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Contact: gregoire.leroy@agroparistech.fr

Gene flows in dog breeds and their impact on heterozygosity

Leroy G., Danchin-Burge C., Verrier E., Rognon X.
INRA, UMR1313 Génétique Animale et Biologie Intégrative, 78350 Jouy-en-Josas, France
AgroParisTech, UMR1313 Génétique Animale et Biologie Intégrative, 16 rue Claude Bernard, 75231 Paris 05, France

Despite the fact that most dog breeders are hobby breeders, there can be a large number of exchanges of reproducers within dog breeds and in particular between countries. Here we investigated reasons why such exchanges may vary from one breed to another, by using the French kennel club registrations data for 182 breeds. International exchanges were negatively correlated with registrations of dog of unknown origins, while several parameters might explain variations in gene flows, such as population size, breed origin, and specific breeding practices in some breeds. By analysing the effects of those gene flows on the genetic diversity of 60 breeds, it was shown that the percentage of stud service made in foreign countries was actually negatively linked to heterozygosity. It might be explained by the fact that breeders tend to use frequently similar foreign origins.

Introduction:

In dog species, more than 350 breeds are recognised by the world canine organisation (FCI: Fédération Cynologique Internationale). Although those breeds are considered as closed populations, they are actually subject to gene flows of different natures. First, a large number of breeds are raised in different countries and are therefore submitted to reproducers exchanges. Then, in several breeds, dogs with unknown origin may be registered as being pure-bred (after passing a morphological exam). It may induce the registration of dogs carrying genes from other breeds. Moreover, this phenomenon may be enhanced by the fact that a small amount of breeders' declarations may also be wrong, for voluntary reasons or not, which could have some genetic impact if the real parents are not pure bred. Finally, the existence of varieties within some breeds may also have an impact on the breeds genetic structure and diversity.

Using molecular markers, several studies showed that dog breeds constitute a generally differentiated and homogeneous genetic structure (Parker et al. 2004, Leroy et al. 2009b). However, it also seems that some differentiated genetic differentiation could be found between European and North american populations of the same breed (Quignon et al. 2008). It was also proved that the existence of varieties could induce genetic differences within some breeds of the same magnitude as it is observed between breeds (Björnerfeldt et al. 2008).

The aim of this study was to evaluate which parameters influence the most gene flows in dog breeds, and to analyse if such gene flows have an impact on within breed genetic variability, based on the example of dog populations raised in France. Using data base of the French kennel club (SCC i.e. Société Centrale Canine), we will focus on dog movements across countries and registration of dogs with unknown origin. The influence of population size, origin, and breed groups will be tested on these parameters, according to breeds. Then, we will analyse if those gene flow impacted the breeds genetic diversity, using heterozygosity rate as an estimator of genetic variability, on a set of 60 breeds.

Material and methods:

The year 2007 SCC registrations were used. In this study, only the 182 breeds having 50 dogs or more registered within a year were used, representing 99% of the 180 903 registrations. For each breed, the following data were extracted for the year 2007: total number of registrations, number of dogs exported, number of dogs imported, number of registered puppies born from a sire of another country (corresponding to stud service, realized either by bringing the dam to the sire, or by artificial insemination), and number of dogs registered with unknown origin. The last four parameters were divided by the total number of dogs registered, in order to have ratios.

In a second step, 60 breeds representing all the groups of the FCI nomenclature were chosen. This nomenclature splits the species into breed groups (see table 1), on the basis of morphology, current use, and historical criteria. In each breed, between 20 and 30 animals were sampled to be representative of their breed, and genotyped, using 21 autosomal microsatellite markers. Non biased heterozygosity H has then been computed within each breed (see Leroy et al. (2009a) for details).

Analyses were performed using the SAS software (2004). Correlations between the following parameters were computed for 182 dog breeds: number of registrations (NR), number of exported dogs / number of registrations (%E), percentage of dogs imported among the registrations (%I), percentage of puppies born from a sire from another country (%Sac), percentage of dogs registered with unknown origin (%Wuo). Effects of population size, breed origin (two categories: local or foreign breed, based from the information of the FCI website) and breed groups were tested (independently and together) for the four last parameters using proc GLM. A generalized linear model was also performed to explain H. The model included the following parameters: breed group, geographical origin of the breed, NR, %I, %Wuo and %Sac.

Table 1: Description of FCI groups, and evaluation of gene flow, based on the 182 breeds having more than 50 dogs registered in 2007: mean value over breeds within group and standard deviation across breeds, within group, in brackets.

Group Nr	Description of the group	Nr of breeds	N° of local breeds	NR *	%E ***	%I **	%Sac ***	%Wuo **
1	Sheepdogs and cattle dogs (except Swiss cattle dogs)	26	4	1231 *(2285)*	7.3 *(7.1)*	2.0 *(2.3)*	5.8 *(6.8)*	0.3 *(1.3)*
2	Pinscher and Schnauzer - Molossoid breeds - Swiss mountain and cattle dogs and other breeds	32	2	819 *(935)*	5.7 *(5.5)*	1.7 *(1.3)*	7.4 *(6.0)*	0.2 *(0.4)*
3	Terriers	18	0	1462 *(1804)*	3.0 *(3.5)*	1.3 *(1.6)*	6.0 *(7.4)*	0.2 *(0.3)*
4	Dachshunds	3	0	1332 *(1185)*	2.3 *(1.2)*	1.6 *(0.7)*	4.5 *(1.3)*	0.0 *(0.0)*
5	Spitz and primitives types	12	1	323 *(299)*	6.5 *(4.1)*	2.0 *(1.4)*	2.8 *(3.2)*	5.5 *(17.7)*
6	Scent hounds and related Breeds	31	21	428 *(501)*	2.5 *(3.8)*	0.5 *(1.5)*	1.6 *(6.5)*	9.1 (17.9)
7	Pointing dogs	21	10	1075 *(1591)*	3.2 *(3.5)*	0.7 *(1.2)*	1.4 *(1.7)*	1.2 *(4.4)*
8	Retrievers - Flushing dogs - Water dogs	9	0	2558 *(3236)*	2.9 *(2.0)*	1.5 *(2.0)*	5.0 *(4.2)*	0.0 *(0.0)*
9	Companion and toy dogs	22	5	1169 *(1614)*	4.5 *(3.5)*	1.8 *(1.6)*	3.2 *(4.5)*	0.3 *(0.5)*
10	Sighthounds	8	0	273 *(311)*	11.3 *(4.3)*	2.6 *(2.1)*	9.9 *(5.9)*	1.1 *(2.3)*
	Total/Average	182	43	985 *(1600)*	4.8 *(5.0)*	1.4 *(1.7)*	4.5 *(6.0)*	2.2 *(9.3)*

NR: number of registrations; %E: number of exported dogs / number of registrations; %I: % of dogs imported among the registrations; %Wuo: % of dogs registered with unknown origin; %Sac: % of puppies born from a sire of another country. Each estimator is averaged over breed groups. (Differences across breed groups: * $P< 0.05$, ** $P< 0.01$, *** $P< 0.001$).

Results:

According to the SCC breed results, a larger number of dogs was exported (equivalent to 4.8% of the registrations) than imported (only 1.4%). However gene flows inside the French populations were not limited to dog importation, as according to the breeds analyzed, 4.5% of dog registered were born from a sire of another country (stud service). The registrations of dogs with unknown origin were not negligible, as it concerned in 2007 an average of 2.2% of the registrations.

These gene flows largely varied across breeds (see table 1), and could be linked to population size, origin, and/or breed groups. Local breeds were found to be not significantly of smaller population size than foreign breeds (683 registrations vs 1077 on average), and %E were found to be not significantly different (3.8% vs 5.1%). On contrary, %I and %Sac were found to be significantly lower in local breed than in foreign breeds (0.4% vs 1.8% (P<0.0001), and 1.2% vs 5.5% (P<0.0001) respectively). %Wuo was found to be significantly higher in local breed (7.7% vs 0.5%, P<0.0001). According to breed groups, some tendencies could be found: indeed scent hounds (group 6) and pointing dogs (group 7) showed a small amount of entries from other countries, which could be partly explained by the fact that there is a large number of local breeds in these two groups. On contrary there were a large number of exportation and importations in sighthounds (group 10), even in comparison with other groups where no local breeds were found (group 3, 4 and 8). The %Wuo was found to be high in two groups (5 and 6), however in group 5, these result was due to only one breed (Cursinu breed), which was recognized recently and therefore had a %Wuo of 61%.

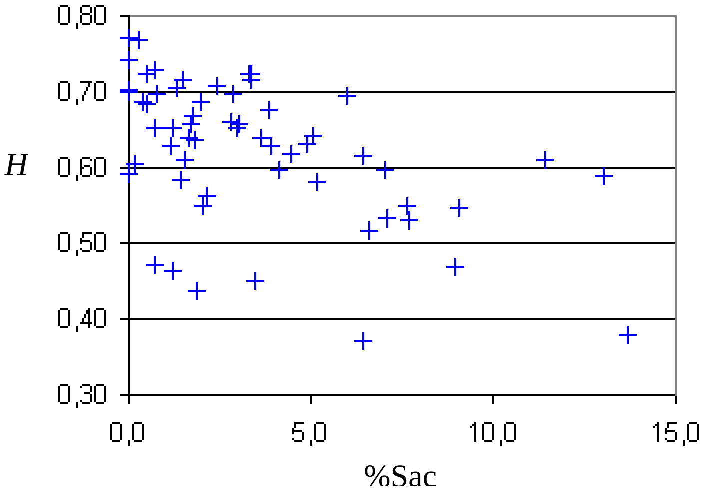
Table 2: Correlations, estimated over the 182 dog breeds, between number of registrations (NR), number of exported dogs / NR (%E), % of dogs imported among the registrations (%I), % of puppies born from a sire of another country (%Sac), and % of dogs registered with unknown origin (%Wuo). Over diagonal: estimated values of the correlations. Under diagonal: P values

	NR	%E	%I	%Sac	%Wuo
NR		-0.29	-0.25	-0.11	-0.12
%E	P<0.0001		0.32	0.34	-0.16
%I	P=0.0006	P<0.0001		0.50	-0.18
%Sac	NS	P<0.0001	P<0.0001		-0.16
%Wuo	NS	P=0.023	P=0.016	P=0.034	

Across variables, if the majority of the correlations were found to be significant (see table 2), they were never higher than 0.50. It was interesting to underline that importations and exportations were negatively correlated with population size, while gene flows with foreign countries (%E, %I, and %Sac) were positively correlated within each others, and negatively correlated with %Wuo. Using NR, breed origin, and FCI group together as explanatory variables, NR showed significant effect on %E (P<0.0001), %I (P<0.0001) and %Sac (P=0.03). Origin showed a significant effect on %I (P=0.001), %Wuo (P=0.004) and %Sac (P=0.03). FCI group showed a significant effect on %E (P<0.0001), and %Sac (P=0.02). The R^2 values were of 0.27 for %E, 0.25 for %I, 0.21 for %Sac and 0.18 for %Wuo (P<0.0001 each).

The only variable that showed a significant effect (P=0.0003) on H in the 60 breeds was the percentage of dogs born from a sire of another country (%Sac) (see Figure 3). Removing all the other explanatory variables, we found a R^2 of 26% (P=0.0001). According to the model, H decreased by 0.47%, when %Sac increased by 1%.

Figure 1: Effect of % of puppies born from a sire of another country (%Sac) on heterozygosity (*H*) of 60 breeds



Discussion:

At national level, dog breeds are subject to different kind of gene flows. Importations and exportations theoretically constitute the most classical way to bring or erode some diversity within a national population. However it is interesting to underline that among breeds where there were few exchanges, the number of dogs registered with unknown origin tended to be higher, as illustrated in table 2.

Results presented here also illustrate quite well the parameters complexity explaining gene flows at a breed level. For instance, some tendencies could be showed by breed groups which are, of course, not independent from origin or population size of the breeds. For instance, it is expected that global importations (%I and %Sac) were found to be lower in local breeds. Therefore, low %Sac found in pointing dogs breeds (group 7), are linked to an important number of French breeds within the group. It is also linked to group specificities, and even among foreign breeds of group 7, %Sac was found to be quite low (2.5% vs 4.5% on average) A more complete model could be designed to explain these gene flows, but it should take into account several other parameters, such as country of origin. For instance some German sport breeds (BOX, GSD, and ROT) showed, each, a very low %I (lower than 0.6%) but a quite high %Sac (higher than 7.5%). This can be explained by the fact that information on German sires is very detailed, on work results, morphology and diseases. In consequences, it can be very interesting for a French breeder to make a mating with such sire, instead of buying a non-controlled male puppy.

The most striking result was the fact that heterozygosity was found to be negatively correlated with the proportion of dogs having a sire from another country. As it was proven that between two different countries, dogs of the same breeds may show genetic differences (Quignon et al. 2008), a contrary result was expected. However we have to remember that the results in the Quignon study were found for a comparison between European and North American populations (which represent only 3% of the importations in France according to SCC). In Europe, exchanges are much more frequent, and populations are probably not differentiated across countries. Moreover a large number of foreign sires are related, and do not constitute a source of different genes. On the contrary, in some case they probably increase bottlenecks phenomena.

In conclusion, importations should not be considered as an obvious solution to increase the diversity within a national population. For instance, to increase the diversity or a least to limit a loss of variability, breed clubs should instead impose some limit in the number of mating made by sires. Such a solution has already been adopted by some clubs in Europe. If the diversity loss is very problematic, maybe clubs should think about allowing a controlled cross with another related breed.

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