

DISSECTING REGULATORY VARIATION IN MAIZE

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Differences in gene expression are central to phenotypic variation and evolution. Such differences can arise from cis-regulatory changes that affect transcription initiation, transcription rate and/or transcript stability in an allele-specific manner, or from trans-regulatory changes that modify the activity or expression of factors that interact with cis-regulatory sequences. Both regulatory changes contribute to divergent gene expression, but their respective contributions remained largely unknown due to difficulties in distinguishing cis-acting components from trans-acting factors. The development of novel methods for the quantification of allele-specific expression has allowed unveiling of relatively frequent occurrence of differential expression that is not due to imprinting phenomena but most likely to cis-acting regulatory variation.

We set out to estimate frequencies and magnitudes of cis- and trans-acting regulatory variation in maize by measuring allele-specific differences in expression levels of genes. Seventy percent of genes tested (11/16) showed differences in expression of at least 1.5 fold due to cis-regulatory variation. On the other hand, only 20% of the genes (2/9) were affected by trans-regulatory activity. Interestingly, variations were tissue specific and influenced by stress. We further examined epistatic effects of trans-acting factors on cis-regulatory variation by assaying allelic expression in a set of 40 Recombinant Inbred Lines (RILs). None of the 10 genes tested showed oscillations in allelic expression across the RILs indicating the rare occurrence of coupled cis- and trans-regulation.

Taken together our data indicate that the majority of gene expression differences in maize are not caused by trans-regulatory changes with widespread effects, but rather by cis-acting changes spread throughout the genome. Depositing heritable variation in the regulation of gene expression within cis-regulatory sequences could be actually favourable since the individual trans-regulatory transcription factors typically interact with a wide network of genes and the variation affecting these proteins would be expected to have pleiotropic effects and rather dramatic phenotypes, therefore trans-regulatory changes are anticipated to be quite rare.