# Selection and genetic variability of the French Angora goat breed: Assessment of a 30 years breeding program

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## Abstract

The French Angora goat breeding program was based on animals imported at the beginning of the eighties mainly from North America, South Africa, Australia and New Zealand. The whole selection program was based on these founders' animals and their offspring as no foreign animals were imported since then. The main selection objectives were to improve the quality and the quantity of the mohair produced. The genetic progress on the three traits selected by the program (fineness, fleece weight and kemp medullation score) over the last decade were calculated. The genetic variability of the breed was also assessed by using its pedigree information, thanks to the PEDIG software (INRA). The pedigree depth can be considered to be good. Various indicators of genetic variability were calculated, such as the effective number of founders and ancestors, average inbreeding and kinship and effective population size. The evolution of the various countries of origin was also assessed and showed a clear selection of the North American genes. Based on the average genetic trends, the breeding program could be assessed as successful. One of its downside would be the rather narrow genetic basis of the breed, which could also be explained by the small number of founders used at the start of the selection program. In order to preserve the future of the breed, specific measures such as cryoconservation of semen were decided.

## Resumen

El programa de selección de la cabra Angora francés estaba fundado en animales importados a principios de los años ochenta principalmente de Norteamérica, Sudáfrica, Australia y Nueva Zelanda. El programa de selección estaba apoyado en estos fundadores y su descendiente ya que ningunos animales extranjeros se importaron desde entonces. Los objetivos de selección principales eran mejorar la calidad y la cantidad del mohair producido. Este artículo presenta el progreso genético en los tres rasgos seleccionados por el programa (fineza, peso de la lana y nota de jarrete) durante la década pasada. La variabilidad genética de la raza se valoró usando información del pedigrí, gracias al software PEDIG (INRA). Se puede considerar que la profundidad del pedigrí está bien. Varios indicadores de la variabilidad genética fueron calculado. Mostró una selección clara de los genes norteamericanos gracias al calculado de la evolución de la contribución de los varios países de nacimiento. Basado en las tendencias genéticas, el programa de selección se podría evaluar como satisfecho. Una de su desventaja sería la base genética bastante estrecha de la clase, que también podría ser explicada por el pequeño número de fundadores usados al principio del programa de selección. A fin de conservar el futuro de la clase, las medidas específicas como el cryoconservation del semen se decidieron.

**Keywords :** Fiber breed – Angora goat – Breeding program – Genetic variability

## Introduction

In France, the case of the Angora breed is quite unique since it is the only ruminant breed selected for fiber production (Allain and Roguet, 2003; Allain and Roguet, 2006). The whole production is oriented toward a niche market for high quality products based on mohair wool. Producers control all the steps from the farm to the final consumer, as the entire French production is marketed directly by the farmers under a common trademark "Le Mohair des Fermes de France" (Allain and Roguet, 2003). In 2010, 16 tons of mohair were produced and sold – after being transformed by various artisans – by 140 farmers (http://www.mohair-france.com/interpro-mohair-france/historique-filiere-mohair-france/, 07/03/13). The breeding program was started at the beginning of the eighties, and based on the selection of animals from nucleus farms. The Angora case is interesting to assess how a breeding program can be efficient despite the limited number of selected animals, as long as the selected traits are highly heritable.

Genetic progress and genetic variability are correlated, and little selection can be done if the genetic variability of a breed for a given trait is limited. It is necessary to have regular assessment of the variability of the breed in order to set up specific management program in case of a sharp decline of its variability. However, if the analysis of genetic variability of various species or industries can be easily found (for instance in French dairy cattle, Danchin-Burge et al. 2011, for sheep, Danchin-Burge et al., 2010, for donkey, Rizzi et al., 2011…) such indicators are scarce for goats (Piacère et al. 2004, Danchin-Burge et al., 2012).

The purpose of this article is to present an update of the Angora fiber selection program, and to perform an extended analysis of the genetic variability of the breed, based on pedigree information.

## Material and Methods

### Breed under study

The Angora breed was probably among the first breed selected for a specific trait since it was identified as early as the 15th century BC in the region of Ankara. The breed was selected for the quality of its long white fleece (Meyer et al., 1998). It is said that Charles V, the first king of Spain, was the first to import the breed in Europe in the 16th, but the breed quickly disappeared. Some goats were imported in France as early as the 18th century but without success (http://www.ansi.okstate.edu/breeds/goats/angora/, Briggs, 1969). In the end, the story of the breed in France is quite contemporary. It results from importations that started in 1978 from various countries: USA (Texas more specifically), Canada, Australia, New-Zealand and South Africa, since it is the world leader in mohair production (Dubeuf et al., 2004). The first herds consisted mostly of purebred animals. However, since the number of pure bred animals was small, some breeders started their herd with Alpine goats that were mated with pure bred Angora bucks.

The first breeders decided from the start to set up a collective organization, which included a breeding program. It led to the creation of a small but successful French mohair industry. As of today, about 4,000 animals are raised by 140 farms, and a group of 35 nucleus herds representing 1,300 breeding females are part of the breeding program. About 60% of the nucleus farms are located in the Western and Southern parts of France. The average herd size is 110 goats; however a large variation exists from 15 to 300 females per farm. Production

**2**

systems are mostly semi-extensive or permanently housed production in order to increase the fiber quality of the fleece. Animals are not necessarily bred each year, since it is not needed for the fleece production. On the contrary, females are usually producing a better quality fleece when they are not expecting. Therefore, the number of breeding animals per year, which is already small since the breed numbers are limited, is quite small.

**Breeding program**

Producers have their animals sheared twice a year and the fleece is sent to a cooperative to be processed and dyed, then returned to the farmer. Since the producer's contribution is evaluated according to the total weight of raw mohair adjusted to quality criteria such as scouring yield, fineness and kemp content, the setting-up of a breeding program to improve the quality and quantity of the mohair was logical. The nucleus animals are evaluated at 18 months of age (male and female) for fleece weight, fiber diameter (ideally lower than 30 mm), absence of kemp and medullated fibers (Allain and Roguet, 2003) with an on-farm recording system where an expert appointed by Capgenes (i.e. the breeding organization in charge of the genetic program) is responsible for the evaluation. Performance, pedigrees and reproduction data are all integrated in a national genetic database (created in 1988). Breeding values are estimated on a national basis.

A buck testing station had been set up in 1995. About 30 bucks were tested on their individual fiber performances every two years. Their recruitment was based upon the breeding values of their parents and the males entered the station at 1 year old. A six month testing period was done, where each buck's fiber performances were evaluated. A culling rate about 20% was applied, and the selected bucks to be kept were sold to the nucleus farms. A total of 105 bucks were evaluated through the station. However the station was stopped in the years 2000 because of new sanitary rules on scrapie that Angora breeders could not comply with at the time.

Since 2002, a global breeding genetic evaluation (undertaken by INRA) is available. Each year Capgenes edits a list of all available bucks for mating with their EBV values, which is transmitted to all the nucleus farmers. Each farmer is then solely responsible for the creation of genetic progress of the breed since no specific mating is programmed by the association to create the next sires generation. There was no specific management of the genetic variability, until 2011. Since then, the Insitut de l'Elevage calculates the average kinship between each male and all the females available in a given herd in order to encourage farmers to buy bucks that are the least related to their herd.

**Methods used to estimate demographic and genetic variability indicators**

The study lays on pedigrees obtained from the national database hosted by Capgenes for the Angora breed. Pedigree depth and estimation of genetic variability based on pedigree information were calculated for an analyzed population ($F_{an}$), i.e. goats born from 2009 to 2012, with both parents known.

The generation intervals on the four pathways (sire-sire, sire-dam, dam-sire, dam-dam) were estimated as the average birth year difference between parents born in the period 2003-2007 and their reproducing offspring, i.e. offspring having themselves at least one offspring known in the national data base. The average generation interval is defined as the average of the four pathways (Lacy, 1989).

The genetic variability of each population and its evolution over time were assessed through indicators derived from pedigree data. The PEDIG software (Boichard, 2002) was preferred over the ENDOG software (Gutiérrez et al., 2005) since animals with offspring born the same year can be used, which is not the case with the ENDOG program. The principles of the methods and the corresponding equations are described in detail in Boichard et al. (1997), and a detailed overview of their application to animal populations is available in several publications (e.g., Leroy et al., 2006, Danchin-Burge et al., 2010, Vosges and Distl, 2009).

Pedigree depth is described by the equivalent generation number $EqG_i$ determined for each animal ($i$) as defined by Boichard et al. (1997). The $EqG$ for each reference population was computed as the mean of the $EqG_i$.

A strong hypothesis of the whole data analysis is that all founders (i.e. animals with offspring and unknown parents) are non-inbred and non-related. The effective number of founders ($f_e$), ancestors ($f_a$), and number of the top contributing ancestors accounting for 50% of the genes ($N_{50}$) as defined by Boichard et al. (1997) were calculated for the $F_{an}$. The effective number of ancestors ($f_a$) is always lower than the effective number of founders ($f_e$) and the comparison of both numbers can be used to appreciate the impact of the bottlenecks that have occurred from the founders to the present population (Boichard et al., 1997): the higher the $f_e/f_a$ ratio, the more stringent the bottlenecks.

The evolution of the contributions of the different original gene pools was assessed also, by using the probability of gene origin and attributing a country or breed of origin to each founder of the Angora breed. The founder animals were pure bred coming mainly from North America (Canada and USA, origin 1) and Australia (origin 2). A small proportion was coming from New Zealand and South Africa: their founder origins were pooled with the Australian animals for analysis purposes (origin 2). Since the number of pure bred animals was quite low, crossbred ones were created with the "alpine" (Alpine and Saanen) breeds (origin 3). The contributions were calculated for all the females with two parents known born between 1980 and 2012 included, and averaged by birth year.

The coefficient of inbreeding $F_i$ of each animal in the file was computed by the method of Meuwissen and Luo (1992). The global inbreeding level ($F$) was simply computed as the average of all individual inbreeding ($F_i$) of animals in the analyzed population. The effective population size ($Ne$) was computed for each breed based on the analyzed population based on the increase in coancestry following the method by Cervantes et al. (2011). Considering the coancestry $c_{ij}$ between two individuals i and j, their increase in coancestry $\Delta c_{ij}$ was calculated as follow:

$$\Delta c_{ij} = 1 - \sqrt[\frac{EqGi_i + EqGj}{2}]{\left(1 - c_{ij}\right)}$$

The kinship coefficients within the analyzed population was computed and compared to the average coefficient of inbreeding and the average coefficient of kinship between their parents. Self-kinships are not included in the calculation of average kinships.

## Results and discussion

Genetic trend average per year is 0.08 µm for fineness, 0.15 kg for fleece weight and 0.11 pt for kemp medullation score when estimated on the last ten years (Figure 1). This gain is equivalent to 0.04 (4.3%/year), 0.04 (4.2%/year) and 0.06 (6.4%/year) genetic standard deviation for fineness, fleece weight and kemp score respectively and a phenotypic trend of 2.7 µm, 0.26 kg, and 2.5 pts over the last ten years for fineness, fleece weight and kemp medullation score respectively. This gain is equivalent to 1.05, 0.36 and 0.65 phenotypic

standard deviation for fineness, fleece weight and kemp score respectively. Mean phenotypic values observed in the last generation born in 2011 are 24.7 µm, 3.7 kg and 42.1 point (over a scale of 45) for fineness, fleece weight and kemp medullation score. Thanks to the different traits medium to good heritability (0.14 for kemp score; 0.25 for fleece weight; 0.51 for fineness, cf. Allain and Renieri, 2010), significant genetic progress were achieved. However, as previously stated in Allain and Renieri (2010), it is somewhat a challenge to improve simultaneously fleece quality and quantity; it implies a multi-trait selection approach.
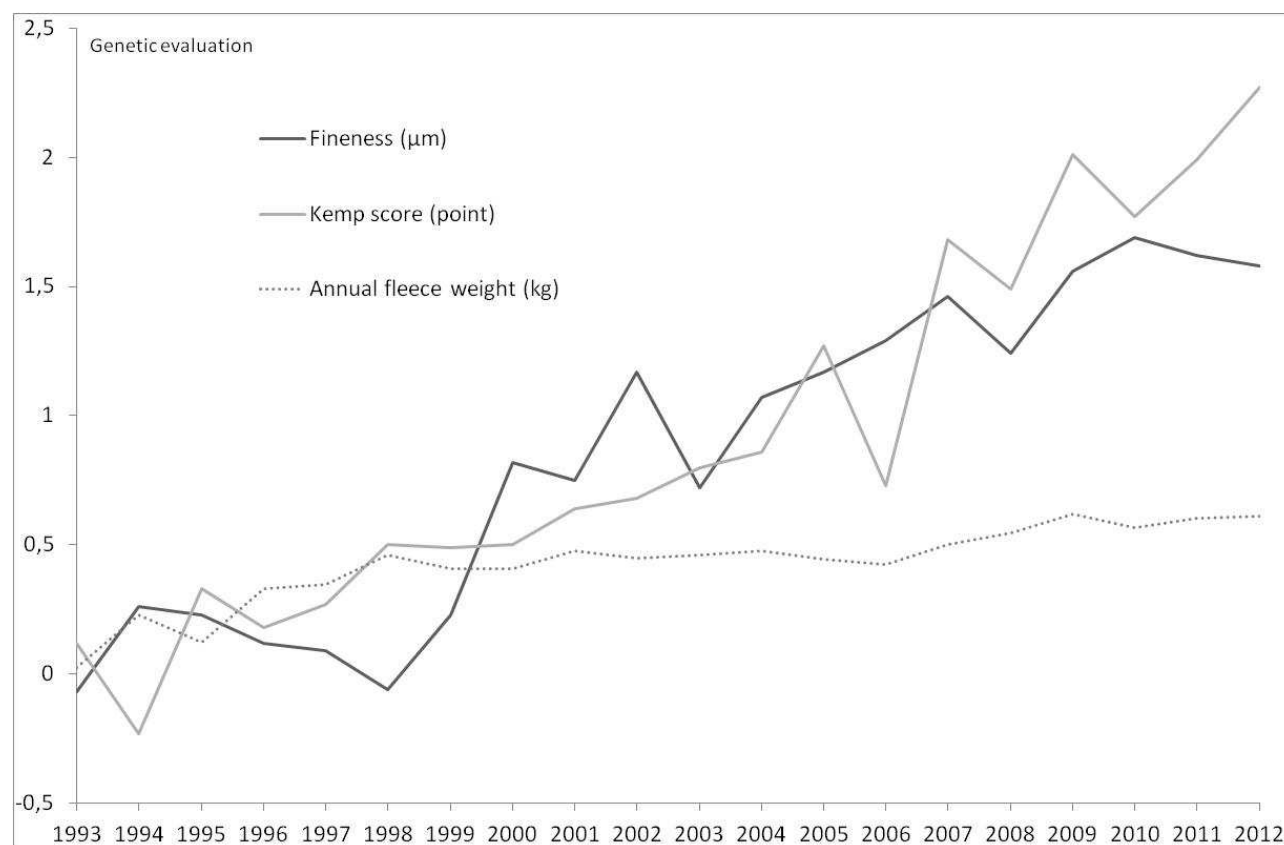


***Figure 1 :*** *Evolution of the genetic evaluation for fineness, fleece weight, and kemp medullation between 1993 and 2012*

When looking at the demographic evolution of the breed, firstly the population (*Figure 2*) showed a constant growth of its number for a five year period, starting in 1984. Since 1991, its number dropped drastically. From 2000 on, the selection basis is slowly declining, with an average over the last 5 years of 284 registered females per year.

5

*Figure 2 : Evolution of the female population per birth year*

The generation intervals is equal to 3.9, the pedigree depth is 6.4 (*Table 1*). The pedigree depth can be considered as good in comparison with other studies for various livestock species (see as an example for sheep, for dogs, Leroy et al., 2006; for sheep breeds, Danchin-Burge et al., 2010). The analyzed population is sired from 108 different males, so the average number of female offspring per male is equal to 9.9 which can be considered as fairly low for a ruminant breed under selection.

*Table 1 : Demographic characteristics, pedigree depth and generation intervals (for the animals born in 1998-2002 and their reproducing offspring) for the Angora breed*

| Total size of the pedigree file | Size of the analyzed population | No of sires of the analyzed population | Pedigree depth of the analyzed population | Generation interval |
|---|---|---|---|---|
| 31,685 | 1,068 | 108 | 6.4 | 3.9 |

The results of the analysis of gene origin probabilities are shown in table2.

*Table 2 : Analysis of the probabilities of gene origin for the Angora breed*

| Total no. of founders | Effective no. of founders $(f_e)$ | Effective no. of ancestors $(f_a)$ | Ratio $f_a/f_e$ | Contribution of the top ancestor | No. of top contributing ancestors accounting for 50% of the genes $(N_{50})$ |
|---|---|---|---|---|---|
| 442 | 65 | 22 | 0.33 | 14.09 | 9 |

The Angora breed has a very small number of founders (442) and the selection bottlenecks are also quite stringent as shown by the small $f_a/f_e$ ratio. A detailed analysis of the main ancestors

(results not published) shows us that most bottlenecks were created at the beginning of the nineties.

*Table 3* :*Average inbreeding level (F) in the analyzed population, average coefficient of kinship (Φ )within the analyzed population ($F_{an}$) and effective population size (Ne) with the Gutiérrez and Cervantes method. All F and Φ values are given in %.*

| F | Φ $F_{an}*F_{an}$ | Φ parents *parents | Ne |
|---|---|---|---|
| 5.5% | 4.3% | 2.80% | 76 |

The inbreeding level of the $F_{an}$ (*Table 3*) is 28% higher than the $F_{an}$ kinship and 186% higher than the parents kinship of the reference population. The percentage of animals with an inbreeding coefficient higher than 6.25% is equal to 30%, which is very high. One of the possible explanation could be the difficulty for breeders to exchange bucks since they are spread in the entire country. Also, some breeders are very close to their animals and might find difficulties to get rid of a male they were particularly fond of.

When looking at the influence of various countries or breeds of origins over time for the Angora breed, it is striking to see that almost no Alpine genes are left in the current population and few of the "Austral" genes (i.e. Australia, New Zealand or South Africa) are leftover. The North American genes were positively selected and are now stabilized around 77%. However it has to be stated that the country of origins were not known for 37% of the founders and these animals were included in an unknown origin category. As of today, the percentage of unknown origin can be estimated to 22% of the analyzed population gene composition.
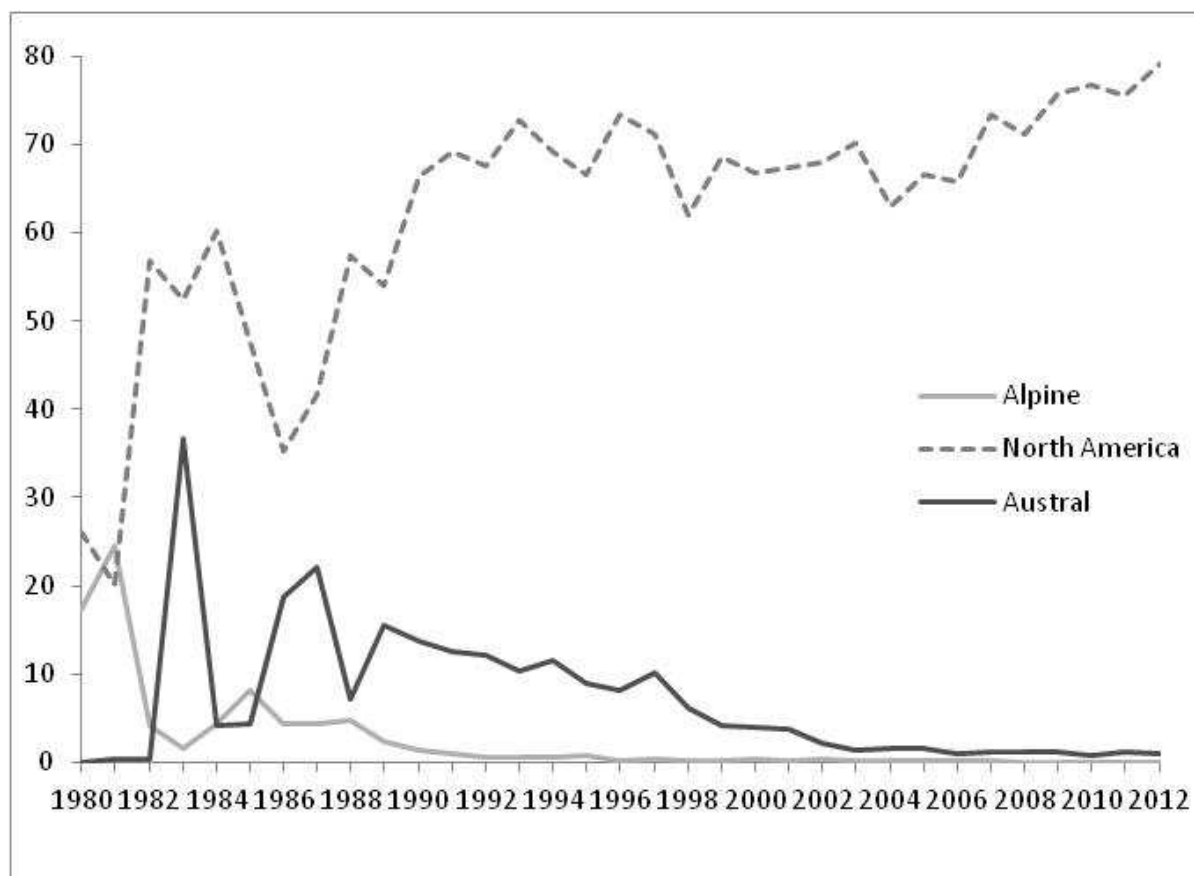
***Figure 3 :*** *Evolution per birth year of three types of genes orgin (North American, Austral and Alpine breed) in the Angora breed*

The Angora breed has a fairly narrow genetic variability which is reflected by both type of indicators, probability of gene origin and probability of gene identity (inbreeding and kinship). At least four different factors are explaining these results. First of all, the breed is quite small, with a declining demography (both census and registered animals) since the nineties. The breed's numbers have been going down steadily since the 1990s which does not help to maintain a good genetic variability. Also the number of founders used to create the French Angora nucleus was quite limited, as indicated by the total number of founders in *Table 2*. Finally, farmers have a tendency to overuse their natural service males, leading to slightly inbred herds.

We also showed that it is possible to set up a successful selection program with a small population in a context where the selection is done on highly heritable trait. The breed has been efficiently selected for thirty years for fiber fineness, which led to the elimination of some of the original strains as shown in *Figure 3*. It seems that all the genes coming from the Alpine breed as well as the New-Zealander, Australian or South-African origins were almost eradicated. This study also clearly indicates that the breeders association would be quite limited in their choice of countries if they wanted to use new origins. It is probable that the extensive conditions used to raise the South African, New Zealand and Australian animals are too rough to get high quality fibers, therefore such animals cannot be used in the French program.

When looking at the effective population size (*Table 3*), the genetic diversity seems within the bracket of the FAO recommendation (FAO, 1998) which is to maintain an effective population size of at least 50 to 100. However, it would appropriate to have a better

management of the genetic variability of the breed by trying to increase the exchange of bucks between farmers.

## Conclusion

The French Angora breed presents an innovative selection program by its selected traits (fiber), its limited size and its genetic progress. However, several handicaps are limiting its genetic variability even though they could be evaluated as remaining at a good level for a small breed under selection. There is still the possibility for the breed of importing animals from other countries, such as Turkey or Canada, to start new origins. Another way to secure the genetic progress and variability of the breed would be by the use of cryoconservation as an *ex situ* conservation of the breed. This is the reason why CAPGENES and the breeder association decided on the sampling of a semi-dozen of bucks over a two year period to safeguard the French Angora breed.

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French Angora goat – Fibre animals 2013

# Selection and genetic variability of the French Angora goat breed:

## Assessment of a 30 years breeding program

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# The French Angora breeding program

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# The French Angora breeding program

**4,000 animals** (males & females)

1,300 animals in 35 nucleus herds

500 animals with perf. recording

BLUP evaluation of the males

No AI

Main selected traits:
Total weight of raw mohair
Fineness
Kemp content

Genetic variability:
No management until 2011
Now: kinship matrix

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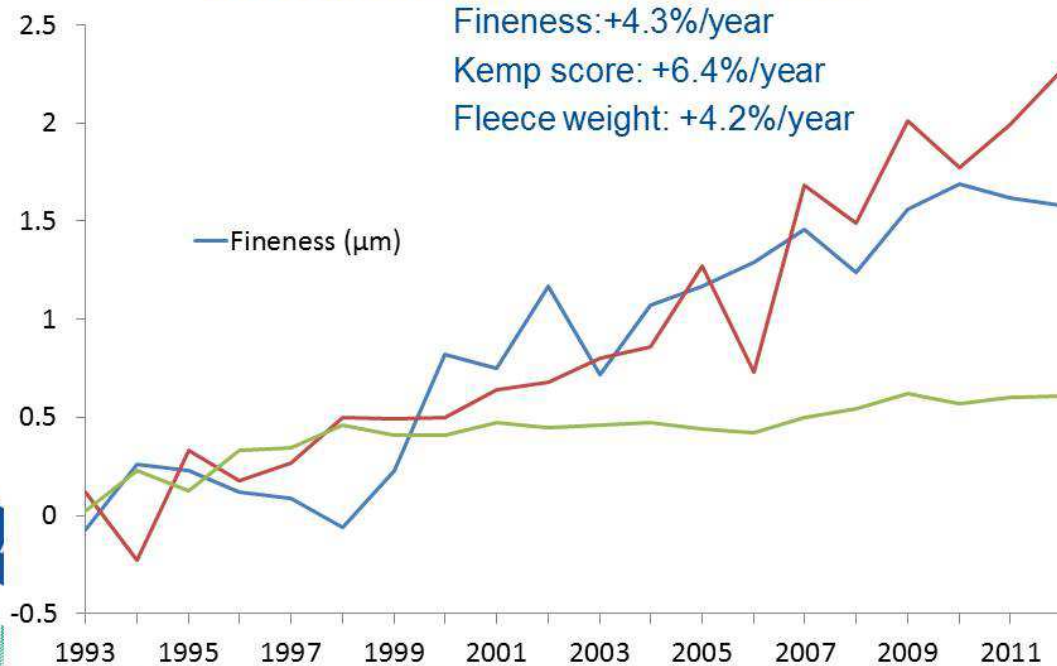16 t/year sold under common trademark:
"Mohair des Fermes de France"

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# Small is beautiful !

## … Provided the traits are highly heritable

Fineness:+4.3%/year
Kemp score: +6.4%/year
Fleece weight: +4.2%/year

Fineness (µm)

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# Analysis of the genetic variability of the breed *(based on pedigrees)*
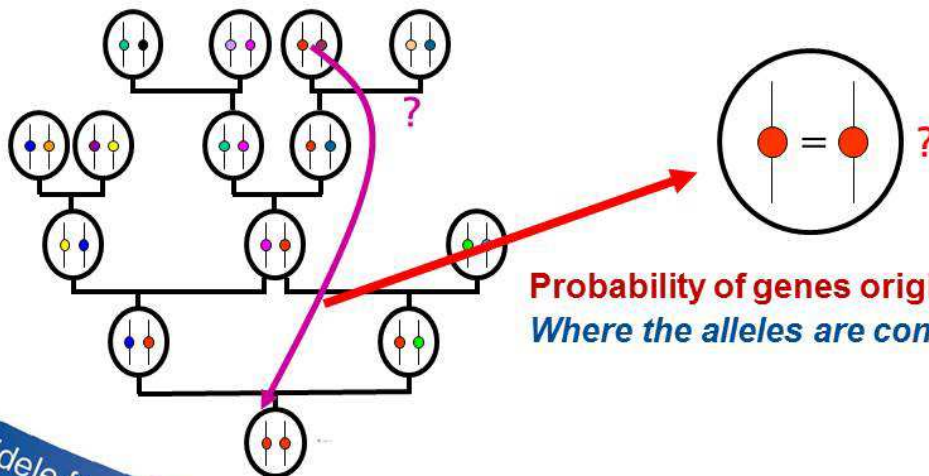
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# Indicators of genetic variability based on two types of probabilities

**Probability of identity**
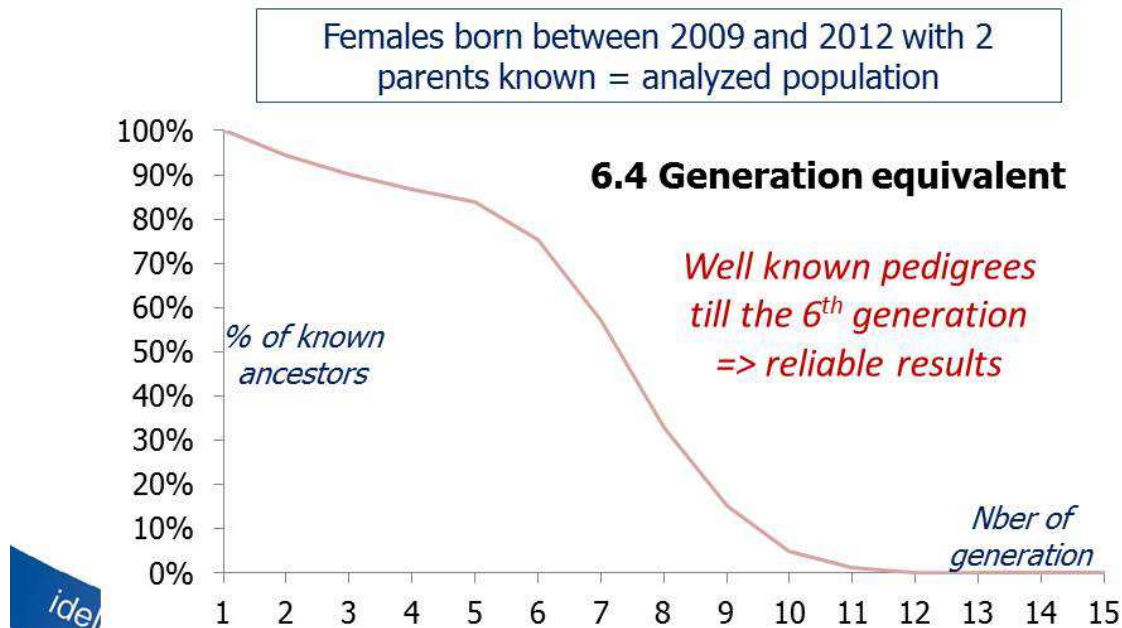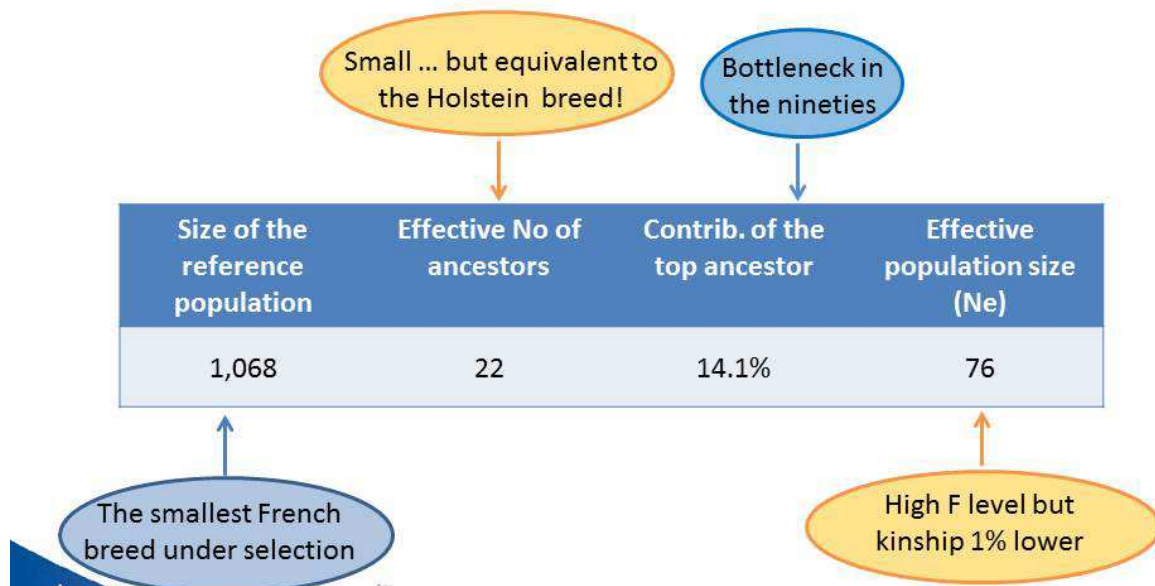*For a given animal, are two alleles identical?*

?

= ?

**Probability of genes origin**
*Where the alleles are coming from ?*

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## Quality of the pedigree information

Females born between 2009 and 2012 with 2 parents known = analyzed population



**6.4 Generation equivalent**

*Well known pedigrees till the 6th generation => reliable results*

% of known ancestors

Nber of generation

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## Probability of gene origin and Ne



Small ... but equivalent to the Holstein breed!

Bottleneck in the nineties

| Size of the reference population | Effective No of ancestors | Contrib. of the top ancestor | Effective population size (Ne) |
|---|---|---|---|
| 1,068 | 22 | 14.1% | 76 |

The smallest French breed under selection

High F level but kinship 1% lower

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**14**

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# Change of genes origin in the Angora breed



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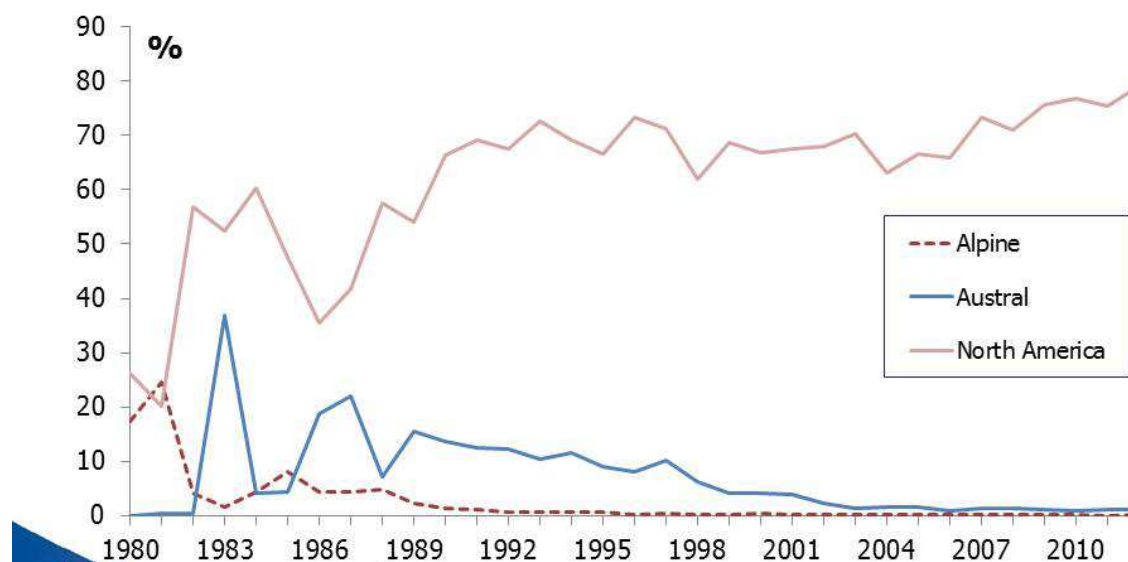
# Conclusions

- Very efficient selection scheme despite the small population size

- Genetic diversity limited due to:
  - ✓ Small number of founders
  - ✓ Small breed with a declining trend
  - ✓ Breeding of highly related animals
  - ✓ Selection program

*Pic. by A.M. Charles*

- Limited choice of countries to diversify the breed origins

- Necessity to implement a specific management of the breed diversity

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# Thank you for your attention



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