

Genomics to estimate additive and dominance genetic variances in purebred and crossbred pig traits

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This study aims at assessing the contribution of the additive and dominance genomic variances to the phenotypic expression of several purebred Piétrain and crossbred (Piétrain × Large White) pig performances. A total of 636 purebred and 720 crossbred male piglets were phenotyped for 22 traits that can be classified into the trait groups growth rate and feed efficiency, carcass composition, meat quality, behaviour, boar taint and puberty. Additive and dominance variances estimated in univariate genotypic models including additive and dominance genotypic effects and a genomic inbreeding covariate allowed us to retrieve the additive and dominance SNP variances for purebred and crossbred performances. These estimated variances were used, together with the allelic frequencies of the parental populations, to obtain additive and dominance variances in terms of genomic breeding values and dominance deviations. Estimates of additive genetic variances across traits were consistent with previous results without dominance indicating that additive and dominance genetic effects were non-confounded. Some traits showed a relevant amount of dominance genetic variance in both populations (i.e. growth rate 8%, feed conversion ratio 9-12%, backfat thickness 14-12%, lean meat 10-8%, carcass lesions 9%, in purebreds and crossbreds, respectively) or increased amounts in crossbreds (i.e. ham cut 8-13%, loin 7-16%, pH semimembranosus 13-18%, pH Longissimus dorsi 9-14%, dressing yield 5-15%, androstenone 5-13% and estradiol 6-11%). Results suggest that accounting for dominance in the models of these traits could lead to an increased GEBV accuracy and that using crossbred information can be beneficial to evaluate purebred candidates to selection for crossbred performance. Further research will compare additive and dominance marker effects between crossbred and purebred performances.