

In Search of Breeder-friendly Markers Linked to *Frl*

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Fusarium crown and root rot (FCCR) can cause severe economic losses in cultivated tomato. A disease resistance gene originating in *L. peruvianum*, designated *Frl*, provides resistance to FCCR. Previous studies with this gene have placed it on the long arm of chromosome 9, near the centromere. We have previously determined through RFLP studies that this gene lies between RFLP markers CT208 and CD3, CD8, TG3A. We have also discovered 146 closely linked AFLP markers by using bulked segregant analysis (BSA).

By creating sequence tagged site (STS) PCR primers from the four RFLP markers and from six of the AFLP markers, we were able to amplify probes to screen through a binary bacterial artificial chromosome (BIBAC) library purchased from the Texas A&M BAC Center. The BIBAC library consists of over 42,000 clones from the FCCR resistant cultivar 'Mogeor'. The screening yielded 82 clones that appeared to be in the region of interest. To create a physical map of the area, these clones were digested with a restriction enzyme, radioactively labeled, and run on a sequencing gel. Three possible contigs resulted from this test.

To further analyze these clones, a series of tests were performed. Of these tests, end sequencing has been the most powerful. Recent end sequencing has allowed us to discard 36 of the 82 clones (they were false positives). Interestingly, all of those discarded were from one the three contigs. We are currently working to analyze the remaining clones. We plan to sequence in from both ends, looking for PCR based polymorphic markers tightly linked to *Frl*.