

Thousands of associated genetic variants have been reported through genome-wide association studies (GWAS). However, the resolution was limited, and the X chromosome and non-additive genetic effects have often been ignored. This thesis carried out GWAS in dairy cattle using high-density SNP chip and whole-genome sequence, explored the imputation of the X chromosome and detection of dominance effects. The results indicate that the resolution of quantitative trait loci detection was increased and meta-analysis of multiple breeds enhanced the power. The X chromosome could be accurately imputed and larger sample size is needed to detect dominance effects.

POPULATION LEVEL GENOME-WIDE ASSOCIATION STUDIES IN DAIRY CATTLE

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