MAKING EVERY SEED COUNT: WHO'S RESPONSIBLE FOR STAND LOSS[1]

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Seedling diseases of soybean and corn can cause significant losses through poor stand establishment and reduced plant vigor. Identifying the causal agent of seedling disease is not a simple process as the soil environment is complex and contains many thousands of microbe species but only a small portion of these actually cause disease. The primary causes of soybean seedling disease are *Pythium* spp., *Phytophthora sojae*, *Rhizoctonia solani* and *Fusarium* spp. In this study it was our objective to identify the predominant oomycete (*Pythium* and *Phytophthora*) species that cause soybean seedling disease. Only by understanding which pathogens cause disease are we are ultimately able to improve disease management.

A survey was conducted over two years across the north central region to identify oomycete species that contribute to seedling disease. The survey was conducted in collaboration with Extension specialists in each state. In each state approximately 6 fields with emergence issues were sampled by collecting 50 diseased soybean seedlings. The soybean seedlings were then taken back to the individual labs at each state, washed thoroughly and isolations were made using agar medium containing antibiotics to limit the growth non-oomycete species.

Overall, 82 different oomycete species were identified across the Midwest, including species of *Pythium, Phytophthora, Phytopythium* and *Aphanomyces*. *Pythium sylvaticum* was the most abundant species across both years. In 2011, a total of 52 *Pythium,* 2 *Phytopythium* and 3 *Phytophthora* spp. were recovered, with *Py. sylvaticum* (16%) and *Py. oopapillum* (12%) being the most frequent. In 2012, a total of 57 *Pythium* spp., 7 *Phytophthora* spp., and 4 *Phytopythium* were found, with *Py. sylvaticum* (15%) and *Py. heterothallicum* (13%) species being most abundant.

Analyses of the oomycete species collected by location have demonstrated that similar geographies group together, i.e. the species identified in one state closely reflect the species collected in a neighboring state. This indicates that fungicide seed treatments may need to be tailored by region to have maximum efficacy. Further analysis to understand these geographic patterns using GIS and metadata are currently being conducted.

We have screened representative isolates of all 82 oomycete species for their pathogenicity to soybean seed and soybean seedlings. Using a combination of this pathogenicity data and the distribution data we will be able to identify the predominant pathogens by region.

By identifying the most significant pathogens that cause seedling and root rot disease we will be able to direct soybean breeding efforts by screening germplasm (cultivars) for resistance against the most appropriate pathogens. The same is true for seed treatments. Understanding which

species are the primary pathogens enables us to work with companies in screening and developing chemical or biological seed treatments to minimize the impact of seedling disease. Using data generated from this study we are also in the process of developing improved diagnostic methods, which will assist in establishing more rapid, specific and accurate diagnoses, which will ultimately improve disease management.

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