

“Genome studies in Soybean” (*Glycine.max.L.*)

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DOI: <https://doi.org/10.63001/tbs.2025.v20.i01.pp481-483>

KEYWORDS

Genome,
Correlation,
Coefficient,
Chromosome Mapping,
Recombination

Received on:

04-01-2025

Accepted on:

04-02-2025

Published on:

08-03-2025

ABSTRACT

Soybean (*Glycine max*) is a vital crop for human nutrition and animal feed. Understanding the soybean genome is essential for improving its yield, quality, and disease resistance. Genome studies in soybean have accelerated in recent years, driven by advances in sequencing technologies and bioinformatics tools. The chromosome number of soybean and other diploid *Glycine* species is $2n=40$, which is doubled relative to its phaseoloid legume relatives (e.g. *Phaseolus*, *Vigna*), most of which are $2n = 20$ or $2n = 22$. Soybean has 20 chromosome pairs that are derived from at least two rounds of genome wide duplication or polyploidy events although, cytogenetically, soybean behaves like a diploid and has disomic inheritance for most loci. In addition, as a diploid evolved from palaeotetraploid, soybean has a highly duplicated genome with about 75% predicted genes maintaining multiple copies, which leads to high genetic redundancy and increases the complexity of elucidating soybean gene function (Schmutz et al., 2010).

Chromosomes studies in soybean were analysis carried out of 18 genotypes of soybean phenotypic coefficient of variation was slightly higher than that of genotype coefficient of variation for all the traits. Present investigation studied the chromosome behavior showed the Generally 40 chromosome in soybean but in tabacina (Labill) Benth contain 80, tomentella Hayata, 78 and tomentella Hayata. 33 chromosome are found The genus *Glycine* consists of two subgenera, *Glycine* and *Soja* (Moench) F. J. Herm. The subgenus *Soja* comprises the cultivated soybean *G. max* (L.) Merrill and its annual wild progenitor, *G. soja* Sieb and Zucc (also known as *Gussuriensis*). These two species have diploid chromosome number, $2n=40$. Prior to 1983, only seven species were recognized in the subgenus *Glycine*. Tindale and Craven added eight new species of *Glycine* from northwestern Australia. The subgenus *Glycine* is thus, composed of 15 wild perennial species (show in Table). Out of these two species namely *G. tabacina* ($2n=40, 80$) and *G. tomentella* ($2n=38, 40, 78, 80$), are polyploidy forms, whereas the other 13 species are diploids ($2n=40$). Hymowitz and Singh, (1992) have assigned genome symbols to several of the species of both the subgenera

INTRODUCTION

The soybean, soy bean, or soya bean (*Glycine max*) is a species of legume native to East Asia, widely grown for its edible bean, which has numerous uses. Traditional unfermented food uses of soybeans include soy milk, from which tofu and tofu skin are made. Fermented soy foods include soy sauce, fermented bean paste and tempeh. Fat-free (defatted) soybean meal is a significant and cheap source of protein for animal feeds and many packaged meals. For example, soybean products, such as textured vegetable protein (TVP), are ingredients in many meat and dairy substitutes.

Soybeans contain significant amounts of phytic acid, dietary minerals and B vitamins. Soy vegetable oil, used in food and industrial applications, is another product of processing the soybean crop. Soybean is a common protein source in feed for farm animals that in turn yield animal protein for human consumption. Soybean was known to Indians since ages. Since soybean was a part of Indian way of life, the present advent of

the crop can be best called as its renaissance. Black-seeded soybean was sporadically grown under the names like Bhatt, Bhatmash or Kalitur in north-Indian Kumaon and Garhwal hills of Uttar Pradesh and scattered pockets of the central India (now Madhya Pradesh). Soybean was being utilized as a source of food in the Kumaon hills and also in the Naga Hills. The earlier documents established that the plant was known to the Angami Nagas as Tsu Dza, a name not unlike *Soja*. The fact that this cultivated plant possesses, even among the aboriginal tribes, names that are original and in no way modern derivatives, points to an ancient cultivation (Watt, 1890). Introduction of soybean in the country dates back to 1000 A. D. It is believed that the crop entered in northern part of Indian sub- continent from central China through the silk-route running across the Tibetan Plateau (Hymowitz and Kaizuma, 1981) and subsequently reached northern India from north-west or directly through northeastern region of the country. Although the origin and early history of soybean is not accurately known, it is believed

that the origin of soybean dates back to 2800 BC in China. The evidences for the antiquity of soybean from the pictographically analysis of the archaic Chinese word of soybean 'Shu', the book of Odes, and bronze inscriptions point to its first domestication in the eastern half of northern China around the 11th century BC (Hymowitz, 1970). The lower and middle yellow river valley is believed to be the primary centre and Manchuria the secondary centre of origin of soybean. Chang Ruzhen, (1989) discussed different hypotheses suggesting a centre of origin in any of four regions: 1. the northeast of China 2. Yangtze River valley and southern part of China, 3. Lower and middle yellow river valley and the Yangtze River valley. It is now widely accepted that the lower and middle yellow river valley is the main centre of origin of soybean. *Glycine soja* Sieb and Zucc. is the probable progenitor of cultivated soybean. In Europe, soybean was known in the 17th century as an exotic plant from the orient. However, it was not until 1712 that the Western world finally recognized soybean as a food plant (Brocks, 1965)

1. Cytogenetic Mapping

Cytogenetic mapping involves the physical mapping of genes and genetic markers to specific chromosomes. In soybean, cytogenetic mapping has been used to identify genes controlling traits such as seed protein content, oil content, and disease resistance.

2. Chromosome Pairing and Recombination

Chromosome pairing and recombination are critical processes during meiosis that determine the genetic diversity of soybean. Studies have shown that soybean chromosomes exhibit a high

degree of pairing and recombination, which can be exploited for breeding purposes.

3. Implications for Breeding

Chromosome studies have significant implications for soybean breeding. By understanding the genetic organization of soybean, breeders can develop more efficient breeding strategies to improve yield, quality, and disease resistance.

MATERIALS AND METHODS

The cultivated soybean, *Glycine max* (L.) Merrill is a member of the family leguminosae and subfamily papilionaceae (Fabaceae). The genus *Glycine* consists of two subgenera, *Glycine* and *Soja* (Moench) F. J. Herm. The genus *Glycine* consists of two subgenera, *Glycine* and *Soja* (Moench) F. J. Herm in the present investigation were procured from Mahatma Phule Krishi Vidyapeeth, Rahuri (Maharashtra) both the cultivars are widely cultivated in Maharashtra. Meiotic studies were made in pollen mother cells from young buds of suitable size the most suitable time for collection is found to be between 8:30 A: M and 11:00A:M. The buds of suitable size were directly fixed in 1:3 Acetic alcohol or in carneys' fluid (Absolute alcohol 6 parts: Chloroform 3 parts: Glacial acetic acid 1parts). After 18 hours of fixation buds were washed in 70% alcohol and stored in same grade on alcohol at 10 degree Celsius. The fixed buds were crushed in drop of 2% aceto-orcin solution. The cytological analysis were made from temporary slide and suitable cells were photographed on 35 mm film with Olympus-PM-6 Microscopic camera at 50 X 12 X and 100 X 12 X magnification.

Table - Species of *Glycine*, their chromosome number and genome (s)

Sr. No	Soybean Species	Chromosome number(2N)	Genomes
1.	<i>alternaria</i> Tind	40	- G
2.	<i>argyrea</i> Tind	40	A2A2 G.
3.	<i>canescens</i> F. J. Herm	40	AA G.
4.	<i>clandestine</i> Wendt	40	A1A1 G.
5.	<i>curvata</i> Tind.	40	C1C1 G.
6.	<i>cyrtioiba</i> Tind.	40	CC G.
7.	<i>falcate</i> Benth.	40	FF G.
8.	<i>G. albicans</i> Tind and Craven	40	- G.
9.	<i>hirticaulis</i> Tind and Craven	80	- G.
10.	<i>lactovilens</i> Tind and craven	40	- G.
11.	<i>latifolia</i> (Benth). Nowell and Hymowitz	40	B1B1 G.
12.	<i>latrobeana</i> (Meissn.) Benth	40	A3A3 G.
13.	<i>microphylla</i> (Benth). Tind	40	BB G.
14.	Subgenus <i>Glycine</i> (x=10)	-	-
15.	<i>tabacina</i> (Labill) Benth	80	Complex G
16.	<i>tabacina</i> (Labill) Benth.	40	B2B2 G.
17.	<i>tomentella</i> Hayata	40	DD G.
18.	<i>tomentella</i> Hayata	78	Complex
19.	<i>Tomentella</i> Hayata.	33	EE G

20 chromosomes of the haploid complement (2n=40) comprise 2 large, 14 intermediate and 4 small chromosomes (Fukuda, 1933). Sen and Vidyabhusan, 1960 identified two metacentric six sub-metacentric and one sub- telocentric (satellite) chromosomes the remaining 11 chromosomes were characterized into classes based on chromosome length and arm ratio. Four satellites, consisting of two each on a pair of long and short chromosomes, have been reported in *G. max* and also in a 40 chromosome *G. soja* (Zheng et al., 1984). Halvankar and Patil, (1990) studied karyotypes of six species of the genus *Glycine* and found that chromosomes were median to sub median. Diploid species had one pair of satellite chromosomes, whereas tetraploid species, namely *G. tabacina* and *G. tomentella* had two pairs of satellite chromosomes. To study chromosomes of soybean, techniques used by Zheng et al.,(1984) for root-tip cells and for mitotic cells from very young leaves have been found suitable. The pretreatment of cells with 8-hydroxyquinoline gives better clarity of chromosome constrictions than that obtained by par dichlorobenzene. Although Giemsa staining appears to have limited scope in soybean chromosome identification, four groups of soybean chromosomes have been distinguished using this

technique. Intra- subgeneric crosses among the subgenus *Soja* are possible except in some combinations where a degree of sterility is obtained in the hybrid. Members of the subgenus *Glycine* possess many desirable agronomic characters like resistance to insect-pests and diseases, drought and salt tolerance, which are not readily found in the subgenus *Soja*. Inter-sub-generic crosses involving the culti gen are however, difficult to realize. Some success has been achieved in crossing *G. tomentella* hayata with the cultigens. Selective elimination of *G. tomentella* chromosome complement, subsequent to introgression of some genes in the cultigens genome, has been indicated in such hybrids (Singh et al., 1990).

CONCLUSION

Chromosome studies have greatly advanced our understanding of the genetic makeup of soybean. These findings have significant implications for soybean breeding and genetic improvement. Further research is needed to fully exploit the genetic potential of soybean.

In present investigation were procured from Mahatma Phule Krishi Vidyapeeth, Rahuri (Maharashtra) both the cultivars are widely cultivated in Maharashtra to begin with pilot experiments

were conducted. *G. tomentella* Hayata 80 Complex *G. soja* Sieb. And Zucc. 40 GG *G. max* (L.) Merr 40 GG Mitotic chromosomes in soybean have been studied by several workers. Four satellites, consisting of two each on a pair of long and short chromosomes, have been reported in *G. max* and also in a 40 chromosome *G.* karyotypes of six species of the genus *Glycine* and found that chromosomes were median to sub median. Diploid species had one pair of satellite chromosomes, whereas tetraploid species, namely *G. tabacina* and *G. tomentella* had two pairs of satellite chromosomes. To study chromosomes of soybean, techniques used by Zheng et al., (1984) for root-tip cells and for mitotic cells from very young leaves have been found suitable.

ACKNOWLEDGMENT

The author is thankful to Head of Department of Botany, Padmashri Vikhe Patil College Pravaranagar, and Principal of P.V.P. College Pravaranagar who provided necessary facilities during research work.

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