

GENETIC EVALUATION OF FRENCH GOATS FOR DAIRY AND TYPE TRAITS

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INTRODUCTION

The beginning of genetic improvement of French dairy goats goes back to the 60's when a selection program was developed at a national scale by the National Institute of Agronomic Research (INRA) for the Alpine and Saanen breeds. The relatively rapid development of milk recording allowed the implementation of typical two-steps selection schemes for both breeds: since 1965, such schemes have included selection of parents, planned mating and progeny testing, and, in the 80's, the initial on-station progeny test evolved towards an on-farm progeny testing based on artificial insemination (Piacère *et al.*, 2000). Since the very beginning of the selection program the main selection objective for both breeds has been the improvement of protein yield and protein content in order to warrant profit for farmers and to improve cheese yield. In 1999, fat yield and fat content were added to the selection objective (Belichon *et al.*, 1999) to avoid an undesirable reduction of the ratio of fat over protein content. Up to 1995, type scores were nonlinear and they were used mainly for culling of dams and sires. In 1995, the "Institut de l'Élevage" and the French Breeders' Association "Caprigène France" defined new linear scores for type appraisal and, since 2000, a new genetic evaluation is being conducted for linear type traits. Methods and software used for genetic evaluation of French dairy goats benefit from the evolutions of dairy cattle genetic evaluation. First methods applied to dairy goats were based on modified contemporary comparison principles (Poutous *et al.*, 1981). Since then, methods and models have evolved: use of BLUP in an animal model with repeated records (Boichard *et al.*, 1992), consideration of heterogeneous variances (Robert-Granié *et al.*, 1999) for dairy traits, and multiple trait genetic evaluation for type traits (Ducrocq, 1992). The objective of this article is to describe the characteristics of present genetic evaluation of dairy goats in France, to report estimates of genetic trends for dairy traits in the Alpine and Saanen breeds, and to discuss perspectives for genetic evaluation.

GENETIC EVALUATION FOR PRODUCTION TRAITS

Data. Dairy performances used in genetic evaluation are recorded by the milk recording organisation "France Contrôle Laitier" and stored in a relational database developed at the Processing Centre of Genetic Information (CTIG, Jouy-en-Josas). In 2000, 303,179 females (156,879 Alpines, 134,672 Saanen, 11,628 crosses) were recorded in 2,613 herds (Institut de l'Élevage, France Contrôle Laitier, 2000). The French recorded populations are the largest for the international breeds Saanen and Alpine. Files used for genetic evaluation in the January 2002 run included 4,328,537 lactations of parity 1 to 10 started after 1978. The available information corresponded to 1,639,056 goats and 45,965 bucks. Traits considered in genetic evaluation are milk yield (kg), fat and protein yields (kg) and fat and protein contents (g/kg). Data are computed in a total lactation basis from monthly record and lactations are adjusted to

250 days. Completed lactations of less than 50 days and in-progress lactations of less than 75 days are excluded from the evaluation. Lactations in-progress shorter than 250 days are extended according to the following formula: $Y_{250d} = Y_{\text{partial}} + w \cdot Y_{\text{last-test-date}}$, where the coefficient w depends on parity and lactation stage (Barbieri, 1992). Terminated lactations are partially pre-corrected for lactation length using $Y_{250d} = Y_{\text{total}} \times (60+250) / (60 + \text{lactation length})$ for lactation shorter than 250 days. Terminated or in-progress lactations longer than 250 days are truncated. Pre-corrections for fat and protein contents are derived from the corresponding total or extended yields.

Method and model. The BLUP based on an homocedastic model (Boichard *et al.*, 1992) was replaced in 2000 by an heteroscedastic model (Robert-Granié *et al.*, 1999). Heritabilities are 0.30 for yields and 0.50 for contents, with corresponding repeatabilities of 0.50 and 0.70. Four environmental fixed effects are included in the model: (1) herd-year-parity (1, 2, 3 and over), (2) kidding month by year-region, (3) days dry classes by year-region, and (4) age by year-region (for 1st, 2nd and 3rd lactations) or parity by year-region (for lactations 4, 5, 6 and over). Genetic groups of unknown parents are defined according to breed and birth year of progeny. The heterogeneity of variances is accounted for by use of a log-linear model for residual variances including a fixed region-year-parity effect and a random herd-year-parity effect. Ratios of additive genetic and permanent environmental variances over residual variances are assumed to be constant.

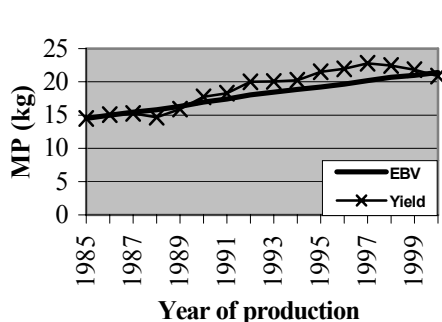
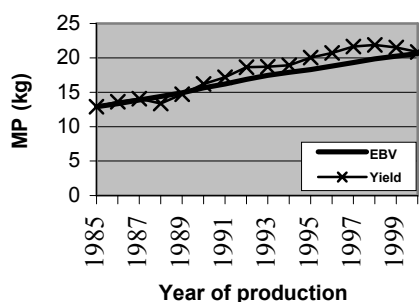
Diffusion of EBV. Genetic evaluation is performed three times a year by INRA. Five elementary EBV are computed: milk yield (IMY), fat yield (IFY), protein yield (IPY), fat content (IFC) and protein content (IPC), as well as a combined index defined as $ICC = IPY + 0.4 IPC + 0.2 IFY + 0.1 IFC$ in usual units, or equivalently $ICC = 0.44 IPY + 0.26 IPC + 0.06 IFY + 0.03 IFC$ expressed in genetic standard deviation units (Belichon *et al.*, 1999). Two groups of herds are distinguished: herds connected via AI (about 1,000 herds included in selection nucleus) for which EBV are published and disconnected herds, for which within-herd rankings are published. Accuracy of EBV is assessed by coefficients of determination (CD or R^2). Minimum CD for publication are 0.30 for natural mating males and females and 0.60 for AI bucks. EBV are expressed as deviations from a floating base updated each year. For year N, this base is the average EBV of does born between N-6 and N-3, with both parents known and a first lactation recorded. This base, common to males and females, is defined within breed.

Estimated genetic trends. Estimates of genetic trends are periodically validated using the method of "daughter yields deviations" proposed by Boichard *et al.*, (1995) and recommended by Interbull. Recent evolutions in the goat genetic evaluation (in particular, the inclusion of an age effect within second and third lactations, and the consideration of heterogeneous variances) yielded a satisfactory validation of genetic trends, with very stable deviations within sire over time. Genetic trends (table 1) were estimated by averaging female EBV (for females with both known parents and a recorded first lactation) by birth year for the last ten years (1990-2000). Genetic and phenotypic trends for protein yield in Alpine and Saanen are presented in figures 1 and 2. Phenotypic trends for protein yield were positive for both breeds. Gains in Alpine were slightly higher than those in Saanen for protein yield as for the other traits, due to a larger population size and higher selection rates practiced in Alpines.

Table 1 : Estimated genetic trends for the last ten years (1990-2000)

		Milk yield (kg/year)	Fat yield (kg/year)	Protein yield (kg/year)	Fat content (g/kg/year)	Protein content (g/kg/year)
Saanen	- usual traits	12.53	0.48	0.46	0.06	0.08
	- σ_g units	0.15	0.15	0.20	0.02	0.06
Alpine	- usual traits	13.65	0.55	0.50	0.09	0.09
	- σ_g units	0.18	0.18	0.22	0.03	0.05

σ_g : genetic standard deviation (as estimated in Belichon *et al.*, 2000)

**Figure 1. Saanen breed****Figure 2. Alpine breed**

GENETIC EVALUATION FOR TYPE TRAITS

Type traits are relative to body (thorax perimeter, back, and rump angle), feet and legs (distance between hocks, feet angle, pasterns), udder (floor position, rear udder attachment, rear udder, fore udder and udder profile), teat dimension (length, diameter, form), and teat location (angle, placement, orientation). Thorax perimeter, teat length and teat diameter are measured while the other traits are scored from 1 to 9. Data used in the January 2002 run included, for the Alpine (or Saanen) breed, 23,385 (15,361) primiparous recorded goats, all sired by 342 (255) AI bucks. A multivariate BLUP animal model (Ducrocq, 1992) is applied to each breed using genetic parameters estimated by Manfredi *et al.* (2001): heritabilities of about 0.5 for measured traits (thorax perimeter, length and diameter of teats), between 0.20 and 0.30 for udder and other teat traits, and lower for feet and legs traits. Fixed effects included in the genetic evaluation model are: herd-year, age classes-year and lactation stage classes-year. For publication, EBV are standardised according to genetic standard deviation. So far, EBV for type appraisal have been published only for AI bucks with at least 30 daughters recorded.

CONCLUSION AND PERSPECTIVES

As in modern dairy cattle genetic programs, EBV for goats in France are used for within herd or within stud selection, and, more importantly, for selection of dams and sires at the population level in planned selection schemes based on AI. This approach is yielding consistent and validated genetic progress in the main French breeds Alpine and Saanen. Estimated genetic trends for the main trait, protein yield, is about 0.2 σ_g , indicating that consistent genetic progress can be generated in dairy goats schemes based on an open nucleus and AI. Methods used for goat genetic evaluation are regularly updated according to available experience in dairy cattle. In perspective, the advantages to move from lactation models to test-date models will be evaluated. Also, the inclusion of molecular information in genetic evaluation will be tested. In particular, the gene of the $\alpha s1$ -casein is highly polymorphic in goats and it has important quantitative effects on solid contents (about three genetic standard deviations between extreme genotypes; Barbieri *et al.*, 1995). This polymorphism is an early partial predictor of progeny test results (Manfredi *et al.*, 1995) and it is used at present as an additional criterion for within-family preselection of young bucks candidates to progeny testing (Piacère *et al.*, 1997). The combination of the $\alpha s1$ -casein polymorphism and performances in genetic evaluation would allow a more efficient across families selection. Other perspectives are oriented towards the inclusion of new traits, such as somatic cell counts as an indicator of subclinical mastitis.

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