



## Wide hybridization in soybean: A Review

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### ABSTRACT

The value of wild species in plant breeding has been known since long as these are valuable gene pools, offer opportunities for enhancing genetic variability and introgressing desired traits, particularly resistance to various stresses. Although, these wild relatives have largely remained under-utilized in grain legumes due to cross ability barriers, however, there are some examples of successful introgression of genes into the cultivated species from their wild relatives, particularly those constituting primary and secondary gene pools. The gene pools of most of the crop plants have less variability compared to the naturally occurring genetic variation of their wild progenitors. Genetic variability of the wild species of soybean could be used for the improvement of the cultivated ones.

### 1. Introduction

The genetic base of modern soybean cultivars is narrow since most of the parents used in crossing are from soybean gene pool 1 (GP 1). To guarantee future global food security and sustainable crop production, there exists a need to broaden the genetic base of soybean cultivars. The wild relatives of soybean are a potential reservoir of diversity for this purpose. The perennial *Glycine tomentella* (Hayata) and the annual *Glycine soja* (Sieb. and Zucc.) have been hybridized successfully with the domesticated soybean to produce breeding lines suitable for yield testing (Ma and Nelson, 2012; Kabelka *et al.*, 2004; Singh *et al.*, 1990). Annual *G. soja* is of particular interest for soybean breeding because it is thought to be the wild progenitor of cultivated soybean (Harlan and deWet 1971). These wild species are an excellent source of genetic variability, agronomically useful genes, biotic and abiotic stresses. These invaluable traits could be utilized to broaden the genetic base of soybean (Chung and Singh, 2008). These species also harbor some

undesirable genetic traits, for example, vining, lodging susceptibility, lack of complete leaf abscission, seed shattering and small black coated seeds. However, desirable ones could be sorted out during the course of selection in successive segregating generations. Of the two, the wild progenitors of soybean, *G. soja*, is the most easily accessible to breeders and has a wealth of diversity preserved in the USDA soybean collection (Carter *et al.*, 2004). Thus, it may be an excellent source of new agronomic genes and traits (Lee *et al.*, 2008). This wild soybean has the same chromosome number as the cultivated soybean, crosses freely via insect or manual hybridization, and the progeny are usually completely fertile (Singh and Hymowitz, 1988; Weber, 1950).

Only three species (*G. argyrea*, *G. canescens*, and *G. tomentella*) have been successfully hybridized with soybean; the F1 hybrids were rescued by embryo culture, were sterile and most researchers could not proceed beyond the amphidiploid stage, with the exception of Singh *et al.*, (1998). Weber (1950) reported seed size data on F1 and F2

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single plants from direct *G. max* and *G. soja* crosses and the calculated heterosis values were -35% MPH in the F1 and -45% MPH in the F2. Resulting F1 and F2 heterosis estimates in this type of cross were highly influenced by the poor undesirable traits of the wild soybean. Ertl and Fehr (1985) crossed two *Glycine soja* accessions with two high yielding *Glycine max* cultivars followed by five backcrosses to the respective *G. max* parent. The F2 plants from the backcross populations were visually examined. They observed significant variation among lines in each backcross generation for the traits, viz. maturity and seed coat colour. The mean yield and lodging resistance of the populations improved from the BC1 to the BC4 generations.

No line from the BC1 generation performed as well as the recurrent parent for all the traits. Three backcrosses to the cultivated parent were necessary to obtain a reasonable number of lines similar to the recurrent parent. The introgression of *G. soja* germplasm into the two soybean cultivars was not very effective method for increasing their yield potential. Carpenter and Fehr (1986) concluded that under no selection, to obtain a high frequency of agronomically acceptable segregates, three backcrosses were needed, which is equivalent to about six per cent *G. soja* alleles in derived populations. Singh and Hymowitz (1988) conducted the study with the objective of determining the genomic relationship between cultivated soybean and wild soybean (*Glycine soja*) of the subgenus soja, genus *Glycine*. Observations on crossability rate, hybrid viability, meiotic chromosome pairing and pollen fertility in F1 hybrids of *G. max* × *G. soja* and reciprocals elucidated that both species hybridized readily and set mature putative hybrid pods, generated vigorous F1 plants, had a majority of sporocytes that showed 18II + 1IV chromosome association at diakinesis and metaphase I and had a pollen fertility that ranged from 49.2% to 53.3%.

Bodanese *et al.*, (1996) employed a different culture strategy and obtained a greatly improved frequency of embryo rescue in inter-sub-generic soybean hybrids. Successful crosses were obtained in 31 different genotype combinations between 9 Brazilian soybean lines as the female parents and 12 accessions from *Glycine canescens*, *G. microphylla*, *G. tabacina* and *G. tomentella*. The hybrid largely unchanged up to the 20<sup>th</sup> day. A total of 90 putative hybrid embryos were rescued using a highly enriched B5 medium to nourish the newly dissected embryos. The growing embryos were then

placed in a high osmotic, modified B5 medium to induce maturation and dormancy. Dorney *et al.*, (1998) carried out interspecific crosses between *Glycine max* × *Glycine soja* and observed that estimates of heterosis over better parent were positive and significant for seeds per plant, pods per plant, pod bearing nodes per plant, plant height and seed yield per plant. Days to maturity, 100-seed weight and internodal length showed negative and significant heterosis over better parent. Days to flowering and number of primary branches exhibited negative heterosis over mid-parent and positive heterosis over better parent. Palmer *et al.* (2000) studied genetics and cytology of chromosome inversions in soybean germplasm. One type of chromosome aberration, an inversion, results in the reverse orientation of genes on a chromosome. Inversions are very useful in genetic linkage tests and have been important in the evolution of certain species of animals and plants.

In soybean, three accessions (PIs) with a paracentric chromosome inversion were identified. Their objective was to determine if the paracentric inversions identified in PI 597651 and PI 597652 (*Glycine max* cultivated species) and in PI 407179 (*G. soja* wild annual species) were identical. The *G. soja* inversion was backcrossed into *G. max* cultivar Hark. The two *G. max* accessions from China were intercrossed, and based on pollen staining F1 and F2 plants were considered identical in chromosome structure. However, the *G. soja* accession had a chromosome structure different from the two *G. max* accessions. Meiotic studies confirmed the presence of paracentric inversions. Crosses of PI 597651 with either cultivar Hark or Hark homozygous inversion gave F1 plants with two to three times as many meiotic cells with chromosome bridges as cells with laggards and fragments. However, crosses of PI 567652 with either cultivar Hark or Hark homozygous inversion gave F1 plants with about equal numbers of meiotic cells with bridges as cells with laggards and fragments. Therefore, cryptic structural differences between these two Chinese accessions might influence chromosome pairing, crossing over and segregation. This might explain the different meiotic behaviors in the crosses of the two Chinese accessions with Hark and Hark homozygous inversion. Yang and Wang (2000) crossed two semi-cultivated (*Glycine gracilis*) and four cultivated (*Glycine max*) cultivars and the resulting F1 and F2 progenies were evaluated for agromorphological and quality characters. The relationship among these traits between intraspecific and interspecific soybean crosses was analysed. Plants derived from interspecific crosses were taller and more vigorous and had more seeds and pods per plant, a lower seed: stem ratio and a lower 100-seed

weight than those from intraspecific crosses. In interspecific crosses, taller and more vigorous plants were closely associated with a lower seed: stem ratio. Nakayama and Yamaguchi (2002) evaluated the frequency of hybridization through pollen flow from the cultivated soybean to the wild soybean to assess the ecological risk of genetically modified crops. The flowering habits of three soybean cultivars and one wild accession were monitored. The seedlings of progeny seeds gathered from individual plants of the wild accession were used for isoenzyme analysis to identify whether they were hybrids or not. In 23 plants of the wild accession, four plants produced hybrids (the incidence of hybridization=17.4%). There was no specific direction in hybridization. The hybridization rate per maternal plant varied from 0 to 5.89% with a mean of 0.73% for all maternal plants. The results indicated that the natural hybrids were easily produced in a certain frequency by pollen flow from the cultivated soybean to the wild soybean under their simultaneous flowering with adequate pollinators.

Wang *et al.* (2004) developed five populations of BC2F4-derived lines using the *G. max* cultivar IA 2008 as a recurrent parent and the *G. soja* plant introduction PI 468916 as a donor parent. There were between 57 and 112 BC2F4-derived lines in each population and a total of 468 lines for the five populations. The lines were evaluated with SSR markers and in field tests for yield, maturity, plant height, and lodging. Marker data were analyzed for linkage and combined with field data to identify QTLs. Chaika *et al.*, 2005 attempted crosses between varietal soybean accessions, interspecific hybrids (*Glycine max* x *G. soja*) and forms of wild soybean. The occurrence in the F1 of recessive and dominant homozygous genes that do not segregate in the F2 and further generations can be explained by the presence of two major genes responsible for the type of growth. A breeding procedure with introgressive hybridization was developed and simple hybrids were inferior to the complex ones in terms of seed yield. The role of introgression of wild soybean genes into cultivated species and individual selection in increasing the seed yield of interspecific hybrids (*G. max* x *G. soja*) and [(*G. max* x *G. soja*) x *G. soja*] was reported. Lee *et al.* (2005) opined that wild soybean (*Glycine soja*) is a useful genetic resource for broadening the genetic background of cultivated soybean and indicated that a single backcross is required to recover a commercially desirable seed-coat color in a population derived from an interspecific cross of *G. max* x *G. soja* when KLG10084 is used as a *G. soja* parent. Therefore,

KLG10084 was considered to be a valuable gene source for overcoming the seed-coat color in interspecific crosses and was particularly useful for shortening soybean breeding program by reducing the number of backcrosses that are required. Siddhu *et al.*(2007) observed the effectiveness of number of pods per plant and dry matter yield per plant as independent selection criteria in early generations of two inter specific crosses of soybean, viz. (PK 472 x *Glycine soja*) x PK 472 and (Bragg x *Glycine soja*) x Bragg and were evaluated for yield improvement. Mean of the selected progenies for dry matter (88.45 and 82.58 g) and pods per plant (255 and 200) were higher as compared to the bulk (77.6 and 60.59 g) and (194 and 172) in respective crosses. Proportions of significantly superior progenies over the better parents were also substantially higher in selected progenies as compared to respective bulks. Barh *et al.* (2014) observed that seed yield had significant and positive correlation with number of pods per plant, number of primary branches per plant, harvest index and dry matter per plant. Tomar *et al.* (2014) found that seed yield had significant and positive correlation with number of primary branches per plant, number of pods per plant, 100-seed weight, harvest index and oil content. It may be summarized that several researchers have attempted to hybridize wild perennial *Glycine* species with the soybean but only few sterile inter-subgeneric F1 hybrid combinations have been reported (Newell *et al.*, 1987, Singh and Hymowitz, 1999). Thus far, only Singh *et al.*, (1990) have successfully produced backcross derived fertile progenies from the soybean and a wild perennial, *Glycine tomentella* (2n=78). Monosomic alien addition lines (MAALs) and modified diploid (2n=40) lines were isolated and identified (Singh *et al.*, 1998). The modified diploid lines could be screened for pests and pathogens. Riggs (1998) reported the introgression of SCN resistance from *G. tomentella* into modified derived diploid soybean lines. These studies set the stage for the exploitation of perennial germplasm to broaden the genetic base of the cultivated soybean.

## 2. References

- Barh A, Pushpendra, Singh K, Gupta MK and M. Joshi, 2014. Genetic divergence and correlation studies on bhat (Black seeded soybean). Mitigating productivity constraints in soybean for sustainable agriculture. Proceedings of SOYCON 2014: International Soybean Research Conference. Society for Soybean Research and Development, Directorate of Soybean Research, Indore (India): p 111-112
- Bodanese MH, Lauxen MS, Richter SNC, Cavalli MS, Lange CE, Wang PJ and CY. Hu, 1996. Wide hybridization between Brazilian soybean cultivars and wild perennial relatives. *Theoretical and Applied Genetics* 93: 703-709
- Carpenter JA and WR. Fehr, 1986. Genetic-variability for desirable agronomic traits in populations containing *Glycine soja* germplasm. *Crop Science* 26: 681-686
- Carter TEJ, Nelson RL, Sneller CH and ZL. Cui, 2004. Genetic diversity in soybean. p. 303-416. In H.R. Boerma, and J.E. Specht (eds.) Soybeans: Improvement, Production, and Uses. Agronomy Monographs 3rd ed. No. 16 ed. ASA-CSSA-SSSA, Madison, WI, USA
- Chaika AK, Ala AY and VA. Tilba, 2005. Use of wild soybean *Glycine soja* in introgressive breeding. *Russian Agricultural Sciences* 22: 16-19
- Chung G and RJ. Singh, 2008. Broadening the Genetic Base of Soybean: A Multidisciplinary Approach. *Critical Reviews in Plant Sciences* 27: 295-341
- Dogney ML, Gour VK and AK. Mehta, 1998. Heterosis of quantitative characters in interspecific crosses of soybean. *Advances in Plant Sciences* 11: 263-267
- Ertl DS and WR. Fehr, 1985. Agronomic performance of soybean genotypes from *Glycine max* x *Glycine soja* crosses. *Crop Science* 25: 589-592
- Harlan JR and de Wet JMJ., 1971. Toward a rational classification of cultivated plants. *Taxon* 20: 509-519
- Kabelka EA, Diers BW, Fehr WR, LeRoy AR, Baianu IC, You T, Neece DJ and RL. Nelson, 2004. Putative alleles for increased yield from soybean plant introductions. *Crop Science* 44: 784-791
- Lee J, Yu J, Hwang Y, Blake S, So Y, Lee G, Nguyen HT and JG. Shannon, 2008. Genetic diversity of wild soybean (*Glycine soja* Sieb. and Zucc.) accessions from South Korea and other countries. *Crop Science* 48: 606-616
- Ma J and R. Nelson, 2012. Evaluation of fertile lines derived from the hybridization of *Glycine max* and *G. tomentella* (2n=78) a wild, perennial relative. M.Sc. thesis, University of Illinois at Urbana-Champaign, Madison, WI, USA
- Nakayama Y and H. Yamaguchi, 2002. Natural hybridization in wild soybean (*Glycine max* subsp. *soja*) by pollen flow from cultivated soybean (*Glycine max* subsp. *max*) in a designed population. *Weed Biology and Management* 2: 25-30
- Newell CA, Delannay X and ME. Edge (1987). Interspecific hybrids between the soybean and wild perennial relatives. *Journal of Heredity* 78: 301-306
- Palmer RG, Sun H and LM. Zhao, 2000. Genetics and cytology of chromosome inversions in soybean germplasm. *Crop Science* 40: 683-687
- Riggs RD., 1998. Possible transfer of resistance to *Heterodera glycines* from *Glycine tomentella* to *Glycine max*. *Journal of Nematology* 30: 547-552
- Siddhu P, Pushpendra, Singh K, Singh BV and MK. Gupta, 2007. Early generation selection for pods per plant and dry matter yield in interspecific crosses of soybean. *Soybean Research* 20: 1-7
- Singh RJ, Kollipara KP and T. Hymowitz, 1990. Backcross-derived progeny from soybean and *Glycine tomentella* hayata intersubgeneric hybrids. *Crop Science* 30: 871-874
- Singh RJ, Kollipara KP and T. Hymowitz, 1998. Monosomic alien addition lines derived from *Glycine max* (L.) Merr., and *Glycine tomentella* Hayata: production, characterization and breeding behaviour. *Crop Science* 38: 1483-1489
- Tomar K, Singh K, Pushpendra, Gupta MK and A. Yadav, 2014. Studies on genetic divergence in advanced breeding lines of soybean [*Glycine max* (L.) Merrill]. Mitigating productivity constraints in soybean for sustainable agriculture. Proceedings of SOYCON 2014: International Soybean Research Conference. Society for Soybean Research and Development, Directorate of Soybean Research, Indore (India): pp 109

- Wang D, Graef GL, Procopiuk AM and BW. Diers, 2004. Identification of putative QTL that underlie yield in interspecific soybean backcross populations. *Theoretical and Applied Genetics* 108: 458-467
- Weber CR., 1950. Inheritance and interrelation of some agronomic and chemical characters in an interspecific cross in soybeans, *Glycine max* x *G. ussuriensis*. Iowa Agric Expt Sta Res Bull 374: 765-816
- Yang Q and JL. Wang, 2000. Agronomic traits correlative analysis between interspecific and intraspecific soybean crosses. *Soybean Genetics Newsletter* 27: 5-8