

Using Perennial *Glycine* to Improve Soybean

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Objectives

To identify high yielding lines derived from backcrosses between the cultivar Dwight and *G. tomentella* PI 441001 and the reciprocal cross.

Materials and Methods

Field of *G. max* × *G. tomentella* backcross lines



G. tomentella



Population development

The *G. max* × *G. tomentella* backcross-derived lines were developed using the maturity group (MG) II cultivar Dwight and the perennial *G. tomentella* PI 441001. PI 441001 was crossed to Dwight and immature seed rescue was used to produce a sterile F₁ plant. Amphidiploid plants (2n=118) were produced by treating the F₁ hybrid with colchicine. Amphidiploid plants were backcrossed to Dwight to obtain BC₁ plants and backcrossing was continued until plants with 2n=40 chromosomes were achieved. The same procedures were followed when PI 441001 was used as the female parent producing derived lines with *G. tomentella* cytoplasm.

Experimental procedures

The lines were initially tested in one of several preliminary tests in MG II, III, or IV beginning in 2014 as part of the breeding program. The best lines were selected in each year and retested the following year. In 2016 we tested 25 MG II lines, 29 MG III lines, and 13 MG IV lines that had been tested in one or two previous years. Because these lines were evaluated in different tests in 2014 and 2015, not all lines could be directly compared over all years and locations. Tests were conducted at two locations in Illinois in 2014 and 2015, and one location in Illinois, Minnesota and Kansas in 2016. All plots were 4 rows wide with the center two rows harvested for yield.

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Results

Table 1. Data collected on maturity group II entries from one location in Illinois in 2014 and 2016, two Illinois locations in 2015, and one location in Minnesota in 2016.

Entry	Pedigree	Yield (kg/ha)	Maturity (days)	Lodging (1 to 5)	Height (cm)
LG13-11138	F3 PI 441001 x Dwight (4)	4481	+1	2.0	87
LG13-10125	F4 PI 441001 x Dwight (3)	4404	0	2.0	90
Dwight	Soybean parent	4169	Sept. 21	2.2	90
LSD (0.05)		173	2	0.4	2

Table 2. Data collected on maturity group IV entries from two locations in Illinois in 2015, one location in Illinois and one location in Kansas in 2016.

Entry	Pedigree	Yield (kg/ha)	Maturity (days)	Lodging (1 to 5)	Height (cm)
LD06-7620	Check	5390	+13	2.3	105
LG13-11006	F5 PI 441001 x Dwight (3)	4890	+6	2.3	100
Dwight	Soybean parent	4280	Sept. 17	2.4	102
LSD (0.05)		420	2	0.5	7

Table 3. Data collected on maturity group IV entries from two locations in Illinois in 2014 and 2015, one location in Illinois and one location in Kansas in 2016.

Entry	Pedigree	Yield (kg/ha)	Maturity (days)	Lodging (1 to 5)	Height (cm)
LD06-7620	Check	4982	+15	2.2	100
LG13-11006	F5 PI 441001 x Dwight (3)	4484	+9	2.3	97
LG12-18375	F7 Dwight (4) x PI 441001	4244	+7	1.9	95
Dwight	Soybean parent	3913	Sept. 18	2.3	98
LSD (0.05)		290	1	0.34	4

Discussion

- Selected lines derived from crossing soybean with *G. tomentella* can yield more than the soybean parent without changes in time of maturity, lodging or plant height (Table 1).
- Most of the lines in this research that yield more than the soybean parent have *G. tomentella* cytoplasm. (Tables 1, 2 and 3)
- Each BC₂ plant has a different, random set of approximately half the *G. tomentella* chromosomes so lines derived from different BC₂ plants are likely to be genetically different. LG12-18375 is the first high yielding line derived from its progenitor BC₂ plant (Table 3).
- The highest yielding lines with *G. tomentella* cytoplasm are all derived from the same BC₂ plant (Tables 1, 2, and 3).
- The highest yielding line (LG13-11006) is approximately a week later but yields 14% more than the soybean parent (Tables 2 and 3).
- Current research is identifying specific genomic regions introgressed from *G. tomentella* that are associated with increased seed yield and quantifying the effects of *G. tomentella* cytoplasm.