

## Short Communication

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### The Genomic Relationships Among *Glycine soja* Sieb. and Zucc., *G. max* (L.) Merr. and '*G. gracilis*' Skvortz.

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With one figure and one table

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#### Abstract

The objective of this study was to establish genomic relationships among *G. soja*, *G. max*, and '*G. gracilis*' based on cytogenetic analyses. All three species hybridized readily, though pod set was low (2.2 %—5.3 %); seeds produced viable, vigorous and totally fertile  $F_1$  plants which were normal in meiotic pairing. This suggests that all three species belong to one gene pool and should be considered as forms of one species.

**Key words:** *Glycine* spp. — gene pool — interspecific hybrids — cytogenetic analysis

The genus *Glycine* Willd. has been divided into two subgenera. The subgenus *Glycine* consists of 12 wild perennial species and they carry mainly diploid ( $2n = 40$ ) and tetraploid ( $2n = 80$ ) cytotypes. The subgenus *Soja* (Moench) F. J. Herm. contains the cultivated soybean, *G. max* (L.) Merr. and its wild progenitor *G. soja* Sieb. and Zucc. (HERMANN 1962). Both species are annual and carry  $2n = 40$  chromosomes. A weedy, intermediate form between *G. max* and *G. soja* with  $2n = 40$  also occurs in the wild and SKVORTZOW (1927) named this variant *G. gracilis* Skvortz. However, HERMANN (1962) removed '*G. gracilis*' from the species rank based on classical taxonomy and incorporated it into *G. max*.

Cytogenetic investigations have revealed that *G. max* and *G. soja* are genomically similar (SINGH and HYMOWITZ 1988). KARASAWA

(1952) reported fertile hybrid plants between *G. max* and '*G. gracilis*', though meiotic pairing was not studied, and a *G. soja* × '*G. gracilis*' cross was not successful. In this paper we report crossability rate, meiotic pairing, pollen fertility and seed set among *G. soja*, *G. max* and '*G. gracilis*' crosses.

Two soybean cultivars, Bonus and Essex, and an accession each of *G. soja* (PI 468916) and '*G. gracilis*' (PI 81766) selected for this study were supplied by R. L. Bernard, USDA/ARS, Urbana/IL. *Glycine soja* accession PI 468916 was included in the crossing program because it does not carry interchanged chromosomes (PALMER et al. 1987). Plant growing conditions, hybridization technique and cytological procedures described by SINGH and HYMOWITZ (1985 a) were used. All the hybrids were identified morphologically and cytologically.

Crossability barrier was not observed in hybrids among *G. soja*, *G. max*, and '*G. gracilis*' because all the putative crossed pods matured in the plants (Table 1). Hybrid seed germinated normally;  $F_1$  plants carried expected  $2n = 40$ , were vigorous in their vegetative growth, were intermediate for several morphological traits such as leaf size, pod length and seed size and color and were totally pollen and seed fertile.

Meiotic pairing in *G. max* × '*G. gracilis*' and the reciprocal crosses was apparently normal, a majority of the sporocytes showed 20 bivalents at diakinesis and metaphase I and chromosome

Table 1. Parents, crossability rate (no. of mature pods set/no. of florets pollinated, with percent pods set in parenthesis), no. of  $F_1$  plants studied, meiotic pairing at diakinesis, pollen fertility (%) and seed set in interspecific  $F_1$  hybrids

Crosses	Crossability	No. $F_1$ plants studied	Chromosome association		Total PMC	Pollen fertility (%)	Seed set
			Univalents	Bivalents			
Essex $\times$ PI 81766 <sup>a</sup>	2/38 (5.3)	2	1.0 (0—4)	19.5 (18—20)	44	86.2	Fertile
PI 81766 $\times$ Essex	3/76 (4.0)	2	0.3 (0—4)	19.9 (18—20)	154	82.5	Fertile
Bonus $\times$ PI 468916	1/28 (3.6)	1	0.1 (0—2)	19.9 (19—20)	69	91.8	Fertile
PI 81766 $\times$ PI 468916	1/45 (2.2)	1	0.8 (0—6)	19.6 (17—20)	46	<sup>b</sup>	Fertile

<sup>a</sup> PI = Plant Introduction number

<sup>b</sup> Cleistogamous pods

migration at anaphase I was normal (Fig. 1a, 1b). In *G. max*  $\times$  *G. soja* cross, an average chromosome association (range) was 0.1 I (0—2) + 19.9 II (19—20) and pollen fertility was 91.8 % (Table 1). This suggests that PI 468916 (*G. soja*) is devoid of translocated chromosomes. This confirms the results of PALMER et al. (1987).

Hybridization of '*G. gracilis*' with *G. soja*, reported for the first time (R. G. PALMER, personal communication), resulted in one mature pod with 2 seeds of the 45 florets pollinated. Both seeds germinated normally, however, one seedling died at an early stage of plant growth and the other seedling reached maturity. At diakinesis, number of univalents

ranged from 0 to 6 (mean 0.8) and the number of bivalents ranged from 17—20 (mean 19.6) and no apparent chromosomal structural changes were recorded in the later meiotic stages. Pollen fertility was not ascertained because of cleistogamous flowers and pod set was completely normal.

In conclusion, this study demonstrates the absence of crossability, cytological and genetical barriers among *G. soja*, *G. max*, and '*G. gracilis*', therefore all three carry the similar genome, GG (SINGH and HYMOWITZ 1985b, 1988), belong to one gene pool — GP 1 of HARLAN and DE WET (1971) and should be considered as forms of one species, *G. max* (LACKEY 1977).

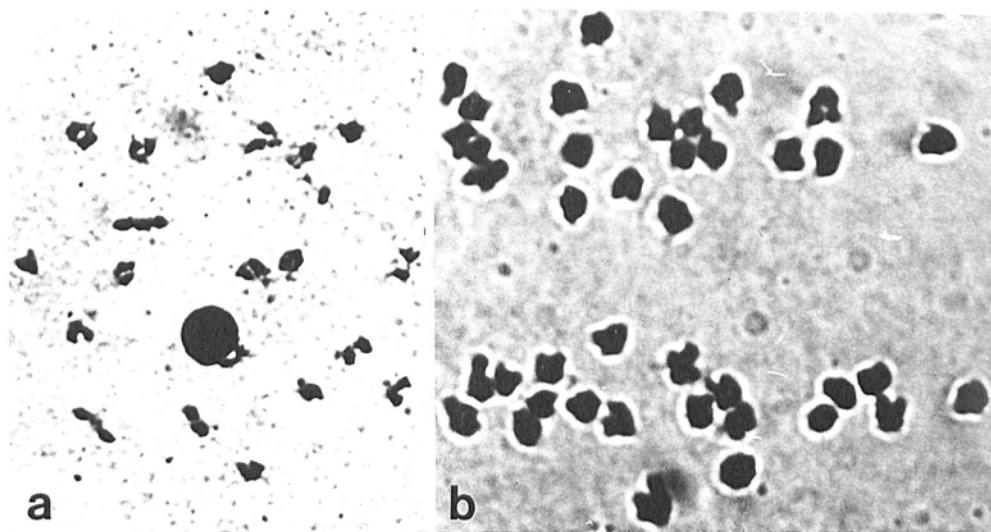


Fig. 1a, b. Meiosis in *G. max* cv. Essex  $\times$  '*G. gracilis*' PI 81766. a. Diakinesis showing 20II; b. Anaphase I with 20—20 chromosome migration

## Zusammenfassung

### Verwandtschaftsbeziehungen der Genome von *Glycine soja* Sieb. und Zucc., *G. max* (L.) Merr. und '*G. gracilis*' Skvortz.

Es war Ziel dieser Untersuchung, anhand von zytologischen Analysen die Verwandtschaftsbeziehungen zwischen den Genomen von *G. soja*, *G. max* und '*G. gracilis*' aufzuzeigen. Alle drei Arten ließen sich gut miteinander kreuzen. Wenn auch der Hülansenatz gering war (2,2—5,3 %), erwuchsen doch aus den Samen lebensfähige, kräftige und vollständig fertile  $F_1$ -Pflanzen mit normaler Chromosomenpaarung in der Meiose. Es liegt nahe, daß alle drei Arten einem Genpool angehören; sie sollten daher als Formen derselben Art *G. max* angesehen werden.

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