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Whole Genome Analysis of Pinkeye Scores in Angus Cattle

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Abstract
Infectious Bovine Keratoconjunctivitis (IBK), known as pinkeye, is a common infectious disease affecting the eyes of cattle. It is characterized by excessive tearing, inflammation of the conjunctiva, and ulceration of the cornea. Although pinkeye is non-fatal, it has a marked economic impact on the cattle industry, due to the decreased performance of infected individuals. Genetic effects on the susceptibility of IBK have been studied and Hereford, Jersey, and Holstein breeds were found to be more susceptible to IBK than Bos Indicus breeds. The objectives of our study were: 1) to estimate genetic parameters of IBK scored in different categories by using genomic threshold model, and 2) to detect markers in linkage disequilibrium with quantitative tract loci (QTL) associated with IBK.

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Whole Genome Analysis of Pinkeye Scores in Angus Cattle

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Introduction

Infectious Bovine Keratoconjunctivitis (IBK), known as pinkeye, is a common infectious disease affecting the eyes of cattle. It is characterized by excessive tearing, inflammation of the conjunctiva, and ulceration of the cornea. Although pinkeye is non-fatal, it has a marked economic impact on the cattle industry, due to the decreased performance of infected individuals. Genetic effects on the susceptibility of IBK have been studied and Hereford, Jersey, and Holstein breeds were found to be more susceptible to IBK than *Bos Indicus* breeds. The objectives of our study were: 1) to estimate genetic parameters of IBK scored in different categories by using genomic threshold model, and 2) to detect markers in linkage disequilibrium with quantitative tract loci (QTL) associated with IBK.

Materials and Methods

Records of IBK were collected from 858 animals born and raised in the Iowa State University Angus research herd from spring 2004 through spring 2008. Both eyes were scored individually by using a scale from 0 to 4. A score of 0 denotes a cornea with no apparent lesions, whereas 1, 2, 3, and 4 denote a cornea with a lesion covering less than 1/3, 1/3 to 2/3, more than 2/3, and perforation of the cornea. The IBK scores were classified for categorical analysis: **Two categories:** 0 for both unaffected eyes (63.7%) and 1 affected in either eye (37.3%). **Three categories:** 0 for both unaffected eyes (63.7%), 1 for single affected eye (26.4%), and 2 for both affected eyes (10.9%). **Nine categories:** 0 (63.7%) to 8 (0.58%) by adding the scores of the left and right eyes.

High-density single nucleotide polymorphism (SNP) genotypes (0, 1, or 2) were obtained using the Bovine SNP50 Infinium II BeadChip (Illumina, Inc., San Diego, CA). The BayesC threshold model was implemented in GenSel software by assuming a fraction (π=0.999) of SNP markers have no effect on IBK scores. In the Markov Chain Monte Carlo (MCMC) implementation, a burn-in period of 5,000 MCMC cycles was used before saving samples from each of an additional 40,000 MCMC cycles. The SNP marker effects were estimated by computing Monte-Carlo means of the posterior distribution of these effects using a Gibbs sampling strategy.

Results and Discussion

Estimated genetic variance components and heritabilities obtained from BayesC threshold model analysis of two-, three-, or nine-category pinkeye scores are given in Table 1. Heritability estimate from two-category analysis were found to be slightly lower than three- and nine-category analysis. However, standard deviations of heritabilities showed that there was no significant difference between heritability estimates from different pinkeye category definitions. Heritability estimates indicated that six or seven percent of observed phenotypic variance was genetic and could be captured and explained by SNP markers.

Genetic variances explained by SNP within each categorical analysis were calculated in the chromosomal regions defined by five contiguous SNP sliding windows and the 1,000 largest genetic variance windows were plotted with respect to their genomic locations (Figure 1). As seen in Figure 1, genome analysis for each categorization of IBK indicated that certain chromosomal region on the genome had a different degree of association to IBK. However, the regions on chromosomes 2, 13, and 23 were found to be common and to have the highest genetic variances in the whole genome analysis of IBK. There are many candidate genes in these regions, which could include a gene or group of genes associated with bacterial disease in cattle. Also, results from the nine-category analysis additionally identified regions on chromosome 1 and 20 including SNP residing within previously identified QTL regions for IBK, pathogenic diseases, and somatic cell count.

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Table 1. Posterior mean estimates of genetic parameter obtained from threshold model analysis of pinkeye scores.

Category	Genetic variance	Heritability ± S.D.
2	0.064	0.060 ± 0.044
3	0.072	0.065 ± 0.043
9	0.072	0.065 ± 0.041

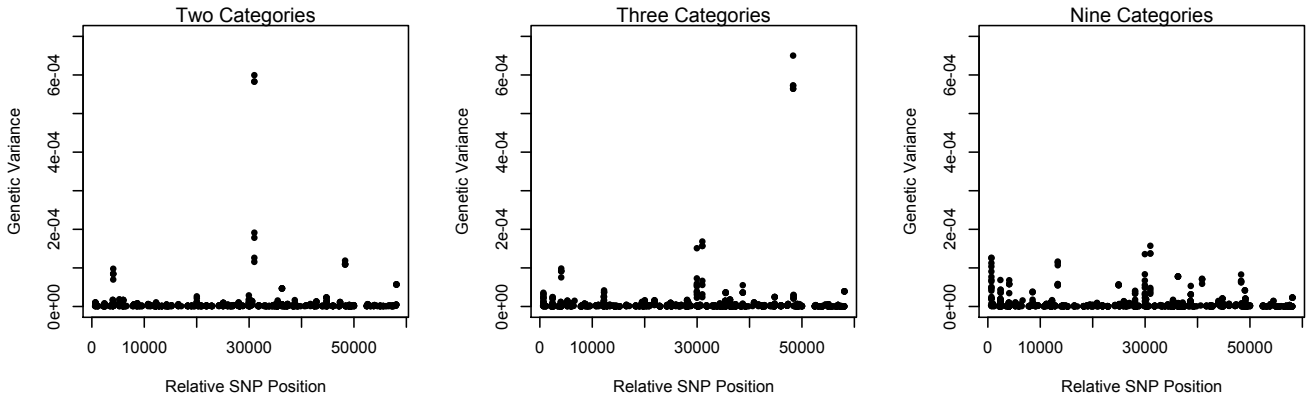

Figure 1. Genetic variance determined in the chromosomal regions by map position from chromosome 1 to 29 and the X chromosome, which were defined by sliding windows of five consecutive SNP through the whole genome for IBK score classified into two, three, or nine categories.