第 28 卷 第 3 期
2009 年 6 月

大 豆 科 学
SOYBEAN SCIENCE

Vol. 28 No. 3
June 2009

Effect of Elite Lines on A Specific Soybean Breeding Program

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Abstract: Genetic variability that arises from genetic diversity benefits the successful soybean breeding program, breeders analyze the pedigree of breeding populations to examine the genetic structure of their populations. The objective of this study was to evaluate the effect of elite entries which had an important role in the yield improvement of the OSU soybean breeding program. The OSU soybean breeding program, usually used the new elite lines from itself breeding program or from other programs as parents to make the new cross in each year, changed the pedigree percentage of elite lines in different years, and the years as the elite line used as parents was limited. However, as there was a lack of breeding materials for food grade soybean breeding, the Ohio FG1 used for a longer time. Kottman, A98-980047, U 97-3114, HS 98-3628, HS 94-4533, Athow, and HS 93-4118 these 7 parents were the best elite lines for the yield improvement of the OSU program. There was a linear relationship between the mean yield of entries with $\geqslant 50\%$ pedigree of elite lines and the mean yield of all tested entries ($P = 0.0002^{**}$). The correlation of the mean yield of entries with $\geqslant 50\%$ pedigree of elite lines and the mean yield of all tested entries was 0.9146, they had a similar trend. There was no linear relationship between the pedigree percentage of elite lines and the mean yield of all tested entries, which meant that making new cross for the yield improvement should consider the combinability of elite line, not just the quantity of elite lines as parents. The mean yield of entries derived from 11 of 26 elite lines was over check, 7 of 11 was from the OSU breeding program, the breeding materials played a key role in the yield improvement. The 7 elite lines were related with five old cultivars (Williams, Essex, Amsoy, Wayne and Corsoy) and a current cultivar A 86-301024. From 1998 to 2008, 17 of 38 parents of the oil-use cultivars, and 14 of 16 parents of the food-grade cultivars were from the OSU program. The elite lines had an important effect on the development of cultivars.

Key words: Soybean; Elite line; Breeding

大豆骨干品系在特定育种程序中的作用

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摘　要: 来源于遗传多样性的变异将有助于提高育种效率, 通过血缘关系分析可以了解后代群体的遗传结构。研究的目的是评估美国俄亥俄州立大学大豆育种程序中对产量改良起过重大贡献的骨干品系的作用。在俄亥俄州立大学大豆育种程序中, 通常采用自己创造的骨干育种材料或来自其他育种程序的优异品种 (系) 做亲本进行常年杂交组配, 这样带来了骨干血缘年度间的差异性, 骨干品种 (系) 做亲本的使用年限也是有限的, 然而, 由于本育种程序中缺乏做豆腐用的骨干亲本, 使 Ohio FG1 品种用作亲本的年限延长。Kottman, A98-980047, U 97-3114, HS 98-3628, HS 94-4533, Athow 和 HS 93-4118 等 7 个骨干品种 (系) 对俄亥俄州立大学大豆产量改良起主要作用。后代群体中含 50% 以上骨干血缘品系的平均产量和所有被鉴定品系的平均产量呈极显著正相关, 相关系数为 0.9146, 含 50% 以上骨干血缘品系的平均产量越高, 所有被鉴定品系的平均产量也越高。但后代群体中骨干品系的血缘百分率和所有被鉴定品系的平均产量间不存在线性关系, 说明在选择骨干品系做亲本时, 除了考虑骨干品系的数量外, 还要考虑骨干品系的配合力。俄亥俄州立大学大豆育种程序中, 26 个骨干品系衍生的后代中有 11 个的衍生后代平均产量超过对照品种, 而且, 这 11 个骨干品系中又有 7 个来自俄亥俄州立大学大豆育种程序, 说明育种中间材料在产量改良中起着关键性作用。血缘分析结果表明, 7 个骨干品系来源于 Williams、Essex、Amsoy、Wayne、Cor-

soy 5 个老品种 和一个现代品系 A 86-301024。1998 至 2008 年俄亥俄州立大学育成的 19 个油用品种和 8 个豆腐用品种中分别有 17 和 14 个亲本来自育种程序本身,进一步说明骨干品系的创造在品种选育中起着重大作用。

关键词: 大豆;骨干品系;育种

In soybean yield improvement breeders have mainly used biparental breeding populations with elite parents[1]. This strategy has gained seed yield increase of cultivars by ≈1.0% yr^{-1}, also better resistance to plant lodging. Recently, the rates of yield improvement have been equal to or greater than those in earlier years[2].

Genetic variability that arises from genetic diversity benefits the successful soybean breeding program. A narrow genetic base of commercial soybean was formed by the predominant use of selected elite parents in the breeding of the United States[3]. Only 11 ancestors accounted for 90% of the parentage of recent elite public and proprietary U. S. soybean cultivars[4], while for the 258 public U. S. cultivars released from 1947 to 1988, only 22 ancestors for 90% of their parentage[5]. Compared with the public cultivars released prior to 1954, the public cultivars released since 1983 had 50% more genes in common[6].

Elite cultivars adapted to the north are quite distinct from southern cultivars in United States [4,6-7]. Among the southern elite cultivars there was less diversity than that of northern elite families. Of the southern elite parentage about 47% was from CNS and S100 ancestors [4,6].

Breeders analyzed the pedigree of their breeding populations, and examined the genetic structure of the populations, which is useful in managing diversity within a population. In the elite North American soybean population pedigree analysis has been applied frequently[4,6-11].

Reducing exchange of germplasm among breeding programs affected the genetic structure of soybean. Before mid 1980s, soybean breeders were free to make cross with any line regardless of its origin. Since some companies have patents on released conventional and RR cultivars as well as additional use restrictions on germplasm beyond that covered by the Plant Variety Protection Act, it is no longer possible for soybean breeders to have the free right. As the imposed restrictions are too severe for acceptance by other breeders,

many lines from proprietary sources are being used only by the company itself, which resulted in that the elite soybean population is becoming subdivided by the source of elite lines [12]. Sneller assessed the genetic structure of the current elite North American soybean population and the current and potential affect of RR soybean and crossing restrictions on this population, and reported that there was a limited diversity among elite lines from some companies, however, the public programs will ensure and expand the diversity[12].

Soybean genetic improvement has produced elite cultivars with high yield potential, good stability, and resistance to important diseases. Elite cultivars have played an important role in commercial soybean production, and also they had a great effect on the genetic improvement of yield. As the limitation of elite cultivar exchange between different breeding programs, it is important to evaluate and keep the best elite entries from a specific breeding program, which will benefit the efficiency of breeding.

From 1984 to 2008, the soybean breeding program conducted at the Ohio Agricultural Research and Development Center of The Ohio State University(OSU) has released 51 cultivars and 6 germplasms[13-28], which showed that the program is productive and efficient. Introduction and assessment of the program would be helpful for other soybean breeders to improve their breeding programs. The objective of this study was to evaluate the effect of elite entries which had an important effect in the yield improvement of the OSU soybean breeding program.

1　Materials and Methods

1.1　The activity of the OSU soybean breeding program

The parents were planted in green house or field for making crosses each year. After harvest the hybrids usually were taken to Puerto Rico or planted in green house as winter nursery to speed up the program.

F_2 plants were planted in nursery, as the plants matured, selected the single plants with the proper ma-

turity.

In the F_3 stage, the progeny of individual F_2 plants were tested in single-row plots approximately 1.5 m long [29]. In most cases, these $F_{2:3}$ lines tests were unreplicated, but some had two replications, one at each of two locations. Most tests contained 83 $F_{2:3}$ lines and 7 check genotypes, for a total of 90 randomized entries. We avoided wide ranges of maturity within a test by classifying F_2 plants as early, medium, or late maturity and assigning to each test progeny from plants of a single maturity class. The experimental lines in each test generally derived from numerous crosses. There were 4 to 26 different tests of $F_{2:3}$ lines annually. Maturity was recorded for each plot as the date when 95% of the pods had reached their mature color. All plots were harvested with a plot combine, and yield was recorded as the weight of air-dry seed per plot at approximately 90 g·kg^{-1} moisture content. We made selections from the F_3 stage by considering the performance of both crosses and individual $F_{2:3}$ lines for maturity and yield. Selection was subjective. Crosses with high mean yields and early maturity were identified first, then superior lines were selected, primarily from superior crosses(Table 1).

Table 1　Overview of the soybean breeding program at Ohio State University-Ohio Agricultural Research and Development Center

Stage	Activity
Parental	Make crosses
F_1	Produce F_1 plants.
F_2	Produce F_2 plants; harvest individual plants.
F_3	Test $F_{2:3}$ lines in single short-row plots, either unreplicated or with one replication at each of two locations.
F_4	Test $F_{2:4}$ lines in two- or three-row plots, two replications per location, two or three locations per test. Also harvest individual F_4 plants from each line.
F_5	Continue test of $F_{2:5}$ lines as in F4 stage. Also, produce and select $F_{4:5}$ lines from selected F_2-derived entries.
F_6	Test $F_{4:6}$ lines in two- or three-row plots, two replications per location, two or three locations per test.
F_7	Statewide tests of selected $F_{4:7}$ lines at 4 to 6 locations, with 2 or (usually) 3 replications per location.
F_8	Continued tests as in F7.
F_9	Continued tests as in F7.
F_{10}	Release of cultivar.

In the F_4 stage, we tested the selected F_2-derived lines in replicated, multiple-row plots. Until 1992, plots consisted of two rows, spaced 76 cm apart. Beginning in 1992, row spacing was reduced to 38 cm and there were three rows per plot. Plots were planted to a length of 4.5 to 5 m, depending upon the year and location, and end-trimmed after physiological maturity to a length of 3 m. Each selection from the F_3 tests was assigned to one of four F_4 tests, depending on maturity(early, i. e., maturity group II or early maturity group III, or late, i. e., late maturity group III or early maturity group IV) and breeding objective. Early and late F_4 tests of lines intended for use as commodity cultivars were conducted at three locations; early and late tests of grain-type or exotic lines were conducted at two locations. There were 25 to 100 entries per test, including 3 to 5 check genotypes. Maturity and yield were measured on each plot as in the F_3 tests, and lodging score was also recorded on a scale of 1(erect) to 5(prostrate). Selection of superior lines from the F_4 test was based on yield, maturity, lodging score, and, in some cases, grain protein content, seed size, and disease resistance.

Selected lines from the F_4 tests were continued for the following year in the same test with newly selected $F_{2:3}$ lines. Thus, $F_{2:4}$ and $F_{2:5}$ selections were in a common test. While continuing to test selected $F_{2:5}$ lines, we also grew $F_{4:5}$ progeny from these lines in a separate nursery, using unreplicated short-row plots. Performance in the $F_{2:5}$ tests was the primary selection criterion, with a small amount of attention to the yield, maturity, and disease resistance of the individual $F_{4:5}$ lines. We saved only $F_{4:5}$ lines for continued testing, discarding all F_2-derived lines after the F_5 generation.

We tested $F_{4:6}$ lines in two- or three-row plots, identical to those used in the F_4 stage, at three locations, with two replications per location. We selected lines primarily on the basis of yield, maturity, and lodging, informally considering F_2 family means along with line performance per se. In the F_7 to F_9, selections were tested statewide at four to six locations in bordered row plots with two or (usually) three replications per location. Row length and spacing varied in the statewide

tests.

1.2 Analysis method

First, use the data of the OSU soybean breeding program from 1997 to 2006, and transfer the yield data of each test(over F_4 stage) in every year to the percentage yield of as check according to the mean yield of check cultivars in each test.

Second, evaluate the top five elite lines which contribute more than 50% the pedigree of entries with the yield of over check cultivars in every year.

Third, combine the top five elite lines from 1997 to 2006 to make the elite lines of this breeding program for the 10 years. And then analyzed the pedigree percentage of the elite lines in different year(Table 2), the mean yield of entries with $\geqslant$50% pedigree of elite lines(Table 3), and the mean yield of all tested entries (data not showed).

Using SAS 9.1 to analyze the relationship between the mean yield of entries with $\geqslant$50% pedigree of elite lines and the mean yield of all tested entries, and relationship between the pedigree percentage of elite lines

and the mean yield of all tested entries.

2 Results

2.1 Effect of elite line on yield

In the OSU soybean breeding program usually used the new elite lines from itself breeding program or from other programs as parents to make the new cross in each year, which changed the pedigree percentage of elite lines in different years, and the duration as the elite line used as parents was limited(Table 2). However, as there was a lack of breeding materials for food grade cultivar, Ohio FG1 used for a longer time.

Entries derived from different elite lines had different yields, some had good yield potentials. The mean yields of entries derived from Kottman, Dilworth, A98-980047, HS 97-5261, U 97-3114, HS 98-3628, IA 3023, HS 94-4533, Athow, HS 93-4118, and HS 90-37100 were over checks, especially the yields of off-springs from Kottman, A98-980047, U 97-3114, HS 98-3628, HS 94-4533, Athow, HS 93-4118 were over checks each year(Table 3), which implied these 7 parents were the best elite lines for the yield improvement of the OSU breeding program.

Table 2   The pedigree percentage of elite lines in different years

Elite line	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006
Kottman	–	–	2.3	2.2	14.4	14	24.9	24.4	29.8	24.5
Dilworth	–	–	–	–	–	–	–	3.6	2.8	16.1
A98-980047	–	–	–	–	–	–	3.5	1.8	8.7	10
HS99-4045	–	–	–	–	0.6	–	–	3.2	0.8	6.8
OhioFG1	4.3	7.5	7.7	9	2.5	3.9	1.3	0.7	5	9.1
HS97-5261	–	–	–	0.4	0.2	3.9	1.3	7.3	5.6	1.3
U97-3114	–	–	–	–	–	2.8	1.3	8.4	3.7	1.3
HS98-3628	–	–	–	–	–	–	0.4	3.7	1.3	0.4
IA3023	–	–	–	–	–	–	–	3.2	0.5	4.1
HS94-4533	–	–	–	1.7	0.5	2.3	3.2	1.7	2.5	0
Athow	–	–	1.1	3.7	1	6.9	3.2	1.7	2.5	0
HS93-4118	–	–	3.1	1.7	14.8	15.1	10.5	2.6	1.8	3.6
Tiffin	–	–	4.3	1.5	11.3	6.1	3.6	0.9	–	–
HS96-3347	–	–	–	–	3	6.4	2.6	0.9	1.4	0.3
Savoy	–	–	2.6	0.4	4	1.6	0.5	–	–	–
General	1.9	7.6	1.9	5.7	4.6	2.3	1.6	3.4	0.6	–
Defiance	3.6	4.5	9.8	3.5	2.3	1.6	3.7	2.6	–	0.3
HS91-4825	5.7	1.3	9.5	2	–	–	–	–	–	–
HS89-3078	3.4	2.8	12.9	9.9	4.5	2.8	–	–	–	–
OhioFG2	3.2	2.8	10	6.6	3.3	1.9	–	–	–	–
IA2007	8.5	14.5	6.4	0.8	0.6	–	–	–	–	–
Macon	1.1	6.6	3.6	1	–	–	–	–	–	–
90-37100	10.1	6.9	3.6	1.3	–	–	–	–	–	–
Resnik	–	7.9	4.3	2.1	1.2	0.6	0.5	0.9	–	–
HS89-5689	6.5	1.1	–	–	–	–	–	–	–	–
Flint	4.8	2.2	3.7	2.3	3	3.9	2.6	0.9	–	–
Total	**53.1**	**65.7**	**86.8**	**55.8**	**71.8**	**76.1**	**64.7**	**71.9**	**67**	**77.8**

Table 3   Mean yield$^{\delta}$ of entries with ≥50% pedigree of elite lines

Elite line	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	Mean
Kottman	–	–	101.6	109.4	104.1	104.8	111.6	102.5	104.7	102.2	105.1
Dilworth	–	–	–	–	–	–	–	103.1	97.1	100.9	100.4
A98-980047	–	–	–	–	–	–	121.2	102	111.5	102.5	109.3
HS99-4045	–	–	–	–	95.3	–	–	102.5	95.6	101.6	98.8
OhioFG1	101.2	91.5	89.5	97.7	98.6	99.1	100.9	84.3	112.4	95.2	97.0
HS97-5261	–	–	–	92	75.7	108.3	115.5	105.8	103.9	98.9	100.0
U97-3114	–	–	–	–	–	108.5	114.3	103.8	106.5	101.6	106.9
HS98-3628	–	–	–	–	–	–	120.4	102.5	111.3	105.6	110.0
IA3023	–	–	–	–	–	–	–	102.5	99.5	99.2	100.4
HS94-4533	–	–	–	112.6	111.8	112.5	123.1	113	103.1	–	112.7
Athow	–	–	107.9	112.7	110.5	108.7	123.1	113	103.1	–	111.3
HS93-4118	–	–	106.2	110.3	105.9	101.7	102.6	100.3	108.2	102.3	104.7
Tiffin	–	–	99	93.1	97.2	102.2	97.5	92.6	–	–	96.9
HS96-3347	–	–	–	–	97.8	97.8	95.9	105.6	105.6	87.1	98.3
Savoy	–	–	98	100.1	102.6	98.1	88.8	–	–	–	97.5
General	98.5	96.2	101.4	99.7	96.7	90.3	91.8	95.3	101.5	–	96.8
Defiance	98.4	99.4	96.6	92.1	99.5	101.8	102.3	93.8	–	99.2	98.1
HS91-4825	96.9	97.7	97	99.1	–	–	–	–	–	–	97.7
HS89-3078	100.3	97.3	93.4	100.9	101.4	103.9	–	–	–	–	99.5
OhioFG2	94.9	95	93.6	98.8	96.9	101.9	–	–	–	–	96.9
IA2007	95.8	97	90.6	100	85.6	–	–	–	–	–	93.8
Macon	98.3	102.8	93.6	93.7	–	–	–	–	–	–	97.1
HS 90-37100	101.2	100.1	98.3	102.3	–	–	–	–	–	–	100.5
Resnik	–	97	93.2	94.8	98.6	82.4	101.7	93.3	–	–	94.4
HS89-5689	99.5	91.9	–	–	–	–	–	–	–	–	95.7
Flint	97.3	97.1	100.8	88.9	105.5	98.6	106.1	101.3	–	–	99.5
Mean	**98.4**	**96.9**	**97.5**	**99.9**	**99.0**	**101.3**	**107.3**	**101.0**	**104.6**	**99.7**	**100.6**

$^{\delta}$ Yield is the % of as check.

There was a linear relationship between the mean yield of entries with ≥50% pedigree of elite lines and the mean yield of all tested entries ($P = 0.0002^{**}$). The correlation of the mean yield of entries with ≥50% pedigree of elite lines and the mean yield of all tested entries was 0.9146. The mean yield of entries with ≥50% pedigree of elite lines and the mean yield of all tested entries had a similar trend (Fig. 1).
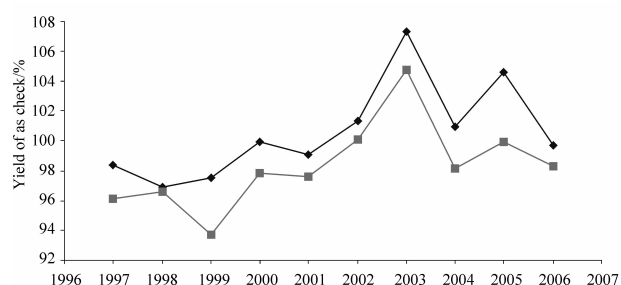

Fig. 1   Yield comparison between the entries (◆) with ≥50% pedigree of elite lines and the all tested entries (■)

The regression of the pedigree percentage of elite lines (Table 2) and the mean yield of all tested entries (data not showed) showed there was no linear relationship between the pedigree percentage of elite lines and the mean yield of all tested entries ($P = 0.5644$), which meant that making new cross for the yield improvement should consider the combinability of elite line, not just the quantity of elite lines as parents.

2.2   Pedigree of elite line

The mean yield of entries from 11 of 26 elite lines was over check (Table 3), 7 of 11 was from the OSU breeding program, which implied that the breeding materials played a key role in the yield improvement of OSU soybean breeding program. The 7 elite lines were related with five old cultivars (Williams, Essex, Amsoy, Wayne and Corsoy) and a current cultivar A 86-301024 (Fig. 2).

2.3   Elite line and breeding efficiency

From 1998 to 2008, the OSU breeding program released 27 cultivars, 19 of them were for oil use, and 8 for food grade (Table 4). 17 of 38 parents of the oil-use cultivars, and 14 of 16 parents of the food-grade cultivars were from the OSU program. The elite lines as breeding materials had an important effect on the development of cultivars.
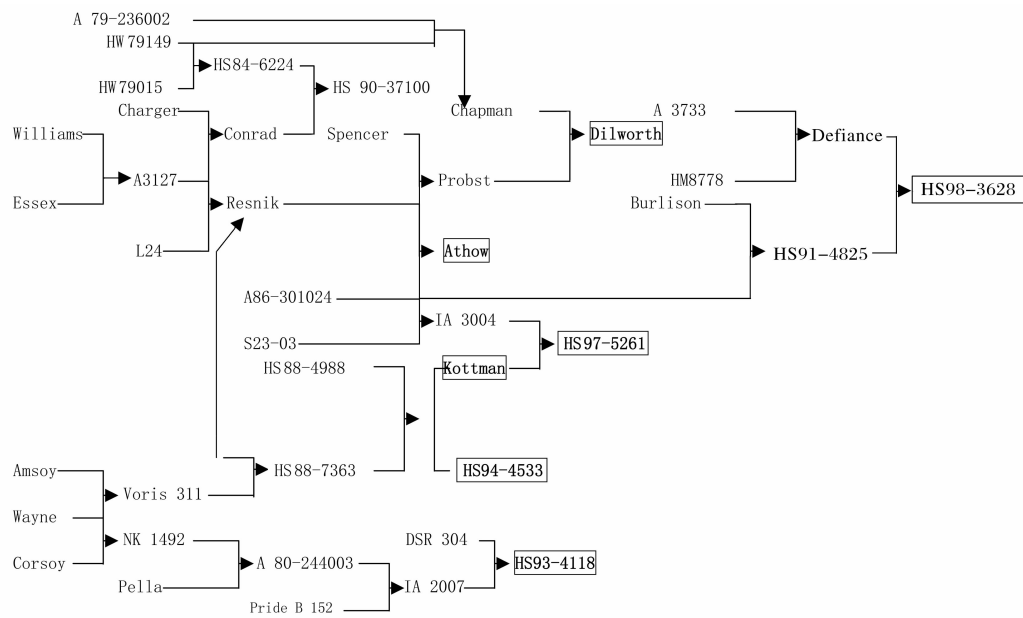
Fig. 2　Pedigree of 7 elite lines from the OSU breeding program

Table 4　Recently released cultivars and its pedigree

Type	Released year	Name	Pedigree
Oil use	1998	Darby	GR8936 × Edison
	1998	HS93-4118	IA2007 × DSR 304
	1998	Tiffin	Haroson × Chapman
	1999	Kottman	HS88-7363 × HS88-4988
	2000	HS95-4907	HS 89-2988 × IA 2003
	2000	HS95-4908	HS 89-2988 × IA 2003
	2001	HS96-3850	HS 89-2966 × HS 89-8843
	2001	HS96-3818	HS 88-7363 × IA 2003
	2002	Dilworth	Chapman × Probst
	2002	HF9667-2-4	General × GXR 9648
	2002	HF9667-2-15	General × GXR 9648
	2002	HF9665-2-15	{（Resnik BC × Flint）× Delsoy 4710} × Resnik BC
	2002	HF9670-3-10	Defiance × GXR 9648
	2005	HS0-3243	Kottman × HS93-4118
	2006	Dennison	Athow × HS94-4533
	2007	OHS 202	A95-581028 × PI 592. 926
	2008	OHS 303	U97-3114 × HS 98-3628
	2008	OHS 304	U97-3114 × HS 97-5261
	2008	OHS 305	A 98-980047 × Kottman
Food grade	2001	Ohio FG3	HS89-8843 × Ohio FG1
	2001	HS96-3136	HS 89-8843 × Ohio FG1
	2001	HS96-3140	HS 89-8843 × Ohio FG1
	2001	HS96-3145	HS 89-8843 × Ohio FG1
	2003	Ohio FG4	OhioFG1 × HS89-3078
	2003	Ohio FG5	OhioFG1 × HS89-3078
	2006	OHS201	OXR-96243 × OhioFG1
	2006	Wyandot	（NK S29-18 × PI 274. 421） × OhioFG1

3　Discussion and Conclusion

For the increase of yield genetic variability, soy-bean breeders have tried for many years to introgress PI germplasm into elite breeding populations. In the development of high‑ yielding cultivars, the use of PI germplasm generally has not been as successful as selection within elite populations. Although some PI germplasms have unique favorable alleles for yield, in a breeding population it was difficult to identify and select for those alleles. To identify these unique favorable alleles at quantitative trait loci（QTL）for yield in PI germplasm, molecular markers may be a useful tool. Also, using PI germplasm to cross with adapted elite cultivars and establish the interbreeding materials would be helpful for developing cultivars. For example, in the OSU breeding program PI399. 073 as a donator of Rps 8 gene to create breeding material HS5W‑ 362 which released as a germplasm in 2008.

Allard pointed out that modern elite cultivars and their close relatives are the most useful genetic resources, especially those adapted in the local environment or closely similar environments[30]. In the OSU breeding program, there were different elite entries as parents in different years, however the top elite cultivars were related with each other in pedigree, For example, Dennison is from Athow HS94‑ 4533, HS94-4533 was released as Kottman, which had a great inference on the program of OSU.

Although yield genetic gain is still being made in U. S. soybean, a lack of genetic diversity may limit breeding progress. Ininda et al. indicated that there was

still sufficient diversity among a large set of northern elite cultivars to maintain yield progress in United States[31]. A lack of diversity may also limit gain from selection. Compared with the populations derived from crosses of parents that are more related, the populations derived from biparental crosses of diverse northern parents were more likely to have higher genetic variance for yield[32-33]. Although populations of some elite × elite crosses had sufficient genetic variation for yield, the limited genetic diversity between parents rendered many crosses useless[32-33]. To maximize diversity within the elite U. S. gene pool multiple pools of diversity will need to be sampled[10,34-35]. In the OSU breeding program, it also existed a lack of genetic diversity, especially for the development of food grade cultivar, most of released cultivars were derived from OhioFG1.

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