

Additive and dominance genomic parameters for backfat thickness in purebred and crossbred pigs

M. Mohammadpanah¹, M. Momen², H. Gilbert³, C. Larzul³, M.J. Mercat⁴, A. Mehrgardi¹, L. Tusell³

¹Dept of Animal Science, Faculty of Agriculture, Shahid Bahonar University of Kerman (SBUK), Kerman, Iran

²Department of Animal and Poultry Sciences, Virginia Polytechnic Institute and State University, Blacksburg, VA, USA 24061

³GenPhySE, Université de Toulouse, INRA, INPT, ENSAT, Castanet-Tolosan, France

⁴IFIP/ALLIANCE R&D, La Motte au Vicomte, 35651 Le Rheu, France

In pig crossbreeding programs, genetic evaluation has been based predominantly on purebred data accounting only for additive genetic effects, whereas improving crossbred performance is the ultimate goal. Theoretically, a combined crossbred and purebred selection method is advised if genetic correlation between purebred and crossbred populations differ from unity. If dominance effects are large enough, assortative mating strategies can enhance the total genetic values of the offspring. Hence, estimates of genetic parameters for purebreds and crossbreds are needed to assess the best selection crossbreeding scheme strategies. In this study, additive and dominance genetic variance components and additive and dominance genotypic correlations between a Piétrain and a Piétrain x Large White populations were estimated for backfat thickness (BFT). A total of 607 purebreds and 620 crossbred BFT records were analysed with a genotypic bivariate model that included hot carcass weight and inbreeding coefficient as covariates, an additive and a dominance genotypic effects, and a pen nested within batch random effect. Genetic parameters were estimated with EM-REML plus an additional iteration of AIREML to obtain the asymptotic standard deviations of the estimates. The additive genotypic correlation between purebreds and crossbreds was high, 0.82, indicating that the genetic progress attained in the purebreds can mostly be transferred to the crossbreds. Dominance genetic variance represented about 10 % of the BFT phenotypic variance in both populations, suggesting that assortative matings could slightly enhance both purebred and crossbred performances. However, the underlying genetic mechanisms responsible for the dominance effects could differ between populations since dominance genotypic correlation was 0.49.