Identification of QTL(s) Associated with Resistance to Sudden Death Syndrome (SDS) in Soybeans

Soybean (*Glycine max* (L.) Merr.) is an economically important crop that is grown worldwide. In the United States, it is the second most cultivated crop with an average of 74 million acres of production (Soy Stats, 2012), and in 2008 was reported to contribute approximately 17 billion dollars to the national economy (Radwan et al., 2011). Soybeans originated in Southeastern Asia, and were domesticated between 1766 and 1125 BCE (Bilyeu et al., 2010). It is an annual diploidized tetraploid species with a total of 20 chromosomes (Li et al. 2010). The estimated size of the soybean genome is 1,115 Mb (Cannon et al. 2009). The crop is grown for several different purposes. Besides being an ingredient in numerous food products, it can be a major component in insecticides, disinfectants, inks (printing), diesel fuel, animal feed, and much more (Pederson, 2007). When a crop of this magnitude suffers a great yield loss from weather or pests, the economy is forced to adjust on a global scale.

Sudden Death Syndrome (SDS), caused by *Fusarium virguliforme* has been recognized to be one of the top four loss-causing diseases for soybeans on a worldwide basis. The disease was first reported in the United States in Arkansas, in 1971. Since then, it has also been reported in Tennessee, Missouri, Mississippi, Illinois, Kentucky, Kansas, Indiana, Iowa, Nebraska, and Minnesota (Navi et al., 2008). Sudden Death Syndrome has been associated with yield losses ranging from only slight to 100% (Diseases and Diseases Management: Sudden Death Syndrome, 2011). Yield loss stems from the characteristic symptoms: root rot, crown necrosis, vascular discoloration of roots and stems, interveinal chlorosis and necrosis of leaves, premature defoliation, and pod abortion (Jin et al., 1996). The SDS symptoms can be categorized into two separate groups that appear to originate from two distinct interactions or components of the pathogen: root rot and leaf scorch. *Fv* is a soil borne root rot pathogen, which has allowed it to have a very wide host range in regards to root infection (Yuan et al., 2008). The leaf scorch is established during the reproductive stages where it is believed that the phytotoxin(s) in the root is translocated to the leaves of the plant (Navi et al., 2008).

SDS resistance was first reported to be controlled by a single gene, but with better understanding of the disease and its various symptoms, several quantitative trait loci (QTL) have been published for only the United States Southern germplasm (Iqbal et al., 2001). In 2007, more than 20 QTLs providing resistance to SDS causing isolates were reported in eight different recombinant inbred line (RIL) populations (Kazi et al., 2008). The various QTLs have been specifically assigned to root rot resistance or leaf scorch resistance (Hnetkovsky et al. 1996;
This study is being conducted to examine the Northern germplasm, the soybean maturity groups that are grown in Iowa, Minnesota, Nebraska, North Dakota, South Dakota, and Wisconsin, for SDS resistance. The overall goals are to: 1) Establish a screening method for SDS of soybeans that provides informative phenotypes for both root resistance and foliar resistance; 2) Identify and map QTL(s) associated with resistance to SDS of soybean in a RIL of the Northern germplasm by utilizing the phenotypic and genotypic data; and 3) Determine the resistance of the identified QTLs for SDS in soybean with other phenotypic traits, such as water use or plant morphology. Ultimately, the newly identified QTLs can be incorporated into new breeding materials of the Northern germplasm to improve breeding efforts associated with SDS.

A RIL population of 230 F₅ derived F₁₂ lines will be utilized in this study, as well as seven specialty lines. Four checks have been grown throughout all of the experiments: Minsoy (RIL parent), Noir1 (RIL parent), AG2107 (susceptible check), and MN1606SP (resistant check). The lines are specific to the Northern germplasm of the United States with the soybean maturity groups 0, I, and II. Experiments were conducted in the greenhouse and field: soil inoculation analysis and phytotoxin analysis. Only one inoculated and irrigated field trial was conducted in the 2012 growing season.

The RIL population was previously genotyped by Dr. Perry Cregan and Yung-Tsi Bolon, USDA. The genotypic files will be coded and statistically analyzed using the program R. The QTL analysis will be conducted with the phenotypic data generated from the greenhouse and field along with the USDA SNP and SSR data utilizing QTL Cartographer.

Upon completion of this study, a better understanding of what the Northern germplasm contains in regards to SDS resistance should be obtained. It will establish a good starting point for further QTL validation and exploration. Overall, it will add to the research that has been conducted on this detrimental disease and provide insights on new phenotypic screening protocols.

**Works Cited**


