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Genomic evaluation of carcass traits of young bulls: comparison of two and single-step approaches

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Meat production has a large economic impact for dual purpose breeds farms, partly through the production of young bulls, slaughtered between 12 and 24 months. In order to implement an appropriate genomic evaluation for carcass traits of Normande and Montbeliarde young bulls, breeding values were estimated for young candidates to selection using different approaches. Records of 159,115 Normande and 154,119 Montbeliarde were used. Evaluation approaches were compared measuring their accuracy (correlation between preadjusted performances and estimated breeding values) and bias (regression coefficient of preadjusted performances on estimated breeding values) on two validation populations: the 20% youngest genotyped young bulls and the 20% youngest AI sires. Genomic approaches were more accurate than BLUP (+0 to +7 points of correlation, except for age at slaughter in the sire validation population evaluated using a GBLUP, where the accuracy was lower), but had worst regression coefficients (regression coefficient of 0.676 to 1.078 with genomic approaches, vs 0.806 to 1.141 with BLUP). Multiple weighting of genomic and pedigree information in the single-step relationship matrix were tested in order to obtain the best single-step evaluation possible. With appropriate correction of the relationship matrix, a single-step evaluation led to similar accuracies than a two-step procedure, but slightly better regression coefficients, except for the low heritability trait (age at slaughter), where the single-step procedure was highly preferable. These results will be used for the development of a routine genomic evaluation of carcass weight, conformation and age at slaughter of young bulls in the Normande and Montbeliarde breeds in France.