

## QTL MAPPING FOR EAR FASCIATION AND KERNEL ROW NUMBER IN TWO CONNECTED RIL POPULATIONS IN MAIZE

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Ear fasciation, originated from excessive proliferation of ear inflorescence meristem has been noticed and studied by researchers for long period of time. However, its molecular developmental basis and inheritance are dissection of this phenotype at the molecular level keeps not yet completely understood and obscure yet due to multigenic control and complex genic interactions complicated regulation mechanism. In this study, two recombinant inbred lines were created by crossing the ear-fasciation donor Lo1016 with two normal-ear inbred lines B73 and Lo964 and genotyped using a high-density SNP array. Here, a total of five traits including kernel row number (KRN), plus four other fasciation-related traits, including evaluation of ear-fasciation index (FAS), degree of ear ovality (OVA), degree of kernel distribution disorder (DIS) and ear diameter ratio (DIA) were phenotyped from 2017 to 2019. Next, QTL mapping was carried out using both linkage and association mapping were applied in order to obtain related QTL. Simultaneously at the same time, the two parent lines Lo1016 and Lo964 were also sequenced by using whole genome shotgun (Illumina). We recorded relatively high heritability values ( $h^2 = 0.60 - 0.79$ ) for all traits except DIA ( $h^2 = 0.31$ ). All ear fasciation-related traits resulted correlated with KRN. As a result, significant correlations between five traits were found, though only four traits have relatively high heritabilities except DIA. When linkage mapping was carried out, a total of 39 QTL were found across all the genome except chromosome 4, mainly distributed with several QTLs on chromosome chr. 7 (10 ten QTL) and 2 (8 eight QTL). Especially, the previously known *ramosa1* locus was included in the supporting intervals of several major ear-fasciation QTLs mapped in this study. A cloned fasciation gene is identified in the clustering region integrated by FAS7.1, DIS7.1 and OVA7.1. Results of variant calling showed that 6 variants were found in Lo1016 around *ra1*, and no difference was present in Lo964. We are investigating the hypothesis that native variation at *ramosa1* locus explains part of the genetic variation for KRN and ear fasciation in our experimental crosses and more generally in maize.