

FINE MAPPING OF *Ol-qt12*, A QTL CONFERRING RESISTANCE TO TOMATO POWDERY MILDEW

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Tomato (*Solanum lycopersicum*) is one of the most important vegetable. Several pathogens are able to infect this specie. Due to the lack of genetic diversity in the cultivated tomato, it is necessary to discover resistance genes by exploring wild tomato species. The tomato powdery mildew is an important disease and one causal agent is *Oidium neolyopersici*. The first observation of tomatoes infected by *O. neolyopersici* was in the late 80's. Although this disease is relatively new, many resistance genes (R-gene) have been identified in wild tomato species, including *Ol-1* and *Ol-3* identified from *S. habrochaites*, the *Ol-4* from *S. peruvianum* and three quantitative traits loci (QTL) from *S. neorickii*. In the last few years efforts has been addressed to the introgression of resistance QTLs (R-QTL) into modern cultivars because it is assumed that the resistance conferred by R-QTLs is more durable comparing with the major R-gene mediated resistance. Three QTLs (*Ol-qt11*, *Ol-qt12* and *Ol-qt13*) have been discovered in *S. neorickii* (G1.1601), which confer resistance to *O. neolyopersici*. *Ol-qt11* is located on the long arm of the chromosome 6 and *Ol-qt12* and *Ol-qt13* are linked and mapped on the short arm of chromosome 12. The aim of this research is to fine-map and to clone the two QTLs on chromosome 12.

For fine-mapping, two BC₂S₁ populations (pop222 and pop242), which are derived from a cross between *S. lycopersicum* cv. Moneymaker and *S. neorickii* G1.1601, have been used. Pop222 harbors the *S. neorickii* alleles of *Ol-qt12* and *Ol-qt13* in a chromosomal region flanked by markers T0659 and TG111. Twenty-one co-dominant markers, spanning the *Ol-qt12* and *Ol-qt13* loci, were generated and applied on 168 individuals of pop222. The results confirmed one QTL, *Ol-qt12* which was mapped in a two-LOD supported interval of 6cM flanked by markers c2At2g06530 and imp3. The highest LOD value was associated with marker CT129. Five BC₂S₁ individuals, which were recombinants in the *Ol-qt12* region, were selected and selfed to produce BC₂S₂ families. By analyzing these five BC₂S₂ families (n=40, per family) with markers and disease tests, *Ol-qt12* could be located in a chromosomal region between two markers A and B at a genetic distance of about 6.5cM. Further, another BC₂S₁ population (pop242) was used to verify the results obtained in pop222. From 580 BC₂S₁ plants, twenty-four were selected as recombinants between the markers A and B and selfed to generate BC₂S₂ families. By using the recombinant BC₂S₂ families (n=30 per family), the localization of *Ol-qt12* flanked by markers A and B was confirmed. Moreover, all the four BC₂S₂ families were genotyped with new BAC specific markers that have been generated from the tomato sequencing project. The results obtained with the new BAC specific markers, localized the *Ol-qt12* locus between markers C and D at a physical distance of about 100Kb. Within the 100Kb 15 coding sequences (CDS) were identified by using FgeneSH, of which six showed

homology to genes involved in resistance. All of these six CDSs were expressed in both parental lines.

In summary, we confirmed the presence of *Ol-qt12* on the short arm of chromosome 12, which is located between the markers C and D in a physical distance of 100Kb where several CDS were identified as candidate genes. In order to clone *Ol-qt12*, we have generated a BAC library of *S. neorickii* G1.1601. Our next step is to identify BACs in the chromosomal region where *Ol-qt12* is located. We expect that sequence comparison between the susceptible and resistant parental lines will facilitate the cloning of *Ol-qt12*.