

Revealing the inheritance of qualitative traits and identification of transgressive segregants for productivity traits in early segregating generation of soybean [*Glycine max* (L.)Merril]

Abstract

The breeding effort was carried out to elucidate information on the inheritance of qualitative traits and identification of transgressive segregants for productivity traits in two crosses viz., DSb 23 x MACS 1575 (Cross 1) and DSb 23 x MACS 1460 (Cross 2) in soybean during *Kharif* 2020 at Botany Garden, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad. The observations were recorded on nine traits viz., days to 50% flowering, days to maturity, plant height, pods per plant, 100 seed weight, seed yield per plant, hilum colour, leaf shape and flower colour. Test for goodness of fit revealed that the traits viz., flower colour and leaf shape are controlled by a single dominant gene (3:1) and hilum colour was controlled by two genes with complementary gene action (9:7). In general, the percent of transgressive segregants obtained for yield-related traits was in a range of 7-17%. The high frequency of favorable segregants was identified for pods per plant (15.33%), 100 seed weight (13.87%) and days to maturity (16.42%) in cross 1, and high frequency of favorable segregants in cross 2 were observed for days to 50% flowering (8.95%), plant height (13.75%) and seed yield per plant (14.17%). These segregants can be further utilized in the breeding programme to develop high-yielding varieties and morphological traits can be used as markers in molecular breeding.

Keywords: Complementary gene action, Morphological traits, Qualitative traits, Transgressive segregants, Soybean.

1. Introduction

Soybean is regarded as the 'miracle crop' or 'Golden Bean' of the 20th century. Soybean belongs to the *Fabaceae* family and is native to north eastern China. The distribution of genotype frequencies illustrates how the F₂ seed, a segregating population, integrates with

a thorough level of segregation in the F₂ generation. The number of genes involved in regulating a qualitative trait and inheritance patterns can both be predicted using the frequency distribution. Massive genetic and phenotypic diversity is caused by maximum segregation in F₂ generation. Development and improvement of new, high-yielding cultivars is greatly aided by high genetic diversity (Kuswanto *et al.*, 2017).

Breeding programs can be effectively directed by using inheritance patterns as a genetic parameter. Gene action and interaction results in different patterns of segregation in plants. The expression of phenotypes is regulated by gene action (Sayama *et al.*, 2017). Three categories of gene actions can be distinguished in plants i.e. additive, dominant and epistasis gene actions. Additive gene action is the result of genes contributing alleles without interacting with other genes to produce a new phenotype that makes parents and their offspring's traits similar (Suh *et al.*, 2000).

A plant's genetic makeup is determined by either a large number of genes or few genes. Characters controlled by a small number of genes (one or two genes) are referred to as qualitative characters because they are typically defined by an erratically distributed frequency distribution. On the other hand, characters controlled by a large number of genes (more than two genes) are known to as quantitative characters because they are characterized by a regularly distributed frequency distribution. The objective of this investigation is to identify the number of genes and inheritance pattern regulating the morphological characteristics of soybean leaves, pods, and seeds.

Studies on transgressive segregants allow us to figure out their proportions for different characters that contribute to the yield. These characters having high variability and heritability will be of more useful in population development and other breeding programs. In any crop improvement programme knowledge of morphology of traits, their inheritance pattern, nature, and number of genes responsible for that trait are important. This ensures a better combination of desirable traits in offspring for any improvement programme. The existence of wide morphological diversity in soybeans offers ample opportunity for genetic studies.

A wide spectrum of variability is expected to be shown by progenies derived from a set of diverse crosses, thereby providing a greater scope for isolating high yielding segregants. Transgressive segregants are generated by the accumulation of favourable genes

from parents involved in hybridization. Studies on transgressive segregants allow us to figure out their proportions for different characters that contribute to the yield. These characters having high variability and heritability will be of more useful in population development and other breeding programs.

Keeping the aforesaid views, an attempt has been made with the following objectives in the present investigation.

1. To study the inheritance of qualitative traits.
2. To identify transgressive segregants for yield and yield attributing traits.

2. Materials and Methods

The experimental material for the present study comprised of F₂ populations of two crosses involving three diverse parents *viz.*, DSb 23, MACS 1575 and MACS 1460 as given in Table 1. Among the parents, DSb 23 is a high yielding variety with broad leaves, brown hilum colour and purple flowers. Whereas, MACS 1575 and MACS 1460 are the genotypes from Agharkar Research Institute, Pune, Maharashtra were low yielders compared to DSb 23. MACS 1575 has narrow leaves and black hilum colour but MACS 1460 has white flowers and black hilum colour. To understand the inheritance of qualitative traits and identification of transgressive segregants, DSb 23 was crossed with MACS 1575 and MACS 1460. The seeds of two F₂ populations *viz.*, DSb 23 x MACS 1575 (Cross 1) and DSb 23 x MACS 1460 (Cross 2) were obtained from AICRP on Soybean, Main Agricultural Research Station, University of Agricultural Sciences, Dharwad. List of F₂ populations under study is given in Table 2.

Table 1: List of parents having contrasting traits

Parents	Shape of leaves	Hilum Colour	Flower colour
DSb 23	Broad leaves	Brown colour	Purple flowers
MACS 1575	Narrow leaves	Black colour	Purple flowers
MACS 1460	Broad leaves	Black colour	White flowers

Experimental site

The present experiment was carried out during *kharif* 2020-21 at Botany Garden, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad. The experiment comprising of F₂ populations of the two crosses *viz.*, DSb 23 x MACS 1575 (Cross 1) and DSb 23 x MACS 1460 (Cross 2) along with the parents DSb 23, MACS 1575, MACS 1460 were sown in a row length of 5 m with spacing 30 cm between rows and 10 cm between plants. The experiment was laid out in an un-replicated trial during *kharif* 2020-21 under *rainfed* conditions. The experimental material was sown on 12th July 2020. The recommended package of practices was followed to raise a good crop. Observations on individual plants were recorded in two F₂ populations. In each F₂ population individual plants were tagged for recording observations on 10 different quantitative and qualitative traits. Observations were recorded on qualitative traits like leaf shape, hilum colour, flower colour and quantitative traits like yield and yield attributing traits.

Table 2: List of F₂ populations under study

Sl. No	Cross	Parents	Number of F ₂ seeds	Plant stand (at harvesting)	Germination (%)
1	Cross 1	DSb 23 x MACS 1575	357	274	76.75
2	Cross 2	DSb 23 x MACS 1460	589	480	81.49

Identification of transgressive segregants

In both the segregating populations, the number of plants that performed better than mean plus (+) one standard deviation for a group of traits *viz.*, plant height, pods per plant, 100 seed weight and seed yield per plant were noted as transgressive segregants and expressed in percentage. Whereas for days to maturity and days to 50% flowering selection criteria for identifying transgressive segregants was mean minus(-) one standard deviation and are also expressed in percentage.

Test for goodness of fit

The chi-square test based on the enumerative data (qualitative) is a valuable tool for the breeder to decide whether the observed data is according to an expected ratio or it agrees well with expected or theoretical frequency distribution. It is done as per the method suggested by Panse and Sukhatme (1967). χ^2 is expressed as follows.

$$\chi^2 = \sum_{i=1}^n \frac{(O-E)^2}{E}$$

Where,

O = Observed frequency of the class

E = Expected frequency of the respective class

The table χ^2 value was taken at (n-1) degrees of freedom and at 0.05 probability level. The null hypothesis H_0 is rejected, if observed χ^2 is found to be greater than the theoretical χ^2 and this difference is said to be significant. Otherwise, the null hypothesis is accepted and the difference between observed and theoretical frequency distribution is not significant.

3. Results

3.1. Inheritance studies for leaf shape and hilum colour in cross 1 (DSb 23 x MACS 1575)

χ^2 value and probabilities for the segregation of leaf shape and hilum colour in cross 1 are presented in Table 3 respectively.

3.1.1. Leaf shape

The parental lines DSb 23 and MACS 1575 differed for leaf shape. DSb 23 was a genotype with broad leaves and MACS 1575 was having narrow leaves. In the F_2 population, 274 individual plants were observed for leaf shape. 210 plants had broad leaf shape whereas 64 plants bore narrow leaves. The calculated chi-square value indicates that the observed value for leaf shape fitted well with an expected ratio of 3 broad: 1 narrow leaf shape which indicates that this character is controlled by a single dominant gene.

3.1.2. Hilum colour

In the cross between DSb 23 x MACS 1575, observations were recorded for hilum colour to study its mode of inheritance. In DSb 23 the colour of hilum is brown whereas in MACS 1575 it is black. In the F_2 population, individual plants were observed for their hilum colour, 167 plants out of 274 plants showed black hilum whereas 107 plants were having brown hilum. The calculated chi-square value indicates that the observed value for hilum colour fitted well with an expected ratio of 9 black: 7 brown. This denotes the character is controlled by two genes with complementary gene action.

3.2. Inheritance studies for flower colour and hilum colour in Cross 2 (DSb 23 x MACS 1460)

χ^2 value and probabilities for segregation of flower colour and hilum colour in cross 2 (DSb 23 x MACS 1460) are presented in Table 4 and Table 5 respectively.

3.2.1. Flower colour

The parental lines exhibited variability in flower colour. DSb 23 has purple flowers, whereas the other parent, MACS 1460 has white flowers. In the cross DSb 23 x MACS 1460, observations were recorded for flower colour to study mode of inheritance of flower colour. In the F₂ population, 480 individual plants were observed for flower colour. 388 plants had purple flower whereas 92 plants bore white colored flowers. The calculated chi-square value indicates that the observed value for flower colour fitted well with an expected ratio of 3 purple: 1 white which indicates that this character is controlled by a single dominant gene.

Table 3: χ^2 value and probabilities for segregation of qualitative traits in Cross 1 (DSb 23 x MACS 1575) and Cross 2 (DSb 23 x MACS 1460)

Cross 1 (DSb 23 x MACS 1575)						
		Observed	Expected	(O-E) ² /E	χ^2	P
Leaf shape	Broad	210	205.5	0.10	0.39	0.53 (0.6-0.5)
	Narrow	64	68.5	0.30		
	Total	274				
Hilum colour	Black	167	154.12	1.08	2.46	0.12 (0.2-0.1)
	Brown	107	119.88	1.38		
	Total	274				
Cross 2 (DSb 23 x MACS 1460)						
Flower colour	Purple	388	360	12.47	49.88	0.003 (0.004-0.003)
	White	92	120	37.41		
	Total	480				
Hilum colour	Black	289	270	1.34	3.06	0.08 (0.09-0.08)
	Brown	191	210	1.72		
	Total	480				

3.2.2 Hilum colour

In the cross between DSb 23 and MACS 1460, observations were recorded for hilum colour to study its mode of inheritance. In DSb 23, the colour of hilum is brown whereas in MACS 1460 it is black. In the F₂ population, individual plants were observed for their hilum colour, 289 plants out of 480 plants showed black hilum whereas 191 plants were having brown hilum. The calculated chi square value indicates that the observed value for hilum colour fitted well with an expected ratio of 9 black: 7 brown. This denotes the character is controlled by two genes with complementary gene action. Similar result was also observed in the cross DSb 23 xMACS 1575 for hilum colour.

3.3. Identification of transgressive segregants

Per cent, transgressive segregants in the F₂ population of both the crosses for days to 50% flowering, days to maturity, plant height, pods per plant, 100 seed weight, and seed yield per plant are given in Table 4. The criterion followed for the selection of transgressive segregants was meanplus (+)one standard deviation. However, for days to 50% flowering and days to maturity, meanminus (–)one standard deviation was considered for identifying the superior segregants.

3.3.1. Frequency of transgressive segregants for six traits in Cross 1 (DSb 23 xMACS 1575)

3.3.1.1 Days to 50% flowering

Among the two parents, MACS 1575 was early flowering (38 days) and DSb 23 was late flowering (45 days). In F₂ segregating generation the average days taken for 50% flowering was 41 days. Twenty-one transgressive segregants with early flowering were obtained which accounted for 7.66%. These transgressive segregants recorded a range of 38-40 days for days 50% flowering.

3.3.1.2 Days to maturity

Among the two parents, MACS 1575 was early maturing with 84 days and DSb 23 was late which recorded 95 days to mature. In F₂ segregating generation the average days to maturity was 95 days with a standard deviation of 17.22 days. The number of transgressive segregants obtained was 45 (16.42%). The mean of superior segregants ranged from 79-90 days for maturity.

3.3.1.3 Plant height

The mean values of parents DSb 23 and MACS 1575 for plant height were 50.4 cm and 41 cm, respectively. In F₂ segregating generation the average plant height was 43.85 cm. The number of transgressive segregants obtained was 33 with a frequency of 12.04 per cent and recorded a range of 55-76 cm for plant height.

3.3.1.4 Pods per plant

It is evident from Table 5 that the parental lines DSb 23 and MACS 1575 recorded mean of 74.6 and 38 pods per plant respectively. In F₂ segregating generation the average number of pods per plant was 66.23 with a standard deviation of 30.19 pods per plant. Pods per plant in cross 1 recorded the highest frequency of transgressive segregants (42 plants out of 274 plants) compared to other studied characters, which accounted for 15.33%. Transgressive segregants for pods per plant ranged from 97-160 pods.

3.3.1.5 100 Seed weight

In F₂ segregating generation the average of 100 seed weight was 11.43 g with a standard deviation of 2.47 g. Data presented in Table 4, showed that the mean value of 100 seed weight in parental lines DSb 23 and MACS 1575 were 12.8 g and 13.7 g, respectively. The number of transgressive segregants in F₂ for 100 seed weight was 38 with a frequency of 13.87 percent and a range of 14-15.5 g.

Table 4: Per cent transgressive segregants for different characters in F₂ populations of the two crosses of soybean

Characters	Cross	Transgressive segregants			
		Mean	SD	Number of plants	%
Days to 50% flowering	DSb 23 x MACS 1575	41	2.89	21	7.66
	DSb 23 x MACS 1460	40	5.56	43	8.95
Days to maturity	DSb 23 x MACS 1575	95	17.22	45	16.42
	DSb 23 x MACS 1460	95	18.23	63	13.12
Plant height (cm)	DSb 23 x MACS 1575	43.85	10.54	33	12.04
	DSb 23 x MACS 1460	41.28	7.54	66	13.75
Pods per plant	DSb 23 x MACS 1575	66.23	30.19	42	15.33

	DSb 23 x MACS 1460	73.87	29.92	65	13.54
100 seed weight (g)	DSb 23 x MACS 1575	11.43	2.74	38	13.87
	DSb 23 x MACS 1460	10.34	2.47	57	11.87
Seed yield per plant (g)	DSb 23 x MACS 1575	16.50	9.26	29	10.58
	DSb 23 x MACS 1460	18.71	10.91	68	14.17

3.3.1.6 Seed yield per plant

From Table 5, it is clear that the mean value for seed yield per plant in parent DSb 23 and MACS 1575 were 28.5 g and 14.7 g, respectively. In F₂ segregating generation the average seed yield per plant was 16.50 g with a standard deviation of 9.26 g. The number of transgressive segregants in F₂ was 29 with a frequency of 10.58 percent and these transgressive segregants ranged from 26.5 g to 52.5 g for seed yield per plant.

3.3.2 Frequency of transgressive segregants for six traits in Cross 2 (DSb 23 xMACS 1460)

3.3.2.1 Days to 50% flowering

Among the two parents, MACS 1460 was early flowering (39 days) and DSb 23 was late flowering (45 days). In F₂ segregating generation the average days taken for 50% flowering was 40 days with a standard deviation of 5.56 days. Forty-three transgressive segregants with early flowering were obtained which accounted for 8.95%. These transgressive segregants recorded a range of 35-39 days.

3.3.2.2 Days to maturity

The mean values of days to maturity, in parents DSb 23 and MACS 1460 were 95 and 86 days, respectively. In F₂ segregating generation the average days to maturity was 95 days. The number of transgressive segregants obtained was 63 (13.12%). Transgressive segregants for days to maturity ranged from 78-88 days for maturity.

3.3.2.3 Plant height

The mean values of parents DSb 23 and MACS 1460 for plant height were 50.4 cm and 43.2 cm, respectively. In F₂ segregating generation the average plant height was 41.28

cm. The number of transgressive segregants obtained was 66 with a frequency of 13.75 percent and recorded a range of 49-60cm for plant height.

3.3.2.4 Pods per plant

It is evident from Table 5 that the mean value of the parental lines DSb 23 and MACS 1460 was 74.6 and 44.2 pods per plant respectively. In F₂ segregating generation the average number of pods per plant was 73.87 with a standard deviation of 29.92 pods per plant. The number of transgressive segregants obtained was 65 (13.54%). Transgressive segregants for pods per plant ranged from 104-175 pods.

3.3.2.5 100 Seed weight

In F₂ segregating generation the average of 100 seed weight was 10.34 g. Data presented in Table 4, showed that the mean value of 100 seed weight in parent DSb 23 and MACS 1460 were 12.8 and 13.3 g, respectively. The number of transgressive segregants in F₂ for 100 seed weight was 57 with a frequency of 11.87 percent and ranged between 16-20.5 g.

3.3.2.6 Seed yield per plant

From Table 5, it is clear that the mean value of parent DSb 23 and MACS 1460 recorded 28.5 g and 15.2 g seed yield per plant, respectively. In F₂ segregating generation the average of seed yield per plant was 18.71 g with a standard deviation of 10.91 g. The number of transgressive segregants in F₂ was 68 with a frequency of 14.17 percent and mean of these superior segregates ranged between 30-55 g.

From the above information, it can be concluded that a high frequency of favorable segregants was identified in F₂ generation of cross 1 for pods per plant (15.33%) followed by 100 seed weight (13.87%) and days to maturity (16.42%) and in cross 2, high frequency of favourable segregants in F₂ generation were observed for days to 50% flowering (8.95%) followed by plant height (13.75%) and seed yield per plant (14.17%).

Table 5: Mean performance of the parents and checks for different characters in soybean

Parents/Checks	Days to 50%	Days to maturity	Plant height	Pods per plant	100 seed weight	Seed yield per
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	flowering		(cm)		(g)	plant (g)
DSb 23	45	95	50.40	74.60	12.80	28.50
MACS 1575	38	84	41.00	38.00	13.70	14.70
MACS 1460	39	86	43.20	44.20	13.30	15.20
JS 335 (check)	40	88	50.40	67.80	10.20	18.10
DSb 21 (check)	42	91	55.60	79.60	13.10	26.10

4. Discussion

4.1. Inheritance of qualitative traits in segregating generation

The present study was aimed at understanding the segregation behaviour for qualitative characters in F₂ generation to understand the population structure with different crosses emerging from the different genetic back-ground used as parents. Among both the crosses, the parents used were having contrasting characters for hilum colour, in addition, parents in cross 1 (DSb 23 x MACS 1575) had contrasting characteristics for leaf shape i.e., DSb 23 was bearing broad leaves and MACS 1575 bearing narrow leaves and in cross 2 (DSb 23 x MACS 1460) parents differed with contrasting characteristics for flower colour i.e., DSb 23 was having purple coloured flowers whereas MACS 1460 was having white flowers which made it easy for identification and recording the data in F₂ generation. From Table 3 it is clear that the calculated χ^2 value indicated that the observed value for leaf shape and flower colour fitted well with an expected ratio of 3 broad: 1 narrow for leaf shape and 3 purple: 1 white for flower colour, respectively, which indicated that these characters are controlled by a single dominant gene. Similar results were observed by Dasriani et al. (2020) for leaf shape in soybean. Nguyen (2012), Vu (2013), and Vu et al. (2017) reported that single gene with a complete dominant effect is responsible for flower colour in mung bean. The calculated χ^2 value for hilum colour fitted well with an expected ratio of 9 black: 7 brown colour which indicated that this character is controlled by two genes with complementary gene action. Pipolo et al. (2015) reported that hilum colour is controlled by two genes segregating independently in soybean. The above information will help the plant breeder to understand the inheritance of various qualitative characters of economic importance and their

use as marker characters in the varietal identification as also in formulating a suitable breeding programme to evolve new superior varieties.

4.2. Identification of transgressive segregants

Recombination breeding is one of the important breeding methods to incorporate and to get the favorable quantitative and qualitative traits for both the parents in their progenies. Transgressive segregation refers to the phenomenon through which we get variation in F₂ or later generation outside the range of both parents. Selection in F₂ generation for transgressive segregants is likely to help the breeder to pick out the most favorable genotypes. In the present investigation, 754 progeny lines from crosses viz., DSb 23 x MACS 1575 and DSb 23 x MACS 1460 have generated greater variability and useful segregants. Transgressive segregants were recorded in each of the two crosses for yield and yield contributing traits based on mean \pm 1 standard deviation. Per-cent transgressive segregants in the F₂ population of both the crosses for days to 50% flowering, days to maturity, plant height, pods per plant, 100 seed weight and seed yield per plant are given in Table 4. In the general, high frequency of favorable segregants were identified in F₂ generation of cross 1 for pods per plant (15.33%), 100 seed weight (13.87%) and days to maturity (16.42%) and in cross 2, high frequency of favourable segregants in F₂ generation was observed for days to 50% flowering (8.95%), plant height (13.75%) and seed yield per plant (14.17%). This could be due to the fact that the parents used in these two crosses were diverse for the characters studied. Karkute and Girase (2002) observed the highest transgressive segregants for plant height (27%) followed by pods per plant and seed yield per plant in chickpea. Massey et al. (2008) reported transgressive segregation in F₂ generations of soybean for days to maturity. Rajavindran et al. (2000) reported high frequency of transgressive segregants for plant height (16.88%) and seed yield per plant (13.92%) in sesame. Aditya et al. (2013) reported transgressive segregants in F₂ and F₃ generations for plant height, number of pods per plant, 100 seed weight, and grain yield per plant in soybean. For yield and its component traits viz., days to 50% flowering, days to maturity, plant height, pods per plant and 100 seed weight considered simultaneously, superior segregants were identified in each of the two crosses. Transgressive segregants for three or more yield component traits were identified as superior transgressive segregants. The possible explanation of simultaneous transgression for two or more yield components is that yield is dependent on yield attributing characters. The details of which are given in Table 6.

Table 6: Superior transgressive segregants identified for productivity traits

Sl. No.	Cross	Plant no.	Days to 50% flowering	Days to maturity	Pods per plant	100 seed weight (g)	Seed yield per plant (g)
1	DSb 23 x MACS 1575	9	38	85	65	13.5	16.5
		26	38	81	96	11.5	28.5
		35	38	80	144	14	35
		38	40	84	108	12.5	29.5
		74	40	86	122	14.5	34
		88	38	80	70	11	16
		92	40	83	99	13.5	30.5
		134	38	82	55	10.5	15
		267	39	84	110	12	33.5
	Mean±SD		41±2.89	95±17.22	66.23± 30.19	11.43± 2.74	16.50±9.26
2	DSb 23 x MACS 1460	21	38	82	111	13	33.5
		23	38	84	123	12.5	37.5
		24	38	85	141	13.5	41.5
		60	35	81	93	11.5	28.5
		85	38	79	114	11	34.5
		201	38	85	100	12.5	31.5
		205	38	79	104	12.5	32
		265	38	81	110	13.5	36
		274	38	83	104	10.5	29.5
	Mean±SD		40±5.56	95±18.23	73.87± 29.92	10.34± 2.47	18.71± 10.91
3	DSb 23 (Parent)	-	41.2	95.6	74.6	12.8	28.5
4	MACS 1575 (Parent)	-	38.4	84.8	38	11.7	12.7
5	MACS 1460 (Parent)	-	39.8	81.8	44.2	13.3	14.2

5. Conclusion

The F₂ populations of the crosses viz., DSb 23 x MACS1575 (cross 1) and DSb 23 x MACS 1460 (cross 2) were grown and observations were recorded on days to 50% flowering, days to maturity, plant height, number of pods per plant, hundred seed weight and seed yield

per plant on individual plants from each cross. In addition to this, observations on some qualitative traits like flower colour, leaf shape and hilum colour were recorded.

From the inheritance study, it was observed that flower colour and leaf shape were under monogenic gene action. Purple flower colour was dominant over white, broad leaf shape was dominant over narrow and hilum colour was controlled by two genes with complementary gene action.

High frequency of favorable segregants was identified in F₂ generation of cross 1 for pods per plant (15.33%), 100 seed weight (13.87%) and days to maturity (16.42%) and in cross 2, high frequency of favorable segregants in F₂ generation were observed for days to 50% flowering (8.95%), plant height (13.75%) and seed yield per plant (14.17%).

Therefore, these qualitative traits can be used as morphological markers in molecular breeding and the superior segregants identified for yield and its component traits need to be further tested for their superiority in replicated trials.

Future scope

Future scope of the present study would be that the identified superior transgressive segregants can be fixed as homozygous lines through continuous selfing to derive advanced breeding lines. Advanced lines can be used as parents in crop improvement programme.

Author's contribution

Data collection, statistical analysis and manuscript writing was performed by Spoorthi S. R. and Dr. Shobha Immadi made corrections in manuscript and approved the final manuscript.

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