P-116

Characterization of components of partial resistance in soybean to Sclerotinia sclerotiorum with ascospore inoculation method

*Jaqueline Huzar Novakowiski**, Department of Plant Pathology, The Ohio State University, Ohio, USA
Anne Dorrance, Center for Soybean Research, The Ohio State University, Ohio, USA

Sclerotinia stem rot of soybean, caused by the fungus *Sclerotinia sclerotiorum* (Lib.) de Bary, can reduce yield by affecting pod fill due to lesions on the base of the stem that result in wilting, lodging and premature plant death. Although complete resistance has not been identified, some soybean genotypes have moderate levels of partial resistance. Inoculation methods with mycelia have been used in many different ways in germplasm screening programs; however, ascospores are the primary source of inoculum for soybean blossoms under field conditions. Based on this, we hypothesize that the characterization of components of resistance with ascospore inoculation could help in development of more reliable methods for germplasm screening. The objective of this study was to determine which component(s) most accurately differentiate the resistance reaction of soybean genotypes to S. sclerotiorum. Ascospores were produced in laboratory and all the experiments were carried out under controlled conditions with inoculations at full flowering (R2) growth stage. Initially, inoculum densities of 1 x 104, 1 x 105 and 1 x 106 ascospores ml-1 were compared for the response on six soybean genotypes with known resistance reactions. Symptoms of SSR developed on all genotypes including the most resistant when 1 x 106 ascospores ml-1 was used. Components of resistance were then measured on a set of 16 genotypes with known resistance reaction at 1 x 105 ascospores ml-1. In a preliminary statistical analysis, resistance reactions could be differentiated based on the level of infection efficiency and lesion length. Although this ascospore method presents some limitations such as the time required to produce ascospores as well as the time and space required for growing the plants until flowering stage, it has the potential to be used for more reliable and accurate identification of resistance reaction of soybean genotypes.