

Apply functional genomics technologies for discovery of soybean genes involved in response to pathogen challenge

(Primary Investigator: Lila Vodkin)

The technology of microarrays (arrays of spotted, partially sequenced genes) can help to identify numerous genes involved in the plant's response to a pathogen. Microarray technology, available today for soybean genetic studies, permit analyses of the role of tens of thousands of genes in any tissue, at any time, under any condition. Soybean arrays constructed in the Vodkin laboratory contain over 18,000 unique genes spotted on glass microscope slides. The number of genes available to spot on microarrays will increase to over 27,000 by the end of 2002. This collection of unique soybean genes has been collected from a variety of plant tissues and developmental stages.

Procedure: Diagnostic gene arrays will be used to detect which of these spotted soybean genes are activated or deactivated when a plant is challenged by the fungus that causes SDS disease (*Fusarium solani*) or with the parasitic cyst nematode (*Heterodera glycines*). This will be accomplished by comparing the fluorescently-labelled mRNA isolated from resistant and susceptible plants. Since the quantity of a given gene's mRNA is indicative of its activity, the changes in their mRNA levels gives a relative indication of gene induction or repression. The research team has already constructed cDNA libraries (gene collections) from tissue induced for SDS symptoms, as well as tissue challenged by other pathogens and stresses. Several thousand newly identified genes from these libraries have recently been sequenced as part of the soybean EST sequencing project and will be included in the microarrays that are used in the analyses.