

GENETIC STUDIES OF FLOWERING AND MATURITY IN INTERSPECIFIC CROSSES OF SOYBEAN

S. S. MALIK^{*} AND B. B. SINGH

Department of Plant Breeding, G. B. Pant University of Agriculture and Technology
Pantnagar 263145

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ABSTRACT

Interspecific crosses between *Glycine max* (L.) Merr. and *G. formosana* (L.) Merr. showed a wide variability for days to flowering, maturity and duration from flowering to maturity. The results indicate that the character days to flowering was governed by polygenes. Earliness in F₂ may be due to the characters less number of days to flowering, and shorter period from flowering to maturity contributed by *G. max* and *G. formosana*, respectively. Heritability of both these characters is high, showing less environmental influences.

Key words: Soybean, interspecific crosses, earliness, heritability.

Interspecific hybridization has been used for the improvement of crop plants by transferring the desirable genes and chromosomes from the wild to cultivated species [1–3]. Although the previous studies reported heritability of maturity in interspecific crosses, no definite conclusion was drawn regarding expression of the genes responsible for days to flowering and maturity. The present study therefore aims to study the extent and nature of genetic variability and heritability for days to flowering, maturity, and duration of the flowering–maturity period in interspecific crosses between *Glycine max* and *G. formosana*.

MATERIALS AND METHODS

Three varieties of cultivated soybean (*G. max*), i.e. UPSM-534, UPSM-533 and Hardee, were crossed with the wild species *G. formosana*. Three F₂ populations (UPSM-534 x *G. formosana*, UPSM-533 x *G. formosana*, and Hardee x *G. formosana*) along with the parents were used for the estimation of variability and heritability for days to flowering, days to maturity, and length of flowering–maturity period. Observations were recorded on individual plant basis during kharif 1978. Twenty random plants from the parents and 1000 plants from each

^{*}Present address: NBPGR, Base Centre, CRR I Campus, Cuttack 753006.

F₂ population per replication in randomized block design were observed for days to flowering, days to maturity and days from flowering to maturity.

Phenotypic variability was studied from the mean, range, and coefficient of variation for the above three characters. Heritability in broad sense (H_b^2) for the three characters was estimated using the mean of parental and the F₂ variances. Genotypic variance (σ_G^2) was calculated by subtracting the average variance of parents (σ_E^2) from the variance of F₂ (σ_P^2) as follows:

$$H_b^2 = \frac{\sigma_G^2}{\sigma_P^2} = \frac{\sigma_P^2 - \sigma_E^2}{\sigma_P^2}$$

RESULTS AND DISCUSSION

The range, coefficient of variability, and heritability of F₂ populations were very high for days to flowering and maturity. Mean number of days to flowering and maturity in F₂ were less than the midparent values (Table 1) due to transgressive segregation towards earliness or due to the partial dominance of earliness. Large portion of F₂ population matured earlier than the parents, although higher limit of F₂ corresponded to the upper limit of the late maturing parent except in the cross Hardee x *G. formosana*. Similar results were reported earlier [1, 3, 4, 5].

Table 1. Range, mean, coefficient of variation (CV), and heritability (H_b^2) for three characters in soybean

Population	Days to flowering				Days to maturity				Days from flowering to maturity			
	range	mean	C.V.	H_b^2	range	mean	C.V.	H_b^2	range	mean	C.V.	H_b^2
<i>G. formosana</i>	69-77	74.1	1.30	—	91-104	101.7	0.50	—	23-33	27.6	1.75	—
UPSM-534	37-43	40.7	0.93	—	89-96	91.4	0.80	—	48-57	50.7	1.70	—
F ₂ (UPSM-534 x <i>G. formosana</i>)	43-61	50.4	7.06	0.85	80-104	88.8	5.22	0.88	26-53	38.4	10.96	0.85
UPSM-533	38-45	43.2	2.11	—	83-89	86.4	0.57	—	40-47	43.1	0.16	—
F ₂ (UPSM-533 x <i>G. formosana</i>)	43-60	51.4	7.16	0.77	79-204	88.8	6.64	0.92	30-38	37.5	10.77	0.91
Hardee	42-47	44.1	0.68	—	100-110	105.4	0.54	—	57-66	61.3	0.99	—
F ₂ (Hardee x <i>G. formosana</i>)	48-65	53.3	5.07	0.81	85-106	95.9	4.03	0.88	33-50	41.5	8.37	0.84

The pattern for the length of flowering-maturity period was different in the three F₂ populations. In the cross UPSM-534 x *G. formosana*, the range in F₂ was towards lower side but in UPSM-533 x *G. formosana* it shifted towards higher side. In the cross Hardee x *G. formosana*, it was between the parental values. However, the mean values of F₂

populations were very close to the midparental values. The heritability was very high in all crosses.

RELATIONSHIP AMONG DAYS TO FLOWERING, MATURITY AND FLOWERING-MATURITY PERIOD

The extreme types were not recovered in F₂ despite normal distribution. The data indicate that a large number of genes must be responsible for governing this trait. The mean number of days to maturity in all F₂ populations was less than both the parents, except in the cross involving UPSM-533. The F₂ distribution skewed towards early parent due to partial dominance of the genes responsible for earliness. The mean duration from flowering to maturity in all F₂ populations was very close to the midparental values. Although the range was wider as compared to days to flowering in all crosses, the F₂ population was normally distributed and indicated that a large number of genes govern this character, showing no dominance effect. In general, the mean number of days to maturity in most of the F₂ populations was less as compared to either parent. Early maturity is the total result of less number of days to flowering and shorter period from flowering to maturity. This study further suggests that the number of days taken up to flowering and from flowering to maturity are governed by independent sets of genes and various combinations involving these two phases should be possible reasons for giving genotypes with different maturity periods. In case of F₂ segregation in all crosses, early maturity was dominant due to the recombination of genes responsible for fewer days to flowering from *G. max* and those for shorter flowering-maturity period from *G. formosana*. It is thus possible to develop very early lines combining these two traits. Similar recombinants were obtained by Nelson [6]. The high heritability values indicate less environmental influence on these characters.

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