

## **DISSECTION OF THE REGULATIVE CONTROL OF MADS69, A GENE UNDERLIES A MAJOR FLOWERING TIME QTL, VGT3**

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Flowering time is an essential adaptative trait for crop breeding to local environments. A major quantitative trait locus (QTL) for flowering time and number of nodes, qVgt3.05 (Vgt3) was previously identified on chromosome 3 using a cross between the elite line B73 and the extremely early flowering Canadian –origin landrace Gaspé Flint. The same locus was shown to control flowering time in independent studies Vgt3 was finely mapped to a 380-kb genomic region including the known flowering time gene *Mads69* by positional cloning. Comparison of genomic sequences between Gaspé Flint and B73 identified no difference in *Mads69* coding sequences. The involvement of *Mads69* in flowering time gene was confirmed by overexpression and downregulation experiments. Comparative genomics analysis showed that *Mads69* RNA expression variation, both in terms of quantity and alternative splicing, associated with structural variation (transposon insertions) at its first intron. The earliness-inducing allele carried by Gaspé Flint appears of ancient origin, is present in tropical maize and likely contributed to adaptation to high-land and high-latitude environments, whereas the late-inducing allele was likely subsequently derived by transposon insertions.