# Novel Sources of Sclerotinia Basal Stalk Rot Resistance from Crop Wild Relatives of Sunflower (Helianthus annuus L.) Science Laboratory Farro ND 58102 USA

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#### Abstract

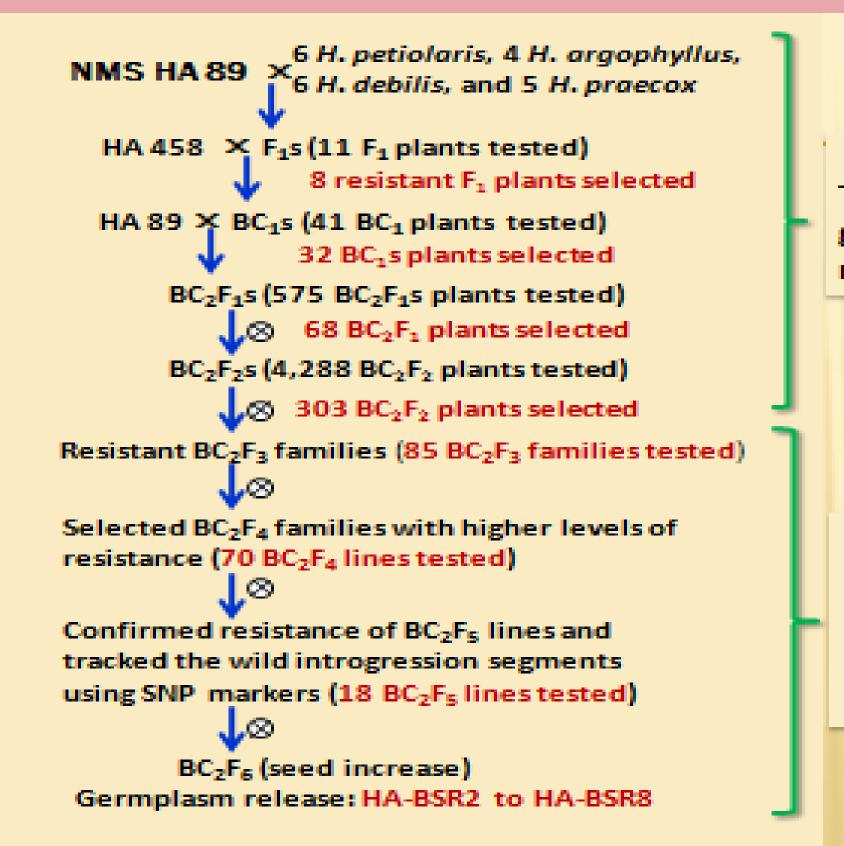
Sclerotinia sclerotiorum is the causal agent of a serious sunflower disease epidemic worldwide. Sclerotinia basal stalk rot is one of the most serious diseases of sunflower. The genetics of resistance to basal stalk rot (BSR) is quantitative, requiring many genes, which complicates breeding efforts. There are 53 species (39 perennial and 14 annual) of sunflower crop wild relatives that represent a considerable amount of genetic diversity available for improvement of cultivated sunflower, which has a very narrow genetic base. The objective of the study was to evaluate interspecific germplasm in various stages of breeding in artificially inoculated field trials for BSR incidence at three locations, Carrington, ND, Grandin, ND, and Crookston, MN. Sclerotinia BSR resistance was successfully transferred from three wild annual *Helianthus* species into cultivated sunflower, with two *H. petiolaris*, six *H. argophyllus*, and five *H. praecox* introgression lines. Whole genome scans using genotyping-by-sequencing (GBS) were used to detect the presence of the wild introgression segments in the selected lines. Single nucleotide polymorphism markers revealed the presence of wild segments in the cultivated sunflower background located on linkage groups (LGS) 1, 3, 8, 9, 10, and 11. Additionally, 411 progeny families from crosses of amphiploid, hexaploid, and diploid perennials with cultivated lines were screened for BSR. More than 150 early generation interspecific families of perennial *H. hirsutus*, *H. salicifolius*, and *H. occidentalis* tested in replicated BSR field trials suggested excellent BSR resistance, further confirming successful gene introgression. Twelve BSR germplasms are in the process of being released based on their higher levels of resistance. Populations of sunflower crop wild relatives from the USDA-ARS-NPGS gene bank continue to contribute specific traits to combat emerging pests and environmental challenges, and at the same time preserve them for future generations.

## Introduction

Sclerotinia sclerotiorum (Lib.) de Bary is the most destructive pathogen of sunflower (*Helianthus annuus* L.), causing basal stalk rot disease. Its mode of infection and the genetics of resistance are completely different from other forms of Sclerotinia infection. Resistance to *S. sclerotiorum* is under polygenic control (Talukder et al., 2014) and no major resistance gene is known against this pathogen in cultivated sunflower. Therefore, breeding for Sclerotinia resistance relies on incorporating genetic factors from partially resistant lines. The genus *Helianthus* is native to North America and comprises 53 species, 14 annual diploids (n=17) and 39 perennial species. Wild annual and perennial species have been an excellent source of resistance genes for economically important sunflower diseases (Seiler and Rieseberg, 1997). Basal stalk rot resistance was identified in wild annual appecies of *H. argophyllus*, *H. praecox*, and *H. petiolaris*, and several wild perennial species. Wild annual and perennial Species were selected to transfer Sclerotinia BSR resistance into cultivated sunflower. In this poster we report the progress of transferring Sclerotinia BSR resistance into cultivated sunflower and monitoring the introgressed alien segments using a high throughput SNP marker resource and the current status of pre-breeding novel Sclerotinia resistance sources from wild annual and perennial species into cultivated sunflower.

#### **Materials and Methods**

Introgression of Sclerotinia resistance from annual crop wild relatives



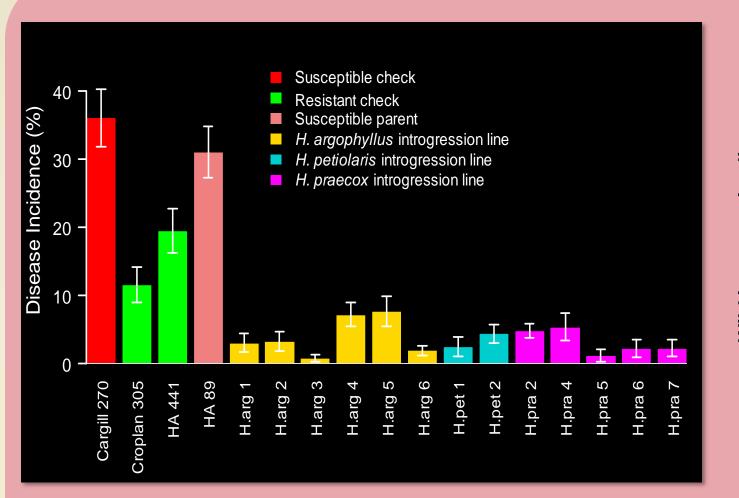
Phase I The individuals in each generation were screened for resistance in the greenhouse

Phase II Families or lines were evaluated for resistance in greenhouse and/or multiple location field trials

Figure 1. Breeding scheme for the development of introgressions lines from annual sunflower crop wild relatives.

## **Results and Discussion**

Transfer of Sclerotinia BSR resistance from wild annual species into cultivated sunflower is moving forward (Fig. 1).



**Figure 3.** Mean BSR disease incidence (DI) of the most resistant wild sunflower introgression lines evaluated in seven environments during 2012-2015.

|               | H.pet 1 | 0    | 0.2 | 0.6  | 0   | 0   | 0.4  | 0    | 4.6   | 0    | 0    | 0.5  | 2.0  | 0.5  | 0.1  | 0.2  | 0    | 0.2  |
|---------------|---------|------|-----|------|-----|-----|------|------|-------|------|------|------|------|------|------|------|------|------|
|               | H.pet 2 | 0.2  | 0.2 | 0    | 0   | 0.5 | 0.8  | 0    | 4.6   | 0    | 0.1  | 0    | 0.3  | 0.8  | 0    | 0.4  | 0    | 0.2  |
|               | H.arg 1 | 1.2  | 2.3 | 2.9  | 1.3 | 1.4 | 0.4  | 0.9  | 20.2  | 6.0  | 4.6  | 20.6 | 3.0  | 0.6  | 0.9  | 1.1  | 2.2  | 0.7  |
| S             | H.arg 2 | 1.2  | 2.1 | 2.9  | 1.5 | 1.1 | 0.4  | 0.3  | 19.7  | 5.5  | 2.3  | 20   | 3.1  | 0.8  | 0.9  | 0.8  | 2.0  | 0.8  |
| line          | H.arg 3 | 1.0  | 1.1 | 1.3  | 0.2 | 1.6 | 0    | 0    | 18.8  | 0.4  | 7.0  | 0.2  | 2.3  | 0.6  | 0.4  | 0    | 0.7  | 0.9  |
|               | H.arg 4 | 1.7  | 0.8 | 1.1  | 0.2 | 0.8 | 0.4  | 0.3  | 19.2  | 0.4  | 1.0  | 0    | 2.3  | 0.6  | 0.6  | 0    | 0.4  | 0.8  |
| introgression | H.arg 5 | 1.2  | 0.6 | 1.1  | 0.2 | 0.9 | 1.7  | 0    | 19.1  | 0.4  | 2.2  | 0    | 1.8  | 0.3  | 0.3  | 1.3  | 0.7  | 0.3  |
| Jre           | H.arg 6 | 0.2  | 0.4 | 11.4 | 0.4 | 0.9 | 0    | 0    | 0     | 0    | 7.2  | 0.5  | 0    | 0    | 0    | 0.6  | 0.7  | 2.2  |
| irog          | H.pra 2 | 0    | 0   | 0.3  | 0   | 0.1 | 3.4  | 0    | 4.6   | 0.6  | 4.9  | 3.4  | 0.2  | 0.5  | 0.6  | 0    | 0.4  | 0    |
|               | H.pra 4 | 0.7  | 0.9 | 0.3  | 0   | 0.7 | 0    | 0    | 0.7   | 0.5  | 5.2  | 0.4  | 0.8  | 0    | 0    | 0    | 0.4  | 0    |
| Wild          | H.pra 5 | 16.5 | 0.8 | 0.6  | 0.2 | 2.8 | 3.0  | 0    | 4.6   | 0.6  | 4.4  | 3.5  | 1.2  | 0.2  | 1.3  | 1.7  | 0.7  | 0    |
| >             | H.pra 6 | 15.0 | 0.8 | 1.0  | 0.2 | 2.8 | 4.2  | 0    | 0.6   | 0.5  | 1.0  | 0.5  | 1.5  | 0    | 1.3  | 1.7  | 0.4  | 0    |
|               | H.pra 7 | 17.5 | 1.7 | 0.5  | 0   | 0.8 | 0    | 0    | 4.4   | 0    | 4.9  | 0.4  | 1.3  | 0.5  | 0.4  | 0    | 0.9  | 0    |
|               |         | LG1  | LG2 | LG3  | LG4 | LG5 | LG6  | LG7  | LG8   | LG9  | LG10 | LG11 | LG12 | LG13 | LG14 | LG15 | LG16 | LG17 |
|               |         |      |     |      |     |     | Linl | kage | e gro | oups | 5    |      |      |      |      |      |      |      |

**Figure 4.** Tracking of *H. argophyllus, H. petiolaris,* and *H. praecox* chromosome segments in highly BSR resistant wild sunflower introgression lines using SNP markers. Intensity of the green color indicates the percentage of polymorphism between the parents and the introgressed lines.

#### Introgression of Sclerotinia resistance from perennial crop wild relatives

Several of the interspecific lines derived from wild perennial species showed very good resistance to BSR. Additionally, 441 families from amphiploid, hexaploid, and diploid perennial crosses were tested for BSR resistance at Carrington, ND and Grandin, ND. Families with better BSR resistance than the recurrent parents and the checks were identified **(Table 2)**. More than 150 early generation interspecific families of perennial *H. salicifolius, H. hirsutus,* and *H. occidentalis* tested in replicated BSR field trials in 2015 suggested excellent BSR resistance, further confirming successful gene introgression **(Table 2)**. Seven Sclerotinia BSR tolerant germplasms from wild annual and five from perennial species field evaluated from 2009-2015 are scheduled for release in 2016-2017 **(Table 3)**.

2015.

**Table 2.** Replicated Sclerotinia stalk rot field evaluation of 2014interspecific lines derived from perennial sunflower crop wild

**Table 3.** Scheduled releases of basal stalk rot tolerantgermplasms in 2016-2017 based on field screening from 2009-

Wild introgressed families consistently showed superior Sclerotinia BSR resistance in the field evaluations tested over the years **(Table 1).** In 2014, 23 BC<sub>2</sub>F<sub>4</sub> families derived from *H. argophyllus, H. petiolaris,* and *H. praecox* were evaluated for BSR resistance in multi-location field trials **(Fig. 2).** Across environments, all the introgressed BC<sub>2</sub>F<sub>4</sub> families showed significantly higher Sclerotinia BSR resistance than both the susceptible checks, Cargill 270 and HA 89 (36% DI). The level of resistance in the introgressed families was similar to the resistant check, Croplan 305 (9.6% DI). However, ten BC<sub>2</sub>F<sub>4</sub> families, five each derived from *H. argophyllus* and *H. praecox* had significantly higher BSR resistance (0 to 3.6% DI) than the other resistant check, HA 441 (18.3% DI).

| Resistance donor201220132014PedigreeBC_F_3PedigreeBC_F_4BC_F_4 $H. petiolaris ssp. fallax11-256-049012F-3405-55.6H. argophyllus11-256-053012F-3406-55.6H. argophyllus11-275-037012F-3416-49.32.9PI 49457311-283-037012F-3424-4010.011-291-016.612F-3438-23.19.511-291-071.512F-3451-43.97.911-291-071.512F-3451-43.97.911-291-571.512F-3456-18.311-291-571.512F-3456-18.311-291-571.512F-3456-18.311-291-571.512F-3456-18.311-291-571.512F-3456-18.311-291-571.512F-3456-18.311-291-571.512F-3456-18.311-291-571.512F-3456-18.311-291-571.512F-3456-13.33.3Susceptible checksCargill 2703.4Cargill 27072.636.011-292-33012F-3482-13.33.3Susceptible checksCroplan 30512.4Croplan 30534.9Resistant checksCroplan 30512.4Croplan 30534.9Resistant checksCroplan 30512.4Croplan 305$  |                           |             | Disea     | se incidence | (%)       |           |  |
|--|---------------------------|-------------|-----------|--------------|-----------|-----------|--|
| H. petiolaris ssp. fallax11-256-049012F-3405-24.08.4PI 43584311-256-053012F-3406-55.6-H. argophyllus11-275-037012F-3416-49.32.9PI 49457311-283-037012F-3424-4010.011-291-016.612F-3438-23.19.511-291-094.512F-3442-16.74.511-291-171.712F-3443-14.26.311-291-571.512F-3456-18.3-11-291-654.212F-3456-18.3-11-291-672.312F-3460-407.911-292-33012F-3467-13.3011-294-213.112F-3482-13.33.3Susceptible checksCargill 27034.8Cargill 27072.6Resistant checksCroplan 30512.4Croplan 30534.9Resistant checksCroplan 30512.4Croplan 30534.99.6  | Resistance donor          | 2012        |           | 2013         | 2013      |           |  |
| PI 435843 11-256-053 0 12F-3406-5 5.6 -<br>H. argophyllus 11-275-037 0 12F-3416-4 9.3 2.9<br>PI 494573 11-283-037 0 12F-3424-4 0 10.0<br>11-291-01 6.6 12F-3438-2 3.1 9.5<br>11-291-09 4.5 12F-3442-1 6.7 4.5<br>11-291-17 1.7 12F-3443-1 4.2 6.3<br>11-291-45 5.3 12F-3451-4 3.9 7.9<br>11-291-57 1.5 12F-3456-1 8.3 -<br>11-291-65 4.2 12F-3459-1 0 0.7<br>11-291-67 2.3 12F-3460-4 0 7.9<br>11-291-67 2.3 12F-3460-4 0 7.9<br>11-292-33 0 12F-3467-1 3.3 0<br>11-294-21 3.1 12F-3482-1 3.3 3.3<br>Susceptible checks Cargill 270 72.6 36.0<br>HA 89 23.7 HA 89 51.6 35.7<br>Resistant checks Croplan 305 12.4 Croplan 305 34.9 9.6  |                           | Pedigree    | $BC_2F_3$ | Pedigree     | $BC_2F_4$ | $BC_2F_4$ | <sup>35</sup> ☐ <i>H. argophyllus</i> introgressed line  |
| PI 49457311-283-037012F-3422-4010.011-291-016.612F-3438-23.19.511-291-094.512F-3442-16.74.511-291-171.712F-3443-14.26.311-291-171.712F-3443-14.26.311-291-571.512F-3456-18.3-11-291-654.212F-3459-100.711-291-654.212F-3460-407.911-291-672.312F-3460-407.911-292-33012F-3467-13.3011-292-33012F-3482-13.33.3Susceptible checksCargill 27034.8Cargill 27072.636.0HA 8923.7HA 8951.635.7Resistant checksCroplan 30512.4Croplan 30534.99.6   | H. petiolaris ssp. fallax | 11-256-049  | 0         | 12F-3405-2   | 4.0       | 8.4       | H. praecox introgressed line   |
| PI 49457311-283-037012F-3424-4010.011-291-016.612F-3438-23.19.511-291-094.512F-3442-16.74.511-291-171.712F-3443-14.26.311-291-455.312F-3451-43.97.911-291-571.512F-3456-18.3-11-291-654.212F-3459-100.711-291-672.312F-3460-407.911-292-33012F-3467-13.3011-292-33012F-3467-13.3011-292-33012F-3467-13.3011-292-33012F-3482-13.33.3Susceptible checksCargill 27034.8Cargill 270HA 8923.7HA 8951.635.7Resistant checksCroplan 30512.4Croplan 30534.9Resistant checksCroplan 30512.4Croplan 30534.99.6   | PI 435843                 | 11-256-053  | 0         | 12F-3406-5   | 5.6       | -         | 30 <sup>−</sup> H. petiolaris introgressed line  |
| PI 49457311-283-037012F-3424-4010.011-291-016.612F-3438-23.19.511-291-094.512F-3438-23.19.511-291-171.712F-3443-14.26.311-291-455.312F-3451-43.97.911-291-571.512F-3456-18.3-11-291-654.212F-3459-100.711-291-672.312F-3460-407.911-292-33012F-3460-407.911-294-213.112F-3482-13.3Susceptible checksCargill 27034.8Cargill 27072.6HA 8923.7HA 8951.635.7Resistant checksCroplan 30512.4Croplan 30534.99.6  | H. argophyllus            | 11-275-037  | 0         | 12F-3416-4   | 9.3       | 2.9       |  |
| H. praecox ssp. runyonii<br>Pl 468853<br>H. praecox ssp. runyonii<br>Pl 468853<br>11-291-45 5.3 12F-3450-1 8.3<br>11-291-65 4.2 12F-3459-1 0 0.7<br>11-291-67 2.3 12F-3460-4 0 7.9<br>11-292-33 0 12F-3467-1 3.3 0<br>11-294-21 3.1 12F-3482-1 3.3 3.3<br>Susceptible checks<br>Cargill 270 34.8 Cargill 270 72.6 36.0<br>HA 89 23.7 HA 89 51.6 35.7<br>Resistant checks<br>Croplan 305 12.4 Croplan 305 34.9 9.6  | PI 494573                 | 11-283-037  | 0         | 12F-3424-4   | 0         | 10.0      | Susceptible check  |
| H. praecox ssp. runyonii<br>Pl 468853<br>H. praecox ssp. runyonii<br>Pl 468853<br>11-291-45 5.3 12F-3450-1 8.3<br>11-291-65 4.2 12F-3459-1 0 0.7<br>11-291-67 2.3 12F-3460-4 0 7.9<br>11-292-33 0 12F-3467-1 3.3 0<br>11-294-21 3.1 12F-3482-1 3.3 3.3<br>Susceptible checks<br>Cargill 270 34.8 Cargill 270 72.6 36.0<br>HA 89 23.7 HA 89 51.6 35.7<br>Resistant checks<br>Croplan 305 12.4 Croplan 305 34.9 9.6  |                           | 11-291-01   | 6.6       | 12F-3438-2   | 3.1       | 9.5       |  |
| H. praecox ssp. runyonii<br>Pl 468853<br>H. praecox ssp. runyonii<br>Pl 468853<br>11-291-45 5.3 12F-3450-1 8.3<br>11-291-65 4.2 12F-3459-1 0 0.7<br>11-291-67 2.3 12F-3460-4 0 7.9<br>11-292-33 0 12F-3467-1 3.3 0<br>11-294-21 3.1 12F-3482-1 3.3 3.3<br>Susceptible checks<br>Cargill 270 34.8 Cargill 270 72.6 36.0<br>HA 89 23.7 HA 89 51.6 35.7<br>Resistant checks<br>Croplan 305 12.4 Croplan 305 34.9 9.6  |                           | 11-291-09   | 4.5       | 12F-3442-1   | 6.7       | 4.5       | . <mark></mark>  |
| H. praecox ssp. runyonii       11-291-57       1.5       12F-3456-1       8.3       -         PI 468853       11-291-65       4.2       12F-3459-1       0       0.7         11-291-67       2.3       12F-3460-4       0       7.9         11-292-33       0       12F-3482-1       3.3       0         11-294-21       3.1       12F-3482-1       3.3       3.3         Susceptible checks       Cargill 270       34.8       Cargill 270       72.6       36.0         HA 89       23.7       HA 89       51.6       35.7         Resistant checks       Croplan 305       12.4       Croplan 305       34.9       9.6  |                           | 11-291-17   | 1.7       | 12F-3443-1   | 4.2       | 6.3       |  |
| $\begin{array}{c} 11. process 33p. runyolini \\ 11-291-57 \\ 11-291-65 \\ 11-291-67 \\ 11-291-67 \\ 11-292-33 \\ 11-292-33 \\ 11-294-21 \\ 11-294-21 \\ 11 \\ 294-21 \\ 3.1 \\ 12F-3482-1 \\ 3.3$ | U pracovice rupuopii      | 11-291-45   | 5.3       | 12F-3451-4   | 3.9       | 7.9       | <u>o</u> 15 –  |
| $\begin{array}{c} 11-291-67 & 2.3 & 12F-3460-4 & 0 & 7.9 \\ 11-292-33 & 0 & 12F-3467-1 & 3.3 & 0 \\ 11-294-21 & 3.1 & 12F-3482-1 & 3.3 & 3.3 \\ \\ Susceptible checks \\ Resistant checks \\ Resistant checks \\ Croplan 305 & 12.4 \\ Croplan 305 & 34.9 \\ 9.6 \end{array}$  |                           | 11-291-57   | 1.5       | 12F-3456-1   | 8.3       | -         |  |
| $\begin{array}{c} 11-291-67 & 2.3 & 12F-3460-4 & 0 & 7.9 \\ 11-292-33 & 0 & 12F-3467-1 & 3.3 & 0 \\ 11-294-21 & 3.1 & 12F-3482-1 & 3.3 & 3.3 \\ \\ Susceptible checks \\ Resistant checks \\ Resistant checks \\ Croplan 305 & 12.4 \\ Croplan 305 & 34.9 \\ 9.6 \end{array}$  | 11400000                  | 11-291-65   | 4.2       | 12F-3459-1   | 0         | 0.7       |  |
| 11 252 35       30       121 3407 1       3.5       6         11-294-21       3.1       12F-3482-1       3.3       3.3         Susceptible checks       Cargill 270       34.8       Cargill 270       72.6       36.0         HA 89       23.7       HA 89       51.6       35.7         Resistant checks       Croplan 305       12.4       Croplan 305       34.9       9.6   |                           | 11-291-67   | 2.3       | 12F-3460-4   | 0         | 7.9       | <u>5.7 6.1 5.5 6.3</u>   |
| Susceptible checks         Cargill 270<br>HA 89         34.8<br>23.7         Cargill 270<br>HA 89         72.6         36.0           Resistant checks         Croplan 305         12.4         Croplan 305         34.9         9.6   |                           | 11-292-33   | 0         | 12F-3467-1   | 3.3       | 0         |  |
| Susceptible checks         HA 89         23.7         HA 89         51.6         35.7           Resistant checks         Croplan 305         12.4         Croplan 305         34.9         9.6   |                           | 11-294-21   | 3.1       | 12F-3482-1   | 3.3       | 3.3       |  |
| HA 89       23.7 HA 89       51.6       35.7         Resistant checks       Croplan 305       12.4       Croplan 305       34.9       9.6  | Suscentible checks        | Cargill 270 | 34.8      | Cargill 270  | 72.6      | 36.0      |  |
|  |                           | HA 89       | 23.7      | HA 89        | 51.6      | 35.7      | 26-1<br>30-1<br>50-1<br>50-1<br>50-1<br>50-1<br>50-1<br>50-1<br>50-1<br>5  |
|  |                           |             |           |              |           |           |  |
| HA $AA1$ 27 $A$ HA $AA1$ 28 $6$ 18 3 HA $AA1$  | Resistant checks          | -           |           |              |           | 9.6       |  |
|  |                           | HA 441      | 27.4      | HA 441       | 28.6      | 18.3      |  |
| <b>Table 1.</b> Evaluation of the 13 most resistant $BC_2F_3$ <b>Figure 2</b> . Mean performance of 23 $BC_2F_4$ famili  | families and deriv        |             |           |              | •         | _ 0       | <b>Figure 2</b> . Mean performance of 23 BC <sub>2</sub> F <sub>4</sub> familie<br>Sclerotinia basal stalk rot resistance at two locat |

stalk rot resistance in the field from 2012 to 2014.

In 2015, six *H. argophyllus*, two *H. petiolaris*, and eight *H. praecox* derived  $BC_2F_5$  wild introgression lines were evaluated for BSR resistance at two North Dakota locations. Wild introgression lines consistently showed superior BSR resistance in the field evaluations tested over the years. A one-way analysis of variance of DI data from seven environments revealed that all the  $BC_2F_5$  introgression lines showed significantly higher BSR resistance than the resistant inbred check, HA 441 (Fig. 3). Most of the introgression lines either showed significantly higher or similar levels of BSR resistance than the resistant hybrid check, Croplan 305.

relatives at Carrington, ND, and Grandin, ND in 2015.

Grandin, ND Carrington, ND Prop Pedigree\* Percent Infected Percent Infected Plants Plants ANN **TEST 2 (Second Retest** % % (NMS HA89 x GIG=PI 547182) HA 410\*2, BC2F3 0 0 HA-BSR (NMS HA89 x GIG=PI 547182) HA 410. BC1F4 10 0 (NMS HA89 x GRO=PI 416793) HA 410, BC1F4 10 HA-BSF CAL 2376 x HA 410\*5, BC4F3-F5 0 HA-BSR (NMS HA89 x GRO=PI 613793) HA 410, BC2F3 4 5 HA-BSR NMS HA89 x GRO=PI 613793) HA 410, BC1F4 2 MAX68 SIB x HA 410\*3, BC2F4 HA-BSR 0 NUT68 x HA 410\*3, BC2F4 15 Checks (NMS HA89 x MAX=PI 586892) HA 410\*2, BC2F2-F3 13 6 Susce STR (68) x HA 410 (3), BC2F4 0 Recurrent parent HA 410 12 11 Resist (NMS HA89 x 1323 (MAX)) HA 441,BC2F4 RHA 4 (NMS HA89 x 1323 (MAX)) HA 441, BC1F5 7 4 PERE (NMS HA89 x 1324 (NUT)) HA 441, BC1F5 0 8 SR MA **Recurrent parent HA 441** 8 5 SR NU **TEST 3 (First Retest)** Recur NMS HA89 X (HIR. X HA 410), F2 3 3 SR CAL NMS HA89 X (HIR. X HA 410), F2 3 2 SR DIV (NMS HA89 X (SAL X HA 410), F2 0 SR STR NMS HA89 X (SAL X HA 410), F2 0 3 Recurr NMS HA89 X (OCC X HA 410), F2 4 0 Checks (NMS HA89 X (OCC X HA 410), F2 0 NMS HA89 X (OCC X HA 410). F2 0 Suscep (NMS HA89 X (OCC X HA 410), F2 0 **Recurrent parent HA 410** 11 12 Resist NMS HA89 X (HIR X HA 451), F2 15 10 NMS HA89 X (HIR X HA 451), F2 \*Num MAX=H (NMS HA89 X (OCC X HA 451), F2 10 4 4 19 (NMS HA89 X (OCC X HA 451), F2 (NMS HA89 X (OCC X HA 451), F2 10 **Recurrent parent HA 451** 22 29 CHECKS 15 25 18 14

| osed Basal Stalk Rot Releases               | Species                   | Disease<br>Incidence (%) |
|---|---------------------------|--------------------------|
| JAL SPECIES                                 |                           |                          |
| R2 (1)*                                     | H. petiolaris ssp. fallax | 4                        |
| 33 (1)                                      | H. argophyllus            | 3                        |
| 34 (1)                                      | H. argophyllus            | 1                        |
| 85 (1)                                      | H. argophyllus            | 2                        |
| 86 (1)                                      | H. praecox ssp. runyonii  | 5                        |
| .7 (1)                                      | H. praecox ssp. runyonii  | 1                        |
| R8 (1)                                      | H. praecox ssp. runyonii  | 2                        |
| s   |                           |                          |
| otible check HA 89 (S) ***                  |                           | 31                       |
| otible check Cargill/Mycogen ( 270/272) (S) |                           | 36                       |
| ant check Croplan 305 (R) ***               |                           | 12                       |
| 41 (R)                                      |                           | 20                       |
| NNIAL SPECIES                               |                           |                          |
| X-1** (7)                                   | H. maximiliani            | 3                        |
| Г-1 (3)                                     | H. nuttallii              | 3                        |
| ent parent HA 441                           |                           | 11                       |
| -1 (23)                                     | H. californicus           | 2                        |
| -1 (1)                                      | H. divaricatus            | 7                        |
| -1 (2)                                      | H. strumosus              | 2                        |
| ent parent HA 410                           |                           | 23                       |
| 5   |                           |                          |
| otible check HA 89 (S) ***                  |                           | 33                       |
| otible check Cargill/Mycogen (270/272 (S)   |                           | 37                       |
| ant check Croplan 305 (R) ***               |                           | 9                        |
| ant check Croplan 343 (R)                   |                           | 17                       |

The first three letters of the *Helianthus* species are used to identify the species source: GIG=H. giganteus; GRO=H. grosseserratus; CAL=H Tralifornicus; MAX=H. maximiliani; NUT=H. nuttallii; STR=H. strumosus; HIR=H. hirsutus; SAL=H. salicifolius; and OCC= H. occidentalis. (S)= Susceptible; (R)=Resistant.

#### Summary

- Replicated field evaluations in 2009-2015 confirmed the successful introgression of Sclerotinia BSR resistance genes from annual and perennial sunflower crop wild relatives.
- GBS revealed the presence of *H. argophyllus* segments in LGs 3, 8, 9, 10, and 11 of the sunflower genome with LG 8 having the highest frequency.
- Progeny families with increased resistance for BSR will be selected for the development of QTL mapping

To detect the presence of *H. argophyllus, H. petiolaris,* and *H. praecox* chromosome segments in the highly BSR resistant wild introgression sunflower lines, a whole genome scan was performed using genotyping-by-sequencing (GBS) approach. Polymorphic single nucleotide polymorphism (SNP) markers revealed the presence of introgressed segments in the cultivated sunflower background predominantly located on LGs 1, 3, 8, 9, 10, and 11. Some of these introgressed segments might be associated with BSR resistance. (Fig. 4).

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North Dakota during 2014.

#### populations.

• Twelve germplasm lines with increased levels of resistance for Sclerotinia BSR will be released in the near future.

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