Registration of Four Soybean Germplasm Lines Containing Defoliating Insect Resistance QTLs from PI 229358 Introgressed into 'Benning'

S. Zhu, D. R. Walker, C. V. Warrington, W. A. Parrott, J. N. All, E. D. Wood, and H. R. Boerma*

The soybean [*Glycine max* (L.) Merr.] germplasm lines, G04-Ben229IR-M (Reg. No. GP-353, PI 647082), G04-Ben229IR-G (Reg. No. GP-354, PI 647083), G04-Ben229IR-H (Reg. No. GP-355, PI 647084), and G05-Ben229IR-MGH (Reg. No. GP-352, PI 647081), were developed by the Georgia Agricultural Experiment Stations at the Univ. of Georgia and released in February of 2006 for use as sources of single and multiple Soybean Insect Resistance (SIR) QTLs. Three of the lines, G04-Ben229IR-M, G04-Ben229IR-G, and G04-Ben229IR-H, are homozygous for PI 229358 alleles at SIRQTL-M, SIRQTL-G, and SIRQTL-H, respectively (Narvel et al., 2001; Warrington, 2006; Zhu et al., 2006). G05-Ben229IR-MGH is homozygous for PI 229358 alleles at all three SIRQTLs. SIRQTL-M, SIRQTL-H, and SIRQTL-G were initially listed as CEW 1-1, CEW 1-2, and CEW 6-1, respectively, in SoyBase (http://soybase.org/ verified 18 July 2007). Previous research has shown SIRQTL-G provides antibiosis (adverse physiological effects on the insect) and SIRQTL-H antixenosis (discouraging insect colonization and/or feeding) forms of resistance against corn earworm [CEW, *Helicoverpa zea* (Boddie)], while SIRQTL-M plants express both antibiosis and antixenosis resistance (Narvel et al., 2001; Rector et al., 1998, 2000). Zhu et al. (2006) reported that the PI 229358 allele from SIRQTL-M was required for the antibiotic effect of SIRQTL-G and the antixenotic effect of SIRQTL-H to be expressed in a Benning genetic background.

S. Zhu, D.R. Walker, W.A. Parrott, E.D. Wood, and H.R. Boerma, Center for Applied Genetic Technologies and Dep. of Crop & Soil Sciences; C.V. Warrington and J.N. All, Dep. of Entomology, Univ. of Georgia, Athens, GA 30602. Current address of D.R. Walker: USDA-ARS Soybean/Maize Germplasm, Pathology and Genetics Unit, Urbana, IL 61801. This work was funded by USDA National Research Initiative Competitive Grants Program (Grants no. 98-01149 and 2002-01460), and by state and federal funding allocated to the Georgia Agricultural Experiment Stations. Registration by CSSA. Received 2 Feb. 2007. *Corresponding author (rboerma@uga.edu).

Published in the Journal of Plant Registrations 1:162–163 (2007).
doi: 10.3198/jpr2007.02.0067crg

677 S. Segoe Rd., Madison, WI 53711 USA

The four germplasm lines are BC_6F_2-derived near-isogenic lines (NILs) from Benning (7) × PI 229358. Benning was initially crossed with PI 229358 in 1999 and was subsequently used as the recurrent parent. Benning is a Maturity Group (MG) VII cultivar which was derived from an F_4 plant descended from the cross 'Hutcheson' × 'Coker 6738' and was released in 1995 (Boerma et al., 1997). The SIRQTL donor PI 229358, known as 'Soden-daizu' in Japan, is a MG VII accession which has been used as a source of defoliating insect resistance in several North American soybean breeding programs (Narvel et al., 2001). For each generation of the backcrosses, F_1 plants were screened and selected for the presence of PI 229358 marker alleles in the three confirmed SIRQTL regions (Zhu et al., 2006). SSR markers surrounding SIRQTL-M (Satt220, Satt536, and Satt175), SIRQTL-G (Satt191, Satt472, and Sct_199), and SIRQTL-H (Sat_118, Sat_122, and Sat_334) were used to identify plants (SoyBase, http://soybase.org; Song et al., 2004). These selected plants provided pollen for the next generation of backcrosses to Benning. The BC_5F_2 progenies were also genotyped in late 2002 to identify individuals that were homozygous at SIRQTL-M, SIRQTL-G, and SIRQTL-H, and the homozygous $BC_5F_{2:3}$ lines were used for insect resistance bioassays (Zhu et al., 2006). The BC_6F_2 progenies were genotyped in early 2003 to identify individuals that were homozygous at the three SIRQTLs. BC_6F_2-derived NILs G04-Ben229IR-M, G04-Ben229IR-G, and G04-Ben229IR-H were evaluated in replicated field experiments in three environments in 2004 (Athens GA 21 May planting, Athens, GA 18 June planting, and Plains, GA), and in two environments in 2005 (Athens and Plains, GA). G05-Ben229IR-MGH was only evaluated at the two 2005 environments (Warrington, 2006). Although the yield trials were conducted in the field with low levels of natural infestation of various insects, the insect infestation and plant damage within each yield trial did not reach the threshold levels recommended for an insecticide application.

G04-Ben229IR-M is genetically similar to Benning, with the exception of an introgressed region containing the PI 229358 allele at SIRQTL-M. In both antibiosis and antixenosis tests, this line was more resistant to CEW and soybean looper [SBL, *Pseudoplusia includens* (Walker)] than Benning (Warrington, 2006; Zhu et al., 2006). Averaged across five environments, G04-Ben229IR-M was not significantly ($P > 0.05$) different in yield (2964 vs. 3074 kg ha^{-1}) from the Benning recurrent parent. For unknown reasons, G04-Ben229IR-M averaged 7% larger seeds than Benning, which averaged 138 mg seed^{-1} (Warrington, 2006).

G04-Ben229IR-G is genetically similar to Benning other than having an introgressed segment of DNA that includes the PI 229358 allele at SIRQTL-G. In antibiosis tests, this line did not reduce CEW or SBL larval weight more than Benning (Warrington, 2006; Zhu et al., 2006). Based on the report of Zhu et al. (2006), this result was expected since G04-Ben229IR-G lacks the PI 229358 allele at SIRQTL-M that is involved in an epistatic interaction with SIRQTL-G. When averaged across five environments, G04-Ben229IR-G yielded 2741 kg ha^{-1}, which was 11% lower in yield than Benning (Warrington, 2006). This line has 8% lower seed weight than Benning (127 vs. 138 mg seed^{-1}), a factor which might contribute to the yield reduction associated with SIRQTL-G.

G04-Ben229IR-H is also similar to Benning, but has the PI 229358 allele introgressed at SIRQTL-H. In antixenosis tests, this line did not show significantly ($P > 0.05$) less defoliation by CEW or SBL than Benning (Warrington, 2006; Zhu et al., 2006). This result was expected based on the report of Zhu et al. (2006), since G04-Ben229IR-H lacks the PI 229358 allele at SIRQTL-M. When evaluated in five environments, G04-Ben229IR-H did not have significantly ($P > 0.05$) different yield (3053 vs. 3074 kg ha^{-1}) from Benning.

G05-Ben229IR-MGH has PI 229358 alleles at the three SIRQTLs introgressed into Benning. In both antibiosis and antixenosis tests, this line was more resistant to CEW than Benning or a Benning BC_5F_2 line containing SIRQTL-M alone (Zhu et al., 2006). The higher resistance of G05-Ben229IR-MGH than the Benning BC_5F_2 line containing SIRQTL-M can be explained by the resistance-enhancing epistasis between SIRQTL-M and SIRQTL-G or SIRQTL-H. Across two environments in 2005, G05-Ben229IR-MGH yielded 3073 kg ha^{-1}, which was 10% lower than that of Benning (Warrington, 2006). This yield reduction is likely due to the presence of SIRQTL-G, which appears to be associated with yield drag.

Like Benning, G04-Ben229IR-M, G04-Ben229IR-G, G04-Ben229IR-H, and G05-Ben229IR-MGH have a determinate growth habit and belong to MG VII. They all have purple flowers, tawny pubescence, tan pods, yellow seed coat, and brown hilum, except that G05-Ben229IR-MGH has brown hila of varying intensity. All of the lines are also similar to Benning in maturity, plant height, lodging score, seed quality score, protein and oil content, and resistance to the southern root-knot nematode [*Meloidogyne incognita* (Kofoid & White) Chitwood] and race 3 of the soybean cyst nematode (*Heterodera glycines* Ichinohe).

Published evaluations of the effects of the PI 229358 SIRQTLs in Benning and 'Jack' (Nickell et al., 1990) genetic backgrounds (Walker et al., 2002, 2004; Zhu et al., 2006) provide breeders with information to help choose which of the NILs would be most suitable for a particular breeding scheme. G04-Ben229IR-MGH would be useful to select for the SIRQTL-M, SIRQTL-H, and SIRQTL-G simultaneously from within one population. The NILs that carry the three SIRQTLs individually would be more useful for backcrossing the SIRQTLs into a recurrent parent one at a time before pyramiding the SIRQTL by inter-crossing the individual SIRQTL-containing backcross lines. Some breeders may wish to exclude SIRQTL-G because of the yield penalty associated with SIRQTL-G in G04-Ben229IR-G.

Seeds of G04-Ben229IR-M, G04-Ben229IR-G, G04-Ben229IR-H, and G05-Ben229IR-MGH will be maintained by the Georgia Agricultural Experiment Stations at the Univ. of Georgia, Athens, GA 30602. A small sample of seeds may be requested from the corresponding author for research purposes, including development and commercialization of new cultivars. It is requested that appropriate recognition be made if a germplasm line contributes to the development of a new breeding line, cultivar, or publication.

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