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Genetic parameter estimation in purebred and crossbred pigs including dominance with kernel and two genomic models

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Recently, we proposed an approach to estimate genetic variance components in an F1 population under a genomic model with additive and dominant gene action (GBLUP-F1). Using GBLUP-F1, genetic variance is partitioned into additive variance (due to substitution effects of the parental gametes) and dominance deviations. Semi-parametric models using kernels (RKHS) to account for dominance may be more flexible and powerful. This work compares variance components estimated with kernel matrices, with “raw” genomic matrices and with the GBLUP-F1.

The genomic matrices involved biological additive (-1/0/1 for the AA/Aa/aa) and dominant (0/1/0) effects of genes. The RKHS model used two Gaussian kernel matrices based on Euclidean distances involving either gene content (additive kernel) or genotypes (dominant kernel). The different variance components were estimated by REML under each model and then referred to the same base population multiplying them by $D_k = \text{avg}(\mathbf{K}) - \text{avg}(\text{diag}(\mathbf{K}))$, being \mathbf{K} the kernel or the “raw” genomic matrices used. We analyzed litter size in pig data provided by Genus plc (Hendersonville, TN, USA) including purebred populations and their crossbreds.

After the correction with D_k , the total genetic variances estimated with kernel and genomic matrices were compared with those obtained with GBLUP-F1; they were identical in all models. Partition of the variance in dominance and additive components was, however, different between the kernel/genomic models and the GBLUP-F1. The partitions using kernel or “raw” genomic matrices are not orthogonal. Semi-parametric models using kernels (RKHS) may be more flexible and powerful, but the results that they produce are much more difficult to interpret. GBLUP-F1 models perform more satisfactorily to explain the partition of the total genetic variance.