

## Abstract

Reproductive health is an important trait in selection of dairy cattle. A genome-wide association study (GWAS) is a powerful tool for annotating phenotypic effects on the genome and to get knowledge of genes and chromosomal regions associated with reproductive performance (Cole et al. 2011). Combining GWAS and genetic profiling of embryos before implantation enables to develop new strategies to select elite breeding genotypes before transfer (Humblot et al. 2010; Ponsart et al. 2013).

## Aim

The aim of the current study was to evaluate the association between single nucleotide polymorphisms (SNP) and estimated breeding values (EBV) for reproductive traits [interval to insemination (EBVII) and interval between calving (EBVIC)].

## Methods

DNA was extracted from 96 sire semen samples. SNP genotyping was performed using the Illumina BovineSNP50 BeadChip (Illumina Inc., San Diego, CA, USA) containing 54609 SNPs.

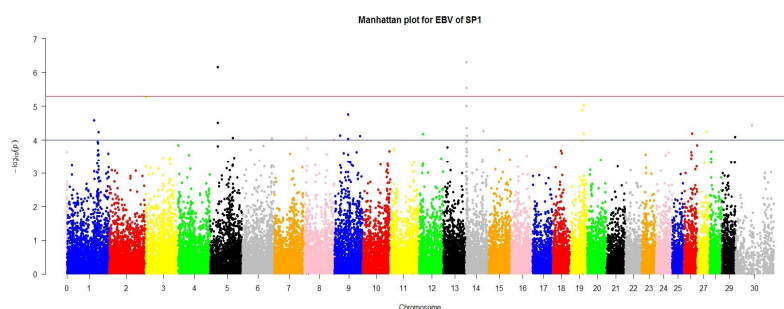
Quality control information was carried out in PLINK (v. 1.07; Purcell et al. 2007 Am. J. Hum. Genet. 81).

Estimations of breeding values of sires were performed by best linear unbiased prediction (BLUP) mixed model equations.

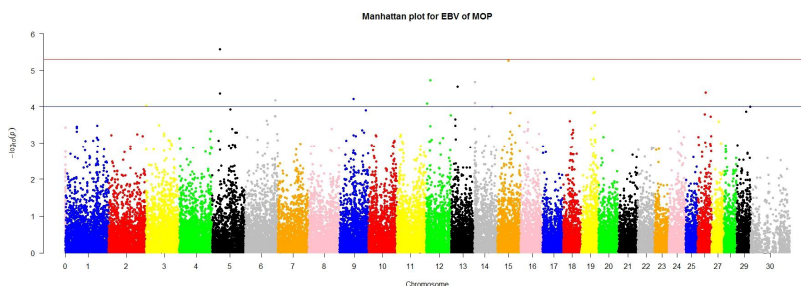
$$y = \mu + BULL + YOB + HERD + MOC + e$$

## Results

Based on the quality control information, 41442 SNPs were selected for subsequent GWAS. We have identified 3270 SNPs having significant effect ( $P < 0.05$ ) on studied traits.



**Fig. 1. Manhattan plot for EBV of interval to insemination.**



**Fig. 2. Manhattan plot for EBV of interval between calving.**

## Discussion

The most significant associations with EBVII were found for SNPs Hapmap38548-BTA-97184 and ARS-BFGL-BAC-11821 with coefficient of determination ( $R^2$ ) of 0.2189 and 0.1937, and P-values  $2.27 \times 10^{-6}$  and  $1.01 \times 10^{-6}$ , respectively.

The most significant effect on EBVIC was detected for SNPs ARS-BFGL-NGS-59769 and ARS-BFGL-NGS-38020 with coefficient of determination ( $R^2$ ) of 0.236 and 0.2421, and P-values  $1.49 \times 10^{-8}$  and  $7.24 \times 10^{-8}$ , respectively.

The highest number of significant associations was found on BTA5, BTA12, BTA19, and BTA14.