

Genome-wide associations for fertility traits in Holstein-Friesian cows using data from four European countries

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The objective was to utilise data on primiparous Holstein-Friesian cows from experimental farms in Ireland, the UK, the Netherlands and Sweden to identify genomic regions associated with fertility. Traditional fertility measures were days to first heat, days to first service, pregnancy rate to first service, number of services and calving interval; post-partum interval to the commencement of luteal activity (CLA) was derived using routine milk progesterone assays. Phenotypic and genotypic data on 37,590 single nucleotide polymorphisms were available on up to 1,570 animals. Genetic parameters were estimated using linear animal models and univariate and bivariate genome-wide association analysis was undertaken using Bayesian stochastic search variable selection performed using Gibbs sampling. Heritability of the traditional fertility traits varied from 0.03 to 0.16; the heritability for CLA was 0.13. The posterior QTL probabilities for the traditional fertility measures were all <0.021. Posterior QTL probability of 0.060 and 0.045 was observed for CLA on BTA2 and BTA21, respectively, in the univariate analyses; these probabilities increased when CLA was included in bivariate analyses with the traditional fertility traits. For example, in the bivariate analysis with calving interval, the posterior QTL probability of the two aforementioned SNPs were 0.66 and 0.12. The results from this study suggest that the power of genome-wide association studies in cattle may be increased by sharing of data and also possibly by using physiological measures of the trait under investigation.