

## Overview of the genetic variability in French selected livestock populations and management approaches

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### **Abstract**

Some results from pedigree analyses of French livestock breeds are reported. Results on both probabilities of gene origin and rates of inbreeding show that 'large' breeds may be small populations from a genetical point of view. Different management methods for selected populations are presented and the efficiency of optimized procedures is illustrated on cases of dairy cattle and pigs breeds. The easiness of application of such methods is discussed.

### **Introduction**

In the last decades selection pressures have increased on all livestock species and selection methods have been improved, leading to more and more efficient programmes. However, due to an intense and accurate selection and to a small number of breeding animals in the selection nuclei, it is expected that within-population genetic variance of the selected traits will decrease and that inbreeding will increase faster than under pure drift (for a review, see Verrier et al. 1991). Preserving the within-population variability and monitoring the rate of inbreeding are necessary for both short- and long-term considerations. The purpose of this paper is two-fold: (i) to demonstrate, using some examples of French livestock populations, how the theoretical predictions are verified; and (ii) to discuss the possible ways and methods to manage selected populations.

### **What can we learn from the analysis of large selected populations of farm animals?**

#### ***Information and methods available for analyzing the within-population genetic variability***

Three kinds of information are available: (i) phenotypes, giving a global view of the variability of the genes (generally unknown) governing the observed traits; (ii) genotypes at genetic markers, giving a detailed view of the variability of the observed loci; and (iii) pedigrees, giving the view of the variability for an anonymous locus (theoretically, a neutral locus with no mutation) anywhere in the genome. Pedigree information is mainly used due to several advantages: easiness and low cost of recording, possibility to trace the history of populations for long periods, and easiness of interpretation. With such information, the genetic variability is assessed in terms of probabilities of

gene identity (coefficients of kinship and of inbreeding) and probabilities of gene origin (for example, see Boichard et al. 1997 and Caballero and Toro 2000).

### **Two case studies: the main French dairy cattle and pig breeds**

Pedigree of the main French dairy cattle and pig breeds were recently analysed (Moureaux et al. 2001; Maignel and Labroue 2001; Delaunay and Mérour 2006). The probabilities of gene origin of the most recent cohort of animals known at the time of the study were analyzed (Table 1). The major ancestors of each cohort were identified by the iterative method proposed by Boichard et al. (1997) and were ranked by decreasing expected genetic contribution. Half of the gene pool was found to originate from a very few ancestors (Table 1). The effective number of ancestors is defined as the reciprocal of the probability that two genes drawn at random in the cohort originate from the same major ancestor (Boichard et al. 1997). In a given locus, the genetic variability of the studied cohort is equivalent to the variability that would originate from the balanced contributions of a number of ancestors equal to the effective number. These results highlight the narrow genetic basis of such populations, due to strong bottlenecks in the pedigrees. In addition, the annual rate of inbreeding was found to be about 0.2% in dairy cattle and between 0.1% and 0.5% in pigs, according to the breed (Delaunay and Mérour 2006). In both species, the changes in the slope of the observed curves have been interpreted as consequences of previous changes in the management of the breeds (Moureaux et al. 2001; Maignel and Labroue 2001; Delaunay and Mérour 2006).

**Table 1.** Analysis of the probabilities of gene origin in the main French dairy cattle and pig breeds.

	Dairy cattle <sup>†</sup>			Pigs <sup>‡</sup>		
	Holstein	Montbéliarde	Normandy	LW <sup>§</sup> Line Nr 1	LW <sup>§</sup> Line Nr 2	French Landrace
No. of animals in the cohort	2 141 261	341 512	326 699	70 551	10 888	40 037
No. of ancestors for a cumulated contribution of 50%	16	12	12	18	28	12
Effective no. of ancestors	33	30	33	31	75	32

<sup>†</sup> Recorded cows born in 1993–1996

<sup>‡</sup> Recorded sows born in 1999

<sup>§</sup> Large-White is the main maternal pig breed used in France. It is divided into two lines differing by the traits on which the most emphasis is given in the breeding goal: litter size in Line Nr 1, growth rate in line Nr 2.

### **Other cases and conclusions from these studies**

In the last decade, extensive pedigree analyses were carried out on French breeds in race or riding horses (Moureaux et al. 1996), draught horses (Vu Tien et al. 1998; Verrier et al. 2005), dairy cattle (Moureaux et al. 2001), sheep (Palhière et al. 2000), beef cattle (Vu Tien et al. 1998), meat sheep (Huby et al. 2003), pigs (Maignel and Labroue 2001; Delaunay and Mérour 2006), rabbit (Kerdiles and de Rochambeau 2002) and dogs (Leroy et al. 2006). From the observed values of the generation length and of the annual rate of inbreeding, the rate of inbreeding per generation and the realised effective size were computed (Table 2). The realised effective size does not depend on the actual population size nor on the status of the breed. On the contrary, there is a strong effect of the management strategy applied by breeders, as revealed by the detailed comparison between national breeds with large population sizes (Moureaux et al. 2001), between separate lines of the same national breed (Palhière et

al. 2000) or between rare breeds (Huby et al. 2003). An extreme case is represented by the Holstein dairy cattle breed, which is simultaneously the largest French cattle breed and the breed with almost the smallest realised effective size, mainly due to a very unbalanced use of artificial insemination bulls, both on the sire–sire and the sire–dam paths (Moureaux et al. 2001). All these studies indicate that 'large' breeds, i.e. those that are widely raised for commercial purposes, may be small populations from a genetic point of view.

**Table 2.** Realised effective population sizes estimated in some French livestock breeds.

Species and production	Breed	Status <sup>†</sup>	Realised effective size	Period analyzed (birth years)	Reference
Horse	Thoroughbred	S I	181	1974–1992	Moureaux et al. (1996)
	Boulonnais	C R	44	1965–2000	Verrier et al. (2005)
Dairy cattle	Holstein	S I	52	1980–1996	Moureaux et al. (2001)
	Montbéliarde	S N	81		
	Normandy	S N	59		
	Abondance	S L	60		
Dairy sheep	Lacaune Line Nr 1 <sup>‡</sup>	S N	278	1970–1999	Palhière et al. (2000)
	Lacaune Line Nr 2 <sup>‡</sup>	S N	167		
Meat sheep	Berrichon-du-Cher	S N	120	1980–2000	Huby et al. (2003)
	Solognot	C R	223		
Pigs	LW Line Nr 1	S N	84	1985–1999	Maignel and Labroue (2001)
	French Landrace	S N	60		

<sup>†</sup> Programme: S = selection, C = conservation; Extent: I = international, N = national, L = local, R = rare.

<sup>‡</sup> The Lacaune dairy sheep breed is divided into two lines, with a few exchanges between lines.

## Methods for limiting the increase of inbreeding and the decrease of within-population genetic variability due to selection

### *Simple demographic rules*

From well-known population genetics principles, an effective way to preserve genetic variability is to breed the largest number of males possible and to equalize their progeny sizes. Males are considered here rather than females due to their smaller number and the easier ability to obtain large differences in their progeny sizes. Due to extra costs and penalties on genetic progress, these rules are rarely strictly applied, except in poultry breeding on the sire–sire path. However, these rules should be kept in mind in order to avoid excess on the selection and the use of breeding males.

### *Splitting the population into groups*

As for the management of some rare breeds (de Rochambeau and Chevalet 1985), the population is split into reproduction groups and the selection works within groups. Such a method has been applied with success in the selection of some rabbit lines (Kerdiles and de Rochambeau 2002). Both lines of the Lacaune dairy sheep breed are managed with rams' groups. By retrospective analyses, it has been shown that these two lines have achieved the same genetic progress for dairy traits but that they differ for realised effective size (see Table 2) due to differences in both the management of the

groups during a round of selection and the stability of the groups from one round of selection to the next (Palhière et al. 2000).

### **Use of modified EBVs**

Many authors have suggested using Estimated Breeding Values (EBVs) different from those deduced from the index theory. Two types of modification have been proposed: (i) reducing the weight given to familial information, either by simple algebra after the EBV has been calculated computation or by inflating the value of genetic parameters; and (ii) including penalties based on the candidate's degree of inbreeding or its kinship with other animals. For a recent list of references, see Colleau et al. 2004b). An example of the possible construction of such EBVs with penalties in pigs is given by Delaunay and Mérour (2006).

### **Optimization methods**

The methods currently considered as methods of choice, from a theoretical point of view, consist of choosing breeding animals and determining their relative contribution to the next generation by optimizing a decision function combining genetic values and inbreeding coefficients, e.g. Toro and Perez-Enciso 1990, Brisbane and Gibson 1995, Meuwissen 1997, Caballero and Toro 2000, Woolliams et al. 2002, Colleau et al. 2004a, Colleau et al. 2005b. In the method proposed by Meuwissen (1997), the genetic progress in one generation of selection is maximized under a constraint on the increase of inbreeding, with no attention paid to the mating plan. Considering that breeders are more familiar with genetic gains than with levels of inbreeding, Colleau et al. (2004a; 2004b) proposed to minimize the increase of inbreeding for a given expected genetic gain, looking also for the optimal mating design between males and females. This method was tested on real data from selection programmes on dairy cattle (Colleau et al. 2005b) and pigs (Colleau and Tribout 2006) and also goat breeding (unpublished results). In each case, the major selection steps were identified and optimized retrospectively. Optimization would have led to kinship and inbreeding coefficients decreased by about 20% at each of the selection steps considered (see Table 3).

**Table 3.** Relative decrease of inbreeding rates ( $\Delta F$ ) and coefficients (F) from using optimized procedures.

Species	Selection step	$\Delta F$	F
Dairy cattle (3 breeds)	Mating for young bulls	15–18%	22–29%
	Young bull selection for sampling	7–20%	
	Use of AI bulls	19–29%	
Pig (1 breed)	Use of boars	19%	17%
	Replacement + use of boars	30%	32%

Sources: Colleau et al. 2005b, Colleau and Tribout 2006.

### **From theory to practice: towards sustainable breeding**

The first step towards sustainable breeding is to regularly provide information to the breeders and their selection organizations de Rochambeau et al. (2003). For instance, from January 2005 in France, each pig breeding organization receives, several times per year, the results for some parameters (probabilities of gene origin, inbreeding, kinship, ...) computed on both its own population and the whole breed considered (Delaunay and Mérour 2006). In dairy cattle, the average coefficients of kinship between the young AI bulls and the old AI bulls are provided yearly.

Optimization methods indicate that at any given time, candidates for selection differ as to their recommended contribution to future generations. Then, corresponding calculations might be achieved with a pre-determined time schedule. Indeed, this new parameter is the most informative one to be transmitted to breeders as guidelines for selection and use decisions. It would not involve any operational complexity for users, exactly the same way as EBVs are just information, not dictating everyday behaviour. Optimal rankings are also useful and these rankings can be predicted by penalized EBVs, although imperfectly, as shown by the experience of dairy cattle and pig breeding schemes. An utmost important topic is to make breeders, at farm level, not departing too much from recommended rates, when using AI males. This might be the objective of renewing the current methodology of the mating plans proposed to them by AI organizations, by integrating the most efficient concepts of population and quantitative genetics.

## Conclusions

Management of animal genetic resources should not only focus on the between-population diversity but also consider the evolution of the within-population variability over time. From that point of view, the situation of some 'large' breeds seems to be more critical than the situation of some rare breeds. Several efficient management methods are available, their use depending on their ease of application and their acceptance by breeders.

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