

INSIGHTS INTO THE REGULATORY MECHANISMS OF A MAJOR FLOWERING TIME QTL IN MAIZE

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Flowering time is an essential adaptative trait for crop breeding to local environments and environmental stresses avoidance. A major quantitative trait locus (QTL) for flowering time and number of nodes, *qVgt3.05 (Vgt3)* was previously identified on chr. 3 by using a mapping population deriving from the cross between B73 and the extremely early flowering Canadian – origin landrace Gaspé Flint. *Vgt3* was finely mapped to a 380-kb genomic region including the already known flowering time gene *Mads69* by positional cloning. The involvement of *Mads69* in flowering time gene was confirmed by overexpression and downregulation experiments. Examination of sequence alignment for the *Mads69* coding sequence of Gaspé Flint and B73 did not reveal polymorphisms. Comparative genomics analysis showed *Mads69* expression variation, both in terms of quantity and alternative splicing, is associated with structural variation. 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.