Assessment of technical and economic efficiency of French dairy sheep genomic breeding programs

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Potential benefits of genomic selection on genetic gain of small ruminant breeding programs

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In conventional small ruminant breeding programs, selection is based on pedigree and phenotypes but now there are prospects of including genomic information. The objective of this study was to predict the potential benefits of genomic selection on the genetic gain in today's French sheep and goat breeding designs. Classic and genomic scenarios were modeled for three breeding programs. The models included decisional variables that were optimized to maximize annual genetic gain (AGG) of: (1) a meat sheep breeding program that improved a meat trait of $h^2=0.30$ and a maternal trait of $h^2=0.09$; and (2) dairy sheep and goat breeding programs that improved a milk trait of $h^2=0.30$. The Bulmer effect was accounted for and the results presented are the averages of AGG after ten generations of selection. Results show that current breeding programs provide an AGG of 0.095 s.d. (genetic standard deviation) for meat and 0.061 s.d. for maternal traits in meat breed, 0.147 s.d. in dairy sheep and 0.120 s.d. in dairy goat breeds. By optimizing decisional variables, the AGG with classic selection methods increased to 0.139 s.d. for meat and 0.096 s.d. for maternal traits in meat breeding programs, and to 0.174 s.d. and 0.183 s.d. in dairy sheep and goat breeding programs, respectively. With a medium-sized reference population of 2,000 individuals (nref), the best genomic scenarios gave an AGG that was 17.9% higher than with traditional selection methods for combined meat and maternal traits in meat sheep, 51.7% in dairy sheep and 26.2% in dairy goats. These results were obtained when scenarios were compared at optimized decisional variables. The superiority of genomic schemes increased with nref and genomic selection gave the best results when nref >1000 individuals for dairy breeds and nref >2,000 individuals for meat breed. Correlation between meat and maternal traits had a large impact on the AGG of both traits.

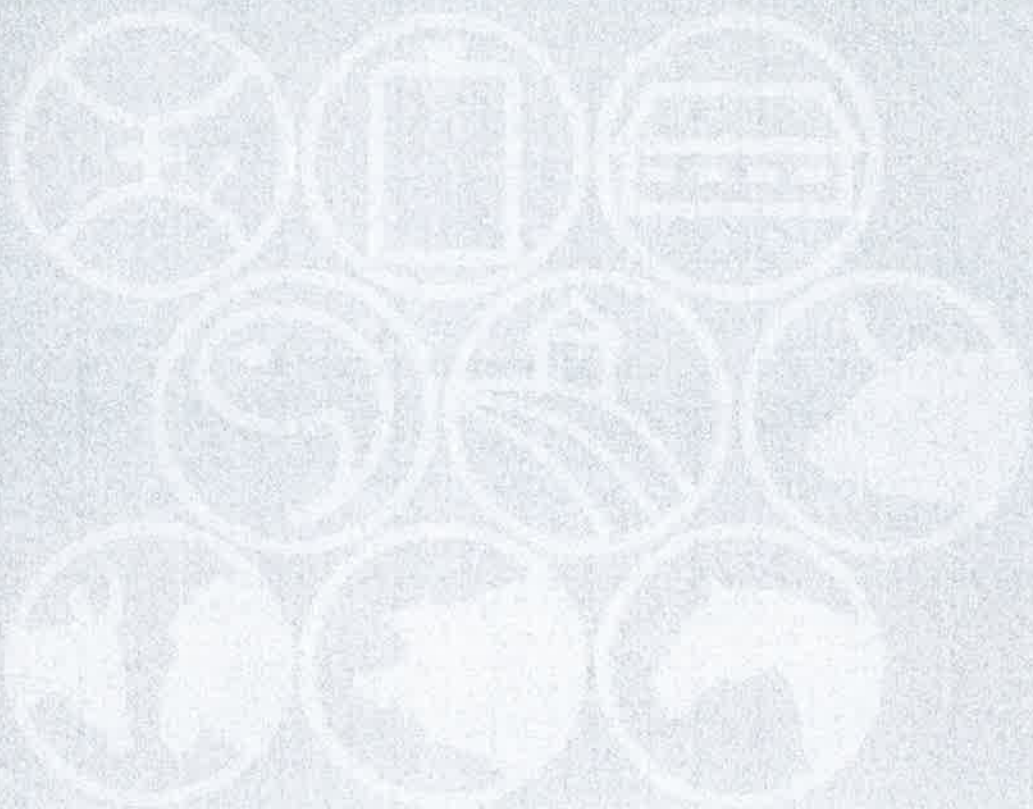**Assessment of technical and economic efficiency of French dairy sheep genomic breeding programs**

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The Roquefort'in and Genomia programs aim at evaluating the feasibility of genomic selection in French dairy sheep breeds. Reference populations of nearly 2,500 (Lacaune) and 1,500 (red-faced Manech) progeny tested AI rams were set up. Genomic predictions exhibit an increase in accuracy compared to parent average, lower than in dairy cattle, but allowing selection of proven rams without progeny-test. The purpose of this work was to model different designs of genomic-based breeding schemes fitting the constraints of dairy sheep: high number of alive rams required to face a high number of fresh semen AI concentrated within a few weeks. The modeling considered a wide range of variations in the management of the rams in the AI center: genomic selection pressure at 3-month-old, semen production of rams, age at culling of rams, selection intensity in the AI centre. The outputs of the models are the annual genetic gain, the total number of alive AI rams and the number of rams to be genotyped. Costs of rams' maintenance are estimated. The technical and economical results are compared to the current situation based on progeny-test. With a genomic selection pressure of around one third, the genetic gain is slightly above the gain of the classical program, close to its optimum, without any extra costs. The sharp decrease in the number of rams in the AI center compensates the costs of the genotypings. A higher genetic gain would be obtained by increasing dramatically the number of genotypings, which would break the economic balance. The capacity of semen production and the cost of genotypings are the key points to make a genomic selection program successful in dairy sheep.

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