Development of PCR-based markers associated with powdery mildew resistance using bulked segregant analysis (BSA-seq) in melon

ABSTRACT

Powdery mildew (PM) is a fungus that causes disease in both the field and the greenhouse. Utilizing resistant cultivars is the most effective approach of disease management. To develop insertion-deletion (InDel) markers associated to this trait, the whole genomes of the PM resistant line M17050 (P1) and the PM-susceptible line 28-1-1 (P2) were sequenced. A total of 1 200 InDels, with an average of 100 markers per chromosome, were arbitrarily chosen from the sequencing data for experimental validation. One hundred InDel markers were ultimately selected due to their informative genetic bands. Further, an F2 segregating population of melons generated from these two parents was inoculated by the PM pathogen. Based on bulk segregant analysis (BSA) using these 100 InDel markers, the powdery mildew resistance was associated with the genomic region LVpm12.1 on the melon chromosome 12. This region overlapped the previously described quantitative trait locus (QTL)-hotspot area carrying multiple PM-resistance QTLs. Moreover, conventional QTL mapping analysis was done, which located LVpm12.1 in the region between 22.72 and 23.34 Mb, where three highly polymorphic InDel markers MInDel89, MInDel92, and MInDel93 were detected. Therefore, these markers could be used to track this resistance locus in melon while the lines carrying this locus could be employed in PM melon resistance breeding programs after validation tests.