

FINE MAPPING AND CHARACTERIZATION OF JAT, A MAJOR LOCUS REGULATING THE TRANSITION FROM JUVENILE TO ADULT PHASE IN MAIZE

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Maize is not only an important crop for grain and forage production but is also one of the most valuable energy crops for biofuel needs. Triggered by different internal and external stimuli, maize goes through a series of three main developmental stages over time, namely juvenile vegetative, adult vegetative, and reproductive. The developmental transition that mostly influences biofuel production is the switch from juvenile to adult phase of development (JAT). In fact, previous analysis of juvenile biomass in maize have shown that it possesses decreased lignin and increased levels of certain sugars, making it a superior substrate for fermentation by reducing the recalcitrant biomass to enzymatic saccharification. The JAT transition generally takes place at leaf 6-7 and can be easily identified by observing the disappearance of epicuticular waxes, the development of hairs and the formation of a thick cuticle.

In this work we report the fine mapping of a locus governing JAT in maize. A B73-nearly isogenic line (39-1-2-33) from a Gaspé Flint/B73 introgression library (Salvi et al. 2011, BMC Plant Biol, 11, 4) showed a prolonged juvenile phase (transition approximately at leaf 9 compared to leaf 6-7 of B73). A B73 x 39-1-2-33 F₂ population of more than 4000 plants was genotyped with SSR and de novo SNP markers and phenotyped by marking the leaf showing the transition between juvenile and adult phase. The fine mapping narrowed down the QTL to a 0,16 cM region corresponding to a 400 kb genomic interval. This region encompasses very few candidate genes potentially involved in promoting juvenile leaf traits. Validation and characterization of the putative functional candidate genes is ongoing by gene expression analysis and sequencing of the Gaspé Flint haplotype. Furthermore, the biomass chemical composition of the 39-1-2-33 line in comparison to B73 is being evaluated.