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Comparison of genomic evaluation in Lacaune dairy sheep using single or multiple step GBLUP

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In Lacaune Dairy sheep, if a genomic breeding scheme is implemented, strong emphasis will be put on selection intensity of the young genotyped rams. Then, in order to keep unbiased GEBV, the pre-selection of candidates based on genomic information would have to be taken into account in genomic evaluation. With recent methodological and software development, the so-called Single-Step (SS) GBLUP gives Genomic Enhanced Breeding Value (GEBV) with such properties. Consequently, an attempt of such an evaluation was carried out in order to test its ability to predict rams genomic breeding value compared to the current multiple-steps (MS) procedure. Available reference population is a subset of 2,614 AI progeny tested rams (belonging to the Lacaune Breeding organisations Confédération Générale de Roquefort and Ovitest), born between 1998 and 2008 which were genotyped with the Illumina Ovine SNP50 BeadChip. After editing 42,039 SNPs were available for genomic evaluation. Depending on the method, phenotypes used were either dairy ewes own performances (SS) or daughter yield deviation weighted by equivalent daughter contribution of rams (MS). Traits studied were milk traits, somatic cell score and udder traits. GEBV computations followed Interbull's recommandations. Finally, predictions were compared to the most recent available EBV. As expected, SS slightly outperforms MS approach across all traits. Moreover its simple implementation and quick computations, except breeding value accuracy, give SS GBLUP better values for routine evaluation. Acknowledgements for French ANR & ApisGene (SheepSNPQTL project), and for FUI, Midi-Pyrénées region, Aveyron & Tarn departements, & Rodez town (Roquefort'in Project).

Genomic predictive ability for growth, carcass and temperament traits in Nelore cattle

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Nelore bulls were genotyped with the Illumina Bovine HD Beadchip to assess genomic predictive ability on weighing traits, scrotal circumference, temperament and carcass traits evaluated through visual scores. After quality control, 685 samples and 320,238 SNPs remained in the analyses. Most SNPs were discarded due to MAF (<0.02), call rate (<0.98) and high correlation (>0.995) with other SNPs. Sires with proofs in 2007 were considered as training group and sires without proofs in 2007 but with proofs in 2011 were considered as testing group. The proportions of sires were 75% (training) and 25% (testing), approximately. Average accuracy of expected breeding values (EBV) was 0.81-0.88 in the training group and 0.73-0.88 in the testing group. Predictive ability was assessed through the correlation between direct genomic breeding values (DGV, using GBLUP) and 2011 EBV for the testing group. Predictive ability based on empirical formula was also calculated and used for comparison. Observed and expected correlations for pre (wG) and post (yG) weaning weight gain, temperament (yT), scrotal circumference (SC), weaning muscling (wM) and precocity (wP), yearling muscling (yM) and finishing precocity (yP) were: 0.38 and 0.51 (wG), 0.53 and 0.50 (yG), 0.16 and 0.41 (yT), 0.60 and 0.47 (SC), 0.55 and 0.50 (wM), 0.52 and 0.50 (wP), 0.69 and 0.49 (yM), 0.70 and 0.49 (yP), respectively. Further analyses suggested that greater than expected predictive abilities were observed for traits affected by genotype stratification. Two subgroups were observed in principal component analyses based on genomic kinship coefficients. The strategy of assessing predictive ability within subgroups will be tested after genotyping more animals.

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