

The role of the blood transcriptome in the prediction of porcine immunity traits

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The blood transcriptome is closely linked to immunocompetence in swine. Incorporating gene expression data in genomic prediction models is thus expected to improve the accuracy of predicting immunity-related traits. This study explores the potential of whole blood RNA-seq data to predict health-related phenotypes in a commercial porcine population. A total of 255 eight-weeks-old Duroc pigs were phenotyped for several health-related traits encompassing both adaptive and innate immunity as well as stress indicators. Animals were genotyped with a commercial chip and imputed to whole genome sequence level (~8 million SNPs). Gene expression levels were obtained by whole blood RNA-seq. Modelling strategies considered in this study were: GBLUP, which used genomic data; TBLUP, which used transcriptomic data; GTBLUP, which considered both as independent random effects; and the models GTCBLUP, GTCBLUPi and MBLUP, which accounted for the shared genetic component between both effects using different strategies. GTCBLUP and GTCBLUPi both conditioned transcriptomic data on SNP genotypes, to make them independent, while MBLUP used a weighed strategy to both random effects. The inclusion of the transcriptome information improved model fitting for all studied traits. Moreover, models considering transcriptomic effects generally captured a higher proportion of phenotypic variance and demonstrated better accuracies in phenotype prediction. Among models considering the interaction between genomic and transcriptomic effects, only GTCBLUPi and MBLUP improved phenotype prediction accuracy, whereas GTCBLUP performed similarly to GTBLUP. Only the GTCBLUPi model showed a tendency towards better breeding value prediction, but the high dispersion prevented conclusive results. In conclusion, whole-blood RNA-seq data improves both model fitting and phenotype prediction of immunity and other health-related traits in pigs, the gain in accuracy depending on adequately modelling of the overlap between genetic and transcriptomic effects.