

Identification and characterization of molecular marker(s) associated with resistance to TSWV and leaf spots in peanuts

Baozhu Guo, Corley Holbrook, Guohao He*, Albert Culbreath, and Craig Kvien

USDA-ARS and the University of Georgia, Costal Plain Experiment Station, Tifton, GA
*Tuskegee University, AL

SUMMARY

In peanut production areas in the southeastern U.S., tomato spotted wilt virus disease caused by tomato spotted wilt tospovirus (TSWV) has become more prevalent and more severe. TSWV has become a major limiting factor for many peanut producers and control methods are limited. Both early (*Cercospora arachidicola*) and late (*Cercosporidium personatum*) leaf spot diseases are also among the worst foliar diseases of the cultivated peanut. Our strategy is to develop peanut cultivars with resistance to these diseases by using marker-assistant breeding and selection. We have been characterizing and developing DNA polymorphic markers associated with the resistant traits in peanut lines resistant or susceptible to TSWV and/or leaf spots, and generating a segregating population to map/clone the resistant loci/gene(s). We have been screening peanut lines, 0013 and 448A (resistant) and GK7 and Coan (susceptible) since 2003.

The progress has been made (2005):

1. One segregating population has been made from the cross between Tifrunner and GT-20 (a Spanish type), and the goal is to develop about 500 RILs (recombined inbred lines).
2. We have screened RAPD SSR markers and have found two RAPD markers showing polymorphism between TSWV between the resistance cultivars (0013 and 448A) and susceptible cultivars (GK7 and Coan).
3. Two PCR primers, Sw5-2 and Sw5-3, have been generated based on the sequences of TSWV resistant genes in pepper and tomato. These two primers have been used to amplify 448A genomic DNA and produced single band with molecular weight ca. 250bp and 900bp, respectively.
4. Over 2,000 ESTs have been sequenced from 2 cDNA libraries, Tifrunner leaf tissues and 013 immature seeds. Total 1345 EST sequences have been deposited in GenBank (accession number CD037499 to CD038843), and 400 unigenes have been generated from these ESTs and used for microarray analysis. Over 40 EST-derived SSRs have been developed.
5. About 5,000 clones have been sequenced from SSR enriched genomic libraries, and total 278 SSR sequences have been deposited in GenBank (accession number AY526357 to AY526456, and AY731521 to AY731698).
6. We have characterized 450 soybean SSRs in cultivated peanuts, GK7, Coan, 0013, and 448A. Total 87 SSRs have been able to amplify peanut genomic DNA.