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Incorporation of blood gene expression data in the genetic prediction of porcine immunity

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The inclusion of health-related traits in porcine breeding programs has been proposed for improving pig robustness. In addition, recent developments in the generation of gene expression data have lowered its cost, making it more feasible to include such information into breeding programs. In the present study we analysed the potential to predict health-related traits in a commercial Duroc population using whole blood RNA-seq data. We used a population of 255 animals, in which 13 health-related traits encompassing both innate and adaptative immunity were measured. Animals were genotyped with a commercial chip and imputed to whole genome sequence level. Transcriptomic data was obtained from whole blood RNA-seq. Modelling was performed with several mixed models: GBLUP, which considered genomic data [1]; TBLUP, which considered transcriptomic data [2]; GTBLUP, which considered both as independent random effects [3]; and the models GTCBLUP, GTCBLUPi and MBLUP, which reduced redundant genetic information between both effects using different approaches [4,5,6]. The inclusion of transcriptome data had a moderate to high impact on the prediction of health-related traits, capturing a large proportion of phenotypic variance and improving the phenotypic prediction accuracy. Considering the redundant information between effects improved both fitting capability and accuracy in the case of GTCBLUPi and MBLUP, whereas GTCBLUP presented similar accuracies that GTBLUP and TBLUP. Regarding genetic evaluation, only GTCBLUPi showed a tendency to higher breeding value accuracies than GBLUP, but results were not conclusive. Our study highlights the relevance of transcriptomic data in improving model fitting and accuracy when predicting immunity and other health-related traits in pigs.

1 - VanRaden 2008, J Dairy Sci 91:4414
2 - Guo et al. 2016, Theor Appl Genet 129:2413
3 - Li et al. 2019, Front Genet 10:126
4 - Perez et al. 2022, G3, 12, jkac258
5 - Haas et al., 2025, pending publication
6 - Liang et al. 2022, J Anim Sci Biotechnol 13:103

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