



# Comparative quantitative trait locus mapping of maize flowering-related traits in an $F_{2:3}$ and recombinant inbred line population

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**ABSTRACT.** Flowering-related traits in maize are affected by complex factors and are important for the improvement of cropping systems in the maize zone. Quantitative trait loci (QTLs) detected using different materials and methods usually vary. In the present study, 266 maize (*Zea mays*)  $F_{2:3}$  families and 301 recombinant inbred lines (RIL) derived from a cross between 08-641 (founding parent from southeast China) and Ye478 (founding parent from China) were evaluated for four flowering-related traits, including days to tasseling (DTT), days to pollen shedding (DPS), days to silking (DTS), and anthesis-silking interval. Sixty-six QTLs controlling the target traits were detected in the  $F_{2:3}$  and RIL populations via single environment analysis and joint analysis across all environments (JAAE). The

QTLs explained 0.8-13.47% of the phenotypic variation, with 12 QTLs explaining more than 10%. The results of meta-QTL (MQTL) analysis indicated that 41 QTLs could be integrated into 14 MQTLs. One MQTL included 2.9 QTLs, ranging from two to ten QTLs for one to three traits. QTLs, including MQTL1-1 and MQTL9-1, were detected across the  $F_{2,3}$  and RIL populations via SAE and JAAE. Among the MQTLs, nine QTLs were integrated into MQTL9-1 and affected DTT, DPS, and DTS, with the favored allele being derived from 08-641. MQTL3-2 showed high phenotypic variation and was suitable for fine mapping to determine the genetic mechanisms of flowering. MQTL3-2 could be applied to improve inbred lines using marker-assisted selection.

**Key words:** Maize; Flowering-related traits;  $F_{2,3}$ ; RIL; QTL; MQTL