# Mapping QTL for bruchid resistance in rice bean (Vigna umbellate)

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ABSTARCT

The damage caused to stored seed by bruchids (Callosobruchus maculatus) is considered to be a major production constraint in rice bean (Vigna umbellata). Breeding for genetically determined resistance is the most environmentally benign and cost-effective means to mitigate the losses to bruchid infestation. Here, a screen of rice bean germplasm identified two sources of resistance, and determined the genetic basis of the resistance using a quantitative trait locus (QTL) mapping approach. The two resistant accessions (LRB238 and JP100304) were each crossed to a common susceptible cultivar (LRB26) to generate F2 mapping populations, one of which (LRB238 × LRB26) was genotyped with a range of Vigna sp. microsatellite assays and by sequence related amplified polymorphism (SRAP) fingerprinting. The resulting linkage map comprised ten linkage groups and covered a genetic distance of 872.1 cM with a mean inter-marker distance of 32.05 cM. The subsequent QTL analysis detected the presence of 11 QTL, distributed over all ten linkage groups, most of which were associated with the % damage caused to the seed. Two major QTL, Cmpd1.5 (flanked by the SRAP markers E2M9-270 and E12M7-311) and Cmpd1.6 (flanked by the SRAP marker E7M10-141 and the microsatellite locus CEDG259) mapped within 11.9 cM and 13.0 cM of the flanking markers, respectively, accounted for, 67.3 and 77.4 % of the variance respectively, for % damaged seeds. A bulked segregation analysis carried out in the JP100304 × LRB26 population revealed that the resistance donor harboured some resistance factors not represented in LRB238.