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**A single-step, multiple-trait genomic evaluation model increase the accuracy for suckling performance in beef cows**

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Suckling performance of beef cows is of major importance for the income of livestock farmers. This trait is estimated with commercial farm data recording by the maternal genetic effect on weaning weight which is lowly heritable (0.09). In the Blonde d'Aquitaine breed, the breeding program includes a progeny testing station where eight sires are tested each year. Milk yield is recorded by the weigh-suckle-weigh technique on daughters and constitute a heritable (0.40) early selection criterion for bulls intended for artificial insemination. A dataset with 2403 milk yield records collected in station and 137,943 weaning weights from field records was used to genetic parameters in relation with suckling performance. A strong genetic correlation (0.75) was obtained and allowed performing a multiple-trait evaluation model. BLUP animal model and single- step genomic BLUP models were tested and theoretical average accuracies on a population of 813 candidates for selection were compared.

The reference population was made of 1 039 animals phenotyped and genotyped or imputed in 50K SNP density. Best correlations (0.20 to 0.30) were obtained with candidates that were moderately or strongly related to the station reference population. For other cases, accuracies were below 0.15.

The combination of farm and station performance is a good way to increase accuracy of candidate for selection, in particular for animal related to the reference population. The single-step GBLUP including performance from many non-genotyped animals leads to a more efficient use of maternal EBV in beef cattle breeding programs. In the near future, this method associated with an increase of genotyped animals will help to improve breeding choice accuracy and genetic progress.

**Keywords:** beef cattle, maternal effect, single step