

GENETICS OF REPRODUCTIVE PHASE DURATION IN SOYBEAN

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ABSTRACT

Genetics of reproductive phase duration (first flower to maturity) was studied in two soybean crosses. In both crosses, the duration of reproductive phase was determined by one major gene, long reproductive phase being dominant to short reproductive phase.

Key words: *Glycine max*, soybean, reproductive phase.

The length of reproductive phase is an important developmental trait [1–4] that could be an effective selection criterion for improvement in seed yield [5]. At present, the major objective in breeding soybeans is the development of early maturing varieties (100–110 days duration) to increase cropping intensity and the total production, especially in the tropics and subtropics. This can be achieved by combining optimum durations of vegetative and reproductive phases within a certain maturity duration. Smith and Nelson [5] reported positive relationship between total reproductive period and seed yield in soybean. Hinson and Hartwig [6] suggested that genotypes with 100 days of growing seasons in the tropics should have a longer time from sowing to flowering (vegetative phase) and shorter time from flowering to maturity (reproductive phase) in soybeans. In the light of such observations, it was considered desirable to obtain information on the genetics of reproductive phase duration in soybean. This is particularly relevant as reports on the genetics of vegetative phase (days to first flower) are available [3, 7–12] but information on the genetics of reproductive phase duration is still not available.

MATERIALS AND METHODS

Three diverse parents were crossed to generate two F₁ populations viz. Bragg (long reproductive phase and short vegetative phase) × Kalitur (short reproductive phase and long vegetative phase) and Kalitur (short reproductive phase and long vegetative phase) ×

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UPSM 534 (long reproductive phase and short vegetative phase). The F₂ seeds of the two crosses (500–800 seeds/cross) were received from the All India Coordinated Research Project on Soybean. Progenies of eighty random F₂ plants in each cross were advanced to F₃ generation. The parents (four rows each), F₁s (one row per cross), and F₃s (78 in the cross Bragg x Kalitur and 74 lines in the cross Kalitur x UPSM 534) were raised together. Each F₁ was planted between four rows of the two parents on either side. The genotype of each randomly selected F₂ plant was ascertained on the basis of its F₃ progeny. The reproductive phase duration was determined as the number of days taken from first open flower to maturity recorded on individual plants of parental, F₁ and F₂ generations. However, in F₃ generation, reproductive phase duration was recorded as range in a particular F₃ line. The data on reproductive phase duration based on daily observations on individual plant in the parental, F₁ and F₂ generations of two crosses were used to classify genotypes into distinct groups. The F₃s lines were classified into true breeding short-reproductive phase, true breeding long-reproductive phase, and segregating type in relation to the parental ranges. The χ^2 test was applied to determine goodness of fit of the segregation ratios obtained in F₂ and F₃ generations.

RESULTS AND DISCUSSION

Reproductive phase duration in the F₁ generation of two crosses. Bragg x Kalitur and Kalitur x UPSM 534, was much higher than the midparental value and almost equal to that of the parents having long reproductive phase (Table 1). This indicates complete dominance of long reproductive phase over short phase. A bimodal frequency distribution observed for reproductive phase in the F₂ generation of these two crosses gave a good fit to 3 (long phase) : 1 (short phase) segregation ratio, which was

Table 1. Range and mean duration of reproductive phase in the parents and F₁s of two soybean crosses

Cross	Parent or generation	Reproductive phase, days	
		range	mean
Bragg x Kalitur	Bragg	60–64	63.0
	Kalitur	55–57	56.0
	F ₁	59–67	63.0
Kalitur x UPSM 534	Kalitur	55–57	56.0
	UPSM 534	58–61	60.0
	F ₁	54–60	59.0

further confirmed by the F₃ progeny test. These results indicate involvement of a single gene in the genetic control of reproductive phase duration (Table 2). It was therefore concluded that short reproductive phase was recessive in *Glycine max*. However, in *Phaseolus vulgaris*, long blooming period (partitioned length of reproductive phase) was reported to be dominant [13] although the segregating generation showed continuous variation instead of discrete variation as reported here for soybean.

The qualitative nature of inheritance of reproductive phase duration, as revealed by the present investigation, will facilitate breeding of soybean varieties having longer

Table 2. Segregation ratios for reproductive phase duration in two crosses of soybean

Cross	Generation	Observed segregation			Total	Expected ratio	χ^2	P
		long phase	segregating	short phase				
Bragg x Kalitur	F ₂ (plants)	149	—	43	192	3:1	0.694	0.5-0.3
	F ₃ (lines)	18	44	16	78	1:2:1	1.385	0.7-0.5
Kalitur x UPSM 534	F ₂ (plants)	143	—	58	201	3:1	1.593	0.3-0.2
	F ₃ (lines)	18	44	12	74	1:2:1	3.621	0.2-0.1

reproductive phase for early and normal sowing in the subtropics [3] and shorter reproductive phase for normal sowing in the tropics [6].

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