Mapping of QTLs conferring to Anthracnose resistance in chili pepper by SNP markers

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ABSTRACT:

Anthracnose in pepper caused by a multiple *Colletotrichum* species is a significant disease damaging chili pepper fruits in the tropical and subtropical climates.

The complexity of the pathogen and lack of resistance in *Capsicum annuum* affected the breeding efforts for anthracnose resistance. *Colletotrichum* is a genus of fungus consisting of ~900 species infecting in a wide range of crops including corn, cauliflower, bitter gourd, cucumber, pumpkin, banana, strawberry, mango, pepper, tomato, and chili pepper. Breeding for resistance by Bioassay due to the complexity of the pathogen-host relationship is not easy. Molecular markers can contribute substantially to the resistance breeding. For the Mapping of QTL's conferring to anthracnose resistance two mapping populations were generated by crossing *Capsicum annuum* variety 'Bangchang' x *C. chinense* 'PBC932', and *C. baccatum* 'PBC80' x 'CA1316'

We created two QTL maps, in the mapping population of 'PBC932', the map contained 12 Linkage groups (representing 12 chromosomes of *capsicum*) with 214 SNPs and total of 824 cM coverage. In the population of *baccatum* 'PBC80' the map consists of 12 Linkage groups with 403 SNPs and 1,270 cM coverage. Two major QTLs were identified in the 'PBC932' and three in the *baccatum* 'PBC80' population.

SNP markers are highly abundant in the genomes and they can provide maps with high resolution compared to the other marker system, therefore have been increasingly used for QTL mapping studies. QTLs are usually located in noncoding regulatory regions such as enhancers, they could be located several megabases away from genes within intergenic spaces

In order to increase the power of the anthracnose QTLs markers we converted the markers which have been mapped in to the Causal markers using the sequence information of Pepper and *C. baccatum* genomes.

For fine mapping the markers flanking anthracnose resistance QTL in *C. baccatum* were mapped to an approximately 12Kbp region on *Capsicum annuum* chromosome 4 (81.8Mbp – 94.3Mbp). Flanking sequences for an additional ten SNPs, roughly equally spaced, spanning the region on *C. annuum* chromosome 4 from 78.6Mbp – 105.7Mbp were mapped to *C. baccatum* chromosome 4. In *C. baccatum,* the region spanned by these SNPs is much larger (84.3Mbp – 150Mbp). A 40Mbp region (80Mbp – 120Mbp) was extracted from the chromosome 4 of the *C. baccatum* draft genome assembly. This region encompasses the region defined by the major chromosome 4 anthracnose resistance QTL identified in this study.

Rna-Seq reads from *two C. baccatum* samples were mapped to the 40Mbp segment. SNPs were called using the Freebayes software package. After filtering for read depth and other quality metrics, a total of 118 SNPs was selected for primer design and testing in the lab. These SNPs were located in several candidate genes and all were causal.

The fine mapping and validation of the markers conducted in a new Population using a resistant *C. baccatum* crossed with a susceptible *baccatum* line.