

DEPARTMENT OF REPRODUCTION, OBSTETRICS AND HERD HEALTH

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GENOME-WIDE ASSOCIATION FOR MILK PRODUCTION, LACTATION CURVE AND CALVING INTERVAL IN HOLSTEIN COWS

INTRODUCTION

Milk production is mainly dependent on the shape of the lactation curve, defined as the graphical representation of milk yield over the course of the lactating period. The shape of the lactation curve is characterized by the slope of the initial rise of the curve, peak yield, time to peak, the slope of the curve after peak yield.

AIM

The aim of this study was use genome-wide association study (GWAS) to identify genetic marker(s) associated with 305-d milk yield, parameters of lactation curve and calving interval in Holstein dairy cows.

MATERIALS AND METHODS

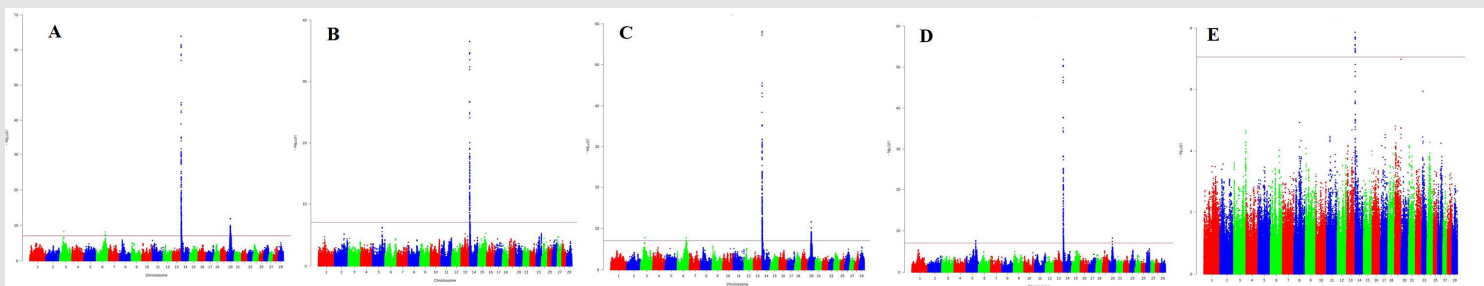
The data were records on 9,917 primiparous Holstein cows, distributed among 118 herds in four countries (Belgium, The Netherlands, Great Britain and Denmark) . To describe the lactation curve, the MilkBot model was used.

$$y_t = a \left(1 - \frac{\exp\left(\frac{c-t}{b}\right)}{2} \right) \exp(-dt)$$

In this function, a represents the theoretical maximum daily yield; b represents the rate of rise in milk production in early lactation; c describes the offset in time between parturition and the start of lactation; and d represents the rate of senescence of production capacity.

Individuals were genotyped using the Bovine LD, Bovine SNP50K or Bovine HD SNP panel. Genotypes of animals were imputed to HD with a reference population of 795 (46 M and 749 F) HD individuals. The genetic analyses were carried out through the restricted maximum likelihood (REML) method. Deregressed estimated breeding values (DEBV) of animals were used as the response variable in the GWAS. The GWAS was performed using a single SNP regression mixed linear model.

RESULTS AND DISCUSSION



Genome-wide association analysis of P-values of SNPs from single SNP regression mixed linear model for 305-d milk yield (A), ramp (B), scale (C), decay (D), and calving interval (E)

In total, 534, 179, 525, 263, and 18 SNPs were found to be associated with 305-d milk yield, ramp, scale, decay, and calving interval, respectively. The most significant SNPs were mapped inside the CPSF1 and DGAT1 gene.

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