Allele-specific expression provides insights into the molecular basis of gene-environment interactions

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Gene-environment interaction (GxE) has been observed in many organisms and is known to be a major driver of phenotypic variation. GxE occurs when distinct genotypes respond differently to changes in the environment. In the face of future environmental change, understanding the effect of GxE is critical, as it may help predict how organisms will respond to new or shifting conditions. However, studying GxE in complex traits using quantitative genetic approaches remains experimentally and statistically challenging. Since organismal phenotypes are driven by molecular changes, molecular phenotypes such as gene expression provide a powerful approach to study GxE. Allelic differences in DNA sequences within populations can cause changes in gene expression. Quantifying allele-specific expression (ASE) by measuring the relative mRNA abundance of each allele at heterozygous loci controls for trans-acting genetic and environmental factors, providing a robust method to characterize gene expression GxE. This study aims to use ASE as a tool to develop a genome-wide framework to study gene expression GxE. To achieve this, we first conducted ASE analysis in a controlled environment, using an experiment on circadian transcription patterns in maize hybrids. This study demonstrated gene-time interactions in the expression patterns of circadian genes, conceptually similar to GxE. Next, we applied this framework to two distinct datasets: a small real-world environmental dataset from one maize hybrid collected at two locations, and a larger population dataset of 1,330 individuals representing 462 genotypes grown across six field environments, to identify gene expression GxE. Overall, these studies provide a systematic understanding of the effects of allelic sequence differences on GxE and show how GxE may contribute to phenotypic variation.