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HERITABILITY AND GENETIC ADVANCEMENT ANALYSIS FOR MAJOR YIELD TRAITS IN SOYBEAN [*GLYCINE MAX* (L.) MERRILL]

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ABSTRACT

The present study was carried out in randomized block design with three replications to examine 20 advanced breeding lines created as part of the All India Coordinated Research Project on Soybeans at RAK College of Agriculture, Sehore (M.P.), India. Heritability estimates in broad sense, include variances due to all types of gene expression. Heritability, which measures the relationship between genotype and phenotype, is an important criterion for success in breeding program, since selective capacity in a population depends upon the amount of heritable variability present. Under present investigation heritability of 30 genotypes of soybean for yield and its contributing traits have been determined. The pooled analysis of variance carried out to know the response of different characters. The high heritability was observed for most of the characters in all the environments except number of primary branches per plant in E-2. Selection of genotypes for these traits may be effective in aforesaid environments. There was noticeable variance in every attribute according to estimates of genetic advancement in various contexts. However, no such trend was discovered. Under E-1, considerable genetic advancement through selection might be anticipated in terms of plant height, number of pods per plant, and number of seeds per plant. It is proposed that varying degrees of genetic advancement for certain qualities could be anticipated in various contexts.

Key words : Heritability, Heredity, Genetic advancement, Stability, association.

Introduction

Raised as a rainfed crop, soybeans in *Rabi* have a large productivity gap because of their diverse surroundings. Therefore, at high sustainable advantages, development stable soybean varieties may reduce the production gap. However, these cultivars still need to be improved in terms of yield, quality and disease resistance in order to produce a sustainable amount of work. Stable fluctuation in the environment is preferred for the maximum potential output levels in Madhya Pradesh, given the variety of conditions in which soybeans are grown. According to Ebert Hard and Russell (1966), stability explains why genotypes' average performance across a wide range of settings is an important characteristic in current breeding lines. The most crucial step in every plant breeding program is selection. The degree of genetic variability in the population and the heritability of the relevant trait are major factors in the effectiveness of a selection program. Characters with a high heredity are typically easier to choose than those with a low heritability. High heritability values were noted by Bhat *et al.* (2012) for two traits: harvest index and number of pods per plant. Hunde (2017) examined sixteen genotypes of soybeans and discovered that, in terms of

biomass output, pod length and plant height, respectively, there was a significant genetic progress and high heritability. On the other hand, it was discovered that days to 95% maturity and the number of pods/ plants had a moderate genetic advance in correlation with high heritability.

Materials and Methods

The present investigation was carried out during the *Rabi* season of 2020-21 at the research field of RAK College of Agriculture; Sehore (M.P.), India. The experiment was conducted in the experimental area of All India Coordinated Research Project on Soybean (AICRPS) at RAK College of Agriculture, Sehore (M.P.), India. The field was fairly uniform with gentle slope, adequate drainage and normal fertility status. The soil of field is clay loam vertisol with 52% clay, 41.3% salt and 6.6% sand with pH ranging from 7.2 to 7.8. Sehore is situated in the eastern part of Vindhyan Plateau in sub-tropical zone at the latitude of $23^0 12'$ North and longitude of $77^0 05'$ East at an attitude of 498.77m above mean sea level in Madhya Pradesh. The annual rainfall varies from 1546.7 mm with major precipitation in the months of July and August. The experiment was carried out in Randomized Block Design with three replications were sown in three environments on 10 November, 20 November and 30 November 2020. Each genotype was planted in row 3m long, 40 cm row to row spacing and 10 cm plant to plant spacing. Fertilizer dose 20:60:20:20 NPKS Kg/ha was applied uniformly over the soil and recommended package of practices were adopted for optimum crop growth and development with proper plant protection under rain fed condition. A random selection of ten plants in each plot was made and various observations were recorded on each selected plant. The Number of days taken from the date of sowing till 50 per cent flowering of the plants, Number of days taken from the date of sowing till 80 per cent maturity of the pods on the plants, The number of primary branches per plant was recorded as total number of primary branches on the main stem, The height of the plant was recorded in centimeters from the ground level to tip of main stem at the time of maturity, The number of effective pods per plant was recorded at the time of maturity for each selected plant, The dry weight of plant along with pods was recorded after cutting root portion for each genotype in grams per plant, after harvesting the bunch of five plants, number of seeds were counted and divided with five and average was taken as number of seeds per plant, The seed yield per plant was recorded from each selected individual after harvest, after threshing and proper drying, randomly drawn 100 seed from the produce of the sample

plants were recorded in grams and the value of harvest index was recorded by dividing the seed yield per plant by biological yield per plant and expressed in percentage.

$$\text{HI (\%)} = \frac{\text{Seed yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

The mean values of each character under study were computed on the basis of ten plants for each genotype from each replication. Heritability in per cent in broad sense was estimated by the following formula given by Singh and Choudhary (1977).

$$\text{Heritability (h}^2) = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

The estimates of expected genetic advance from selection, G (s), was obtained by the formula suggested by Robinson, Comstock and Harvey (1949).

$$G(s) = k \times h^2 \times \sigma_p$$

where,

k = Selection differential in standard deviation units which is 2.06 for 5% selection intensity,

h^2 = Heritability in broad sense and

σ_p = Phenotypic standard deviation

Experimental material

The experimental material comprised of 20 advance homozygous breeding lines of All India Coordinated Research Project on Soybean (AICRPS) RAK College of Agriculture, Sehore (M.P.)

S. no.	Genotype	Pedigree
1	RVS2012-3	JS20-63XJS95-60
2	RVS2012-10	JS20-09XPS1475
3	RVS2012-8	JS20-29XJS95-60
4	RVS2012-7	JS20-88XJS20-34
5	RVS2012-21	JS20-53XJS20-34
6	RVS2013-13	JS20-29XJS93-05
7	RVS2012-10	JS20-88XJSM-96
8	RVS2012-12	JS97-52XJS20-9
9	RVS-28	JS20-29XJS20-22
10	RVS2012-15	JS20-57XJSM-259
11	RVS2012-29	RVS2012-29XJS20-9XPSIV
12	RVS2012-6	JS20-89XJS-2034
13	RVS2012-5	JS2059XJS-2034
14	RVS2012-29	RVS2012-29XJS20-9XPSIV-
15	RVS2012-26	JS20-29XPS1475
16	RVS-18	JSM-110XJSM-66
17	RVS2011-35	JS335XPK1042
18	JS21-72	SL738XJS95-60
19	JS20-94	NRC127XJS20-94
20	Himso-1689	Himso1689XRVS11-35

Results and Discussion

Estimates of heritability (%) in broad sense

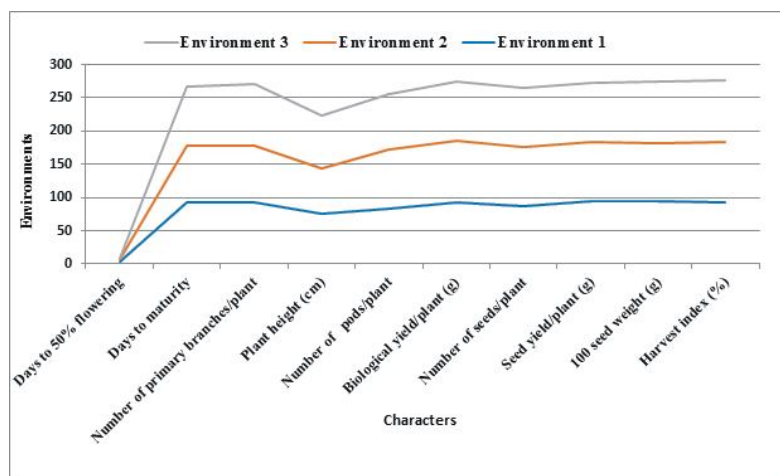Estimates of heritability in broad sense for different traits under the all three environments are reported in

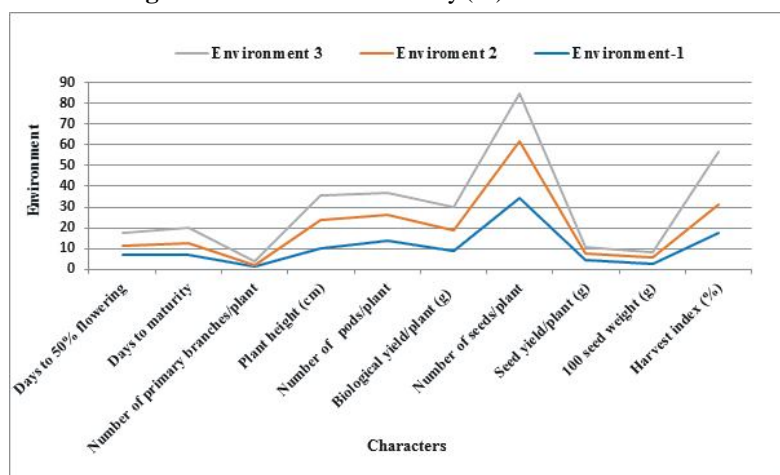**Fig. 1 :** Estimates of Heritability (%) in Broad Sense.

Fig. 2 : Estimates of Genetic advance in (%).

(Table 1 and Fig. 1). Number of days to 50% flowering showed the highest heritability (92.6%) in E-1 and lowest (84.8%) in E-2, days to maturity found the highest (92.0%) in E-1 and lowest (86.8%) in E-2, number of primary branches per plant recorded the highest (79.6%) in E-3 and lowest (69.7%) in E-2, plant height showed the highest (89.6%) in E-2 and lowest (82.8%) in E-1, number of pods per plant the highest (93.0%) in E-1 and lowest (89.7%) in E-3, similarly biological yield per plant noticed highest (89.8%) in E-2 and lowest (87.1%) in E-1, number of seeds per plant found the highest (94.0%) in E-1 closely followed by E-2 (90.1%) and lowest (88.6%) in E-3, seed yield per plant the highest (94.6%) in E-1 and lowest (88.0%) in E-2, 100 seed weight exhibited the highest (93.2%) in E-1 and lowest (91.3%) in E-2 & harvest index showed highest heritability (89.0%) in E-3 and lowest (79.4%) in E-2. Gupta and Punetha (2007), Yadav (2007) and Karnwal and Singh (2009) also reported similar findings.

Estimates of genetic advance in percent:

Genetic advance estimates in percent' expect. all the three environments are reported for days to 50% flowering the highest value noticed (6.87%) genetic advance was expected from E-1 and lowest (4.74%) from E-2, for days to maturity the highest value found (7.21%) from E-3 and lowest (5.88%) from E-2, for number of primary branches per plant the highest figure observed (1.56%) from E-3 and lowest (1.02%) from E-2, for plant height the highest (13.27%)

Table 1 : Estimates of Heritability (%) and Genetic advance (%) in Broad Sense.

Characters	Heritability (%) in Broad Sense			Genetic advance (%)		
	Environments			Environments		
	E1	E2	E3	E1	E2	E3
Days to 50% flowering	92.6	84.8	88.9	6.87	4.74	5.72
Days to maturity	92.0	86.8	92.0	6.95	5.88	7.21
Number of primary branches/plant	74.8	69.7	79.6	1.32	1.02	1.56
Plant height (cm)	82.8	89.6	82.9	10.35	13.2	12.28
Number of pods/plant	93.0	92.2	89.7	13.76	12.47	10.52
Biological yield/plant (g)	87.1	89.8	88.3	8.75	10.26	11.16
Number of seeds/plant	94.0	90.1	88.6	34.56	27.31	23.13
Seed yield/plant (g)	94.6	88.0	91.3	4.59	3.18	3.06
100 seed weight (g)	93.2	91.3	92.7	2.92	2.73	2.78
Harvest index (%)	86.10	79.40	89.00	17.46	13.81	25.56

E1 = Enviroment-1 (Date of sowing 10 November 2020) **E2** = Enviroment-2 (Date of sowing 20 November 2020)
E3 = Enviroment-3 (Date of sowing 30 November 2020)

from E-2 and lowest (10.35%) from E-1, for number of pods per plant the highest magnitude recorded (13.76%) from E-1 and lowest (10.52%) from E-3, for biological yield per plant the highest value found (11.16%) from E-3 and lowest (8.75%) from E-1, for number of seeds per plant the highest value noticed (34.56%) from E-1 and lowest (23.13%) from E-3, for seed yield per plant the highest value observed (4.59%) from E-1 and lowest (3.06%) from E-3, for 100 seed weight the highest value found (2.92%) from E-1 and lowest (2.73%) for E-2 and for harvest index the highest value recorded (25.56%) from E-3 and lowest (13.81%) from E-2. Similar findings in respect of plant height, number of pods and seeds per plant were also reported by several researchers namely Gupta and Punetha (2007), Yadav (2007), Karnwal and Singh (2009) (Table 1 and Fig. 2).

Conclusion

Gene expression variations are included in heritability estimations in a broad sense. Heritability, which gauges the correlation between genotype and phenotype, is a crucial success factor in breeding program since it indicates the degree of heritable variability that determines a population's ability to be selected. With the exception of E-2's number of primary branches per plant, all environments showed substantial heritability for the majority of the traits. In such circumstances, genetic selection for these features might be beneficial. These traits were therefore largely inherited and less influenced by the surroundings. In the E-2 environment, the number of primary braches per plant showed minimal heredity. When choosing genotypes in the conditions mentioned above, this feature may be avoided. High estimates of heritability accompanied by high genetic advance were recorded for plant height, number of pods per plant, number of seeds per plant over environments suggested that direct selection on these traits can improved the seed yield.

Acknowledgement

Future scope

The adaptive capability and phenotypic stability of the genotypes require additional assessment in a variety of contexts. To create stable, high-yielding varieties, one might take use of the heterogeneity seen in soybean genotypes. The genotypes that have been identified must be used for both commercial growth and as parents to create improved cultivars. A deeper comprehension of the real links among features through path analysis necessitates more investigation into correlation at the phenotypic and genotypic levels. To evaluate the consistency of performance, evaluation of additional minor yield and qualitative attributes of genotypes should be done throughout the course of seasons and years.

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