CHARACTER ASSOCIATION AND PATH ANALYSIS STUDIES FOR YIELD AND YIELD CONTRIBUTING TRAITS IN SOYBEAN MUTANT PROGENIES

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ABSTRACT

The experimental material comprised of 30 soybean mutant lines along with 3 checks TAMS-38, AMS MB 5-18, and JS-335. The experiment was carried out at the research farm of the All India Coordinated Research Project on Linseed and Mustard, College of Agriculture, Nagpur during *kharif* 2021. Mutant lines with checks were evaluated for days to 50% flowering, days to maturity, plant height, number of branches plant^{-1}, pods plant^{-1}, 100 seed weight, days to 1st flower, clusters plant^{-1} and seed yield plant^{-1}. The data were analysed for GCV, PCV, heritability, genetic advance, inter relationship among the components for yield i.e. character association and to estimate the direct and indirect influences of the component traits i.e. path analysis. Results of GCV and PCV showed medium to high GCV and PCV for number of pods plant^{-1}, cluster plant^{-1} and number of branches plant^{-1} indicating high variation in these characters, predicting greater scope for improvement. Medium to high heritability along with high genetic advance were exhibited by number of pods plant^{-1}, cluster plant^{-1}, number of branches plant^{-1}, 100 seed weight and seed yield plant^{-1}. Also the results of path analysis suggested that number of pods plant^{-1}, followed by plant height and days to 50% flowering recorded highest positive direct effect on seed yield plant^{-1}. Correlation study had strong positive correlation with number of pods plant^{-1}, number of branches plant^{-1}, cluster plant^{-1} and 100 seed weight with seed yield plant^{-1}. So from the present research work, mutants NSM-21-16 and NSM-21-18 were isolated as superior lines for further soybean breeding programme.

(Key words:Character association, path analysis, heritability, variability, soybean, mutants)

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is considered as a miracle crop due to its extraordinary qualities. It is a wonderful crop gifted by the nature to mankind which is one of the richest sources of oil as well as protein. It belongs to the family Leguminoceae, sub-family Papilionoidea (*Fabaceae)* and is a self-pollinated crop having chromosome number of 2n=40. It contains about 37-42% of good quality protein, 6% ash, 29% carbohydrate and 17-24% oil comprising 85% unsaturated fatty acid with two essential fatty acids (linoleic and linolenic acid) which are not synthesized by the human body, so it is highly desirable in human diet. Soybean protein is rich in valuable amino acid lysine (5%) in which most of the cereals are deficient (Gopinath and Pavadai, 2015).

India is on the 5th position with respect to area and production. As we compare the productivity of India and Maharashtra it appears high but it is still far less than the USA, Brazil and China. It is because of the lack of high yielding varieties and susceptibility of available varieties to biotic stress like viral disease (YMY), root rot, etc. so there is a need to increase productivity by developing high yielding and diseased resistance varieties.

Direct selection for increasing soybean yield is frequently misleading. Thus, understanding existing variability and the degree of association between yield contributing characters and their relative contribution to yield is critical for developing high yielding soybean genotypes. However,In this regards,mutation breeding has been use to generate genetic variability and have been successfully utilised to improve yield and yield component of various crops. (Lande *et al.*, 2018).

Kalpande *et al.* (2020) state that mutation breeding have been found promising to induced variability for qualitative and quantitative traits in various crops. The different genetical and breeding problem can be solved by inducing the artificial mutation in the organism and plants. Therefore, the technique of mutation breeding has been adopted as a valuable supplement to conventional breeding to create additional genetic variability. The variability created through mutations is utilised for further crop/genotype

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improvement Chavhan *et al.* (2020).The existing variability is a combination of genetic and environmental factors. Environmental variability is not heritable, whereas genetic variability is passed down from generation to generation. As a result, heritability and genetic advance can help breeders to determine the direction and magnitude of selection (Prajapati *et al.,* 2020). Similarly, correlation studies provide an opportunity to study the direction and magnitude of association of yield with its components and also among various components. Path coefficient is essential to accumulate optimum combination of yield contributing characters and to know the implication of interrelationship of various characters in a single genotype. Therefore, putting these view, the present study was framed and was implemented by selecting M_7 mutant progenies for evaluation and identification of high yielding mutant lines.

MATERIALS AND METHODS

The 30 soybean mutants (M_6 generation) identified alongwith 3 checks (TAMS-38, JS- 335 and AMS MB 5 -18) were planted in RBD with three replications in *kharif* 2021 to raise M_7 generation. The research was conducted at Research farm of All India Coordinated. Research Project on Linseed and Mustard, College of Agriculture, Nagpur. All the recommended cultural practices were followed to raise a good crop. The observations on nine characters recorded *viz.*, days to 1st flower, days to 50% flowering, days to maturity, plant height, number of branches plant[-1], number of pods plant[-1], 100 seed weight, cluster plant[-1] and seed yield plant[-1] in M_7 generation.

The analyses of variance was performed to test the significance of different among the genotypes for the different characters studied as per the methodology suggested by Panse and Sukhatme (1954). Partitioning the variance into genotypic, phenotypic and environmental components were done a ssuggested by Fisher andYates (1958). The genotypic and phenotypic coefficients of variations were computed according to Burton and Devane (1953). Heritability in broad sense which is the heritable variation were estimated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage (Hanson *et al.*,1956). The extent of genetic advance expected by selecting five per cent of the superior genotype was calculated by using the following formula given by Robinson *et al.*(1949). The phenotypic and genotypic correlation co-efficient were estimated between two characters using the variance and covariance between them as per the procedure suggested by Sharma (1998) and path coefficient analysis was done by method given by Dewey and Lu (1959).

RESULTS AND DISCUSSION

The analysis of variance for experimental design was worked out for nine characters (Table 1), The mean sum of squares due to genotypes were highly significant for all the characters studied. This reveals that the genotypes had significant amount of genetic variability among themselves for seed yield plant[-1] and other yield components, which allow the further estimation of different parameters for all nine characters.The study revealed that estimates of phenotypic coefficient of variation (PCV) were higher than their corresponding values of genotypic coefficient of variation (GCV) for all the nine characters under consideration indicating that, the apparent variation was not only due to genotypes but also due to the influence of environment in the expression of genotypes. The results were in accordance with the results of Jandong *et al.* (2020), Khadka *et al.* (2021) and Khan *et al.* (2022) in soybean, who also observed higher value of PCV than their respective value of GCV due to the influence of environment. Amongst all the characters studied, the highest GCV and PCV were recorded for number of pods plant[-1] and cluster plant[-1]. Medium value for number of branches plant[-1] indicating high variation in these characters and predicting greater scope for improvement of these three characters. Similarly, high variability has been recorded by Mahbub *et al.* (2019) and Kumari *et al.* (2022) for number of pods plant[-1], number of branches plant[-1] and cluster plant[-1] in soybean.

The heritability estimated for the nine characters using 30 mutants and three checks of soybean are presented in Table 2. High heritability were recorded for number of pods plant[-1] (78.63%), cluster plant[-1] (71.40%), number of branches plant[-1] (66.25%) and 100 seed weight (63.71%) reflecting the importance of these traits in selection programme. This indicated that these characters were less governed by a few major genes or additive gene effect even, if they were under polygenic control and therefore, selection of these characters would be more effective for yield improvement. Moderate estimate of heritability were observed for seed yield plant[-1] (33.46%) and days to 50% flowering (33.14%). Low heritability was recorded for days to maturity (28.06%), days to first flower (26.44%) and plant height (24.75%). In accordance to these results Chandrawat *et al.*(2017) and Kumari *et al.* (2022) found high heritability coupled with high genetic advance for pods plant[-1], plant height and yield plant[-1]. Uiekey *et al.* (2018) also found high heritability along with high genetic advanced for number of mature pods plant[-1] in groundnut.

Genetic advance as percentage of mean value were high for number of branches plant[-1] (799.34%), seed yield plant[-1] (82.37%), number of pods plant[-1] (70.57%) and 100 seed weight (54.93%). Moderate genetic advance as percentage of mean value was not observed, whereas low genetic advance as percentage of mean value was found for plant height (9.64%), days to first flower (9.03%), days to 50% flowering (6.73), cluster plant[-1] (5.79) and days to maturity (1.43%). Similar to these results high genetic advance as percentage of mean were also reported by Chandrawat *et al.* (2017) and Kumari *et al.* (2022). In the present study number of branches plant[-1], number of pods plant[-1] and 100 seed weight showed the high heritability

along with high genetic advance. While seed yield plant[-1] exhibited medium heritability with high genetic advance. Estimate of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. High heritability along with high genetic gain indicated in these characters was due to considerable additive gene effects and selection may be effective. Thus, selection on the basis of these characters would be more effective for further breeding programs. Similar results to these were found by Aditya *et al*. (2011) for number of primary branches plant[-1] and 100 seed weight and Kumari *et al*. (2022) for seed yield, biological yield, number of pods plant[-1] number of branches plant[-1] and 100 seed weight in soybean.

Correlation and path coefficient analysis

In the present study, results of correlation analysis showed that cluster plant[-1] exhibited highly positive and significant correlation (0.61, 0.53) at both genotypic and phenotypic levels with seed yield plant[-1]. Number of pods plant[-1] exhibited positive significant correlation at both genotypic and phenotypic level (0.5290, 0.4260) with seed yield plant[-1]. 100 seed weight exhibited positive and significant correlation with seed yield plant[-1] at genotypic level (0.37), number of branches plant[-1] exhibited highly positive significant correlation at genotypic and level (0.45) with seed yield plant[-1]. These results are in accordance with the study of Kumar *et al*. (2018) and Deshmukh (2020),who observed plant height, number of pods[-1], plant[-1]100 seed weight had strong positive correlation with seed yield plant[-1.]

In the present investigation, it was found that number of pods plant[-1] (0.858) recorded magnitudinally the highest positive direct effect on seed yield plant[-1]followed by plant height (0.062) and days to 50% flowering (0.046). The character days to maturity (-1.184) recorded highest but negative direct effect on seed yield plant[-1] followed by days to 1st flower (-0.988), number of branches plant[-1](-0.160), cluster plant[-1](-0.636) and 100 seed weight (-0.121) (Table 4).

In the present investigation path coefficient analysis (Table 4) revealed that number of pods recorded magnitudinally the highest positive direct effect on seed yield plant[-1] followed by plant height and days to 50% flowering. These direct effects are mainly responsible for significant positive association of these characters with seed yield plant[-1]. These results similar to findings of Balla

and Ibrahim (2017), Deshmukh *et al*. (2020) and Mehra *etal*. (2020), who observed higher possitive direct effect of number of pods plant[-1] and number of seeds pod[-1] on seed yield plant[-1]in soybean.When any character recorded negative direct effect on seed yield plant[-1] but character exhibited positive significant correlation with seed yield plant[-1], then the indirect causal factors are to be considered simultaneously for selection. Based on findings of present investigations it could be enforced that the most desirable plant type in soybean should possess characters number of pods plant[-1] 100 seed weight and plant height.

Genotypic path coefficient analysis was carried out by taking seed yield plant[-1] as a dependent character and data are presented in Table 4 and 5. The residual effect was found to be -0.5674 which reveals that sufficient characters were included in the path coefficient and hence the information drawn can be used.The partitioning of positive genotypic correlation of seed yield plant[-1] with different traits into direct and indirect effects revealed that number of pods plant[-1] (0.858) contributed highest positive direct effect followed by plant height (0.062) and days to 50% flowering. The research findings are in accordance with Mehbub *et al*. (2019),who reported substantially high positive direct effect and number of pods plant[-1] and number of seeds pod[-1] on seed yield plant[-1] in soybean. In term of percentage maximum direct effect contributed toward positive significant genotypic correlation was number of pods plant[-1] (162.19%). However, negative direct effect on seed yield plant[-1] was attributed by days to maturity (-1.184), days to first flower (-0.988), cluster plant[-1] (-0.636), number of branches plant[-1] (-0.160) and 100 seed weight (-0.121).The residual effect determines how best the causal factors account for the variability of the dependent factor the seed yield in this case. In present study, residual effect was low (-0.5674) indicating that characters studied considered sufficient for the variability in seed yield of soybean. Silva *et al*. (2015) also reported the similar results in which they also found low residual effect.

In the present investigation, based on high GCV, PCV, high heritability along with genetic advance, positive significant genotypic correlation with yield and path coefficient analysis studied in this experiment, suggested only one character i.e., number of pods plant[-1] was useful. Considering this character, mutants NSM 21-16 and NSM 21-18 are isolated as superior lines over all the lines for further soybean breeding programme.

Table 1. Analysis of variance (mean sum of squares) for different characters under study in soybean

Sources of variation	D.F.	Mean sum of squares								
		Days to 1st flower	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches plant⁻¹	No. of pods plant⁻¹	100 seed weight (g)	Cluster plant⁻¹	Seed yield plant⁻¹ (g)
Replications	2	10.74	4.74	4.53	66.58	0.15	27.91	0.45	0.41	5.78
Treatments	32	9.85**	7.53**	9.30**	47.97**	0.37**	397.34**	1.00**	5.36**	5.91**
Error	64	4.74	3.03	4.29	24.14	0.05	32.90	0.16	0.63	2.35

*Significant at 5% level, **Significant at 1% level

Table 2. Estimates of genetic variability, heritability, genetic advance and genetic advance per cent of mean for different traits in the soybean genotype

Sr. No.	Characters	GCV(%)	PCV(%)	Heritability (%)	G.A.	G.A. (% mean)
1	Days to first flower	3.38	6.49	26.44	3.535	9.03
2	Days to 50 % flowering	2.64	4.58	33.14	3.130	6.73
3	Days to maturity	1.30	2.46	28.06	1.424	1.43
4	Plant height	5.15	10.35	24.75	5.279	9.64
5	No. of branches plant⁻¹	12.50	15.30	66.25	20.863	799.34
6	No. of pods plant⁻¹	20.63	23.26	78.68	37.700	70.57
7	100 seed weight	4.21	5.27	63.71	6.922	54.93
8	Cluster plant⁻¹	20.43	24.18	71.40	35.537	5.79
9	Seed yield plant⁻¹	8.68	14.99	33.46	10.338	82.37

Table 3. Genotypic and phenotypic correlation of different traits

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches plant⁻¹	No. of pods plant⁻¹	100 seed weight (g)	Cluster plant⁻¹	Seed yield plant⁻¹
Days to first flower	G	0.87**	-0.08	0.40*	-0.12	0.09	-0.53	-0.07	-0.61
	P	0.68**	-0.013	0.23	-0.11	0.05	-0.34	-0.10	-0.38
Days to 50% flowering	G		0.04	0.98**	-0.12	0.17	-0.25	0.08	-0.60
	P		0.10	0.52**	-0.13	0.10	-0.14	-0.01	-0.38
Days to maturity	G			0.34*	-0.24	-0.24	-0.08	-0.51	-0.91
	P			0.13	-0.20	-0.16	-0.08	-0.30	-0.45
Plant height (cm)	G				-0.06	0.25	0.17	0.05	-0.51
	P				-0.02	0.18	0.16	0.02	-0.20
No. of branches plant⁻¹	G					0.45**	0.03	0.25	0.46**
	P					0.39*	0.04	0.22	0.33
No. of pods plant⁻¹	G						0.01	0.74**	0.52**
	P						-0.02	0.72**	0.42*
100 seed weight (g)	G							0.21	0.37*
	P							0.15	0.30
Cluster plant⁻¹	G								0.61**
	P								0.53**

Table 4. Direct and indirect effects of eight variables of soybean mutant lines

Characters	Days to first flower	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches plant⁻¹	No. of pods plant⁻¹	100 seed weight (gm)	Cluster plant⁻¹	Genotypic correlation with seed yield plant⁻¹
Days to first flower	**-0.988**	0.040	0.097	0.024	0.019	0.081	0.065	0.051	-0.613
Days to 50% flowering	-0.860	**0.046**	-0.058	0.071	0.020	0.148	0.031	-0.005	-0.607
Days to maturity	0.081	0.002	**-1.184**	0.021	0.039	-0.206	0.011	0.325	-0.911
Plant height(cm)	-0.388	0.052	-0.409	**0.062**	0.010	0.216	-0.021	-0.033	-0.512
No. of branches plant⁻¹	0.118	-0.006	0.290	-0.004	**-0.160**	0.390	-0.004	-0.165	0.460
No. of pods plant⁻¹	-0.093	0.008	0.284	0.016	-0.072	**0.858**	-0.001	-0.471	0.529
100 seed weight (gm)	0.529	-0.012	0.105	0.011	-0.005	0.008	**-0.121**	-0.138	0.377
Cluster plant⁻¹	0.079	0.002	0.605	0.003	-0.041	0.635	-0.026	**-0.636**	0.618

* Values in the bold are the direct effect   Residual effect = - 0.5674

Table 5. Estimates of direct and indirect effect of different traits in soybean in terms of percentage

Characters	Genotypic correlation with seed yield plant[-1]	Direct effect	% Direct effect	Total indirect effect	% indirect effect	Character contributing toward indirect effect
Days to first flower	-0.613	-0.988	161.17	0.377	-61.50	NPPP, 100SW, DTM
Days to 50% flowering	-0.607	0.046	-7.570	-0.653	107.57	PH, NPPP, 100SW
Days to maturity	-0.911	-1.184	129.96	0.273	-29.96	CPP, DTFF
Plant height(cm)	-0.512	0.062	-12.100	-0.573	111.91	NPPP, NBPP
No. of branches plant[-1]	0.460 **	-0.160	-34.780	0.619	134.56	NPPP, DTM, DTFF
No. of pods plant[-1]	0.529 **	0.858	162.19	-0.329	-62.19	DTM, PH
100 seed weight (gm)	0.377 *	-0.121	-32.09	0.498	132.09	DTFF, DTM
Cluster plant[-1]	0.618**	-0.636	-102.91	1.255	203.07	DTM, NPPP

DTFF = Days to first flowering NBPP = Number of branches plant[-1]

NPPP = Number of pods plant[-1] D 50% F = Days to 50%f lowering

100 SW = 100 seed weight DTM = Days to maturity

CPP = Cluster plant[-1] PH = Plant height

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