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COMPOSITION OF GENETIC COVARIANCE BETWEEN TRAITS USING HIGH DENSITY SNP INFORMATION, A QUANTITATIVE PERSPECTIVE

Roel F. Veerkamp, Mario P. L. Calus

Animal Breeding and Genomics Centre, Wageningen Livestock Research, Wageningen, The Netherlands

Genetic association between traits, and correlated responses resulting from those associations, are generally predicted using genetic correlations. However, depending on the composition and magnitude of the genetic covariance, asymmetry of correlated responses might occur and predictions may last for one generation only (Bohren et al. 1966). Genome-wide association studies with denser marker genotypes might be useful to investigate the makeup of the genetic covariance between traits. Therefore, the objective was to investigate the makeup of the genetic covariances between quantitative traits in more detail. Phenotypic records of 1737 heifers of farms in four different countries were used after homogenizing and adjusting for management effects. All cows had a genotype for 37,590 SNPs. Initially, only the milk yield traits were considered, with a univariate Bayesian Stochastic Search Variable Selection (BSSVS) model including a separate polygenic effect. SNP estimated heritability and covariances differed from pedigree based estimates for some of the traits and the SNPs without a significant association explained most of the genetic variances and covariances of the traits. Ten regions were found with an

association with multiple traits, in one of these regions the DGAT1 gene was previously reported with an association with multiple traits. DGAT1 explained up to 41% of the variances of four traits and explained a major part of the correlation between fat yield and fat% and contributes to asymmetry in correlated response between fat yield and fat%. Some of the prior assumptions of the model (few QTL assumed and fitting a polygenic effect), and using a univariate model might have favoured the infinitesimal model like description of the covariances. Therefore, subsequently, a multi-trait BSSVS model was used and prior model assumptions were varied to investigate the effect on the estimated composition of the underlying the covariances.