

Transferring Sclerotinia Resistance Genes from Wild *Helianthus* Species into Cultivated Sunflower

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Abstract

Wild perennial *Helianthus* species are highly resistant to Sclerotinia stalk and head rot. In order to introgress the resistance genes from wild *Helianthus* species, crosses and backcrosses have been conducted between amphiploids, hexaploid, tetraploid and diploid perennials with cultivated sunflower (HA 410, HA 441, HA 451 or NMS HA 89). The backcross progenies with 2n=34 chromosomes derived from different crosses were evaluated in replicated trials in 2009-2015. In 2015, 411 families were tested for stalk rot at Carrington, ND and Grandin, ND, and 336 families for head rot at Carrington, ND and Staples, MN. The results indicated successful gene introgression. Seed was increased in the field for more than 500 progeny families in 2015, including eight Sclerotinia head and stalk rot tolerant germplasms bulks based on field screening from 2009-2015. Progenies with 2n chromosome number=34-37 derived from various crosses were backcrossed with HA 410, HA 451 or NMS HA 89 to stabilize chromosome numbers and enhance further recombination. These materials will provide a potential pool of resistance genes and increase the probability of identifying useful resistance QTLs. The eight Sclerotinia head and stalk rot resistant germplasm bulks derived from five perennial species will be released.

Introduction

Sclerotinia, caused by the fungus *Sclerotinia sclerotiorum* (Lib.) de Bary, attacks sunflower (*Helianthus annuus* L.) causing root, stalk, and head rot, and is one of the most damaging and difficult-to-control sunflower diseases (Gulya, 2004). Many wild perennial *Helianthus* species have been confirmed to be highly resistant to this fungus (Block et al., 2011; Feng et al., 2007a, b). In the last 11 years, our lab has focused on the introgression of resistance genes from the wild perennial *Helianthus* species and interspecific amphiploids into cultivated sunflower, via the traditional backcross method (Liu et al. 2011, 2013, 2015). The objectives of this study were to: (1) evaluate stalk and head rot resistance of progeny families using field testing to identify progenies with new and high levels of resistance; and (2) continue to transfer Sclerotinia stalk and head rot resistance from wild perennial *Helianthus* accessions, and interspecific amphiploids into cultivated sunflower.

Materials and Methods

1. Head rot resistance evaluation: Replicated field evaluation for 20 families of 2014 retests derived from Phase 1 crosses, and 316 early generation families derived from Phase 2 crosses were conducted at Carrington, ND and Staples, MN in 2015.

2. Stalk rot resistance evaluation: Replicated field evaluation for 39 families of 2014 retests derived from Phase 1 crosses, and 372 early generation families derived from Phase 2 crosses were conducted at Carrington, ND and Grandin, ND in 2015.

3. Seed increase and backcrosses: Seeds of 552 backcross families derived from previous crosses were increased in the field in 2015. Nearly 300 other families with high chromosome numbers and poor seed set were backcrossed with HA 410, HA 451 or NMS HA 89 in the greenhouse in 2015.

Results

1. Sclerotinia head rot resistance evaluation of 2014 retests and new selections

Table 1. Replicated Sclerotinia head rot field evaluation of 2014 retest (Tests 2 and 3) and new interspecific crosses (Test 4) at Carrington, ND and Staples, MN in 2015.

Pedigree*	Carrington, ND 2015		Staples, MN 2015	
	Disease Rating	Infected Plants	Disease Rating	Infected Plants
TEST 2 (Second Retest)				
((NMS HA 89 x H. GRO=PI613793) HA 410*2), BC2F3 (47)	2.21	58	0	0
((NMS HA 89 x H. GRO=PI613793) HA 410), BC2F3 (66)	2.76	74	0	0
((NMS HA 89 x H. GRO=PI613793) HA 410), BC1F4 *new 69*	1.87	58	1.46	33
Recurrent parent HA 410	3.67	92	0.25	6
((NMS HA 89 x 1323(MAX)) x HA 441) BC1F5 (7)	1.91	53	0	0
((NMS HA 89 x 1324(NUT)) x HA 441) BC1F5 (8)	2.7	60	0	0
((NMS HA 89 x 1008 (NUT)) x HA 441) HA 441, BC2F4 (9)	0.81	17	0.19	4
((NMS HA 89 x 1018 (MAX)) x HA 441) BC1F6 (10)	1.82	38	0.37	12
((NMS HA 89 x 1324 (NUT)) x HA 441) BC1F5 (11)	0.68	21	0.50	11
((NMS HA 89 x 1008 (NUT)) x HA 441) HA 441) BC2F4 (15)	1.16	35	0.76	20
((NMS HA 89 x 1008 (NUT)) x HA 441) HA 441) BC2F4 (16)	1.91	54	0.65	15
Recurrent parent HA 441	1.94	55	0.51	11
TEST 3 (First Retest)				
NMS HA 89 X (H. SAL X HA 410), F2 (1011)	0.50	13	-	-
NMS HA 89 X (H. SAL X HA 410), F2 (1014)	0.92	22	-	-
NMS HA 89 X (H. SAL X HA 410), F2 (1063)	-	-	0.34	10
NMS HA 89 X (H. SAL X HA 410), F2 (1069)	-	-	0	0
NMS HA 89 X (H. SAL X HA 410), F2 (1072)	-	-	0.32	12
NMS HA 89 X (H. SAL X HA 410), F2 (1074)	-	-	0	0
NMS HA 89 X (H. SAL X HA 410), F2 (1077)	-	-	0.33	8
NMS HA 89 X (H. OCC X HA 410), F2 (1047)	1.24	31	-	-
NMS HA 89 X (H. OCC X HA 410), F2 (1085)	-	-	0.25	8
NMS HA 89 X (H. OCC X HA 410), F2 (1097)	-	-	0.21	7
NMS HA 89 X (H. OCC X HA 410), F2 (1098)	-	-	0.18	7
Recurrent parent HA 410	4.71	97	0.20	5
TEST 4 (New Selections)				
NMS HA 89 x ((SAL) x HA 410), F2 (1120)	2.33	62	-	-
NMS HA 89 x ((SAL) x HA 410), F2 (1121)	2.10	50	-	-
NMS HA 89 x ((SAL) x HA 410), F2 (1137)	-	-	0.29	7
NMS HA 89 x ((SAL) x HA 410), F2 (1138)	-	-	0.29	7
NMS HA 89 x ((SAL) x HA 410), F2 (1139)	-	-	0	0
NMS HA 89 x ((OCC) x HA 410), F2 (1163)	1.08	25	-	-
NMS HA 89 x ((OCC) x HA 410), F2 (1195)	-	-	0.27	7
NMS HA 89 x ((OCC) x HA 410), F2 (1208)	-	-	0.29	7
Recurrent parent HA 410	4.89	100	0.29	7
Checks				
Susceptible check HA 89 (S)	4.54	96	1.38	37
Susceptible check Mycogen (Cargill) 272 (S)	1.83	45	2.58	67
Resistant check Croplan 305 (R)	2.97	72	0.55	14
Resistant check Croplan 343 (R)	1.08	26	0.0	0.0

* The first three letters of the *Helianthus* species are used to identify the species source: GIG=*H. giganteus*; GRO=*H. grosseserratus*; CAL=*H. californicus*; MAX=*H. maximiliani*; NUT=*H. nuttallii*; DIV=*H. divaricatus*; STR=*H. strumosus*; HIR=*H. hirsutus*; SAL=*H. salicifolius*; and OCC=*H. occidentalis*. (S)= Susceptible; (R)=Resistant. The number(s) in parenthesis at the end of each pedigree is the family ID of the selected family.

2. Sclerotinia stalk rot resistance evaluation of 2014 retests

Table 2. Replicated Sclerotinia stalk rot field evaluation of 2014 retests (Tests 2 and 3) at Carrington, ND and Grandin, ND in 2015.

Pedigree*	Carrington ND		Grandin, ND	
	Percent Infected Plants	%	Percent Infected Plants	%
TEST 2 (Second Retest)				
(NMS HA 89 x GIG=PI547182) HA 410*2, BC2F3 (49)	0	0	0	0
(NMS HA 89 x GIG=PI547182) HA 410, BC1F4 (68,72)	0	10	10	10
(NMS HA 89 x GRO=PI 416793) HA 410, BC1F4 (66)	10	0	0	0
CAL 2376 x HA 410*5), BC4F3-F5 (39,40,42,25,27,26, 28,34,43)	2	0	0	0
(NMS HA 89 x GRO=PI 613793) HA 410, BC2F3 (58,85,86,76,78,74,77)	4	5	5	5
(NMS HA 89 x GRO=PI 613793) HA 410, BC1F4 (87,88, 80, 81, 82)	2	2	2	2
MAX68 SIB x HA 410*3, BC2F4 (95,96)	0	0	0	0
NUT68 x HA 410*3, BC2F4 (89-105)	0	15	15	15
(NMS HA 89 x MAX=PI586892) HA 410*2, BC2F2-F3 (47,103)	6	13	13	13
STR (68) x HA 410 (3), BC3F3 (100)	13	0	0	0
STR (68) x HA 410 (3), BC2F4 (38,106)	0	0	0	0
Recurrent parent HA 410	11	12	12	12
(NMS HA 89 x 1323(MAX)) HA 441,BC2F4 (20,21)	0	3	3	3
(NMS HA 89 x 1323(MAX)) HA 441,BC1F5 (9,10)	4	7	7	7
(NMS HA 89 x 1324(NUT)) X HA 441., BC1F5 (11)	0	8	8	8
Recurrent parent HA 441	8	5	5	5
TEST 3 (First Retest)				
NMS HA 89 X (HIR. X HA 410), F2 (523)	3	3	3	3
NMS HA 89 X (HIR. X HA 410), F2 (524)	3	3	3	3
NMS HA 89 X (HIR. X HA 410), F2 (545)	3	2	2	2
(NMS HA 89 X (SAL X HA 410), F2 (584)	2	0	0	0
(NMS HA 89 X (SAL X HA 410), F2 (600)	5	5	5	5
(NMS HA 89 X (SAL X HA 410), F2 (667)	0	3	3	3
(NMS HA 89 X (OCC X HA 410), F2 (713)	4	0	0	0
(NMS HA 89 X (OCC X HA 410), F2 (728)	3	0	0	0
(NMS HA 89 X (OCC X HA 410), F2 (744)	5	0	0	0
(NMS HA 89 X (OCC X HA 410), F2 (762)	3	8	8	8
(NMS HA 89 X (OCC X HA 410), F2 (785)	0	0	0	0
Recurrent parent HA 410	11	12	12	12
NMS HA 89 X (HIR X HA 451), F2 (508)	6	15	15	15
NMS HA 89 X (HIR X HA 451), F2 (511)	6	10	10	10
(NMS HA 89 X (OCC X HA 451), F2 (915)	4	10	10	10
(NMS HA 89 X (OCC X HA 451), F2 (917)	4	19	19	19
(NMS HA 89 X (OCC X HA 451), F2 (925)	3	10	10	10
Recurrent parent HA 451	22	29	29	29
CHECKS				
Susceptible check HA 89 (S)	15	25	25	25
Susceptible check Mycogen (Cargill) 272 (S)	8	4	4	4
Resistant check Croplan 305 (R)	8	8	8	8
Resistant check Croplan 343 (R)	5	4	4	4

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3. Scheduled releases of Sclerotinia head and stalk rot resistant germplasms

Table 3. Scheduled releases of Sclerotinia head and stalk rot resistant germplasms in 2016 based on field screening from 2009-2015.

Release Name	Disease Rating	Infected Plants
HEAD ROT RELEASES	0-5	%
HR MAX*-1 (4)**	0.9	23
HR NUT-1 (3)	1.1	24
Recurrent parent HA 441	2.3	52
Checks		
Susceptible check HA 89 (S)	3.4	71
Susceptible check Mycogen (Cargill) 272 (S)	3.3	70
Resistant check Croplan 305 (R)	2.7	59
Resistant check Croplan 343 (R)	1.7	46
STALK ROT RELEASES		
SR MAX-1 (7)	-	3
SR NUT-1 (3)	-	3
Recurrent parent HA 441	-	11
SR CAL-1 (23)	-	2
SR DIV-1 (1)	-	7
SR MAX-2 (1)	-	0.4
SR STR-1 (2)	-	2
Recurrent parent HA 410	-	23
Checks		
Susceptible check HA 89 (S)	-	33
Susceptible check Mycogen (Cargill) 272 (S)	-	37
Resistant check Croplan 305 (R)	-	9
Resistant check Croplan 343 (R)	-	17

** Number of families in the release.

Summary

1. Replicated field evaluation in 2015 of 2014 retests for head and stalk rot resistance confirmed successful introgression of resistance genes.
2. Nearly 400 new early generation families from Phase 2 crosses tested in 2014 suggested excellent stalk rot resistance.
3. Seed was increased in the field for more than 500 progeny families in 2015, including eight Sclerotinia head and stalk rot resistant germplasms bulks, which will be released in 2016.
4. The families with good resistance will be selected for the development of QTL mapping populations.

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