

# Incorporating genomic and transcriptomic effects in linear and structural models for predicting complex traits in pigs.

I. T. Vourlaki, M. Ballester, T. Jové-Juncà, Y. Ramayo-Caldas, and M. Piles\*

*IRTA, Institute of Agrifood Research and Technology, Barcelona, Spain.*

Phenotypes are influenced by genetic, epistatic and downstream biological regulation effects. Since transcriptome data serve as intermediate layers between phenotypes and genomic information, their incorporation in genomic prediction framework can be beneficial as other studies have shown. The objective of this study was to evaluate whether the integration of transcriptomics data can increase the prediction ability of single nucleotide polymorphisms (SNPs). Furthermore, we aim to compare the phenotypic variance explained by the additive genetic effect of SNPs alone with that explained by the combined contributions of SNPs and gene expression levels. The analysis was carried out for 6 traits, related to immune response and to porcine production, using blood transcriptomic data from 255 Duroc pigs. We compared the predictive performance of 2 Bayesian regression methods, BayesC and RKHS, with the extended neural network linear mixed model (NNLMM), which structurally incorporates omics data as intermediate layers between phenotype and genotypes. The 3 methods were implemented testing various input strategies using full set of transcripts or subsets selected through feature selection with Partial Least Square. Furthermore, we conducted a functional analysis to study whether the selected subset of transcript features have a biological relevance. The results showed that gene expression levels can explain a substantial fraction of phenotypic variance across all the traits, surpassing the variance explained by SNPs alone. Moreover, integrating gene expression data into the genomic prediction framework significantly boosts prediction accuracy. Our findings indicate that for 5 out of the 6 traits, combining transcripts and SNPs in a joint linear model improves prediction accuracy in animal breeding. Finally, among the selected subsets of transcripts we identified genes and biological processes directly related to the analysed traits.

**Key Words:** pig, immunology, machine learning, genomic prediction, RNA-seq.