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Evaluation of *Helianthus* germplasm for resistance to *Plasmopara halstedii* (downy mildew) and *Puccinia helianthi* (rust)

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Introduction

Two of the most economically important diseases that occur on sunflower in the north central United States are downy mildew caused by *Plasmopara halstedii* and rust caused by *Puccinia helianthi*.

Downy mildew is a seedling disease facilitated by periods of high moisture and cool soil temperatures (15-20°C). Systemic infections occur 3-15 days after planting when motile zoospores infect sunflower radicles. Systemically infected plants may damp-off either pre- or post- emergence, but in many cases may survive. Symptoms of surviving infected plants include dwarfing, chlorosis along the leaf mid-veins, and puckering of the leaf tissue. White zoosporangia are produced on the underside of the chlorotic leaf tissue, which is often the tell-tale sign associated with the disease. Yield losses occur when water saturated areas (i.e. low spots) in fields create conditions conducive for systemic infection which results in significant stand reductions (Friskop et al. 2009; Gulya et al. 1997).

Rust is a foliar disease capable of overwintering on wild and volunteer sunflowers in the northern United States. Overwintering telia serve as the source of primary inoculum for the next cropping season. Rust development is favored by moderate to warm (13-30°C) temperatures and frequent periods of leaf wetness. During these conditions, uredinia are formed and produce repeating urediniospores that continue to infect healthy tissues. Signs and symptoms of rust include dusty, cinnamon-brown pustules on the leaves, stems, and bracts that can be rubbed off and sometimes appear with a chlorotic halo surrounding them. Rust inhibits photosynthetic processes which results in seed quality and yield reductions (Friskop et al. 2011; Gulya et al. 1997).

Both diseases are capable of causing significant economic losses if not managed properly. One of the most effective tools used to manage both downy mildew and rust is genetic resistance. Historically, resistance genes are frequently overcome and as a result of this, new sources of resistance are needed. In the past, wild, annual *Helianthus* germplasm has provided numerous sources of resistance that have been introgressed into commercial hybrids. Previous screenings of wild *Helianthus* germplasm found that a disproportionate amount of resistance genes were identified in germplasm originating from Texas (Gulya et al. 2000; Gulya 2005). Therefore, the objective of this research was to screen wild *Helianthus* germplasm derived from Texas for new potential sources of resistance to both common and highly virulent races of *P. halstedii* and *P. helianthi*.

Materials and Methods

<u>Host and pathogen material.</u> One hundred eighty-two wild *H. annuus* and 33 wild *H. argophyllus* accessions were obtained from the USDA North Central Regional Plant Introduction Station (NCRPIS) in Ames, IA for screening. All *P. halstedii* and *P. helianthi* isolates used in the studies were originally collected from North Dakota.

<u>Downy Mildew.</u> Initially, all 215 accessions were screened in a greenhouse environment to a common race of *P. halstedii*. Seed was pre-germinated so seedlings could be artificially inoculated with *P. halstedii* zoosporangia and then hand-planted. Trials were arranged as a completely randomized design (CRD) with four replicates. Incidence was evaluated 11 days post-inoculation by visually examining plants for signs and symptoms consistent with systemic infection. The number of systemically infected and non-systemically infected plants were recorded. Data was converted and reported as percent resistance, which was calculated by taking the number of non-systemically infected plants divided by the total number of plants screened for the accession. Once completed, the most resistant 10% of accessions from both *H. annuus* and *H. argophyllus* were screened a second time to a highly virulent race of *P. halstedii* using the same methods mentioned previously.

<u>Rust.</u> All 215 accessions were initially screened in a greenhouse environment to a common race of *P. helianthi*. Seeds were planted and allowed to grow for 14 days before they were artificially inoculated with fresh urediniospores. The trial was arranged as a CRD with six replicates. Infection types were evaluated 14-15 days post inoculation by visually examining pustules on the first true leaves. Infection types including 0, ;, 1, and 2 were considered a resistant reaction, while infection types of 3, 4, and 5 were considered a susceptible reaction. From this, the percent resistance was calculated by taking the number of plants with a resistant reaction divided by the total number of plants screened for the accession. Once completed, the most resistant 10% of *H. annuus* and *H. argophyllus* accessions were screened a second time to a highly virulent race of *P. helianthi* using the same methods mentioned previously.

Results and Discussion

<u>Downy mildew.</u> Results from the initial screening of 182 *H. annuus* accessions to a common race of *P. halstedii* found 92 accessions having greater than 70% resistance with the percent resistance ranging from 27-97% for all 182 accessions. Twenty-two accessions were selected and included in the advanced screening. Of the 33 *H. argophyllus* accessions, 23 accessions had greater than 70 percent resistance with the percent resistance ranging from 46-97%. Three accessions were selected and included in the advanced screening. Results from the advanced screening of 22 *H. annuus* to a combination of highly virulent races found 18 accessions with greater than 70% resistance. Of the three *H. argophyllus* accessions, all had greater than 70% resistance.

<u>Rust.</u> Results from the initial screening of 182 *H. annuus* accessions to a common race of *P. helianthi* found 71 accessions having greater than 70% resistance with the percent resistance ranging from 3-100% for all 182 accessions. Twenty-two accessions were selected and included in the advanced screening. Of the 33 *H. argophyllus* accessions, 33 had greater than 70% resistance with the percent resistance ranging from 77-100%. Four accessions were selected and included included in the advanced screening. Results from the advanced screening of 22 *H. annuus* to a

combination of highly virulent races found all 22 accessions had greater than 70% resistance. Of the four *H. argophyllus*, all had greater than 70% resistance.

Summary. All of the data from the four screenings to both pathogens were combined in order to look for accessions that had greater than 70% resistance to both pathogens in all four screenings. From this, seven *H. annuus* and three *H. argophyllus* accessions were identified and included PI 435432, PI 468456, PI 494566, PI 468449, PI 468525, PI 468460, PI 413161, PI 494578, PI 649863, and PI 494579. Future work will focus on characterizing the genes conferring resistance in these accessions.

References

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