Genomic selection in French dairy sheep: Main results and design to implement genomic breeding schemes

J.-M. Astruc[1], *F. Barillet[2], G. Baloche[2], D. Buisson[2,3,4], G. Lagriffoul[1], X. Aguerre[3], P. Boulenc[5], F. Fidele[3], G. Fregeat[4], B. Giral-Viala[5], P. Guibert[6], P. Panis[6], C. Soulas[3], H. Larroque[2], A. Legarra[2]

[1]*Institut de l'Elevage, Castanet-Tolosan, France*
[2]*INRA, Castanet-Tolosan, France*
[3]*CDEO, Ordiarp, France*
[4]*OS Lacaune, Rodez, France*
[5]*Ovitest, Rodez, France*
[6]*Confédération Roquefort, Millau, France*

The selection of the French dairy sheep breeds is presently based on the annual progeny-test of around 440, 50, 30 and 150 AI rams, respectively in Lacaune (LL), Basco-Bearnaise (BB), black-faced Manech (BFM), and red-faced Manech (RFM) breeds. The 2009 release of the Illumina Ovine SNP50 BeadChip enabled to carry out programs to study the feasibility of genomic selection in the above breeds.

The main results are the following: (1) the size of the reference populations reached in 2013 4841 (LL), 509 (BB), 331 (BFM), 1424 (RFM) AI rams; (2) as accuracies of different genomic methods were quite comparable, in agreement with the probable absence of large QTL or major genes for the selected traits, the single step GBLUP method was chosen; (3) gain in accuracy of genomic predictions over parent average ranged from 0.10 to 0.20, depending on the trait and breed, in agreement with the reference population size of LL and RFM breeds, however unexpectedly high for BB breed; (4) gain in accuracy was more limited than in large dairy cattle breeds, in agreement with larger effective population size in sheep (200 to 370 in dairy sheep breeds); (5) blending populations, such as Manech and Latxa (Spain) whose proximity is known and assessed by conservation of LD patterns, did not increase the accuracy of genomic evaluations.

Given the moderate gain in accuracy of genomic predictions and the constraints of fresh semen for AI, the design of a genomic breeding scheme in dairy sheep will be quite different from the one in a large dairy cattle population. Dairy sheep breeding schemes requires a significant AI livestock, whose size may be reduced by 20 % to 40 % in genomic situation where males do not attend first proofs to be used. With a genomic selection pressure between 1/3 and ¼ in young rams, the annual genetic gain will be increased by 10% to 20%, with reduction of the AI livestock hardly balancing genotyping costs. Finally, the breeding organizations decided to move towards genomic selection in 2015 in Lacaune and in a near future in Pyrenean breeds, expecting a greater flexibility of the genomic scheme.

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