United States Department of Agriculture
Research, Education, and Economics
Agricultural Research Service

UNITED STATES DEPARTMENT OF AGRICULTURE
Agricultural Research Service
Washington, D.C.

and

North Dakota Agricultural Experiment Station
North Dakota State University
Fargo, North Dakota

NOTICE OF RELEASE OF THE SUNFLOWER (HELIANTHUS ANNUUS L.) GERMPLASM, HA-BSR1

The most significant disease threat to sunflower (Helianthus annuus L) production in humid temperate, as well as tropical and sub- tropical regions of the world is Sclerotinia sclerotiorum (Lib.) de Bary, a necrotrophic fungus that causes three distinctly different diseases on sunflower; basal stalk rot or wilt, mid-stalk rot, and head rot. Basal stalk rot (BSR) is a serious problem in sunflower-growing areas of the USA that starts by root infection resulting from myceliogenic germination of sclerotia. BSR resistance is genetically complex and quantitatively conditioned by multiple genes, each having a small effect. Low levels of resistance are available in some inbred lines and hybrids, but greater levels of resistance are needed to combat this emerging pathogen.

A sunflower (Helianthus annuus L.) germplasm, HA-BSR1 was selected for Sclerotinia BSR resistance from an F7-derived recombinant inbred line (RIL) population developed from the cross HA 441/RHA 439. HA 441 (PI 639164) and RHA 439 (PI 639162) were developed and jointly released in 2003 by the USDA-ARS and North Dakota Agricultural Experiment Station at Fargo, ND for their tolerance to Sclerotinia head rot caused by Sclerotinia sclerotiorum. RHA 439 is a restorer line selected from the cross RHA 377/AS 3211. RHA 377 (PI 560145) is a restorer line jointly released in 1990 by the USDA-ARS and North Dakota Agricultural Experiment Station at Fargo, ND, and AS 3211 is a hybrid developed in France. HA 441 is a maintainer line selected from the cross HA 412/SD. HA 412 (PI 603993) is a maintainer line jointly released in 1995 by the USDA-ARS and North Dakota Agricultural Experiment Station at Fargo, ND. SD is a maintainer line obtained through a germplasm exchange with National Institute for Agricultural Research (INRA), France.

The cross of HA 441/RHA 439 was made in 2004, and the seed of a single head was used as the progenitor of the F2 population. The RIL population was advanced from the F2 through the F7 in

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the greenhouse by single-seed descent. Each F7 line was grown in one row of 25 plants at Fargo, ND, in 2010 and the harvested F8 seeds were bulked to form individual RILs. Both the parents, HA 441 and RHA 439, were moderately tolerant to Sclerotinia BSR. The selected RIL line, HA-BSR1 (RIL25) was tested for resistance to BSR along with the parents, and both susceptible and resistant checks in inoculated field screening nurseries across seven environments in North Dakota and Minnesota during 2012 to 2015. HA-BSR1 consistently showed high levels of BSR resistance across all environments with a mean disease incidence (DI) of 2%, which was significantly lower than the parents RHA 439 (DI 14%) and HA 441 (DI 21%) and the resistant hybrid check Croplan 305 (DI 10%). The susceptible checks, HA 89 (DI 31%) and Cargill 270 (DI 33%) had the highest DI across all environments. Genetic analysis of the HA-BSR1 line confirmed the presence of alleles associated with two major quantitative trait loci (QTL), QTLbsr-10.1 and QTLbsr-17.1 conferring resistance against Sclerotinia BSR identified in the RIL population. The resistance allele of QTLbsr-10.1 was contributed by the RHA 439 parent, while the resistance allele of QTLbsr-17.1 was contributed by HA 441, each explained 32 and 20% of the BSR variation in the RIL population, respectively. The combined effect of these two resistance alleles significantly reduced the BSR disease incidence in the HA-BSR1 line.

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Signatures:

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8/1/16
Date

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8/10/16
Date