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A network of genes involved in steroid metabolism as potential molecular markers for ovulation-related fertility in Holstein cattle. The present study was conducted to evaluate potential markers for ovulation-related fertility in Holstein cattle by identifying and analyzing genes involved in the steroid metabolism pathway. A total of 185 Holstein sires were classified into four groups (by estrus/cyclic, pregnant, not pregnant and nonpregnant) based on the records of their inseminations to 242 fertile cows and 36 nonfertile cows. Fourteen candidate genes involved in steroidogenesis and metabolism were selected from a previous study. In total, 1,123 single nucleotide polymorphisms (SNPs) were identified in 17 candidate genes. In the screening of the candidate SNPs, a comparison of allele frequencies between the two groups by a chi-square test revealed no significance ($p > 0.05$). However, a stepwise linear discriminant analysis (LDA) for the group classification revealed that the SNP genotype of the gene BEX4 (S17I) and CYP11A (T286N) could effectively discriminate the fertile and nonfertile cows. The relative contribution for LDA and the area under receiver operating characteristic (ROC) curve (AUC) of the LDA model were 0.848 and 0.857, respectively. The efficiency of the SNPs for the classification of fertile and nonfertile cows by LDA was lower than that of the microsatellite markers reported previously. The results of the present study suggest that a network of genes involved in steroid metabolism could be used to identify potential markers for the classification of cow fertility.

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