Proceedings of the LXVI SIGA Annual Congress Bari, 5/8 September, 2023 ISBN: **978-88-944843-4-2**

Poster Communication Abstract - 1.33

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

TASSINARI A.*, FORESTAN C.*, BERTOLINI E.**, EMANUELLI F.*, TUBEROSA R.*, SALVI S.*

*) University of Bologna**) Donald Danforth Plant Science Center

maize, QTL, flowering time, transposable elements

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 Gaspe Flint and B73 did not polymorphisms. Comparative genomics analysis reveal 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.