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**Genomic selection experiment in Lacaune dairy sheep : progeny test results of rams initially selected either on parent average or on genomic prediction**

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**ABSTRACT:** A genomic selection experiment was carried out for the AI dairy Lacaune rams born in 2011: within 46 sires, 200 and 128 sons have been progeny tested, respectively after usual parent average preselection (classical rams), or after a genomic preselection of around one third (genomic rams). The superiority of the genomic rams (GR) compared to classical rams (CR) for the total merit index (TMI) was underestimated by 58 % using BLUP versus using single-step GBLUP: the true breeding value superiority of GR compared to CR was estimated to 0.52 TMI standard deviation, so that only 24 % of GR were eliminated versus 48 % of CR according to the TMI threshold used to select the proven rams.

Keywords:

dairy sheep

Lacaune Breed

Genomic Selection

Experiment

### Introduction

French Lacaune, Basco-Bearnaise and Manech dairy sheep breeds benefit from efficient conventional breeding schemes using extensively artificial insemination (AI), which allows the progeny testing of around 700 AI rams per year on the whole (Astruc et al. (2010)). Therefore two research programs (Roquefort'in and Genomia) have been carried out over the last four years to give us time to investigate carefully the feasibility of genomic selection (GS) in these French dairy sheep breeds. We performed the four following tasks: 1. Setting-up of reference populations using the Illumina Ovine SNP50 BeadChip (Barillet et al. (2012)); 2. Testing increase in reliability of GEBV compared to the parent average reliability, most of our GEBV computations being based on GBLUP methods (Barillet et al. (2012); Duchemin et al. (2012); Baloche et al. (2014); Legarra et al. (2014)) 3. Conceiving genomic breeding schemes suitable for these dairy sheep populations and assessing their technical and economic efficiency compared to the conventional breeding programs (Buisson et al. (2013); Buisson et al. (2014)); 4. Implementing a genomic selection experiment to check in actual condition true efficiency of GS in these dairy sheep populations before possible evolution to GS breeding schemes. We expected also that this fourth task could provide us with relevant results or parameters for the third modeling task.

Given that 400 AI rams are progeny tested each year in Lacaune breed by 2 companies (Confédération Générale de Roquefort and Ovitest), it was decided to implement this genomic selection experiment in this breed, in the framework of the Roquefort'in project, for 2 batches of AI rams born in 2011 and 2012. The experimental design concerned a set of elite sires, for which sufficient sons entered breeding centers of young rams as candidates to be progeny tested by AI. Each group of sons within each elite sire was divided into 2 sub-groups: a sub-group of classical rams (CR) preselected as usual only on parent average prediction, and a second sub-group of genomic rams (GR) with the same parent average superiority plus a genomic preselection based on genomic prediction.

The objectives of this experiment were to compare progeny test results for the males of these two groups, CR and GR, which entered the AI centers. The aim was, on the one hand to validate the relevance of our genomic predictions, and on the other hand to verify the efficiency of the genomic preselection, which was of around one third. Indeed, according to our modeling results (third task), such a selection rate could allow, at about the same costs, an annual genetic gain increased by 15 % compared to a conventional breeding scheme, itself close to its optimum (Buisson et al. (2013); Buisson et al. (2014)).

### Materials and Methods

We will present in this paper only the results of the AI rams born in 2011, since the first progeny test results of the rams born in 2012 will be available only at the end of 2014.

**Breeding goal.** The current Lacaune breeding objective chosen by the breeders in 2005 gives the same relative weights to milk production traits (milk yield, fat and protein contents) and mammary functional traits (somatic cell count and udder scores) combined in a total merit index (TMI) (Barillet, (2007)). At the beginning of the selection in the years 60s, TMI included only milk yield expressed in deciliters (dl). TMI as described above includes now 9 production or functional traits, but it is always expressed in equivalent dl, like milk yield, since the breeders got used to its dimension and scale.

**Experimental design.** In 2011, 1,285 young Lacaune rams, born from assortative matings with 46 elite sires, entered breeding centers of young rams at one-month

old, i.e. on average 28 sons per sire. They were divided into two sub-groups of 482 and 803 candidates, respectively for the classical rams (CR) and genomic rams (GR), with the same TMI parent average predictions: 498 dl in both sub-groups CR and GR (table 1). This constraint of similar TMI parent average prediction was achieved within each elite sire, including on average 10 CR and 18 GR per sire. Given the TMI genomic prediction at 3 months of age, a preselection of around 1/3 was applied within each sub-group of about 18 GR per sire. After discarding males based on breed standard and male functionality (feet, etc), the final number of young 6-month-old rams that entered AI centers to be progeny tested was 200 and 128 respectively for CR and GR (table 1). TMI parent average predictions of these 328 AI young rams, 498 and 506 dl respectively for CR and GR, were comparable to values of candidate sons for these 2 sub-groups at the entrance in the breeding centers (498 dl), illustrating that selection for standard and male functional traits was independent from TMI selection (table 1).

#### **Pedigree and Genomic predictions.**

In 2011, we did not yet compute single step genomic BLUP (ssGBLUP) using all performances, animals in pedigree and including genotyped rams (Baloche et al. (2014)).

Thus, in March 2011, at 3-month-old for these young rams, we estimated TMI parent average using BLUP (4,278,634 performances and 1,392,483 animals in pedigree) and TMI genomic prediction using Pseudo-ssGBLUP (8,917 rams with daughter yield deviations (DYD), including 2,620 genotyped rams) to achieve a genomic preselection within the 803 candidate GR.

In September 2013, at the arrival of progeny test results for the AI rams born in 2011, which were 2.5-year-old, we computed both BLUP and ssGBLUP, including in both cases 4,643,878 performances and 1,511,343 animals in pedigree. For ssGBLUP, 4,768 genotyped rams were also included, of which the 803 candidate rams from the GR sub-group and the 200 progeny tested rams from the CR sub-group. The genotypes of the 803 GR candidates allowed with the ssGBLUP to account for the genomic preselection (at 3-month-old) effectively performed when choosing the 128 GR to be progeny tested (table 1).

**Criteria used to compare the results of the CR and GR.** Two criteria were used: first, the superiority of the GR compared to CR corresponding to the difference between average EBV or GEBV for the GR and CR sub-groups, expressed in TMI standard deviation; second, the culling rate according to the TMI threshold of 100 used to select the rams at the reception of their first proof results.

### **Results and Discussion**

**Progeny test results.** Table 2 shows the progeny test results of the 328 AI Lacaune rams involved in the first experimental 2011 batch. TMI distributions for polygenic EBV (BLUP) or genomic EBV (ssGBLUP) are comparable for CR and GR: EBV standard deviation for TMI of 220

and 215 for BLUP, of 259 and 269 for ssGBLUP, respectively for the 200 CR and the 128 GR. But the TMI superiority of GR versus CR is highly significant and estimated to 59 dl ( $P=0.0183$ ) and 141 dl ( $P < 0.0001$ ) respectively for BLUP and ssGBLUP TMI evaluations (figure 1), i.e. 0.27 and 0.52 TMI standard deviation (table 2).

**Evidence of biases in polygenic BLUP evaluations due to genomic preselection.** TMI parent average was not able to account for TMI genomic preselection carried out for the sub-group of GR: the predictions were the same, around 500 dl, for the 2 CR and GR sub-groups (table 1). The proof of 30 daughters per ram was not enough, since TMI BLUP evaluations for GR were significantly underestimated by 58 % (table 2), in agreement with Patry's simulations (Patry et al. (2011)). Conversely the results of this genomic selection experiment illustrate the ability of ssGBLUP evaluations to account for the fact that the 128 progeny tested GR had a better Mendelian sampling contribution, given that the genotypes of the 803 candidates were included in the ssGBLUP evaluations. Bias in polygenic BLUP evaluation appears quite high, even with a moderate genomic preselection of around one third for GR: genomic preselection needs to be accounted for in polygenic BLUP evaluations, in a transition period from a conventional to a GS breeding scheme, when only a part of the AI young rams could present a GS preselection.

#### **Useful parameters for GS design in dairy sheep.**

In the present GS experiment, we got on average three six-month-old GR per elite sire entering AI centers to be progeny tested. Since we did not compute ssGBLUP in 2011 to perform the genomic preselection for the GR sub-group, we checked *a posteriori* possible consequences on the present experimental results by computing now a 2011 ssGBLUP evaluation: the conclusion was that 33% of GR young rams per elite sire would have been replaced by best candidates, i.e. one GR within the three preselected young ram per elite sire. Such results are in agreement with highest accuracies and lowest bias when using regular ssGBLUP (Baloche et al. (2014)).

In other words, the present GS experiment could have been more efficient: the culling rate of 24 % for the GR sub-group versus usual 48 % for the CR sub-group, to select the proven rams at the reception of the results of their first proofs, must therefore be overestimated.

### **Conclusion**

To our knowledge, very few GS experiments have been published and none in sheep. It was the fourth task of our research programs carried out over the last four years to give us time with the managers of the French dairy sheep breeding schemes to investigate carefully the efficiency of GS in French dairy sheep populations. The present results are very useful and confirm key parameters of our design of suitable GS breeding schemes to French dairy sheep populations: a moderate genomic selection rate at 3-month-old completed by a null or low phenotype selection at 2 or

3-year-old for the AI rams, at the reception of the results of the first proofs, would allow an annual genetic at least equal to the gain of a conventional breeding scheme at its optimum (Buisson et al. (2013); Buisson et al. (2014)). This design is in complete agreement with our first GS experiment results, i.e. a phenotype selection culling of around 20 % at 2.5-year-old, after an initial genomic preselection of one third at 3-month-old for the AI rams. If these experimental results are confirmed at the end of 2014 for the second batch of Lacaune AI rams born in 2012, there is no doubt that GS will be implemented in 2015 in French Lacaune and in a near future in Basco-Bearnaise and Manech breeds.

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**Table 1. Design of the genomic selection experiment for the AI Lacaune rams born in 2011.**

	Classical rams (CR)	Genomic rams (GR)
# sires	46	
Candidate sons	at one-month-old <sup>1</sup>	
# candidate sons <sup>1</sup>	482	803
TMI <sup>2</sup> parent average	498 dl (a)	498 dl (a)
Genomic preselection	at three-month-old	
	no	yes
Genomic selection rate	0	1/3
Sons chosen as AI rams	at six-month-old	
# sons progeny tested <sup>3</sup>	200	128
TMI <sup>3</sup> parent average	498 dl (a)	506 dl (a)

<sup>1</sup> candidate sons born from assortative mating entering breeding center of young rams at one month old

<sup>2</sup> total merit index (TMI) expressed as equivalent milk yield in dl

<sup>3</sup> sons entering AI center to be progeny tested at 6-month-old

**Table 2. Progeny test results (at 2.5 year old) for the 328 AI Lacaune rams (born in 2011) in the experimentation**

	Classical rams (CR)	Genomic rams (GR)
# sires	46	
# sons progeny tested	200	128
TMI <sup>1</sup> parent average	498 dl (a)	506 dl (a)
Progeny test results	at 2.5-year-old	
# daughters per son	30	29
TMI <sup>1</sup> BLUP : mean	124 (a)	183 (b)
std	215	220
Superiority of GR	0.27 TMI std <sup>2</sup>	
% sons above TMI 100 dl <sup>3</sup>	45 %	32 %
TMI <sup>1</sup> ssGBLUP : mean	133 (a)	274 (c)
std	259	269
Superiority of GR	0.52 TMI std <sup>2</sup>	
% sons above TMI 100 dl <sup>3</sup>	48 %	24 %
BLUP underestimation for GR	58 %	

<sup>1</sup> total merit index (TMI) expressed as equivalent milk yield in dl

<sup>2</sup> standard deviation (std)

<sup>3</sup> Culling rate when using the TMI threshold of 100 to select the proven rams at the arrival of their first proof results.

**Figure 1 : distribution of TMI ssGBLUP for CR and GR**

