Fine mapping and Potential for PCR Based Markers for *Frl*

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Genetic resistance to fusarium crown and root rot (Fusarium oxysporum f.sp. radicis-lycopersici) was previously introduced into tomato (Solanum lycopersicum) from the wild species S. peruvianum on three separate occasions from three unique accessions. All three sources contributed the same single dominant allele, Frl. These three PI sources were PI 126944, PI 128650, and PI 126926. Previous work suggested that Frl was located on the long arm, near the centromere, of chromosome 9 of tomato. However, our recent studies have placed Frl near the centromere on the short arm of chromosome 9 between SSR70 and T1212 (42 cM and 48 cM on Tomato-EXPEN 2000 Sol Gen map). We have tested the following lines known to be resistant to FCRR, Ohio 89-1 (PI 126944), FL 7464 (PI 126944), FL 7226 (PI 126944), Momor (PI 128650), Mogéor (PI 128650), Mopérou (PI 126926), and Mocis (PI 128650). Additionally we studied both a BC1 and F2 population which as segregating for Frl in relationship to the following markers known to reside in the above described chromosomal region. The actual disease resistance response was confirmed by screening the BC1S1 and F3 progeny of the plants determined to have unique molecular marker/disease phenotype interaction. The markers we are using are UBC 194, UBC 655, TG101, LeOH31, SSRB63839, T1212, c2at2g38025, cTOB-1-K3, c2at5g02230, and SSR70. Some of the markers we have been able to determine each plants genotype by basic PCR/gel studies while others we are only able to determine the genotype by sequencing. At present, our data suggest that Frl resides somewhere between SSRB63839 and c2at5g02230, which appears to approximately reside between the 42 and 46 cM area on the Tomato-EXPEN 2000 map. Our data do clearly show that there are polymorphisms between each marker representing the independent introgressions of Frl mentioned above. Thus, it is possible to design PCR protocols to: 1) determine the origin of a given Frl gene found in specific germplasm; 2) determine the approximate amount of introgression involved in a given line; and 3) create flanking markers surrounding the gene.