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**Genomic breeding schemes in French Lacaune and Manech dairy sheep:
design and expected genetic gain**

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ABSTRACT: French dairy sheep breeding schemes require a significant number of alive AI rams due to the fresh semen constraints. This number may be reduced significantly (by 25% to 45%) in the case of genomic selection (GS). For the AI rams, in a *GS design*, a genomic selection rate ($r1$) at 3-month-old, completed by a progeny selection rate ($r2$) at 2.5-year-old, is replacing the only progeny selection rate (r) at 2.5-year-old performed in a classical scheme. Compared to actual optimum (r) of 0.5, $r1$ and $r2$ values of respectively 0.3 and 0.8 allow an annual genetic gain increased by 15%, at same breeding cost of the AI rams. Genomic selection will be implemented in 2015 in Lacaune and in a near future in Manech breed.

Keywords:

Dairy sheep Lacaune, Manech

Genomic breeding scheme

Introduction

Both the availability of the Illumina Ovine SNP50 BeadChip since 2009 and the rapid improvements in genomic evaluations in dairy cattle were incentives for the managers of the French breeding companies to assess the technical and economical relevance of genomic selection (GS) in the dairy sheep populations. Two major research programs (Roquefort' in and Genomia) have been implemented since 2010 to study GS feasibility, respectively in the French Lacaune and Manech breeds (Astruc et al. (2012)). Reference populations of nearly 4,800 (Lacaune (LL)) and 1,500 (Manech red-face (MRF)) progeny tested AI rams (progeny rams - PR) were set up by the end of 2013. A significant gain in accuracy of genomic prediction over parent average (Baloche et al. (2014a); Legarra et al. (2014)), although lower than in large dairy cattle populations, allowed utilization of young rams (YR) without progeny-test. Based on a single step genomic BLUP, a routine genomic evaluation is now available for French dairy sheep breeds (Baloche et al. (2014a)). In addition, the first results of a GS experiment conducted in the LL breed confirmed its efficiency (Baloche et al. (2014b)), and provide us with useful informations and parameters for the present study.

The purpose of this study was to model different genomic breeding schemes and to compare their annual genetic gain (AGG) with classical breeding schemes close to their optimum (Buisson et al. (2013)). The modeling of GS scenarios takes into account the specific constraints of French dairy sheep breeding, where a significant number of

alive AI rams is required to face a high demand of fresh semen AI concentrated within a few weeks. This practical modeling approach was implemented with the balance between cost increase due to genotyping of YR to be genomically selected and cost decrease allowed by the reduction of the size of the AI rams in GS. Model outputs comprised AGG, the total number of alive AI rams, the number of rams to be genotyped and the breeding cost of the AI rams.

Materials and Methods

Classical AI breeding schemes. AI data from 2008 to 2011 were provided by the breeding companies and a precise description of AI along the year was carried out in order to produce the parameters of semen production needed for modeling (Table 1): number of AI doses in the top week ranged from 14,000 AI in MRF to 26,000 AI per company in LL; AI production per ram and per week ranged from 18 to 115 AI doses depending on the breed and the age of the ram; the elimination rate of bad semen ranged from 0 to 20 %, and the yearly mortality was around 5 % (Table 1). For the classical current breeding scheme of a given company, there are 200 (MRF) to 220 (LL) AI rams, born each year from around 30 ram sires, to be progeny tested. The total number of AI rams is nearly 600 in MRF and 700 rams in LL per company (Table 2).

The AGG of all 4 selection paths (MM, MF, FM and FF for males to males, males to females, females to males, and females to females, respectively) was then calculated in a deterministic model as:

Δ is the average genetic superiority of selected animals compared to the average genetic value of available candidates for each path, u is the percentage of ewes inseminated with sampling rams (for a GS scheme, $u=0$) and L the generation interval for each path (Lindhe (1968)).

The AGG is computed in overlapping generations by truncation on EBV omitting the within sire families selection (AGGt). Based on selection intensities, computed from actual selection differentials in classical LL or MRF breeding schemes, including in practice selection of ram sires within families, AGG values (AGGd) were 0.23 and 0.16 genetic standard deviation (σ_g). The homologous

AGGt results, equal to 0.27 and 0.20 σ_g respectively in LL and MRF classical breeding schemes, overestimated by 17 % (LL breed) to 25 % (MRF breed) actual AGGd results (Table 2). In other words, AGGt results must be used only for relative comparisons between classical and GS breeding schemes, and not as absolute AGG results.

Genomic breeding scheme designs. Different genomic scenarios were studied using a deterministic modeling. YR are first selected on their genomic evaluation (GEBV) at 3-month-old ($r1$) and then on their progeny phenotypes ($r2$), at 2.5-year-old or later at the arrival of their first proof, to move from the status of YR to the one of PR (Figure 1). In their first year of AI, YR are used with the aim of updating the reference population.

The following scenarios were modeled with $r1$ ranging from 1/2 to 1/7 and $r2$ from 0.7 to 1 :

GS-0.5: all the YR are first used at 6-month-old for updating the reference population. Then, at 1.5-year-old, they are used as dam or ram sires according to their GEBV (without daughters). YR become PR at 2.5-year-old (Figure 1).

GS-1.5: According to the difficulties of using 6-month-old rams in AI in MRF, YR are first used as AI rams at 1.5-year-old to update the reference population. They become PR at 3.5-year-old.

GS-mix: 80% of YR are first used at 6-month-old and the 20% left at 1.5-year-old. This scenario allows integration of late-born rams within a year.

The maximum ages at culling were fixed at 4.5-year-old in LL and 5.5-year-old in MRF.

Breeding Cost of the AI rams. The costs considered are those impacted by a genomic program: costs of genotyping, costs of maintenance of AI rams, purchase and sales of rams. Moreover the breeding scheme managers fixed the following cost constraints: to start GS at the same cost than the one of the classical breeding scheme.

Results and Discussion

Genomic breeding schemes. There are few differences between GS-0.5 and GS-mix in LL schemes. The number of AI rams per generation is reduced by almost 50% in LL and by 35% in MRF. This reduction is less important in MRF because of a lower AI dose production capacity per ram in this breed. On the other hand, for a given genomic selection rate ($r1$), the number of genotyped candidate rams per generation (NG) compared to the number of young AI rams (YR) selected per generation (NO) is higher in LL than in MRF (Table 2), because of a higher culling rate in breeding center of YR on standard and functional defaults (50% in LL and 15% in MRF) occurring before genomic selection. Finally, total number of AI rams (Ntot) is reduced by 45% and 25%, respectively in LL and MRF, thanks to lay off suppression in GS. The sharp decrease in the number of rams in the AI centers will partly compensate costs of genotyping. Despite the livestock reduction, the number of ram sires tends to increase (by 2.3

to 3 times in LL and MRF), which is a positive trend regarding the evolution of the genetic variability (Table 2).

Annual Genetic Gain. In the LL GS-0.5 scenario, except when $r1=1/2$, AGG is higher in GS than in the classical scheme (Figure 2). AGG increases when $r1$ and $r2$ increase (values decrease). However, the impact of $r1$ (genomic selection *per se*) is much higher than the impact of $r2$ (selection after progeny testing). Furthermore, Table 2 shows small variations for AGG between the two LL genomic schemes. In the genomic scenario where $r1=1/3$ and $r2=0.8$, AGG is increased by 10-15% in LL and 20% in MRF compared to optimum classical breeding schemes.

Annual cost. Figure 3 illustrates the impact of $r1$ on annual cost in the LL GS-0.5 scenario ($r2$ set at 0.8). Actual cost is set at 100. The more $r1$ increases (value decreases), the more the cost increases. With $r1=1/3$, the costs of both genomic and classical schemes are quite the same, in agreement with starting cost constraints defined by the breeding scheme managers. From $r1$ at 1/4 up to 1/7, costs become high (+25 to +90%) which does not comply with the constraints of starting GS at the same cost. When searching a consensus between AGG and cost, it appears that, with the current genotyping cost, the case $r1=1/3$ is the scenario economically relevant to face the constraints of no extra cost defined by the managers for GS starting. In Table 1, we observe that both genomic schemes modeled in LL allow an increase in AGG for the same annual cost. In MRF, with $r1=1/3$, the genomic cost is 40% higher, because of a smaller reduction of AI rams and a weaker utilization of YR.

Conclusion

Our modeling highlights that AI rams are used successively as YR then PR in an optimum dairy sheep GS breeding scheme (Figure 1). The same results are obtained in small dairy cattle populations, for which such a scheme is called hybrid scheme (Thomasen et al. (2014)). GS appears technically and economically relevant in French dairy sheep breeds, although it is clearly less cost-effective than in dairy cattle. This study shows that a genomic breeding scheme applying a genomic selection rate $r1=1/3$ at 3-month-old completed by a progeny selection rate $r2=0.8$ at the arrival of the first proof and at the following proofs provide an AGG increased by 15%, at same costs in LL. In MRF breed, the 40% higher costs could be balanced by a 20% increase in AGG. Any expected decrease of genotyping cost could also improve the cost balance. According to these results, the breeding organizations decided to implement GS in 2015 in LL and in a near future in Pyrenean breeds.

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Table 1. Parameters used for modeling scenarios of GS breeding schemes in Lacaune (LL, for one breeding company) and Manech Red Face (MRF) dairy sheep breeds.

	LL	MRF
# AI doses at the top week	26,000	14,000
AI production per ram and per week ¹	25-90-115	18-45-55
Elimination rate for semen production, % ²	10-5-0	20-5-5

¹ AI dose production per ram and per week depends on age of rams. The three values correspond to the AI production at 6-month-old, 1.5-year-old and ≥2.5-year-old rams

² The percentages of culling based on semen production are given, in order, at 6-month-old, at 1.5-year-old and at ≥2.5-year-old. It concerns rams whose semen of poor quality never allows AI dose production.

Table 2. Key parameters for classical (C) and genomic breeding schemes (GS-0.5, GS-mix and GS-1.5) in Lacaune (LL) and Manech Red Face (MRF) breeds. Genomic results are presented with $r1=1/3$ and $r2=80\%$.

	LL C	LL GS-0.5	LL GS-mix	MRF C	MRF GS-1.5
NG ¹	-	703	672	-	456
N0 ²	220	117	112	200	129
Ntot ³	700	392	391	595	451
Nrs ⁴	35	81	83	30	90
AGGd ⁵	0.23	-	-	0.16	-
AGGt ⁶	0.27	0.31	0.30	0.20	0.24
Cost, %	100	103	99	100	140

¹ NG = Number of genotyped candidates rams per generation

² N0 = Number of young AI rams (YR) selected per generation for AI

³ Ntot = AI rams present at the AI center (all generations)

⁴ Nrs = Number of ram sires

⁵ AGGd = Annual genetic gain using estimation of phenotypic selection differentials (in genetic standard deviation)

⁶ AGGt = Annual genetic gain using truncation method (in genetic standard deviation)

Classical AI scheme	Age	GS-0.5 scheme
		703 Genotyped rams
		$r1 = 1/3$
240 Sampling rams [£]	0.5	117 Young rams [£]
		$r2 = 0.8$
Lay-off (230 rams)	1.5	101 Young rams *
		$r2 = 0.8$
115 Progeny-tested rams *	2.5	74 Progeny-tested rams *
		$r2 = 0.8$
70 Progeny-tested rams *	3.5	57 Progeny-tested rams *
		$r2 = 0.8$
45 Progeny-tested rams *	4.5	44 Progeny-tested rams *
		Culling

[£] Used as dam sires in the nucleus flocks to maintain the reference population

* Used as dam or ram sires according to their EBV or GEBV

Green : progeny-testing of SR ; Red : Genomic use of YR ; Orange : classic utilisation of PR.

Figure 1. Design of a GS selection scheme (LL ; GS-0.5 ; $r1=1/3$; $r2=0.8$) and a classical breeding scheme.

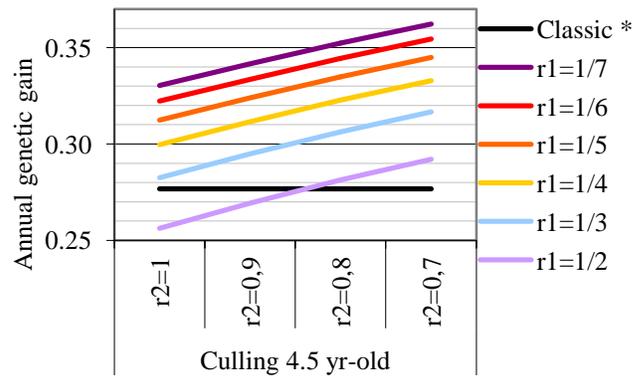


Figure 2. Annual genetic gain (AGGt) in genetic standard deviation according to $r1$ (genomic selection of newborns) and $r2$ (selection after progeny test) for the Lacaune breed and the scenario GS-0.5.

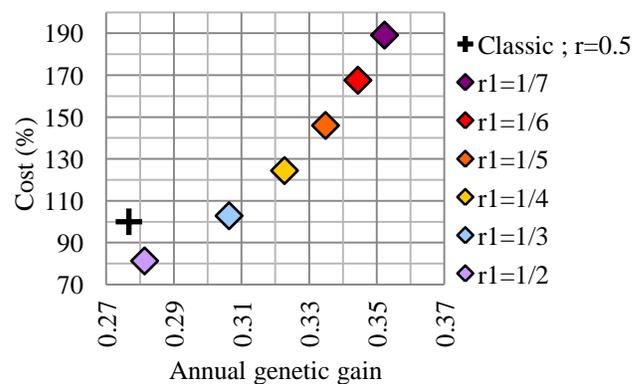


Figure 3. Co-evolution of AGGt and costs according to the genomic selection rate ($r1$) [Lacaune ; scenario GS-0.5 ; $r2=0.8$]. The costs are expressed as a percentage of classical scheme cost. The black cross indicates the current AGG and cost of the classical breeding scheme.