why, such measures could be applied only if breeders and owners are motivated and implied in the process.

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