Registration of the Essex × Forrest Recombinant Inbred Line Mapping Population

A genetic map of soybean [Glycine max (L.) Merr.] constructed with a recombinant inbred line (RIL) mapping population (Reg. no. MP-2, NSL 431663 MAP) from the cross ‘Essex MAP’ (PI 636326 MAP) by ‘Forrest MAP’ (PI 636325 MAP) has been used extensively worldwide. Essex was registered by Smith and Camper (1973) and Forest by Hartwig and Epps (1973). Since most morphological traits do not vary greatly, the RIL population has been used extensively worldwide to map genes underlying biochemical and physiological traits (Table 1). The genetic marker data encompass thousands of polymorphic markers and tens of thousands of sequence-tagged site (STS) that were collected at SIUC by Dr. Lightfoot’s group (Table 2). Several genetic maps of ExF94 have been constructed (Chang et al., 1997; Iqbal et al., 2001; Kassem et al., 2004b) and will continue to be developed.

The population is used to identify quantitative trait loci (QTL; Table 3) including those underlying biochemical and physiological traits that include resistance to soybean sudden death syndrome (SDS) [caused by Fusarium solani (Mart.) Sacc. f. sp. glycines (Fsg)]; soybean cyst nematode (SCN), Heterodera glycines Ichinohe (Hnetkovsky et al., 1996; Chang et al., 1996, 1997; Iqbal et al., 2001); seed yield (Njiti et al., 1997b; Yuan et al., 2002); seed quality traits (Njiti et al., 1999; Meksem et al., 2001b, 2004); water deficit (Cho et al., 2002); and manganese toxicity (Kassem et al., 2004b). Soybean genome analysis is underpinned by the population (Meksem et al., 2000, 2001a, 2001c, 2001d; Shultz et al., 2001; Wu et al., 2004a, 2004b). The map and RILs were used to anchor a physical map of soybean (Wu et al., 2004a, 2004b). The map and RILs were used for positional cloning of nts1, GmNARK (Searle et al., 2003), Rpg5 (Ashfield et al., 2003), Rhg1, Rhg4, and Rs2 (Lightfoot and Meksem, 1999). The population was used to develop an assay for marker-assisted selection for SDS resistance in the greenhouse (Njiti et al., 2001). Near-isogenic line populations have been created from each RIL for fine mapping and verification of QTL detected in the RIL population (Table 2; Njiti et al., 1998; Meksem et al., 1999; Triwitayakorn et al., 2005).

Forrest has been used as a source of DNA for three bacterial artificial chromosome (BAC) libraries (Meksem et al., 2000; Wu et al., 2004a). The set of materials has been used by many additional collaborators (unpublished to date). The population is very important for the analysis of yield QTL and other agronomic traits because it does not segregate for maturity and growth habit. The registration of this population allows public access to the population and data generated from it. Joint efforts in combating many agronomic problems in the future are expected.

Parents

Forrest is an F1-derived line from the cross ‘Dyer’ × ‘Bragg’, and Essex is an F7-derived line from the cross ‘Lee’ × ‘Forrest’. Essex MAP is an F8-derived line from the cross ‘Essex’ × ‘MAP’ by ‘Forrest MAP’ × ‘MAP’. Essex MAP is an F2-derived line from the cross ‘Essex’ × ‘MAP’ by ‘Forrest MAP’ × ‘MAP’.

Development of the Population

The cross was made in 1983 at Southern Illinois University at Carbondale using seed obtained from the cross ‘Lee’ × ‘Forrest’. About 4500 F2 plants were inbred to F6 by modified single seed descent (Brim, 1966). The RILs were harvested of which 150 were randomly selected for use in the greenhouse (Njiti et al., 1997a), and will continue to be developed. Thirty-five RILs were released as disease resistant (DX 100%) by F. solani f. sp. glycines (Njiti et al., 1997a), and F. tucumaniae (Aoki et al., 2003). Forrest has excellent pod-shatter resistance (Hartwig and Epps, 1973).

Essex is an F7-derived line from the cross ‘Lee’ × ‘Forrest’ and released by the Virginia Experiment Station in 1973. It was subsequently found to be resistant to Phytophthora root rot, as is Forrest. It has been grown as a source of DNA for three bacterial artificial chromosome (BAC) libraries (Meksem et al., 2000; Lightfoot et al., 2001). The population is used to identify quantitative trait loci (QTL) in the greenhouse (Njiti et al., 2001). Near-isogenic line populations have been created from each RIL for fine mapping (Table 2; Njiti et al., 1998; Meksem et al., 1999; Triwitayakorn et al., 2005).

Description of the Population

The population has a 7-d spread in maturity (from early to late group V in maturity and is characterized by determinate growth habit). The population ranges from 71 to 106 cm for full season planting. All RILs have a determinate growth habit. Plant height varies from 2.9 to 3.9 Mg ha−1.

The population is used to identify quantitative trait loci (QTL) in the greenhouse (Njiti et al., 2001). Near-isogenic line populations have been created from each RIL for fine mapping (Table 2; Njiti et al., 1998; Meksem et al., 1999; Triwitayakorn et al., 2005).

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