

ASSESSMENT OF GENETIC VARIABILITY PARAMETERS IN MAGIC POPULATION OF SOYBEAN [*Glycine max* (L.) MERRILL]

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ABSTRACT

The present investigation was carried out to assess the genetic variability present in 95 soybean MAGIC lines along with six checks for 10 different quantitative traits. The analysis of variance revealed significant variation among all the characters. The higher estimates of PCV and GCV were found for seed yield plant⁻¹(29.1, 27.3), pods plant⁻¹(28.9, 27.5) and the number of branches plant⁻¹(23.9, 23.2) and a lower value was observed for protein content (3.94, 3.36) and oil content (6.9, 6.56). The measure of broad sense heritability was found high for most of the traits and the lowest (51.4 %) for harvest index. High heritability coupled with high genetic advance was observed for number of pods plant⁻¹, number of branches plant⁻¹, seed yield plant⁻¹ and 100 seed weight indicating that these traits are governed by additive gene effects and direct selection of soybean MAGIC lines based on these traits would be effective.

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill), (2n = 2x = 40) is a globally cultivated leading oilseed crop, otherwise known as “golden bean” or “miracle bean”. The centre of origin of the crop is considered to be Yellow river valley of China (Wang *et al.*, 2006). The major soybean producing countries are Brazil, Canada, China, India and USA. Globally India stands fifth with a production capacity of 13.78 MT (FAO STAT, 2018). The soybean seed contains about 38 to 44 % protein and 18-23 % oil. Moreover, it contains vitamin B, fibre, iron, calcium, zinc and isoflavones such as genistein and daidzein (Rizzo and Baroni, 2018). The crop was introduced in India in 1000 AD (Dupare *et al.*, 2008). Whereas, major commercial cultivation started after the launch of AICRP on soybean in 1967 (Tiwari, 2014).

Variability in the plant population is a pre-requisite for initiating any crop improvement program in order to adopt proper selection techniques (Dhanwani *et al.*, 2013). Selection based on phenotypic variation alone is misleading as it is influenced by environmental factors. So, partition of overall variability into different components is necessary to understand the genetic makeup of experimental population. The genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are highly useful in the estimation of variability at its genotypic and phenotypic levels. Moreover, partitioning of observed variability into heritable and non-heritable components is essential to carry out selection effectively (Yadawad *et al.*, 2015). Thus, the parameter heritability is used to measure the heritable portion

of total variation but, alone is not sufficiently informative for the proper selection process. Hence heritability along with genetic advance is useful in predicting genetic gain under selection (Johnson *et al.*, 1955). The genetic variability of the crop has become limited due to frequent inbreeding and natural selection process. Furthermore, Indian soybean cultivars have a very narrow genetic base due to the repetitive use of the same parents during hybridisation program (Bharadwaj *et al.*, 2002). Hence, A multi-way hybrid such as MAGIC (Multi-parent Advanced Generation Inter Cross) can contribute variability to the crop gene pool as these are highly variable and diverse source of germplasm which undergoes heavy genetic recombination events.

The genetic parameters in various soybean cultivars were studied by Chandrawat *et al.* (2017), Guleria *et al.* (2019), Jain *et al.* (2018), Joshi *et al.* (2018), Koraddi and Basavaraja (2019), Kumar *et al.* (2018) and Neelima *et al.* (2018). But, an in depth study is required on soybean MAGIC lines which is of current importance. Hence, the present study was carried out which deals with the assessment of phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance in soybean MAGIC lines for yield and its attributing traits.

MATERIALS AND METHODS

The present study was carried out at ARS (Agricultural Research Station) Adilabad, PJTS Agricultural University, Hyderabad during *Kharif* 2019. The experimental material consisted of 95 soybean MAGIC lines (F5 generation) with six

checks namely EC333901, EC546882, EC572109, NRC 86, JS 335 and Basara. All the entries were evaluated in Randomised Block Design (RBD) with two replications by keeping inter and intra-row spacing of 45 and 10 cm respectively. The observations were recorded for ten yield and its attributing traits and subjected to statistical analysis. The protein and oil content were estimated as per protocols of AOAC (1990).

Statistical Analysis

All the statistical analyses were carried out using INDOSTAT software version 9.2 and the methods adopted are mentioned as follows.

Analysis of variance

Analysis of variance (ANOVA) is a statistical tool used to split the total variation into different components. Analysis of variance was performed as per standard procedure suggested by Panse and Sukhatme (1985).

Genotypic and phenotypic coefficient of variation

The coefficient of variation (GCV and PCV) gives an overall idea about the magnitude and nature variability present in the population and was calculated as per Burton (1952).

$$GCV = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100$$

$$PCV = \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

\bar{x} = Grand mean for the character

Estimates of GCV and PCV were categorized as low (< 10%), moderate (10-20%) and high (> 20%) as suggested by Sivasubramanian and Madhavamenon (1973).

Broad sense heritability (h^2_{bs})

Heritability in the broad sense was calculated as the proportion of genotypic variance to total phenotypic variance as suggested by Johnson *et al.* (1955a).

$$h^2_{bs} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

The estimates of h^2_{bs} were classified as low (0-30%), medium (30-60%) and high (>60%) as suggested by Johnson *et al.* (1955)

Genetic Advance (GA)

Genetic advance was calculated by the following formula given by Johnson *et al.* (1955).

$$GA = Kx(h^2_{bs})\times\sigma_p$$

Where,

K = Selection differential at selection intensity (2.06), assuming 5 percent population selected.

σ_p = Phenotypic standard deviation

Genetic advance as percent of mean (GA %)

For performing relative comparison among the characters, Genetic advance as percent of mean was computed using the formula suggested by Johnson *et al.* (1955).

$$GA(\%) = \frac{GA}{\bar{x}} \times 100$$

The estimates of the range of genetic advance as percent of mean were classified as low (< 10 %), moderate (10%-20%) and high (> 20%) as given by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The analysis of variance revealed a significant treatment mean sum of squares for all the studied characters (Table 1). It indicates the presence of sufficient genetic variation in the experimental material which can be utilized in the selection of better performing lines. This is in agreement with the result obtained by Koraddi and Basavaraja (2019). A wide range of variation was observed among the MAGIC lines for all the traits (Table 2). It provides ample opportunity for the breeder in the selection of lines having traits in the desirable direction.

The magnitude of variability is estimated by the parameter PCV and GCV which suggests the phenotypic and genotypic components of variation respectively. The value of PCV was found higher than the corresponding GCV for all the characters. But, a narrow gap between the PCV and GCV was observed indicating a lower influence of environmental factor in the expression of selected traits. Thus, selection of the genotypes for these characters would be beneficial. Similar results were obtained by Neelima *et al.* (2018).

Higher estimates of PCV and GCV were recorded in seed yield plant⁻¹(29.1, 27.3), number of pods plant⁻¹(28.9, 27.5) and number of branches plant⁻¹(23.9, 23.2). The results suggesting the presence of sufficient variability among the MAGIC lines for these traits which can be selected directly or may be utilised in future breeding programs. Similar findings were obtained by Chandrawat *et al.* (2017), Dubey *et al.*

Table 1: Analysis of variance and mean sum of square for yield and its attributing traits in Soybean

Source of variation	D.F	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of branches plant ⁻¹	Number of pods plant ⁻¹	100 seed weight (g)	Seed yield plant ⁻¹ (g)	Oil content (%)	Protein content (%)	Harvest Index (%)
Replication	1	2.62	15.52	64	0.22	26.96	0.98	2.61	0.29	0.89	10.83
Treatment	100	14.12**	49.27**	145.8**	2.45**	343.96**	6.28**	21.69**	3.05**	4.07**	32.62**
Error	101	2.46	6.01	32.8	0.18	17.55	0.67	1.38	0.15	0.64	10.46

Note: * significance at 5 per cent probability level, ** significance at 1 per cent probability level

Table 2 :Estimates of genetic variability parameters for yield and yield attributing characters in soybean

Sl. No.	Characters	Range		Mean	PCV	GCV	ECV	h ² (bs)	GA%
		Minimum	Maximum						
1	Days to 50 % flowering	35	47	40.51	7.1	5.96	3.87	70.3	10.3
2	Days to maturity	91	114	105	5	4.43	2.33	78.2	8.06
3	Plant height (cm)	40.6	88.6	62.28	15.2	12.1	9.19	63.3	12.78
4	Number of branches plant ⁻¹	3	11	4.8	23.9	23.2	8.96	86	43.31
5	Number of pods plant ⁻¹	20.35	77.95	46.48	28.9	27.5	9.01	90.3	53.8
6	100 seed weight (g)	10.065	17.38	13.55	13.8	12.4	6.03	80.8	22.88
7	Seed yield per plant (g)	4.94	19.54	11.67	29.1	27.3	10.1	88	52.8
8	Oil content (%)	16.15	21.1	18.35	6.9	6.56	2.14	90.4	12.86
9	Protein content (%)	36	42.15	38.96	3.94	3.36	2.05	72.8	5.9
10	Harvest Index (%)	30.41	47.64	38.73	12	8.59	8.35	51.4	12.69

(2015), Guleria *et al.* (2019), Joshi *et al.* (2018) and Neelima *et al.* (2018). A moderate value of PCV and GCV was recorded for plant height (15.2, 12.1) and 100 seed weight (13.8, 12.4) which is similar to the result obtained by Karnwal *et al.* (2009) and Kumar *et al.* (2018). The trait harvest index exhibited a moderate PCV and a lower GCV which is in accordance with the result of Koraddi and Basavaraja (2019).

The measure of PCV and GCV was found lower for days to 50 percent flowering (7.1, 5.96), days to maturity (5, 4.43), oil content (6.9, 6.56), and protein content (3.94, 3.36). It shows presence of lower variability in the selected MAGIC lines for these traits indicating a good scope for their further improvement. Similar results were obtained by Chandrawat *et al.* (2017), Dubey *et al.* (2015), Guleria *et al.* (2019) and Mahbub *et al.* (2015) for days to 50 percent flowering and days to maturity. Whereas, Baraskar *et al.* (2014), Neelima *et al.* (2018), Karnwal *et al.* (2009) and Ramteke *et al.* (2010) obtained similar findings for oil and protein content.

Variability exists among the genotypes for several traits can be better exploited when they are heritable in nature. Broad sense heritability measures the proportion of total phenotypic variability that arises due to genetic causes. It suggests the extent up to which a character is transmitted to the next generation. The result revealed high broad sense heritability for most of the traits (Table 2). It shows that these traits are least influenced by environmental effects and genetic improvement through selection may be effective. The findings are in conformity with the earlier reports of Akram *et al.* (2016), Chandrawat *et al.* (2017), Guleria *et al.* (2019) and Malek *et al.* (2014). Similarly, a moderate value (51.40 %) of heritability was observed in harvest index which is in conformity with the findings of Jain *et al.* (2018) and Koraddi and Basavaraja (2019).

Genetic advance refers to the improvement of the mean genotypic value of the selected lines over the mean genotypic value of the parental population. It is usually expressed as a percent of the mean. Selection based on broad sense heritability alone is misleading as it is not sufficiently informative about the existence of gene action (additive/non-additive) and involvement of other factors in the expression of traits. Thus heritability along with genetic advance together is helpful in predicting genetic gain under selection (Johnson *et al.*, 1955). The estimates of genetic advance as percent of mean was found highest for number of pods plant⁻¹ (53.8 %) followed by seed yield plant⁻¹ (52.76%), number of branches plant⁻¹ (43.31%), 100 seed weight (22.88%) and oil content (12.86%) and the lowest value was observed in protein content (5.9%)

followed by days to maturity (8.06%), days to 50 % flowering (10.3%), harvest index (12.69%) and plant height (12.78%). The present findings are in partial agreement with the findings of Akram *et al.* (2016), Baraskar *et al.* (2014), Koraddi and Basavaraja (2019), Kumar *et al.* (2018) and Neelima *et al.* (2018).

Among all the characters, high heritability along with high genetic advance as percent of mean was observed for number of pods plant⁻¹, number of branches plant⁻¹, seed yield plant⁻¹ and 100 seed weight indicating predominance of additive gene action and a limited role of environment in the expression of these traits. Hence, these traits are fixable in nature and selection on the basis of these traits would be effective. The result is in accordance with the result of Chandrawat *et al.* (2017) and Neelima *et al.* (2018) and in partial agreement with the result of Koraddi and Basavaraja (2019) and Kumar *et al.* (2018).

Traits like oil content, plant height and days to 50 percent flowering exhibited high heritability with moderate genetic advance as percent of mean suggesting the combining or conditional role of additive and non-additive gene action in governing these traits and high heritability may have resulted from favourable influence of environmental factors. Thus, the selection of these traits may not be beneficial. Similar findings were reported by Akram *et al.* (2016) for days to 50 percent flowering, Dhillon *et al.* (2005) for plant height and Neelima *et al.* (2018) for oil content.

A higher estimate of heritability with lower estimates of genetic advance as percent of mean was observed for protein content and days to maturity indicating predominance of non-additive gene action and direct selection for these traits may not be rewarding. Hence, recombination breeding may be useful for the improvement of these traits. Similar findings were obtained by Neelima *et al.* (2018) for protein content and Akram *et al.* (2016), Chandrawat *et al.* (2017) and Guleria *et al.* (2019) for days to maturity. A lower value of broad sense heritability was observed with a moderate genetic advance as percent of mean for harvest index indicating that the trait is highly influenced by environmental effects and selection for it would be ineffective. The result is in agreement with Joshi *et al.* (2018).

From the findings of the present investigation, it can be concluded that a substantial amount of genetic variation exists in the selected soybean MAGIC lines since they exhibited a wide range of variation and a significant treatment sum of

square for all the characters. Higher estimates of genetic parameters like PCV, GCV, broad sense heritability and genetic advance were observed for seed yield plant⁻¹, number of pods plant⁻¹ and number of branches plant⁻¹ indicating predominance of additive gene action. Thus, these traits can be fixable and should be given priority in the selection of soybean MAGIC lines in future crop improvement programs.

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