

FINE MAPPING OF *JAT-1*, A LOCUS CONTROLLING 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 it is also one of the most valuable energy crops. For this purpose, improved maize lines specifically tailored to serve as energy crops are needed. The developmental transition that mostly influences biofuel production is potentially the switch from the juvenile to adult phase of development (JAT). Previous analysis of juvenile biomass in maize showed that it possessed decreased lignin and increased levels of certain sugars making it a superior substrate for fermentation and a faster biomass-to-enzymatic saccharification. Triggered by different internal and external cues, maize undergoes three main development stages over time, namely juvenile vegetative, adult vegetative and reproductive. Each phase displays unique morphological and physiological characteristics that change when the plant undergoes a transition to the next phase. The transition to adult phase, a genotype-dependent event that generally takes place at the 6-7 leaf stage, can be easily identified by observing the disappearance of epicuticular wax, the development of hairs and the formation of a thick cuticle.

In this work, we report the fine mapping of *JAT-1* a locus governing transition from the juvenile to adult phase in maize. A B73-Near Isogenic line (NIL) from a Gaspé Flint/B73 introgression library (Salvi et al. 2011. BMC Plant Biology) showed a prolonged juvenile phase (transition at approx. leaf 9-10, compared to leaf 6-7 of B73). Two B73 x B73-NIL F2 population of almost 2,000 plants each were scored in 2014 and 2015 respectively by marking the leaf showing transition between juvenile and adult phase. Analysis of trait inheritance showed that early (B73-like) transition was incompletely dominant over late (Gaspé Flint-like) transition. Fine mapping carried out using SSR and SNP markers has narrowed down *JAT-1* to a 150 kb genomic region. Validation and characterization of the positional and putative functional candidate genes is ongoing.