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What future for the rare French goat breeds ?

Some answers thanks to a pedigree analysis on three breeds

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Abstract - In France, the goat is one of the species with the least diversity of breeds. Only ten breeds are recognized (versus more than forty in cattle and sixty in sheep), and two of them represent over 99% of the total French goat population.

In this article, we propose first to describe how conservation programs were implemented in the goat species. The key mark of the French programs is their pragmatic side. We also give a first assessment of the genetic variability of three rare breeds, namely the Poitevine, Provence and Fossés breeds, which were chosen as test cases because their demography and dynamic represent various and interesting situations. Our purpose was to check if simple management rules are efficient to maintain a low inbreeding level.

The genetic variability of the breeds was estimated via pedigree analysis. Some results illustrated that low number of females per male or using males from new bloodlines have a positive impact on genetic variability and, on the contrary, drastic demographic bottlenecks have a negative impact. More interesting, we showed that in the case of small ruminants, where both the sex ratio and the generation interval are generally small, straightforward management rules at the population level are enough to maintain a slow rate of inbreeding, at least on a short/mid term level. These results are preliminary and simulation models should be implemented in order to check and refine our conclusions.

Management of genetic variability / rare goat breeds / pedigree analysis

1 INTRODUCTION

There is nowadays a general agreement on the need to conserve the biodiversity of farm animals, and the consensus is also clear on the fact that this biodiversity is decreasing extremely rapidly (Scherf 2000). In order to stop this regression, conservation programs for endangered breeds were initiated in Europe as early as the beginning of the seventies. In France, the first conservation programs were started forty years ago in sheep and were followed by actions mostly in the cattle, horse and pig species. In our time these programs can be assessed as being successful, since the rare breeds population size has increased and the analysis of their genetic variability generally provided a favorable figure (see, for example, in cattle, Avon and Colleau, 2006; in sheep, Huby et al., 2003). In goats, conservation programs were set up much later, during the nineties only.

The purpose of this paper is to present the first results of a pedigree analysis performed on three local and rare goat breeds and to show that, under some conditions, very simple management rules are efficient to preserve the breeds genetic variability. To begin with, the goat conservation programs set up in France will be briefly presented (the evolution of goat breeding in France and the principles of conservation programs will be analyzed in a more details in another article to come).

2 CONTEXT AND BREEDS UNDER STUDY

2.1 Goats conservation programs

The implementation and the management of conservation programs in goat is under the responsibility of the *Institut de l'Elevage*, which is a technical institute dealing with the breeding of domestic ruminants species. Due to an extremely fast evolution of goat breeding during the sixties and seventies, two breeds, namely the Alpine and Saanen breeds, represent nowadays more than 99% of the national stock. All the other French breeds, more or less standardized, can be classified as "local" and/or "rare".

The process of identification of the breeds or populations to be preserved was rather tricky since the reliable sources were scarce and the only way to identify these populations was an in-field investigation.

Currently, seven French goat breeds are under conservation: the Chèvre des Fossés, Poitevine, Provençale, Rove, Pyrénéenne, Chèvre du Massif-Central and Chèvre des Savoie breeds. The first five ones only are accredited by the French Ministry of Agriculture. In each case, the program first step was to inventory the population's remaining breeders and animals, in an as

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comprehensive way as possible. The second step was to build up a breed database by merging the data collected in field and the ones available in the national performance recording system.

In situ management of these populations was implemented at the flock level. The accumulation of data allowed to follow the demography of each breed as well as its genetic variability. These information are used in order to give personalized advices to farmers on the choice of natural service males. Attention is given to some rules that are known to be efficient ways of preserving genetic variability (see, for example, Rochambeau and Chevalet, 1990; Verrier, 1992) such as (i) balancing family sizes, (ii) avoiding to mate a too large number of females to the same male (40 females per male being a maximum), (iii) quickly changing males (e.g. every two years in small ruminants), (iv) not using a male born in its own farm.

Ex situ conservation was also developed, despite the fact that artificial insemination (AI) is seldom used in the rare French goat breeds. Whenever specific funding was found, semen was cryopreserved to conserve the genes of the population for long term and safeguarding purposes. The ambition is to collect 200 doses of 25 unrelated males, with 100 doses for the French National Cryobank and 100 doses as a working stock (Ollivier et al, 1995 and Verrier et al., 2003). Due to difficulties of different nature, the semen collection varies greatly depending on the breed considered. The number of doses collected per male varies from 80 to 200, and the number of males collected per breed[†] from two (Rove) to thirty (Poitevine). An assessment of the goat French National Cryobank collection can be found hereafter: http://www.cryobanque.org/.

2.2 Breeds under study

Among the seven breeds under conservation, the present paper focuses on the three breeds with the largest amount of genealogical data: the Chèvre des Fossés, Poitevine and Provencale breeds. They also represent an interesting range of breeding system, since it goes from a breed raised mainly by farmers (Provençale) to a breed kept only by fancy breeders or communities (Fossés), while the Poitevine breed presents an intermediate situation: half its breeders are farmers and the other half fancy breeders.

The Chèvre des Fossés breed – hedge goat (hereafter abbreviated as FOS) – is a non standardized population raised traditionally in the North-West of France (Brittany and Normandy). Its conservation program started in 1995. In 2006, 515 live females and 170 males were registered in the *Institut de l'Elevage* database.

The Poitevine breed (POIT) is an old standardized breed raised in the in the Poitou-Charentes regional administrative district (West of France). The conservation program for this dairy breed was initiated by its last farmers in 1986 when only 600 goats were remaining. Twenty years later, around 2 600 females and 200 males are registered.

The Provençale breed (PROV) is a non standardized population that was traditionally bred in Provence (South-East of France) for milk and kid meat. This is the French rare goat breed with the highest milk yield. In 2006, there were about 900 females and 65 males in this breed, still considered at risk.

3 PEDIGREE ANALYSIS

3.1 Data analyzed and methods

The pedigree files, managed by the *Institut de l'Elevage*, were used for the genetic analysis. A total of 1 097 animals are registered in the FOS file, 13 569 in the POIT one and 2 240 in the PROV breed. Indicators of the within-population genetic variability were based on probabilities of gene origin, in reference to founder animals or major ancestors, and probabilities of gene identity (for details, see, for instance, Boichard et al., 1997). The analysis of probabilities of gene origin was performed on groups called the female reference population, formed by goats with both parents known during the 2003-2006 period, such a period representing about one generation interval in these breeds. Since the Poitevine breed is the one with the oldest pedigree data recording, a comparison was made with the females born in 1993-1996. All pedigree analyses were performed using the PEDIG software (Boichard, 2002).

3.2 Pedigree completeness level

Since the variability genetic of the breeds will be estimated thanks to pedigree information, the meaning of the results depends on the pedigree completeness level. This parameter was assessed by the equivalent complete generations traced (EqG) from the female reference population (Boichard et al., 1997) and by the maximum number of generations traced.

Table 1: Level of completeness of the pedigrees for the reference population

Breed	Period of birth	No of females in the reference population	No of equivalent generations traced (EqG)	Maximum No. of generations traced	Average No.of ancestors per female
FOS	2003-2006	431	2.7	8	18
POIT	1993-1996	1 274	4.1	13	127
POIT	2003-2006	1 231	4.9	18	619
PROV	2003-2006	727	3.6	10	48

[†] *No males were collected yet for the Massif-Central and the Savoie breeds.*

The basic characteristics of the reference populations are shown in Table 1. On average, EqG was found to be quite lower than French selected breeds in dairy cattle (Mattalia et al, 2006) or dog (Leroy et al, 2006). However EqG was similar to what can be found for other French rare breeds in cattle (Avon and Colleau, 2006) or sheep (Huby et al, 2003). The EqG is directly linked to the starting date of the pedigree collections, therefore it is the highest for the POIT breed.

When the EqG is small, for populations with comparable information, the interpretation is quite different between breeds such as FOS and PROV and a selected breed. In the case of a selected breed, it is expected that recent animals with no pedigree information are indeed quite closely related to the rest of the population, therefore that the population inbreeding is likely to be underestimated. In the case of FOS and PROV, the EqG was small due to a short history of pedigree recording and to the fact that the founders of the population were recorded only recently. In most cases the founders were found in different flocks that were quite isolated from each other and were not exchanging animals. It is probable that the assumption that the founders are not related is true, so forth the genetic variability indicators calculated are probably not too far from reality.

On the other hand, these indicators are underestimated in the case of POIT, since the missing information is mostly due to gaps at a period where all the POIT population was known: the EqG of a reference population between the 1993/1996 period is very similar (4.1) to the 2003/2006 one (4.9) while ten years represent about three generations interval in goat.

3.3 Probabilities of gene origin

Table 2 : Criteria calculated from the probabilities of gene origin

Breed	Total No of founders	Effective No of founders	Effective No of ancestors	Contrib. of main ancestor	Contrib.of the 5 main ancestors	No of ancestors contrib. for 50%
FOS	153	41	34	10.8%	30.2%	15
POIT 1993/1996	404	83	47	7.3%	24.9%	17
POIT 2003/2006	547	120	63	5.5%	21.6%	24
PROV	242	28	18	16.8%	44.3%	7

In the POIT breed, the genetic basis of the current population, as indicated by criteria derived from probabilities of gene origin, seems wider than a decade earlier. A probable explanation – other than the fact that a lot of pedigree information was lost between the two periods, as stated earlier – is how the male population was managed now and then, which is underlined by the contribution of the most important ancestors. In the previous decade a very limited number of breeders were selling most of the sires. Males were managed as in a scheme, with a pyramidal structure. This practice was quite harshly reproved by the person who did the first breed inventories for the *Institut de l'Elevage*, and breeders, even though quite shocked at first, changed the way they worked. In the following years all the potential sires, whatever the flocks they were coming from, including non farmers, were inventoried by the association and posted for sale. This very simple rule was enough to change completely the structure of the population.

The results in FOS reveal a rather good preservation of its genetic variability, considering the size of the population and the number of founders that were left when the breed was rediscovered. On the contrary the values of the indicators in PROV are similar to those found in rare cattle breeds (Avon and Colleau, 2006) and reveal quite a narrow genetic basis. These results may be explained by the history and the demographic evolution of the FOS and PROV breeds. Both populations started with a limited number of founders. However, the flock structure of the FOS breed seems to be favourable to the preservation of its genetic variability: the average flock size is small (3 in 2000, 6 en 2006 – reference: *Institut de l'Elevage*) and the sex ratio was always extremely low (one male for three goats on average). Also most of the remaining sires were unrelated. Meanwhile, since the PROV is raised mostly by "professional" farmers, the average size of the flock is much higher (45 in 2006) and so is the sex ratio. Also, when the conservation program started in 1999 all the dairy farmers were using bucks from the same origin, which were sons and grand-sons of the same sire: this buck was found to be the ancestor with the largest contribution to the breed (cf. Tab. 2).

3.4 Inbreeding and kinship

Table 3 : Inbreeding (F) in the reference female population and average kinship (Φ) between parents of these females

Breed	% of inbred animals	% of animals with F > 6,25%	Average coefficient of inbreeding (%)	Average coefficient of kinship between the parents (%)	Ratio $F / \Phi_{(parents)}$
FOS	34%	20%	4.3%	1.5%	2.9
POIT 1993/1996	60%	9%	2.1%	1.2%	1.8
POIT 2003/2006	68%	22%	4.1%	1.1%	3.7
PROV	60%	18%	4.1%	2.8%	1.5

Since inbreeding is much more sensitive to pedigree information than criteria calculated from the probabilities of gene origin (Boichard et al., 1997), the comparison of inbreeding results in different breeds should take into account the differences of pedigree completeness level. As an example while the POIT showed the best results for the criteria of probabilities of origin, the inbreeding value of the reference population is almost the same as the other breeds (Tab. 3): the higher EqG of the POIT (Tab. 1) probably explains most of the result.

Inbreeding can be caused by the narrow genetic variability of a population, when there is actually no choice other than to breed related animals, but it is also caused by breeders practices. Farmers may breed related animals more or less on purpose. When the conservation program started in PROV, the defiance of the farmers toward traditional breeders led them to use their own bucks born in their farm instead of buying them to other farms. In FOS, one of the main breeder – which is also one of the main provider of sires and dams – used inbreeding in its flock in order to homogenize its animals phenotype. The role of any organization that supervises conservation program is to track down such behaviors and try to change them.

Since the kinship between two animals is equal to the inbreeding of their possible offspring, a way to know if inbreeding is caused by the limited genetic variability of a population or by management practices is to compare the kinship of the parents of the reference population to the reference population inbreeding (Tab. 3). In FOS, the results show a large discrepancy between inbreeding of females and kinship between their parents, probably due to the management practice of the breeder mentioned just above. In POIT a decade earlier the same problem existed: a few breeders, who used to mate related animals, were impacting negatively the rest of the population. Since the breeder association was careful to have as many people as possible selling and buying bucks, the population is much more homogenous (which is shown also by the fact that kinship between males, females, and males and females is the same: 1.1% - results not shown). However inbreeding is still higher than kinship since several farmers are still using mating between close relatives in their flock, as it is shown by the percentage of animals with coefficient higher than 6.25% (22% of the reference population).

The PROV breed shows the highest result for the parents kinship: it reflects once again the small number of founders the population started with (Tab. 2). However, it is the population with the smallest ratio between inbreeding and kinship of the parents, as well as the smallest percentage of animals with an inbreeding superior to 6.5% . These are signs that farmers, as a group, pay attention to the management of the breed and that they avoid mating between related animals.

4 DISCUSSION

When the conservation program started, the three goat breeds under study were considered at great risk. The POIT was undergoing a decrease of its number and both the FOS and the PROV had a very small number of pure breed animals left. Also, the management practices used by the last breeders in FOS and PROV were big threats for the genetic variability of the breeds. In FOS, one flock that was using inbreeding to homogenize the standard of its animals, was also the main contributor of future breeders (males and females). In PROV, the average size of the flocks and the sex ratio were high in comparison with a breed raised only by fancy breeders such as FOS. Mostly, all the dairy farmers were using related bucks and several of them used the same males for several years.

However when evaluating the genetic variability of these breed the situation is not as bad as what it could have been feared. When comparing the results with rare cattle breeds (Avon and Colleau, 2006) with similar EqG and demography, such as Nantaise or Maraîchine breeds, the genetic variability of these three goat breeds seems better. The results are quite similar with rare sheep breeds (Huby et al, 2003).

The difference between the management of small ruminants and cattle lays mostly in the male management, and more specifically the use of AI, which is hardly or never used in rare small ruminant breeds: it is too costly and difficult to implement. On the contrary, between 20% to 93% of the cows in rare breeds are inseminated (Avon and Colleau, 2006): in the end the number of offspring left by male is much higher in cattle, which greatly impact its genetic variability. A main reason of the use of AI in cattle is the fact that raising a bull is very costly, and even dangerous, while raising a buck (or a ram) is fairly easy (even fancy breeders are doing it). Since in small ruminants most farmers are raising at least one male, it lowers the sex ratio which impacts favorably the breeds genetic variability.

Another reason for these fairly good results is the farmers awareness towards inbreeding. Most of them are willing to set up simple management practices to try to lower the inbreeding at the population level, even if it might jeopardize their income at short term. As an example, in PROV, since in 1999 all the dairy farmers were using males coming from the same bloodline, several of them decided to buy non related bucks from non farmers flock. It was a brave decision to do since they had no information on the milk production level of the flock they were buying their males from. Also, most farmers started to renew frequently their sires. These simple rules were started in 2000 and they had a significant effect on the inbreeding level of the population: it went from an average of 4.8% over the 1999/2002 period (results not shown) to 4.1% over the 2003/2006 period.

In FOS and POIT, the fast growth of the populations probably explains a good part of the results. In both breeds all females are kept for mating, therefore no bottleneck is created on the female part. Another important point is that all breeders sell and buy animals from each other: as we saw previously, since the Poitevine's breeder association organized exchange among males the inbreeding situation improved. On the contrary, a single breeder may influence negatively the genetic variability of a population when its number are low, as we saw in FOS.

Last but not least, another management practice helped the maintenance of the PROV genetic variability: absorbing mating has been used widely in this breed. The reason of such practice was the lack of availability of pure bred females and it certainly helped to maintain some variability in the population, both in term of probability of gene origin (the total contribution of foreign genes to the reference population is equal to 10%) and inbreeding, by increasing the number of unrelated sires and dams. However the use of an exogenous population in a rare breed should not be advocated unless the situation is critical: it is not always well perceived and it can generate conflicts between breeders, which is always dangerous from a social point of view in a rare breed (Lauvie et al, 2008).

5 CONCLUSION

There are numerous ways of managing the genetic variability of small populations (Rochambeau and Chevalet, 1990, Verrier, 1993). However, on a practical level, these solutions are often too constraining for the breeders. As an example, the rotational scheme is usually advocated to lower a small population inbreeding level. However this type of conservation program was rarely successfully implemented since farmers don't have much choice for their replacement sires: they are allowed to buy animals from one farm only. On the long run farmers find these rules too strict and they either cheat by buying animals from another farm without telling the breeder's association, or they give up the breed.

In France, conservation programs in goat were very recently implemented. One of the main action was to record pedigree information, when possible, for all the animals of the breed. Thanks to the information gathered a pedigree analysis was performed for three rare breeds. Results showed that in the goat species, where sex ratio is low and AI is seldom used, very simple rules – such as promoting a systematic male exchanges from all breeders, including non farmers, and a fast male renewal - are sufficient to maintain a rather good genetic variability.

However, if these rules work on a short term basis, it is necessary to assess their efficiency on the long run. There is still an acute need to find a scientific and practical way to manage the genetic variability of breeds with poor pedigree information and where several males are used at the same time to service a large number of females - which is often the case in small ruminants under extensive farm systems. The implementation of a software, SAUVAGE, (Raoul et al, 2004) is actually under work and it is hoped that it will achieve both targets, simple management and scientific thoroughness.

Since the implementation of intensive farming system, over the last forty years hundred of breeds have disappeared or at close from extinction even if France, despite a fairly long history of conservation programs, lot of breeds are still under threat. As an example, the Poitevine breed was known for having "naturally" good milk protein level and it is one of the reason why it survived. However, after 30 years of improvement, the selected breeds (Alpine and Saanen) have reached and even overtaken the Poitevine abilities. Yet, when comparing the genetic variability of rare and selected breeds (Mattalia and al, 2006) it is impressive to realize that breeds with thousands or even million numbers may have a lesser variability than rare breeds. In the end, the agriculture intensification achieved to endanger both between and within breeds genetic variability. It is probably time that efficient conservation programs are implemented, to preserve our farm breeds at a global level.

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Fossés Buck	**Fossés Goat**
	
Poitevine Buck	**Poitevine Goat**
	
Provençale Buck	**Provençale Goat**
	

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