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Yield prediction based on QTLs for yield components using crop eco-physiological models
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Topic(s): Growth and physiology of crops (plant factories, greenhouses, open field, food, ornamentals)

Keywords: QTL, crop model, yield, yield components, prediction

Abstract: When studies on quantitative trait loci (QTL) for yield are conducted, number of harvestable organs and the weight of a harvestable organ are often included. Yield can be constructed from these two components and this is therefore a simple dissection of yield. However, there are more dissections of yield possible, with varying degrees of complexity. Next to the dissection mentioned above, simulation models can also help with dissecting yield. The goal in the present study is to compare different dissections of yield with varying complexity and see how well yield can be predicted based on the QTL of the components of the dissection. The first dissection of yield, called F, was into number of fruits and average fruit weight. The second dissection divided yield into total biomass and partitioning into the fruits, and was called dissection PS (partitioning static). A third dissection was called partitioning dynamic (PD) and involved a simple eco-physiological model (Lintul-type) with components partitioning into the fruits, light use efficiency and increase rate of leaf area index. We hypothesize that prediction of yield based on the QTL of the dissection PD is better than other dissections, as the yield components are rates rather than states, and the effect on yield of the environmental factors light and temperature, as well as duration of the growth, are removed from the components. Three experiments with a RIL-population of pepper were conducted in Spain to obtain yield and yield components: one training experiment T and two validation experiments V1 and V2. Experiment T and V1 included 149 genotypes and were conducted in autumn and spring, respectively. Experiment V2 included 37 genotypes, and was conducted in autumn. The genetic map consisted of 455 markers on 12 linkage groups. QTL analyses were performed on yield and the components of the three dissections obtained in experiment T. For yield, 3 QTL were found, which explained 37% of the variation. Dissection F and PS resulted in 7 QTL, dissection PD resulted in 10 QTL. On average 35% of the variation in components was explained by the QTL. Prediction of yield in experiment T was best with dissection PS (38% explained), closely followed by dissection PD (36% explained). Yield in experiments V1 and V2 using QTL from experiment T was best predicted by dissection PD (41% and 46% explained, respectively). Prediction of yield by dissection F (number of fruit and average fruit weight) was always the worst, especially in the validation experiments. This study shows that proper dissection of a complex trait using a (simple) simulation model can lead to better predictions in new environments.

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