



## **Second Annual Soybean Biotechnology Symposium**

**March 22, 2006**

**MU Christopher S. Bond Life Science Center**

**Sponsored by the National Center for Soybean Biotechnology**

### **Schedule of Events**

#### **9:00 am**

Registration & Opening Reception

*Bond LSC Monsanto Auditorium Foyer*

#### **10:00 am**

Welcoming Remarks

*Bond LSC Monsanto Auditorium*

#### **10:30 am**

Dr. Tom Clemente, "Transgenes and Soybeans"

*Bond LSC Monsanto Auditorium*

#### **1:00 pm**

Poster Session

*Bond LSC McQuinn Atrium*

#### **2:30 pm**

Reception

*Bond LSC McQuinn Atrium*

#### **3:00 pm**

Dr. Brian Diers, Poehlman Lecturer, "SCN Resistant QTL: Confirmation Testing and Associated Effects on Agronomic Traits"

*Bond LSC Monsanto Auditorium*

#### **4:00 pm**

Closing Reception

*Bond LSC McQuinn Atrium*

### **Dr. Tom Clemente**

#### **The Plant Transformation Core Research Facility, University of Nebraska**

Tom Clemente received a BA degree from Indiana University of Pennsylvania in Biology. Dr. Clemente then obtained a M.S. and Ph.D. in Plant Pathology at Oklahoma State University and North Carolina State University, respectively. After a post-doctoral position at Monsanto, he joined the University of Nebraska as a Research Assistant Professor in Biotechnology. Dr. Clemente's current role is Director of the Plant Transformation Core Research Facility and Associate Professor of Agronomy & Horticulture. Dr. Clemente's research interests are in developing tools for functional genomics and implementing genetic engineering for plant germplasm enhancement targeting value added and disease control traits. His laboratory has research programs on soybean, wheat, maize, sorghum, and turf grasses. The Plant Transformation Core Research Facility is a state-of-the-art facility that provides services for vector constructions, plant transformations and characterizations of the derived transformants. Dr. Clemente instructs a laboratory class, Plant Genetic Engineering.

### **TRANSGENES IN SOYBEANS**

#### **BRIEF:**

Genetic transformation is one of the tools biotechnologists can employ toward the genetic improvement of soybean. Transformation is the step in the genetic engineering process where a new gene (transgene) is delivered into the nucleus of a plant cell and inserts into a chromosome where it is passed on to progeny. There is great interest in genetically transforming soybean for such traits as improved protein quality, altered lipid content, and herbicide resistance. This seminar will discuss the regulations pertaining to the handling and release of transgenic plants and the research that is coordinated through the Plant Transformation Core Research Facility at the University of Nebraska.

#### **ABSTRACT:**

The University of Nebraska's Plant Transformation Core Research Facility has been evaluating a number of novel input and output traits in soybean. These include such phenotypes as, herbicide tolerance, increased resistance towards iron deficiency chlorosis and perturbation of seed-oil fatty acid profile. Testing of transgenic alleles for stability of expression of the novel trait and potential impact on the agronomic performance of soybean requires extensive field-testing of the respective transgenic events. To this end field tests of regulated transgenic material must be carried-out in accordance with the Federal guidelines governing movement and release of transgenic seed. To complement the Plant Transformation Core Research Facility and strengthen its field-testing capabilities with regulated transgenic seed

the University has established the infrastructure to ensure identity preservation, containment and chain of custody tracking of the regulated seed. These resources include dedicated fully irrigated acreage, isolated storage facility along with separate planting and harvesting equipment. In addition a Field Coordinator is assigned whose responsibilities include training of personnel and oversight of the operation. More recently the University has set-up a down-stream processing facility, which includes an Insta Pro 2000 extruder coupled with a continuous horizontal oil press. This infrastructure permits a researcher to evaluate transgenic traits from the bench to the field down to processed oil and meal suitable for feed applications under strict identity preservation.

**Dr. Brian Diers**

**Department of Crop Sciences, University of Illinois**

Brian Diers received a BS degree from the University of Minnesota in Agronomy. Dr. Diers then obtained a M.S. and Ph.D. in Plant Breeding at Iowa State University. He received post-doctoral training at the University of Wisconsin, before joining Michigan State University as an Assistant Professor. Dr. Diers' is currently an Associate Professor in the Department of Crop Sciences at the University of Illinois. Dr. Diers' research interests are developing new soybean varieties for general use and specialty markets through applied plant breeding. He uses genetic markers to evaluate how much diversity is present in U.S. and exotic germplasm and whether markers can predict which crosses should be made in breeding programs. He is currently mapping cyst nematode resistance genes with genetic markers in a number of plant introductions with the goal to identify the location of new resistance genes and deploy them in cultivars through marker aided selection. Dr. Diers is the 2001 recipient of the Young Crop Scientist Award presented by the Crop Science Society of America.

**SCN RESISTANT QTL: CONFIRMATION TESTING AND ASSOCIATED EFFECTS ON AGRONOMIC TRAITS**

**BRIEF:**

When soybeans are parasitized by nematodes yield is often reduced. The soybean cyst nematode (SCN) is estimated to cause the greatest yield losses of any soybean disease worldwide. This seminar will present our findings from studies examining the effect of an important SCN resistance gene named *rhg1*.

**ABSTRACT:**

Soybean cyst nematode (SCN; *Heterodera glycines* Ichinohe) is estimated to cause the greatest yield losses of any soybean [*Glycine max* (L.) Merr.] disease worldwide. Although many SCN resistance genes have been mapped, the most important SCN resistance gene is *rhg1*. We have conducted studies to investigate the magnitude of the effect of this gene from PI 88788, determine whether the segregation of this gene is associated with other traits, and determine if different resistance sources carry different functional alleles at this locus. The testing of near isogenic lines (NIL) populations for resistance in a greenhouse showed that *rhg1* can act as a qualitative resistance gene with lines carrying the resistant allele having almost complete resistance and those with the susceptibility allele being almost completely susceptible. In field tests, there was significantly less SCN reproduction in plots of NILs carrying the *rhg1* resistance allele than the susceptible NILs. This reduced reproduction allowed the resistant NILs to out yield the susceptible NILs in the SCN infested plots. In plots with a low level of SCN infestation, there was little difference in yield detected between the resistant and susceptible NILs, suggesting that there is little yield drag associated with *rhg1*. We found that segregation distortion is frequently associated with *rhg1*, with significantly fewer homozygous resistant plants than expected in populations. Further studies showed that the distortion is at least partially caused by resistant NILs having a reduced level of plant emergence compared to susceptible NILs. To determine whether different alleles of *rhg1* exist in soybean germplasm, populations segregating for resistance alleles at this locus from PI 88788 and PI 437654 were screened for resistance to *H. glycines* isolates in a greenhouse and evaluated with molecular markers linked to *rhg1*. These tests revealed that alleles from each source gave differential resistance to two isolates and for one isolate, the PI 437654 allele gave complete resistance and the PI 88788 allele resulted in complete susceptibility.