

Genetic and QTL analyses of yield and a set of physiological traits in pepper

An interesting strategy for improvement of a complex trait dissects the complex trait in a number of physiological component traits, with the latter having hopefully a simple genetic basis. The complex trait is then improved via improvement of its component traits. As first part of such a strategy to improve yield in pepper, we present genetic and QTL analyses for four pepper experiments. Sixteen traits were analysed for a population of 149 recombinant inbred lines, obtained from a cross between the large-fruited pepper cultivar 'Yolo Wonder' (YW) and the small fruited pepper 'Criollo de Morelos 334' (CM334). The marker data consisted of 493 markers assembled into 17 linkage groups covering 1,775 cM. The trait distributions were unimodal, although sometimes skewed. Many traits displayed heterosis and transgression. Heritabilities were high (mean 0.86, with a range between 0.43 and 0.96). A multiple QTL mapping approach per trait and environment yielded 24 QTLs. The average numbers of QTLs per trait was two, ranging between zero and six. The total explained trait variance by QTLs varied between 9 and 61 %. QTL effects differed quantitatively between environments, but not qualitatively. For stem-related traits, the trait-increasing QTL alleles came from parent CM334, while for leaf and fruit related traits the increasing QTL alleles came from parent YW. The QTLs on linkage groups 1b, 2, 3a, 4, 6 and 12 showed pleiotropic effects with patterns that were consistent with the genetic correlations. These results contribute to a better understanding of the genetics of yield-related physiological traits in pepper and represent a first step in the improvement of the target trait yield.

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