

# Genome-wide association analyses identify genotype-by-environment interactions of growth traits in Simmental cattle

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## Abstract

Understanding genotype-by-environment interactions ( $G \times E$ ) is crucial to understand environmental adaptation in mammals and improve the sustainability of agricultural production. Here, we present an extensive study investigating the interaction of genome-wide SNP markers with a vast assortment of environmental variables and searching for SNPs controlling phenotypic variance (vQTL) using a large beef cattle dataset. We showed that  $G \times E$  contribute 10.1%, 3.8%, and 2.8% of the phenotypic variance of birth weight, weaning weight, and yearling weight, respectively.  $G \times E$  genome-wide association analysis (GWAA) detected a large number of  $G \times E$  loci affecting growth traits, which the traditional GWAA did not detect, showing that functional loci may have non-additive genetic effects regardless of differences in genotypic means. Further, variance-heterogeneity GWAA detected loci enriched with  $G \times E$  effects without requiring prior knowledge of the interacting environmental factors. Functional annotation and pathway analysis of  $G \times E$  genes revealed biological mechanisms by which cattle respond to changes in their environment, such as neurotransmitter activity, hypoxia-induced processes, keratinization, hormone, thermogenic and immune pathways. We unraveled the relevance and complexity of the genetic basis of  $G \times E$  underlying growth traits, providing new insights into how different environmental conditions interact with specific genes influencing adaptation and productivity in beef cattle and potentially across mammals.

## Biograph :

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