

IDENTIFICATION OF QTLS FOR EAR PROLIFICACY AND TILLERING IN MAIZE USING TWO CONNECTED RIL POPULATIONS

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maize, QTL, ear prolificacy, Tillering

The presence of multiple ears on the same stem node (Prolificacy) and number of tillers (Tillering) are important traits shaping maize plant architecture and affecting yield. In this study, two connected F6:7 RIL populations sharing one parent line (B73 × Lo1016 and Lo964 × Lo1016) were genotyped using a highly-dense SNP array and phenotyped in the field over two seasons for plant architecture and phenology traits. Lo964 is a high prolificacy - low tillering line, while Lo1016 is low prolificacy - high tillering. We performed quantitative trait loci (QTL) mapping by joint inclusive composite interval mapping. Across populations, prolificacy ($h^2 = 0.47 - 0.67$) and tillering ($h^2 = 0.61 - 0.64$) showed nearly normal distribution suggesting polygenic control. Mild correlations were observed between plant height and tillering ($r = 0.24$) and prolificacy and lowermost ear position ($r = 0.26$) or number of leaves ($r = 0.18$). Four QTLs for tillering were detected on chromosome 1, 2, 4 and 9. The tillering QTL on chr 1 overlaps with a known major tillering QTL formerly identified in maize × teosinte crosses. Based on literature review, one new prolificacy QTL was identified on chr 2 explaining 14.0% of the phenotypic variance. Our study revealed novel loci associated to prolificacy and tillering, providing support for cloning the corresponding genes and shedding light on the genetic control of maize plant architecture.