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442. Implementing genomic management of diversity and selection in French dairy goats

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Abstract

Optimal contribution selection (OCS) is a selection method that optimises genetic gain and diversity simultaneously. It has been implemented in French dairy goat breeding programmes since 2006. When genomic evaluation was applied in 2018, genomic OCS replaced pedigree OCS, accounting for genomic coancestries and differences of GEBV accuracies between progeny tested sires and untested sires. The genomic OCS efficiency was assessed based on the actual matings scheduled in 2021. Compared to candidates, selected sires had a higher genetic level despite a lower coancestry. Contribution of untested sires was only 30-35%. The future offspring showed a high genetic level and a genomic inbreeding from 3.0 to 3.6%. The survey of the AI bucks born between 2000 and 2022 confirmed the long-term efficiency of OCS: the annual genetic gain was about 0.17 genetic standard deviation on the total merit index whereas the annual rate of inbreeding only ranged between 0.05 and 0.07%.

Introduction

The implementation of genomic selection in many species generates additional genetic gain but raises questions about its impact on genetic diversity. For a large international breed like the Holstein breed, many studies (Doekes *et al.*, 2018; Forutan *et al.*, 2018; Doublet *et al.*, 2019) showed that genetic diversity was dramatically reduced once genomic selection was introduced. OCS is a powerful method (Meuwissen, 1997) maximising genetic gain at restricted rate of inbreeding. Colleau *et al.* (2004) developed an alternative method where the coancestry rate was minimized at fixed genetic gain. In France, two main dairy goat breeds are raised: the Alpine and the Saanen breeds. A total of 600 breeders and 175,000 females is involved in both breeding schemes. Since 2018, genomic selection has been implemented with two main changes: breeding values (GEBV) have been estimated with single step GBLUP (Legarra *et al.*, 2009; Carillier *et al.*, 2014) and 5 month-old AI bucks have been eligible for selection based on their GEBV. Their GEBV accuracy is not high enough to stop progeny testing, unlike dairy cattle. The management of genetic diversity has always been a major concern for the goat breeding schemes. In 2006, pedigree OCS (Colleau *et al.*, 2004) was introduced for producing young AI bucks, born from elite sires and dams. From the start of genomic evaluation in 2018, GOCS has been implemented, accounting not only for genomic coancestries, but also for GEBV accuracies. It was due to the very lower accuracy of not yet progeny-tested sires (NT) compared to progeny tested sires (PT). The goal of this paper was first to present the principles and results of the GOCS actually implemented in the two French dairy goats in 2021. The evolution of the genetic gain and the genetic diversity of AI bucks born between 2000 and 2020 was also analysed, in order to evaluate the long-term impact of OCS.

Materials & methods

Animals involved. GOCS is applied once a year for both breeds, in order to produce the new generation of young AI bucks. The result is a list of matings between elite sires and dams. To perform the optimisation, the breeding organisation provided different datasets and information. The list of candidates dealt with ungenotyped dams (871 Alpine / 822 Saanen) and genotyped elite sires (151 Alpine/ 76 Saanen). Because GOCS should produce minimal coancestry within the pool of males likely to perform AI in the future, the

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four last cohorts of young bucks (4C) born form OCS the four last years, were also considered (415 Alpine / 302 Saanen). GEBVs for the total merit index (ICC) and 16 other GEBVs were included, in reference with minimum thresholds in order to compute the number of defects for each mating. Genomic data corresponded to 2,901 Alpine and 1,980 Saanen 54K Illumina genotypes for the 46,707 SNP used in the official genomic evaluation. The overall pedigree included 41,557 Alpine and 34,678 Saanen animals.

The survey of AI bucks included 959 AI progeny-tested bucks in Alpine breed and 694 in Saanen breed, born between 2000 and 2020. For cohorts 2021 and 2022, progeny testing was not completed so that their statistics were those of the corresponding mating cohorts (about 700-750 per breed and per year). Trends in genetic gain, inbreeding and coancestry were analysed. Genetic gain was measured for ICC, expressed in σA. GEBV came from the French official genetic evaluation, performed in June 2021.

Genomic coancestry and optimisation methods. Genomic coancestries between pairs of genotyped individuals were computed according to Van Raden's method (2008). Otherwise, they were estimated by the method described by Colleau *et al.* (2017). Finally, SNP genomic coancestries and inbreeding were expressed in a converted scale, established once for all in 2018, based on data not influenced by genomic selection, as proposed by the same authors.

The optimal contributions of candidates and the corresponding mating design were computed based on the simulated annealing Monte-Carlo method (Metropolis *et al.* 1953, Kirkpatrick *et al.,* 1983). Constraints were accounted for by a constrained simulated annealing (CSA), according to the method proposed by Colleau *et al.* (2009), Chapuis *et al.* (2016). For computing optimal contributions, the corresponding CSA considered two major nuisances: the average coancestry coefficient (in a rolling window including 4C and future progeny) and the average inaccuracy (1-CD) of sires. These nuisances were expressed on a 0-1 scale from the minimum to the maximum values. Extreme values were given by dedicated CSA procedures, of course accounting for the constraint imposed for the average ICC of future progeny. Afterwards, scaled nuisances were minimized, while constrained to be equal, because considered of equal importance by the breeding organisation. The mating design basically minimized a linear function involving inbreeding coefficient and number of defects, standardized in reference to the whole variability of possible matings. A special sampling procedure was introduced to avoid extreme percentages of NT sires in the farms holding the selected dams and, thus, to increase acceptability by breeders.

Results

GOCS selected 60 sires (40% of candidates) in the Alpine breed and 37 sires (48%) in Saanen breed. Among them, about 60% were NT sires but their contribution to matings were only 39% in Alpine breed and 34% in Saanen breed. Each PT sire contributed to 19 matings, on average, in the Alpine breed and 33 in the Saanen breed, whereas NT sires contributed to 8 and 10 matings, respectively. The difference of contribution between PT and NT sires was explained by the gap of GEBV accuracy: NT sires had a much lower CD than PT sires (0.56 vs 0.90 on average). In contrast, candidate NT sires showed a genetic superiority over candidate PT sires of 1.12 ICC units (0.36 σA) in the Alpine breed and 0.70 ICC units (0.22) in the Saanen breed. Globally, GOCS selected sires (PT+NT) with a selection differential of 0.29 ICC unit (0.09 σA) in Alpine breed and 0.70 (0.22) in Saanen breed. In comparison with candidates, the average coancestry of selected sires with 4C was decreased by 15% in the Alpine breed and 9% in the Saanen breed. Table 1 shows the results for the 760 matings in the Alpine breed and 700 in the Saanen breeds. The mean ICC was fixed by the breeding organisation. The average genomic coancestry of offspring with 4C was 4.70% in the Alpine breed and 5.35% in the Saanen breed. The average genomic inbreeding reached 2.96% in the Alpine breed and 3.58% in the Saanen breed. Compared to all possible matings between selected sires and dams (before mating optimisation), the average inbreeding was reduced of 40% in the Alpine breed and 35% in

Table 1. Genetic gain, genetic diversity and number of defects of offspring.[1]

Breed	Alpine	Saanen
ICC	7.00 (0.65 / 5.57-9.93)	6.90 (0.58 / 5.58-9.04)
Inbreeding (%)	2.96 (0.57 / 1.16-4.51)	3.58 (0.63 / 1.90-5.57)
Coancestry[2] (%)	4.70	5.35
# defects	0.19 (0.43 / 0-3)	0.09 (0.31 / 0-2)

[1] Mean (standard deviation / min-max.

[2] Average genomic coancestry coefficient between offspring and 4C.

the Saanen breed. The average number of defects was very low, ranging between 0 and 3 depending on the mating. Consequently, offspring had balanced GEBV profile for all the traits.

The annual rate of inbreeding for AI bucks born between 2000 and 2022 (Figure 1) was 0.07% in the Alpine breed and 0.05% in the Saanen breed. It corresponded to an increase of 0.26% per generation in the Alpine breed and 0.21% in the Saanen breed. Before the implementation of OCS (2000-2006) the rate of inbreeding reached 0.30%/year in the Alpine breed and 0.22%/year in the Saanen breed, whereas after the implementation of POCS (2007-2018) it decreased to 0.14%/year and 0.17%/year, respectively. When focusing on the GOCS period (2019-2022), we observed that the rate of inbreeding dramatically decreased: -0.08%/year in Alpine and 0.07%/year in Saanen. The trend in annual coancestry rate was the same, decreasing from 0.01 to -0.19% in the Alpine breed and from 0.01 to -0.06% in the Saanen breed, between POCS and GOCS. The annual genetic gain on ICC was 0.165 σA in the Alpine breed and 0.169 σA in the Saanen breed during the 2000-2022 period. No major difference was observed before or after POCS. But, under the GOCS period, the preliminary results showed that the annual genetic gain substantially increased by 30% (Alpine) to 46% (Saanen).

Discussion

The implementation of genomic evaluation in dairy goat breeding programmes led to modifying OCS. Accounting for genome-based coancestries was necessary, as demonstrated by Sonesson *et al.* (2012). Otherwise, the inbreeding rate would have been underestimated. Including NT sires had contradictory

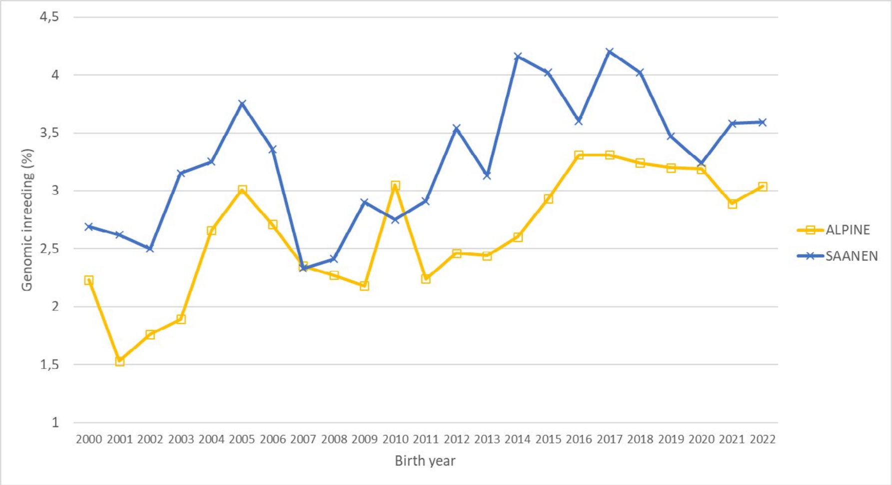

Figure 1. Genomic inbreeding trend for AI bucks between 2000 and 2022.

effects because the value of their genetic superiority for the breeding scheme was tempered by a low at-birth-GEBV accuracy. Currently, goat breeders have not been yet ready to use a high percentage of NT sires. But, the breeding organisation plans in the near future to use 60% of NT sires, still under the current GEBV accuracy, in order to reduce the generation interval. This could generate more genetic gain without decreasing genetic diversity, thanks to GOCS.

Our first results illustrated the efficiency of GOCS that combined moderate inbreeding and balanced GEBV profile of offspring, customized allocation for each NT sire while respecting desired genetic gain. Consequently, the rate of inbreeding for AI bucks remained reasonable, and much lower than in dairy cattle (Doekes *et al.*, 2018; Forutan *et al.*, 2018; Doublet *et al.*, 2019).

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