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STUDIES ON GENETIC VARIABILITY AND RUST RESISTANCE IN SOYBEAN (*GLYCINE MAX* L.)

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ABSTRACT

In the present investigation, F_4 generation of two crosses, cross 1 (DSb 23 x MACS 1575) and cross 2 (DSb 23 x MACS 1460) were assessed during *kharif* 2021 for genetic variability and rust resistance. Compared to check DSb 21, the genotypes from cross 1 were significantly early maturing and were on par for yield. Whereas, the cross 2 genotypes were similar in performance for days to maturity but significantly superior for yield compared to DSb 21. PCV and GCV values were high for seed yield per plot followed by productive pods per plant and branches per plant. High heritability associated with high response to selection was showed by productive pods per plant and seed yield per plot. None of the genotypes exhibited highly resistant reaction to rust. However, fourteen genotypes from cross 1 and nine genotypes from cross 2 showed moderately resistant reaction to rust.

***Keywords*:** Soybean, Phenotypic coefficient of variation, Genotypic coefficient of variation, Heritability, Rust resistance

Introduction

Soybean [*Glycine max* (L.) Merrill] is considered as “Yellow Jewel” and “Great Treasure” for its nutrition value. It contains about 40% protein, 20% oil, 80% soybean meal, and eight essential amino acids. Because of two important parameters (oil and protein) in a sole crop, soybean plays a vital role in the global agricultural economy. Global soybean production for 2023-2024 was 350.72 million tonnes (Anonymous 2024b). Brazil surpassed the United States as the biggest soybean producer, with a production level of 144 million tonnes in 2023-2024 (Anonymous 2024c). In India, the crop covers 12.19 million hectares and yields 12.72 million tonnes per hectare, with a productivity of 1042.8 kg/ha. In Karnataka the crop covers 0.382 million hectares and produces 0.384 million tonnes per hectare, with a productivity of 1004 kg per hectare. Soybean cultivation is mostly concentrated in the northern districts of Karnataka namely Belgaum, Bidar, Dharwad, Haveri, Kalburgi and Bagalkot, which occupy 95 percent of the state's total land. Bidar is the leading state in Karnataka, which occupies an area of 0.174 million hectares and production of 0.23 million tonnes per hectare, with a productivity of 1331 kg/ha during 2023-2024 (Anonymous 2024a).

One of the limiting factors in soybean production and productivity is unavailability of biotic/abiotic stress resilient lines with early maturity and good yielding capabilities. To improve the production potential of soybean, appropriate use of parental lines in the crossing programme and selection of superior lines in segregating material is very important. This requires precise knowledge on the degree and nature of genetic variability present in soybean and breeder has to formulate criteria for isolating superior genotypes from segregating populations.

Rust disease caused by *Phakopsora pachyrhizi* is another major constraint for soybean output in India, especially in south India including Karnataka. Chemical fungicides and specialised production procedures, such as the eradication of secondary hosts and the introduction of soybean-free growth periods, are among the rust management and control strategies (sanitary periods). In addition, cultivars with resistant genes have been developed to investigate genetic resistance. Therefore, using resistant cultivars is not only the most sustainable approach for managing soybean rust over time, but it may also be the utmost cost-effective option for subsistence farming systems in developing countries.

In this direction, to develop lines with high yield coupled with earliness and rust resistance, the study was emphasized by using suitable parental lines in the breeding programme and selection from the segregating generations and evaluating their performance in the advanced generations.

Material and Methods

The breeding material for the current study encompassed of F_4 generation of two crosses, cross 1 (DSb 23 x MACS 1575) and cross 2 (DSb 23 x MACS 1460) involving three diverse parents *viz.,* DSb 23, MACS 1575 and MACS 1460. The salient features of the three parental lines and checks used in the current study are deciphered in Table 1. Superior F_4 families selected from F_3 generation, were assessed in *Kharif* 2021 at Botany Garden, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, for yield associated traits and reaction to rust disease. From cross 1, 22 genotypes and from cross 2, 14 genotypes were evaluated.

The experiment was directed using RCBD design with two replications. To ensure optimal crop growth, the recommended package of practices was followed. Observations were taken on five healthier plants for yield attributing traits. Additionally, lines were screened under natural epiphytotic conditions during the *Kharif* season of 2021 for rust disease. Each line from both crosses was appraised in a single row under uncontrolled conditions for rust disease, alongside parental lines and check varieties.

Results and Discussion

A highly significant mean sum of square for genotypes was detected in both crosses, suggesting a substantial amount of genetic variability present in the genetic materials studied, as revealed in Table 2 and Table 3. Similarly, Jandong *et al.* (2019) registered significant variation for all the yield parameters among the soybean genotypes signifying the persistence of variability. The genotypes of cross 1 were on par (89 to 95 days) with early maturing parents MACS 1575 (86 days) and MACS 1460 (87 days) and were significantly superior than DSb 23 (94 days) and DSb 21 (92 days) for days to maturity. However, the genotypes of cross 2 were on par (86 to 95 days) with the superior parents DSb 23 and DSb 21 for attaining maturity (94 days). Least and extreme height of the plant was observed in cross 1 and cross 2 was 24.8 cm and 52.9 cm, 42.05 cm and 54.20 cm respectively. Less variation was registered for number of branches per plant (8 branches per plant) in both the crosses. Productive pods per plant ranged from 79-141 pods and 83-151 pods in cross 1 and cross 2. The greater number of pods were observed in genotypes of cross 2 compared to cross 1, which reflected in higher yield of cross 2 genotypes. Test weight was high in genotypes of cross 2 with a range from 14.57g - 15.90 g. The genotype 21-7 had highest test weight (15.90 g).

Among the parents, DSb 23 recorded 14.40 g followed by MACS 1460 (13.70 g) and MACS 1575 (13.20 g). Among the checks, DSb 21 had 13.65 g and JS 335 had 12.45 g for weight of 100 seeds. Highest yield of 2.21 kg/plot was recorded in cross 1, however in cross 2 highest yield was 2.61 kg/plot with a range of 1.87 kg/plot to 2.61 kg/plot. The genotypes of cross 1 showed significant superiority for early flowering and maturity. However, did not observe significant supremacy for seed yield per plot compared to superior check DSb 21. Whereas, the cross 2 genotypes were highly substantial for seed yield per plot and did not exhibit superiority for days to maturity as they were on par with late maturing check DSb 21. High range was observed among the lines in both the crosses for different quantitative traits studied, indicating the existence of vast genetic variability among the lines for these characters as described in Table 4. High range with superior *per se* performance will aid in identifying superior genotypes. The above results are in harmony with Neelima *et al.* (2018) who also reported a range of 35-44 days for early flowering, days to maturity, 47.67-65.27 cm for plant height and 10.7-13.5 g for test weight and also observed highest yield of 1.56 kg/plot in soybean.

For all the yield attributing traits, the PCV values was higher than the GCV values, signifying that environmental factor influenced trait expression to some extent. These research findings make even with the reports of Neelima *et al.* (2018) and Ravindra *et al.* (2017). As per Deshmukh *et al.* (1986), PCV and GCV values above 20% are considered high, values below 10% are regarded as low, and those between 10% and 20% are classified as medium. The variability values for different yield component traits in the F_4 generations of soybean crosses 1 (DSb 23 × MACS 1575) and 2 (DSb 23 × MACS 1460) are presented in Table 5.

In cross 1, PCV and GCV values were high for seed yield per plot, followed by plant height. Similarly, in cross 2, coefficient of variability values was uppermost for seed yield per plot, tailed by the number of productive pods per plant. This suggests the dominance of additive gene action, indicating that applying selection pressure on these traits could effectively enhance their improvement. The high GCV observed for seed yield reflects substantial genetic variation, allowing for further improvement through selection (Jandong *et al.* 2020). The variances between PCV and GCV across all studied traits in both crosses were minimal, suggesting a low impact of environmental factors on phenotypic performance. According to Akram *et al.* (2016), selection based on characters with minimal environmental influence is more effective. PCV and GCV values were moderate for branches per plant and the productive pods per plant, while they were least for days to 50% flowering, days to maturity, and test weight.

Prediction of positive selection becomes more precise if it is based on estimations of broad sense heritability allied with response to selection because it gives estimates not only of genetic contribution of each trait but of projected genetic gain out of selection as well. The results from the current investigation on additive genetic variance and response to selection for different characters are summarized as below,

In cross 1, high heritability shared with high response to selection was observed for productive pods per plant, seed yield per plot, height of the plant, and the number of branches per plant. In cross 2, the same trend was renowned for productive pods per plant and seed yield per plot, signifying that these traits are chiefly controlled by additive gene action. Amrita *et al.* (2013) reported similar findings for seed yield, while Akram *et al.* (2016) observed this pattern for productive pods per plant and seed yield per plot in soybean. Traits with high heritability and moderate response to selection were observed by days to 50% flowering and test weight in cross 1, and plant height and the number of branches per plant in cross 2, indicate a combination of additive and non-additive gene action. These results align with the findings of Osekita and Olorunfemi *et al.* (2014) and Kwusantoro *et al.* (2018). Additionally, traits such as days to 50% flowering, days to maturity, and test weight, which exhibited high heritability but less response to selection, suggest a prevalence of non-additive gene action. Similar conclusions were drawn by Baraskar *et al.* (2014) and Chandrawat *et al.* (2017).

During the evaluation for rust disease i.e., *kharif* 2021, under natural conditions, due to congenial environmental conditions for the growth and spread of the disease, the scoring for disease was very effective. In the current study, 22 genotypes of cross 1 (DSb 23 x MACS 1575) and 14 genotypes of cross 2 (DSb 23 x MACS 1460) along with parents and checks, were curtained for rust resistance under natural uncontrolled field conditions and the results of which are offered in Table 6 and the reaction of genotypes of cross 1 and cross 2 for rust disease are depicted in Figure 1 and 2.

Among the three parents, DSb 23 is a rust resistant variety and other two parents *viz.,* MACS 1575 and MACS 1460 are susceptible to rust. Similar inferences were also observed in the present investing as DSb 23 recorded moderately resistant with rust score 3 and DSb 21 exhibited moderately susceptible reaction to rust with score of 5, whereas JS 335, MACS 1575 and MACS 1460 unveiled highly susceptible reaction with rust score of 9 [Genotypes with score of 0, 1, 3, 5, 7 and 9 were grouped as absolutely resistant, highly resistant, moderately resistant, moderately susceptible, susceptible and highly susceptible, respectively according to Mayee *et al.* (1986)].

The results of rust reaction in of both the crosses are summarized as follows

Rust reaction	**DSb 23 X MACS 1575 (Cross 1)**	**DSb 23 X MACS 1460 (Cross 2)**
Moderately resistant	14	9
Moderately susceptible	7	5

Results of natural epiphytotic condition from the two crosses of F_4 generation revealed that fourteen genotypes from cross 1 and 9 genotypes from cross 2 recorded moderately resilient reaction to rust with score of 3 and percent disease index of 12.22 to 33.33. Moderately susceptible rust reaction was recorded by 9 genotypes of cross 1 and 5 genotypes of cross 2 with rust score of 5 and percent disease index of 34.44 to 55.5. Only one genotype of cross 1 recorded susceptible reaction to rust with rust score of 9 and percent disease index of 56.6 to 77.7. Genotypes in both the crosses, which recorded moderately resilient reaction to rust can be used as donor parents in crossing programme. Similar results were observed by Rahangdale and Raut (2004), Iwo *et al.* (2012), Kiryowa *et al.* (2009) for disease reaction in soybean.

Conclusion

Variability study deciphered vast significant variation among the lines in both the crosses for all the yield related traits studied. Considerable range of variation was observed for all the yield contributing traits under study signifying adequate choice for bringing about improvement in the positive direction. Simple selection scheme would be enough for the traits, productive pods per plant followed by number of branches per plant and plant height to bring genetic improvement in desired direction. The reaction of lines from cross 1 and cross 2 for rust reaction revealed that in cross 1, fourteen genotypes (9-4, 7-1, 176-1 etc) and in cross 2, 9 genotypes (23-15, 58-1, 21-7 etc) recorded moderately resistant reaction to rust. Hence, we can utilize moderately resistant genotypes in crossing programme to develop breeding populations for identify genes/QTLs governing the soybean rust and further can also be used in marker assisted backcrossing for developing rust resilient genotypes.

9-4 (MR) **JS-335 (HS)** **7-1 (MR)**

Fig. 1: Reaction of genotypes of cross 1 (DSb 23 x MACS 1575) for rust disease

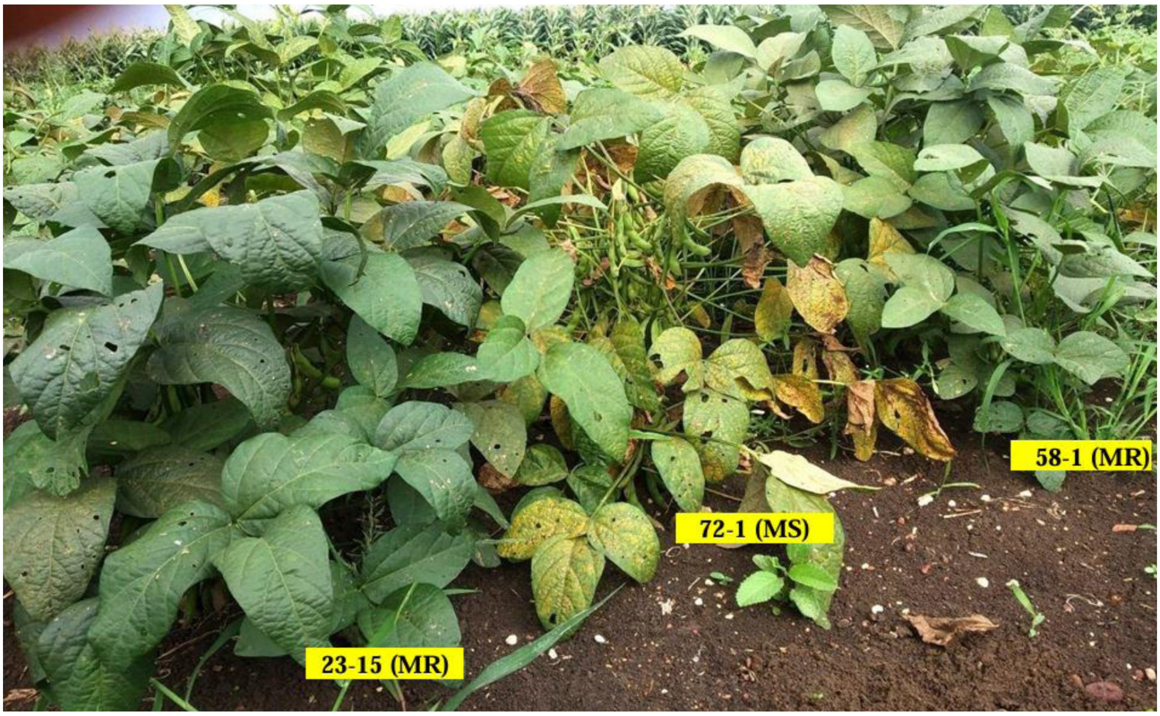

Fig. 2: Reaction of genotypes of cross 2 (DSb 23 x MACS 1460) for rust disease

Table 1: The salient features of the three parental lines and checks used in the present study

Genotypes	Days to maturity	Yield potential (q/ha)	Salient features
DSb 23	95-100	32-35	High yield potential and highly resistant to rust but late maturing
MACS 1575	80-85	24-26	Early maturing, susceptible to rust and low pod yield
MACS 1460	80-85	25-28	Early maturing, susceptible to rust and low pod yield
JS 335	85-90	25-35	Early maturing, susceptible to rust and high pod yield
DSb 21	90-95	32-35	High yield potential and highly resistant to rust but late maturing

Table 2: Analysis of variance in F_4 generation for seven quantitative characters in Cross 1 (DSb 23 x MACS 1575) of soybean

Source of Variation	d.f.	Mean sum of squares						
		Days to 50% flowering	Days to Maturity	Plant height	Number of branches per plant	Productive pods per plant	test weight (g)	Pod yield (kg/plot)
Genotypes	26.00	09.69**	14.56**	156.22**	01.69**	645.97**	02.85**	00.17**
Replications	1.00	03.63	01.85	22.47	00.15	221.23	01.85	00.03
Error	26.00	01.28	01.58	09.45	00.24	55.88	00.60	00.01
CV (%)		03.16	01.41	07.31	07.65	07.09	05.51	06.14

Table 3: Analysis of variance in F_4 generation for seven quantitative characters in Cross 2 (DSb 23 x MACS 1460) of soybean

Source of Variation	d.f.	Mean sum of squares						
		Days to 50% flowering	Days to Maturity	Plant height	Number of Branches per plant	Productive pods per plant	test weight (g)	Pod yield (kg/plot)
Genotypes	18.00	06.74**	27.98**	26.74**	01.00**	836.04**	01.64**	00.56**
Replications	1.00	04.45	05.16	11.13	00.15	04.52	01.40	00.01
Error	18.00	01.39	01.71	04.36	00.16	41.34	00.51	00.02
CV (%)		03.09	01.39	04.19	05.76	05.07	04.92	07.64

Table 4: *Per se* performance and range for seven quantitative characters in Cross 1 (DSb 23 x MACS 1575) and Cross 2 (DSb 23 x MACS 1460) of soybean

Traits	**Generation**	**Mean**	**Range**		**CV**	**CD**	**Mean**				
			Min	**Max**			**DSb 23**	**MACS 1575**	**MACS 1460**	**JS 335**	**DSb 21**
Days to 50% flowering.	Cross 1	36.00	34.00	45.00	03.16	02.33	45.00	36.00	38.00	38.00	41.00
	Cross 2	38.00	36.00	44.00	03.09	02.48	44.00	36.00	38.00	39.00	42.00
Days to Maturity	Cross 1	89.00	86.00	97.00	01.41	02.59	94.00	86.00	87.00	88.00	92.00
	Cross 2	94.00	85.00	98.00	01.39	02.75	94.00	86.00	87.00	88.00	92.00
Plant height (cm)	Cross 1	93.00	85.00	98.00	02.12	04.19	94.00	85.00	87.00	88.00	92.00
	Cross 2	48.07	42.05	54.20	04.19	04.39	50.40	44.40	42.20	50.50	51.60
Number of Branches per plant	Cross 1	05.00	6.00	08.00	07.65	01.00	08.00	05.00	06.00	07.00	08.00
	Cross 2	07.00	05.00	08.00	05.76	00.84	08.00	05.00	06.00	07.00	08.00
Productive pods per plant	Cross 1	106.00	79.00	141.00	07.09	15.37	110.00	86.00	81.00	97.00	105.00
	Cross 2	127.00	83.00	151.00	05.07	13.51	110.00	86.00	83.00	97.00	106.00
test weight (g)	Cross 1	13.26	10.70	14.95	05.51	01.60	14.20	13.20	13.65	12.55	13.50
	Cross 2	14.51	12.45	15.45	04.92	01.51	14.45	13.25	13.65	12.60	13.55
Pod yield (kg/plot)	Cross 1	01.37	00.93	02.21	06.14	00.17	01.35	00.93	01.04	01.12	01.31
	Cross 2	01.87	00.96	02.61	06.39	00.25	01.34	00.96	01.03	01.18	01.36

Table 5: Estimates of variability parameters for seven quantitative traits in Cross 1 (DSb 23 x MACS 1575) and Cross 2 (DSb 23 x MACS 1460) of soybean

Traits	**Generation**	**PCV**	**GCV**	**h^2**	**GAM**
Days to 50% flowering.	Cross 1	06.53	05.72	76.60	10.31
	Cross 2	05.27	04.28	65.78	07.15
Days to Maturity	Cross 1	03.17	02.85	80.39	05.26
	Cross 2	04.10	03.86	88.46	07.48
Plant height (cm)	Cross 1	21.64	20.37	88.60	39.50
	Cross 2	07.91	06.71	71.94	11.72
Number of Branches per plant	Cross 1	15.45	13.42	75.47	24.02
	Cross 2	11.05	09.42	72.77	16.56
Productive pods per plant	Cross 1	17.76	16.28	84.08	30.75
	Cross 2	16.52	15.72	90.58	30.83
test weight (g)	Cross 1	09.32	07.52	70.24	12.49
	Cross 2	07.12	05.15	52.30	07.68
Pod yield (kg/plot)	Cross 1	21.70	20.81	91.99	41.12
	Cross 2	28.78	27.75	92.96	55.12

Table 6: Rust score, percent disease index and rust reaction of genotypes in F_4 generation of soybean

Cross 1 (DSb 23 x MACS 1575)					**Cross 2 (DSb 23 x MACS 1460)**				
Sl. No.	**Genotype**	**Rust score**	**Percent Disease Index**	**Rust reaction**	**Sl. No.**	**Genotype**	**Rust score**	**Percent Disease Index**	**Rust reaction**
1	129-12	3	22.10	MR	1	479-1	3	28.1	MR
2	172-5	7	60.10	S	2	58-8	3	32.6	MR
3	74-8	5	54.10	MS	3	217-7	5	52.4	MS
4	249-8	3	25.10	MR	4	23-15	3	30.8	MR
5	178-2	3	22.80	MR	5	129-4	7	56.7	MS
6	176-1	3	31.40	MR	6	58-1	3	29.4	MR
7	9-4.	3	24.04	MR	7	439-4	3	25.9	MR
8	133-10	5	51.40	MS	8	205-4	5	52.4	MS
9	202-1	5	46.50	MS	9	92-6	3	31.6	MR
10	7-1.	3	26.40	MR	10	92-1	3	26.2	MR
11	74-3	5	51.90	MS	11	72-1	5	51.2	MS
12	64-2	5	50.90	MS	12	21-7.	3	33.1	MR
13	172-1	3	30.40	MR	13	60-2	5	50.4	MS
14	38-2	3	24.50	MR	14	377-10	3	30.1	MR

15	9-2.	3	29.70	MR	Checks	JS 335	3	29.5	MR
16	8-12.	3	22.40	MR		DSb 21	3	51.7	MS
17	8-7.	3	31.90	MR	Parents	DSb 23	9	83.4	HS
18	224-1	3	23.40	MR		MACS 1460	9	86.7	HS
19	249-11	5	52.80	MS		MACS 1575	9	79.5	HS
20	14-6.	3	33.20	MR	MR – Moderately resistant, MS – Moderately susceptible HS – Highly susceptible and S – Susceptible				
21	74-10	5	50.40	MS					
22	86-1	3	29.60	MR					

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References

Akram, S., Hussain, B.N., Al Bari, M.A., Burritt D.J. and Hossain M.A. (2016). Variability and association analysis of soybean (Glycine max (L.) Merrill) for yield and yield attributing traits. *Plant Gene and Trait.*, *7*(13).

Amrita, B., Shrivastava, A.N., Bisen R. and Mishra S. (2013). Genetic variability, association and path analysis in advanced generation of fixed lines of soybean (*Glycine max* (L.) Merril). *Soybean Research.,* **12** (1): 20-27.

Anonymous (2024a). The Soybean Processors Association of India, Area, Yield and Production for the year 2023-24. http:// www.sopa.org.

Anonymous (2024b). United state department of agriculture, Area, Yield and Production for the year 2023-24. http://www. usda.gov.

Anonymous (2024c). Indian Institute of Soybean Research. Indore, Area, Yield and Production for the year 2023-24. http://www.iisriindore.icar.gov.in

Baraskar, V.V., Kachhadia, V.H., VachhanI, J.H., Barad, H.R., Patel M.B. and Darwankar M.S. (2014). Genetic variability, heritability and genetic advance in soybean [*Glycine max* (L.) Merrill]. *Electron. J. Plant Breed.*, **5** (4): 802-806.

Chandrawat, K.S., Baig, K.S., Hashmi, S., Sarang, D.H., Kumar A. and Dumai, P.K. (2017). Study on genetic variability, heritability and genetic advance in soybean. *Ind. J. Pure App. Biosci.*, **5** (1): 57-63.

Deshmukh, S.N., Basu M.S. and Reddy P.S. (1986). Genetic variability, character association and path coefficients of quantitative traits in Virginia bunch varieties of groundnut.

Jandong, E.A., Uguru M.I. and Okechukwu E.C. (2020). Estimates of genetic variability, heritability and genetic advance for agronomic and yield traits in soybean (*Glycine max* L.). *Afr. J. Biotechnol.*, **19** (4): 201-206.

Kiryowa, M., Tukamuhabwa P. and Adipala E. (2009). Genetic analysis of resistance to *Phakospora pachyrhizi*. *Afr. J. Crop Sci.,* **16** (3): 211-217.

Kuswantoro, H., Artari, R., Rahajeng, W., Ginting E. and Supeno A. (2018). Genetic variability, heritability, and correlation of some agronomical characters of soybean varieties. *Biosaintifika: J. Biol*, **10** (1): 9-15.

Mayee C.D. and Datar V.V. (1986). Phytopathometry technical bulletin-1 (special bulletin-3). Maratwada Agricultural University, Parbhani, Maharashtra, India: 48.

Neelima, G., Mehtre S.P. and Narkhede G.W. (2018). Genetic variability, heritability and genetic advance in soybean. *Ind. J. Pure App. Biosci.*, **6** (2): 1011-1017.

Osekita O.S. and Olorunfemi O. (2014). Quantitative genetic variation, heritability and genetic advance in the segregating F3 populations in soybean (*Glycine max* (L.) Merril. *J. Adv. Res.*, **2** (7): 82-89.

Rahangdale S.R. and Raut V.M. (2004). Genetics of rust resistance in soybean (*Glycine max* (L.) Merrill). *Ind. J. Genet. Plant. Breed.,* 64:121-124.

Ravindra, K.J., Arunabh, J., Hem, R.C., Abhay D. and Champa L.K. (2017). Study on genetic variability, heritability and genetic advance in soybean [*Glycine max* (L.) Merrill]. *Legume Res.*, **41**: 532-536.