

ABSTRACT

QTL ANALYSIS AND MARKER ADDITION IN A RECOMBINANT INBRED POPULATION OF PEPPER (*CAPSICUM* *ANNUUM* L.)

Regions of the pepper (*Capsicum annuum*) genome controlling germination rate, days to germination, days to flowering, yield, fruit weight, fruit length, fruit width, fruit shape, fruit number, pericarp thickness, plant height, and leaf level water use efficiency were analyzed through quantitative trait loci (QTL) and candidate gene approaches. This was performed utilizing a recombinant inbred line (RIL) population of pepper. This population was previously characterized by Ogundiwin et al. (2005), where 183 markers were used in concert with *Phytophthora capsici* resistance screening to locate QTLs for disease resistance. These same RILs were screened for the phenotypes listed above, and 13 QTLs controlling these traits were mapped to 6 linkage groups. In addition, cloned candidate genes that may be the source of the QTLs found were screened for polymorphism. The candidate gene markers along with internal simple sequence repeats (ISSR) markers could increase the marker density of the genetic map created by Ogundiwin et al. (2005), and help in fine-scale mapping of the QTLs found, should polymorphisms be found. The QTLs conferring the traits of interest will help plant breeders integrate resistance and agronomic traits in their pepper improvement breeding schemes.

Chad Michael Jorgensen
August 2009