Identification of seedling resistance in wild oat relatives against oat crown rust

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Abstract

Oat crown rust, caused by the plant pathogenic fungus *Puccinia coronata* f. sp. *avenae* (*Pca*), is a devastating disease that threatens global oat production. One of the best methods to manage this disease is to grow oat varieties (*Avena sativa*) that contain genetic resistance against *Pca*. To provide breeding programs with genetic material for introgression, we are working to identify new resistance genes in domesticated oat and wild relatives. In this experiment, 40 accessions of oats were screened using two highly virulent *Pca* races, 15MN15-3 and 15MN21-3, collected in Minnesota in 2015. Selections were made from a collection of 191 oat accessions based on their previous resistance to a broadly virulent *Pca* isolate 12SD80. Physiological race assignments of 15MN15-3, 15MN21-3, and 12SD80 were completed after scoring disease phenotypes in a set of 40 oat accessions. Assessment of genetic resistance to *Pca* identified 30 oat accessions that are resistant to 15MN15-3 and/or 15MN21-3, in comparison to the susceptible checks 'Marvelous' and 'Saber'. To map resistance-associated genes and study the mechanisms of oat immunity, several crosses between resistant oat accessions and the high yielding variety Saber were performed. Current work includes selfing F1 progenies and screening F2 and F3 offspring for resistance with each *Pca* isolate.

Introduction

Genetic resistance to *Pca* and other fungal plant pathogens is investigated mainly because of the expense and environmental consequences of the alternative treatment, fungicides. Unfortunately, genetic resistance to *Pca* in oat follows a sine-like curve called a boom and bust cycle. When novel resistance is widely deployed, Pca isolates that can overcome the resistance are discovered, usually within a few years. Again new resistance is deployed and the cycle continues. This should not discourage investigation of novel genetic resistance, however; a combination of many seedling resistance genes and a recently characterized type of adult plant resistance may slow the boom and bust cycle and prevent yield losses.

Materials and Methods

40 accessions were planted in 9 cm plastic pots, with eight seeds planted per pot, in 2/3 MVP RSi soil and 1/3 vermiculite. The pots were treated at 4.5 °C for five days and moved to a locked greenhouse. After 7 days of growth, seedlings were inoculated using 3 mL of isopar oil and 9 mg of *Pca* spores. Inoculated plants were left to dry for 30 minutes, then transferred to a darkened mist chamber with continuous mist for 30 minutes. The following day lights were turned on and mist treatment intensified. Humidity and darkness followed by light and warmth provide *Pca* with the best conditions for infection. Plants were then moved to a growth chamber and scored for infection phenotype at eight days post inoculation.

Crosses between commercial cultivar Saber and 8 resistant accessions were performed in a locked greenhouse. Saber was chosen for its importance in the Midwestern United States as an early-maturing, high-yielding, and publicly available cultivar.

Modified Murphy Scale with Sample Infection Types

Figure 1. Modified Murphy scale (0-4) used for scoring seedling resistance to oat crown rust.

Bar Charts of Infection Type for isolates 15MN15-3 and 15MN21-3

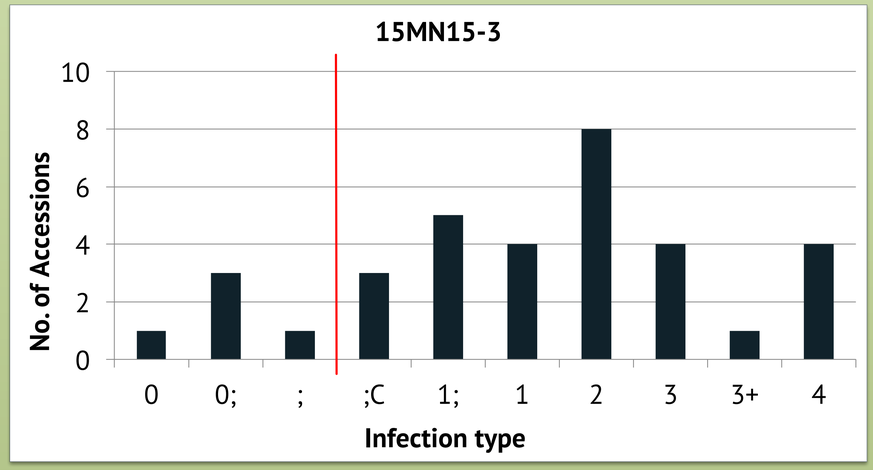

Figure 2. Bar chart showing frequency of infection types for accessions inoculated with *Pca* isolate 15MN15-3. The red line indicates the cutoff of what was considered a highly resistant reaction phenotype.

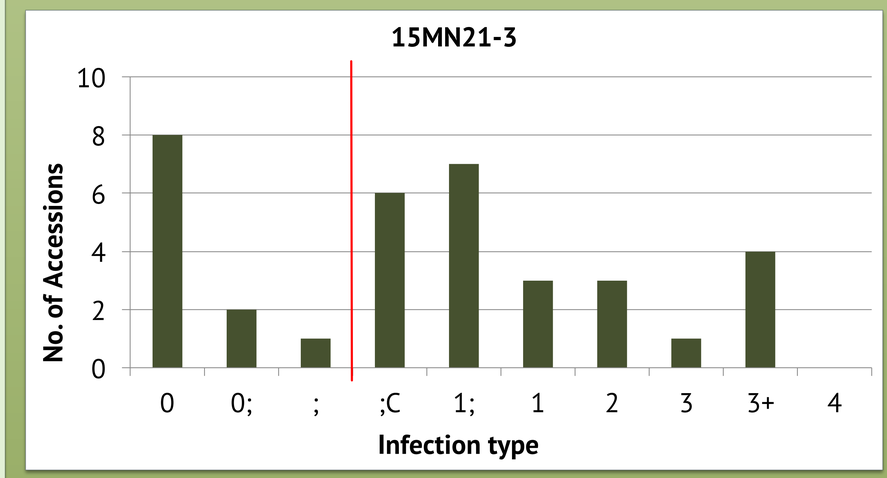

Figure 3. Bar chart showing frequency of infection types for accessions inoculated with *Pca* isolate 15MN21-3. The red line indicates the cutoff of what is considered a highly resistant reaction phenotype.

Results

- Physiological race assignments of 15MN15-3, 15MN21-3, and 12SD80 were completed after scoring disease phenotypes in a set of oat differentials.
- 40 accessions were resistant to isolate 12SD80.
- Approximately 30 accessions are resistant to either 15MN15-3, 15MN21-3, or to both.
- 5 highly resistant and 6 resistant accessions from species *A. strigosa*, *A. sterilis*, *A. sativa*, *A. atlantica,* and *A. brevis* were selected for crossing with either Saber or a susceptible parent of their species.
- Successful crosses to date:

Susceptible parent	Resistant Parent
Saber	*A. sterilis*, PI 411559
Saber	*A. sativa*, UPF97H300-2-11
Saber	*A. sterilis*, PI 324815
Saber	*A. sterilis*, Clav 8321
Saber	*A. sterilis*, PI 378792
Saber	*A. sativa*, SASK-14
Saber	*A. sativa*, OT3044
A. brevis, Clav 1783	*A. brevis*, PI 83719
A. strigosa, Clav 2921	*A. atlantica*, PI 657393

Current Conclusions

- Wild relatives of *A. sativa* may be able to provide novel genetic resistance to highly virulent *Pca* races
- Resistance to 15MN15-3 and 15MN21-3 may be correlated to 12SD80 resistance

Next Steps

- Complete crosses:
  - Saber x *A. sativa*, FL0115-J2
  - *A. strigosa*, Clav 2921 (S) x *A. strigosa*, PI258731 (R)
- Plant F1 seed from completed crosses
- Self F1 and plant F2 seed
- Collect DNA and screen F2 population with 15MN15-3 and 15MN21-3

References

Chong, J., Leonard, K.J., and Salmeron, J.J. 2000. A North American system of nomenclature for *Puccinia coronata* f. sp. *avenae*. Plant Dis. 84: 580-585.

Dinoor, A. "Sources of oat crown rust resistance in hexaploid and tetraploid wild oats in Israel." *Canadian Journal of Botany* 48.1 (1970): 153-161.

Tan, M. Y., & Carson, M. L. (2013). Screening Wild Oat Accessions from Morocco for Resistance to *Puccinia coronata*. *Plant Disease, 97*(12), 1544-1548.