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## **Virulence update for downy mildew of sunflowers**

Michelle Gilley and Samuel Markell

Department of Plant Pathology, North Dakota State University, Fargo, ND

### **Introduction**

Downy mildew, caused by the obligate biotrophic pathogen, *Plasmopara halstedii* (Farl.) Berl. and de Toni, is an economically significant seedling disease in cultivated sunflowers, *Helianthus annuus* L., grown in temperate regions. Yield losses to downy mildew are dependent on cool, wet weather between germination and emergence, as well as a combination of percentage of infected plants and their location in the field (Gascuel et al. 2015; Friskop et al. 2009). Qualitative genetic resistance is one of the most important management tools of sunflower; however, many single dominant resistance genes denoted *Pl* have been overcome by the pathogen and the incorporation of additional resistance genes into commercial hybrids is needed (Tourvieille de Labrouhe et al. 2008). Assessment of pathogen virulence is critical for determining what resistance genes should be incorporated into hybrids. The objectives of this study were to monitor race changes and effectiveness of downy mildew resistance genes.

### **Materials and Methods**

Field samples were collected in 2014, 2015, 2016 and 2018 in North Dakota, South Dakota, Minnesota and Nebraska (Gilley et al. 2016). Susceptible sunflower seedlings were inoculated with a spore suspension prepared with symptomatic leaves to increase *P. halstedii* inoculum using similar methods to those described by Gulya in 1996. Each isolate was increased on a susceptible hybrid for virulence phenotyping (race determination). Inoculated differential seedlings were placed in rows, covered with sand and watered daily. After 11 to 14 days, when true leaves were visible, flats were misted then placed for 16 to 48 hours at 100% relative humidity at 16-18°C to cause sporulation. Flats were left on a counter to let plants dry completely before rating susceptibility and resistance to each gene that was screened.

### **Results and Conclusions**

In 2014 and 2015, the first reported virulence was identified on the *Pl<sub>8</sub>* resistance gene (Figure 1). Virulence was not observed on the *Pl<sub>Arg</sub>*, *Pl<sub>15</sub>*, and *Pl<sub>17</sub>* resistance genes. In 2016 and 2018, five isolates at three locations with virulence on both the *Pl<sub>6</sub>* and *Pl<sub>8</sub>* genes were identified, as well as five additional isolates with virulence on the *Pl<sub>8</sub>* gene (Figure 2). Virulence was not observed on the *Pl<sub>Arg</sub>*, *Pl<sub>13</sub>*, *Pl<sub>15</sub>*, *Pl<sub>16</sub>*, and *Pl<sub>17</sub>* resistance genes. The sunflower industry has at least three resistance genes, *Pl<sub>Arg</sub>*, *Pl<sub>15</sub>*, and *Pl<sub>17</sub>*, which are believed to be completely effective as well as two resistance genes, *Pl<sub>13</sub>* and *Pl<sub>16</sub>*, for which little virulence has been observed.

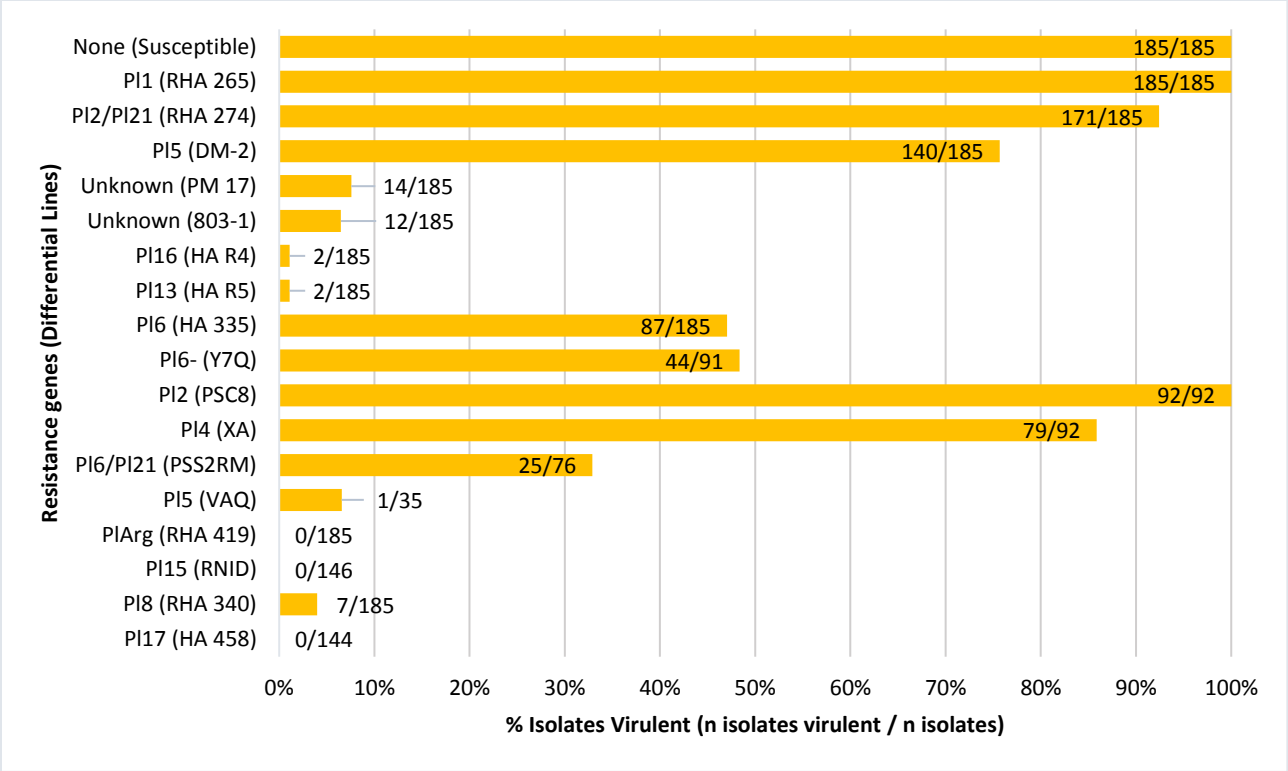


Figure 1. Percentage of 2014 and 2015 downy mildew isolates virulent on differentials.

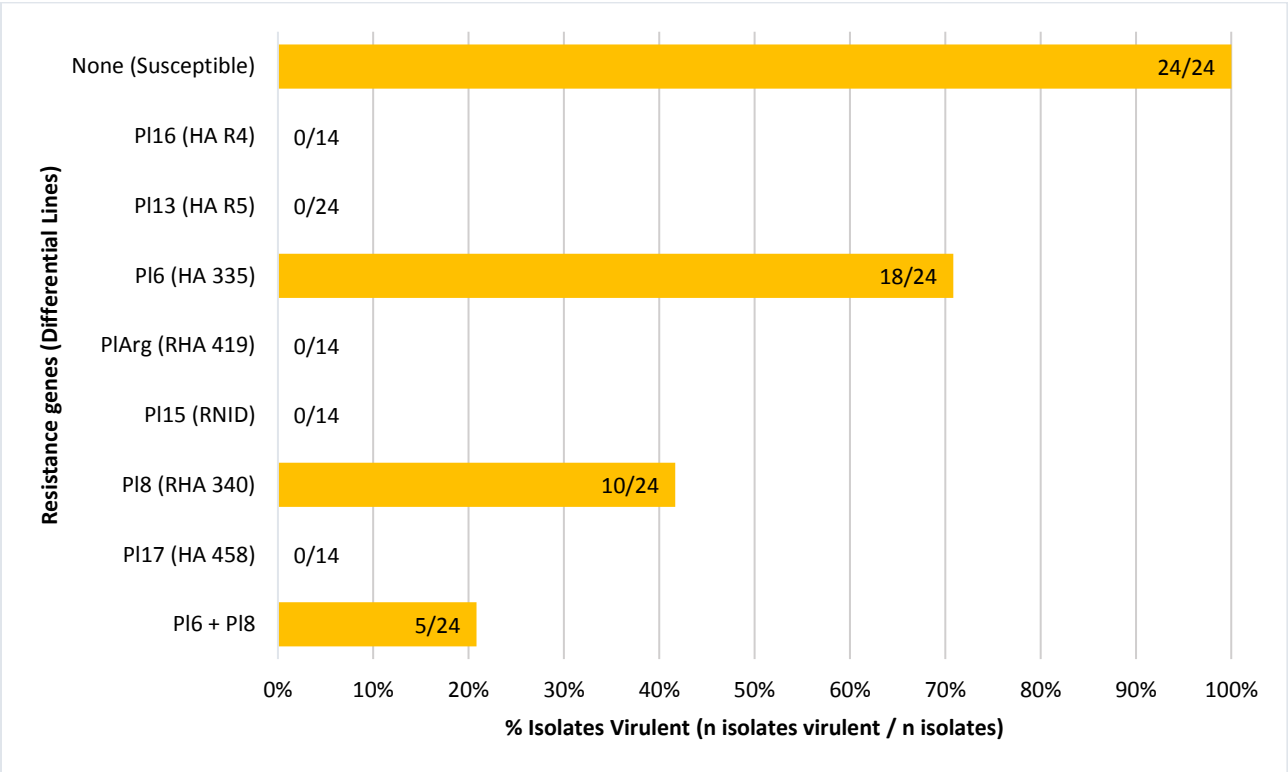


Figure 2. Percentage of 2016 and 2018 downy mildew isolates virulent on differentials.

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