

Confirmation of quantitative trait loci using a low-density single nucleotide polymorphism map for twinning and ovulation rate on bovine chromosome 5

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Abstract :

Traditional genetic selection in cattle for traits with low heritability, such as reproduction, has had very little success. With the addition of DNA technologies to the genetic selection toolbox for livestock, the opportunity may exist to improve reproductive efficiency more rapidly in cattle. The US Meat Animal Research Center Production Efficiency Population has 9,186 twinning and 29,571 ovulation rate records for multiple generations of animals, but a significant number of these animals do not have tissue samples available for DNA genotyping. The objectives of this study were to confirm QTL for twinning and ovulation rate previously found on BTA5 and to evaluate the ability of GenoProb to predict genotypic information in a pedigree containing 16,035 animals when using genotypes for 24 SNPs from 3 data sets containing 48, 724, or 2,900 animals. Marker data for 21 microsatellites on BTA5 with 297 to 3,395 animals per marker were used in conjunction with each data set of genotyped animals. Genotypic probabilities for females were used to calculate independent variables for regressions of additive, dominance, and imprinting effects. Genotypic regressions were fitted as fixed effects in a 2-trait mixed model analysis by using multiple-trait derivative-free REML. Each SNP was analyzed individually, followed by backward selection fitting all individually significant SNPs simultaneously and then removing the least significant SNP until only significant SNPs were left. Five significant SNP associations were detected for twinning rate and 3 were detected for ovulation rate. Two of these SNPs, 1 for each trait, were significant for imprinting. Additional modeling of paternal and maternal allelic effects confirmed the initial results of imprinting done by contrasting heterozygotes. These results are supported by comparative mapping of mouse and human imprinted genes to this region of bovine chromosome 5.

Key Word :

GenoProb, multiple-trait derivative-free restricted maximum likelihood, single nucleotide polymorphism, twinning

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