Breeding and Genetics (BG)

Dissecting Multiflower Male Truss Character in Melon (*Cucumis melo* L.)

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Male flowers in melon are usually found alone or in groups of 1-3 flowers per node. However, Zimbabwean melon line TGR-1551 has been identified to exhibit multiflower male trusses. In a previous study, one major QTL on linkage group 6 associated with the character in a poorly saturated region of a map of a RIL population derived from a cross between TGR-1551 and the Spanish melon cultivar 'Bola de Oro'. Now, a dissection of the character through the construction of a high-density map and the addition of one more phenotypic character has been carried out. High resolution QTL analysis was performed using genotyping by sequencing (GBS) of the same RIL population derived from the cross between TGR-1551 and 'Bola de Oro'. Genotypic data included approximately 1600 SNP markers and phenotypic data were based on the presence or absence of multiflower male trusses in 2012, 2013, and 2014 evaluations. In 2014, the number of flowers/node in the RIL population was also recorded. A major QTL on chromosome 6 (LOD score 12.89 for 2012, 19.9 for 2013, and 22.7 for 2014), which could explain up to 51.7 % of the phenotypic variability observed for multiflower male truss has been confirmed; the same QTL has been also identified for the number of flowers per node (LOD score 6.64 and R^2 17.4). This QTL collocated with the QTL described in our previous study although this time the level of phenotypic variation explained was higher and the stability of the character across three years has been confirmed. In addition, other two minor QTLs on chromosomes 6 and 4 were detected, explaining 7.1% and 9.5% of the phenotypic variance respectively. While the candidate gene MELO3C006888 had already been detected in our previous study, three novel candidates genes (MELO3C006880, MELO3C006860, and MELO3C006940) have been identified in the same QTL region. Further research through gene sequencing and gene expression profiling is needed to confirm the exact role of the found candidate genes on the character.

Session Topic
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