Mapping of resistant loci for *Fusarium solani f. sp.glycines*

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Introduction

Sudden death syndrome (SDS) of soybean (*Glycine max* L. Merr.) is an important soybean disease caused by the soil-borne fungus *Fusarium solani* f. sp. *glycines*. Yield loss from SDS in severely affected areas can range from slight to nearly 100 percent. The most viable option for SDS disease management is to develop cultivars with field resistance to SDS. The main objective of the research was to identify simple sequence repeat (SSR) markers linked to SDS resistance in two populations.

Plant material

•106 F2:3 lines from a cross between PI 507531 (resistant) and Spencer (susceptible)
•70 F2:3 lines from parents PI 243530 (resistant) and Spencer (susceptible)

Greenhouse study

Figure 1. Plants prior to symptom development, 1.5 weeks old

Figure 2. Plants showing symptoms, 3 weeks after inoculation

•Greenhouse plants were inoculated in cones using a layer inoculation method with infested sorghum.

•Experiment was set up as a randomized block design with three replications.

•Young tissues from individuals were collected prior to the onset of foliar symptoms.

•Plants were evaluated for disease severity approximately three weeks after inoculation.

1 3 5 7 9

Figure 3. Plants were rated for foliar disease severity from 1 (resistant) to 9 (susceptible).

Figure 4. Electrophoresis setup. 3% metaphore agrose gel was stained with ethidium bromide.

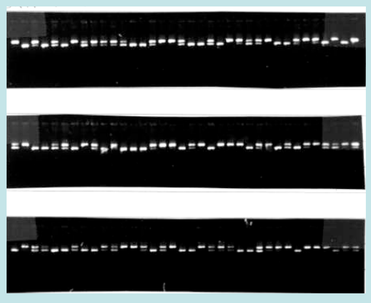

Figure 5. The polymorphic segregation of Satt187 on population PI 507531 x Spencer.

Co-segregation study

Parent screening

•295 SSR primers from all 20 linkage groups were selected at 20-cM intervals from the soybean genetic linkage map for each parent.
•70 primers between PI 507531 and Spencer showed polymorphism.
•68 primers between PI 243530 and Spencer showed polymorphism.

Co-segregation

•DNA isolation was performed on the collected tissues from both populations using the CTAB extraction protocol with slight modifications.
•The primers were used to amplify DNA using PCR.
•The PCR products were analyzed with electrophoresis.

Analysis and results

•A linkage map was made for the PI 243530 x Spencer population and for the PI 507531 x Spencer population with JoinMap 3.0 (Kyazma Software, Wageningen, Netherlands).

•SDS resistance QTL were mapped in both populations with plabQTL software.

•Significant association of disease severity for marker Satt187 on Linkage group A2 in population PI 507531 x Spencer.

•Preliminary results showed no association between the markers linked to previous identified QTL and resistance.

Table 1. One location of QTL significantly associated with sudden death syndrome disease severity in population PI 507531 x Spencer

Location	LG[a]	LOD[b]	R^2	a[c]
Satt187	A2	3.03	13.4	-0.394

[a]Linkage group on which the QTL maps, based on the integrated soybean map.
[b]Likelihood of odds (LOD) at the QTL peak.
[c]Additive effect of an allele substitution for the QTL based on the disease severity ratings.