

Genome Wide Association Study for Heifer Pregnancy in Nellore Cattle

A.S. Leaflet R3063

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Summary and Implications

Considering the economic importance of sexual precocity in Brazilian beef cattle production systems, we were interested in a genome wide association study (GWAS) to find genomic regions that might explain the genetic variability of precocity assessed from heifer pregnancy rates. Given each suggestive region of large effect, we were interested in contrasting the two paternally-inherited haplotype alleles to identify sires that were heterozygous for the effect caused by that region. The database consists of reproductive information on 1,337 *Bos indicus* Nellore heifers, from three different herds in Brazil. GWAS results identified genomic regions on chromosomes 5, 14 and 18 that explained more than 1% of the total genetic variance. Haplotype analysis for the chromosome 5 region showed heterozygote sires with significant differences in reproduction between their half-sib progenies.

Introduction

Reproductive traits in livestock production systems directly influence the number of animals for sale and can constrain attempts to reduce the generation interval of the population. The understanding of the genomic regions explaining variation in these traits could help better define selection criteria for more efficient animals, allow reductions in the generation interval, increase the supply of surplus animals for finishing, and collectively improve the profitability of producers. The presence of haplotypes blocks that segregate together in the population make it possible to contrast the effects of paternal haplotype alleles, which can assist fine-mapping in relation to using only SNP genotypes. Favorable haplotypes for heifer pregnancy should be detected and selected to increase genetic value of the population.

Materials and Methods

The project called “Genomic Improvement of Fertilization Traits in Danish and Brazilian Cattle” is a

partnership between the University of Copenhagen (Denmark) and University of Sao Paulo (Brazil). The database comprises information on 1,337 Nellore heifers from three different herds in Brazil representing the offspring of 48 sires.

Sexual precocity was measured in terms of pregnancy in Nellore heifers after being exposed to bulls or artificial breeding at about 15 months old. Pregnancy diagnosis was made by ultrasound examination some 40 days after the start of the breeding season. The pregnancy status was analyzed as a categorical trait using GenSel software.

The animals were genotyped using the *Bos indicus* GeneSeek Genomic Profiler (GGP-HDi) that features nearly 78,000 SNPs. A total of 1,254 animals and 64,800 SNPs passed quality control filters and were used in the analyses. Bayes-B methodology was used for GWAS by characterizing the proportion of variance accounted for by each non-overlapping one megabase (Mb) window. Haplotypes blocks were defined by Findhap software considering a frequency filter of 3%. Contrast analyses ($p < 0.10$) were made in order to compare the posterior effects of alternate paternal alleles inherited by each set of half sib daughters when these were fitted as fixed effects in a Bayes-B model that fitted as random effects all SNPs outside the window.

Results and Discussions

The heritability was estimated to be 0.09. The GWAS results showed regions on chromosomes 5, 14, and 18 that explained $>1\%$ of total genetic variance. The chromosome 5 region explained 4.89% (Figure 1).

A haplotype block of approximately 4 Mb was defined centered on the most significant window on chromosome 5. The contrast analysis identified four different haplotype alleles that significantly affected heifer pregnancy.

The results suggest regions on chromosomes 5, 14, and 18 affect heifer pregnancy in Nellore cattle. The significant haplotypes at chromosome 5 could be used for selection to increase heifer pregnancy rates, and for additional fine-mapping studies to determine the causal mutation.

Acknowledgements

We would like to thank Dr. Pietro Sampaio Baruselli (USP) and his group for collecting and sharing the reproductive data allowing this research to be done.

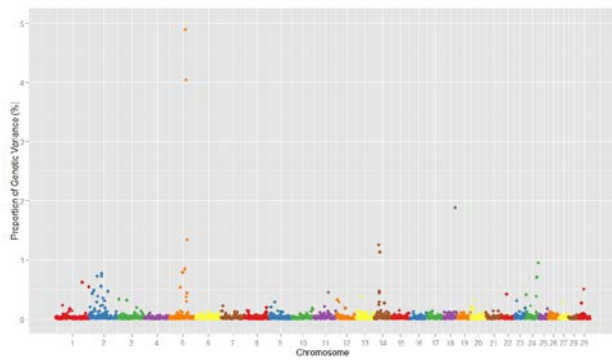


Figure 1 – Manhattan plot of Genomic Wide Association Study for heifer pregnancy in Nellore cattle.