B-24

Role of Rhg1 and other resistance genes in controlling SCN in soybean

*Brian Diers**, Department of Crop Sciences, University of Illinois, Illinois, USA
Matt Hudson, Department of Crop Sciences, University of Illinois, Illinois, USA
Andrew Bent, Department of Plant Pathology, University of Wisconsin, Wisconsin, USA

Soybean cyst nematode is estimated to cause the greatest yield loss of any soybean disease or pest in the USA. Genetic resistance is the most economical form of SCN control and genetic markers have been used to map SCN resistance genes. The most important SCN resistance gene used by breeders in the USA is *Rhg1*, which is a complex locus that contains tandem repeats of a 31.2 kb unit. Within these repeats, there are four genes and three have been implicated in contributing to resistance. Across soybean germplasm, one to ten repeats and different repeat types have been reported. Our research has shown that repeat number significantly impacts resistance and as the number of repeats increase, resistance is generally enhanced. Repeat type is important as it has also been shown that the *Rhg1* allele from the resistance source Peking interacts with the SCN resistance gene *Rhg4*, but this interaction was not observed for the *Rhg1* allele from PI 88788. DNA based assays were developed to quantify *Rhg1* repeat number in soybean germplasm to help predict resistance levels. Our research also has focused on identifying new SCN resistance genes that can be used to diversify resistance in soybean cultivars. Two major quantitative trait loci (QTL) from wild soybean, *Glycine soja*, that confer SCN resistance have been a focus of these efforts. These two QTL were fine mapped onto 212 and 103 kb intervals on soybean chromosomes 15 and 18, respectively. These interval sizes are based on the genome assembly of the SCN susceptible cultivar Williams 82. We showed that by combining these *G. soja* genes with resistance alleles at *Rhg1*, we can improve resistance levels. As an effort to develop more durable SCN resistance, research to identify gene combinations that can provide optimal resistance is continuing.