**Genome-wide association study for milk fatty acid composition using cow versus bull data**

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So far, few genome-wide association studies (GWAS) have been performed on milk fatty acid composition (FAC) in dairy cattle. Those studies used single SNP models applied to cow data. The objective of our study is to perform a GWAS for FAC, using either predicted FAC on a few hundred genotyped cows or 226 genotyped bulls with estimated breeding values (EBV) for predicted FAC or both. FAC in milk (g/dl) for both the genotyped cows and the daughters of the genotyped bulls was predicted from mid-infrared profiles using calibration equations developed notably within the RobustMilk project. The following groups of FA were included: saturated, monounsaturated, polyunsaturated, unsaturated, short chain, medium chain and long chain. EBV for FA for the 226 bulls were obtained from a dataset including 345,723 Walloon Holstein cows using a series of 4-trait (milk, fat, and protein yields plus one of the FA traits) 3-lactation random regression models. The 226 bulls had FA EBV with reliabilities ≥0.44. Of the 226 bulls, 44 had no daughters with predicted FA, so their FA EBV were only based on the yield traits. Of the other 182 bulls, 140 had between 10 and 1,691 daughters with predicted FA. A Bayesian model was used to estimate the effects of all SNP simultaneously. Genotypes were available for 36,346 SNPs after usual edits. When both cows and bulls were included, the traits were analysed as separate traits, using a bivariate model. It is expected that combining the cow and bull data will increase the power of the analysis.