

REPETITIVE ELEMENTS: A SOURCE OF *CIS*-ACTING REGULATORY VARIATION IN MAIZE

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The maize genome is characterised by high nucleotide diversity within single copy regions, including genes, and lack of colinearity in intergenic regions due to the presence of different LTR-retrotransposons. These features may affect gene regulation and gene expression levels. By allele-specific quantification of transcript levels for a random set of genes in F1 hybrids we estimated that 70% of genes show differences in expression of at least 1.5 fold due to *cis*-regulatory variation. The differences were tissue specific and influenced by stress.

To assess the effects of the lack of colinearity in intergenic regions on allelic expression we estimated allelic expression imbalance in genes within 5 fully sequenced genomic regions from both alleles. We observed that the repetitive sequences content of intergenic regions significantly influences ($P < 0.01$) allelic expression. Conversely, there was no correlation between nucleotide diversity in the proximal promoter and differential allelic expression.

Retroelements are usually inactive but can be induced by various stresses and may affect the expression of neighbouring genes by producing single, chimeric or anti-sense transcripts. To investigate the potential role of epigenetic chromatin silencing in regulation of expression we are at the moment examining the methylation state of the analysed genes and their promoters within fully sequenced regions.

The results presented emphasize the importance of the genomic environment on gene expression and indicate repetitive elements as liable for expression regulation. Different sequence environments could therefore affect tissue specificity or temporal regulation of expression ensuring optimal gene expression in a wide variety of environmental conditions.