



Genetic dissection of agronomic traits in *Capsicum baccatum* var. *pendulum*

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ABSTRACT. Genetic mapping is very useful for dissecting complex agronomic traits. Genetic mapping allows for identification of quantitative trait loci (QTL), provide knowledge on a gene position and its adjacent region, and enable prediction of evolutionary mechanisms, in addition to contributing to synteny studies. The aim of this study was to predict genetic values associated with different agronomic traits evaluated in an F₂ population of *Capsicum baccatum* var. *pendulum*. Previously, a reference genetic map for *C. baccatum* was constructed, which included 183 markers (42 microsatellite, 85 inter-simple sequence repeat, and 56 random amplification of polymorphic DNA) arranged in 16 linkage groups. The map was used to identify QTL associated with 11 agronomic traits, including plant height, crown diameter, number of days to flowering, days to fruiting, number of fruits per plant, average fruit weight, fruit length, fruit diameter, fruit

pulp thickness, soluble solids, and fruit dry weight. QTL mapping was performed by standard interval mapping. The number of small QTL effects ranged from 3-11, with a total of 61 QTL detected in 9 linkage groups. This is the first report involving QTL analysis for *C. baccatum* species.

Key words: Chili Pepper; Complex trait; Genetic map; Molecular markers; Quantitative trait loci