Chromosomal partitioning of correlations among dairy and beef traits in dual purpose Fleckvieh breed

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Understanding genetic correlations among traits is important for multi-trait breeding. In this study we partition correlations among dairy and beef traits by chromosomes in dual purpose Fleckvieh breed. The data comprised 4,105 progeny-tested bulls genotyped with Illumina BovineSNP50K. Dairy traits were milk yield (MY) and fat yield (FY), while beef traits were net daily gain (NG) and carcass grading (CG). To partition correlations we performed a two-step analysis. First, we estimated allele substitution effects of SNP markers with a multivariate marker model (ridge regression). For this step we used a Monte Carlo Markov Chain method and saved samples from posterior distribution of allele substitution effects. Second, we used these samples and marker genotype data to obtain samples from posterior distribution of breeding values, which were in turn summarized to obtain samples from posterior distribution of genetic covariances and correlations among traits. We performed the second step for the whole genome as well as for different chromosomes, which enabled us to partition overall correlations among traits by chromosomes. Allele substitution effects were positively correlated among all traits (rMY:FY=0.30, rMY:NG=0.17, rMY:CG=0.15, rFY:NG=0.17, rFY:CG=0.15, and rNG:CG=0.28). Overall correlations within dairy and beef traits were high and positive (rMY:FY=0.76, rNG:CG=0.46), while they were low between these two groups of traits (rMY:NG=0.16, rMY:CG=-0.06, rFY:NG=0.11, and rFY:CG=-0.10). Chromosome specific correlations ranged between -0.03 and 0.02 for all pairs of traits. The chromosomal partitioning of the overall trait correlations indicated a positive contribution from within chromosomes and a substantial negative contribution from between chromosomes. For example, the negative correlation between MY and CG of -0.06 had the contribution of 0.41 from within chromosomes and the contribution of -0.47 from between chromosomes. This methodology will be used for further fine partitioning in the future.