Bayesian stochastic search variable selection using phenotypes collected across research herds in EU

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Genome-wide association studies (GWAS) for difficult-to-measure traits are generally limited by the sample size with accurate phenotypic data and are usually carried out considering individual single nucleotide polymorphism (SNPs) one at a time. The objective of this study was to compare variance components from a linear animal model with those estimated using BSSVS. Phenotypic data on primiparous Holstein-Friesian cows from experimental farms in Ireland, the UK, the Netherlands and Sweden (FPCM, DMI, BCS and LW) were available on up to 1,629 genotyped animals (37,590 SNPs). Genetic parameters from the two analysis were comparable, but not equivalent. For some traits, SNPs explained a larger part of the total genetic variances than for other traits. This was also reflected in the genetic correlations between the traits. The variation explained by SNPs on each chromosome was related to the size of the chromosome and was relatively consistent for each trait with the possible exceptions of BTA4 for BCS, BTA7, BTA13, BTA14, BTA18 for LW, and BTA27 for DMI. For LW, BCS, DMI, and FPCM, 266, 178, 206 and 254 SNPs had a Bayes factor >3, respectively. Olfactory genes and genes involved in the sensory smell process were over represented in a 500 kb window around the significant SNPs. Potential candidate genes were involved with functions linked to insulin regulation, epidermal growth factor and tryptophan.