GENETIC USEFULNESS OF MULTI-PARENTAL CROSSES VIS-À-VIS BI-PARENTAL CROSSES IN SOYBEAN

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Advanced breeding lines from seven different crosses were evaluated in randomized Block Design during *Kharif* 2016 and 2017 for the study of genetic parameters. High broad sense heritability (H_{bs}) and genetic advance as per cent of mean (GA_{PM}) were observed for seed yield per plant, biomass per plant and number of pods per plant that depicts additive gene action and hence selection based on these traits would be more reliable. Multi-parental crosses had in general higher estimates of heritability and genetic advance as compared to bi-parental crosses. Genetic usefulness (U) for yield contributing traits like pods per plant, 100 seed weight was higher in cross 2 whereas bi-parental crosses had high genetic usefulness for seed yield and biological yield per plant. Susceptibility of parental lines might have resulted in lower genetic usefulness in multi-parental crosses. Selection of diverse parents to be used in breeding programme should be undertaken while considering the susceptibility of parental lines to various biotic and abiotic factors responsible for yield losses.

Key words: Genetic advance, genetic usefulness, heritability, multi-parentalsoybean

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is an important source of protein and oil for food and feed worldwide (SHARMA *et al.* 2013, HOSSAIN and KOMATSU 2014; POPOVIĆ *et al.,* 2016; 2020). After introduction of yellow seeded soybean in 1970s from USA, in next three decades, it became number one oilseed crop of India. However, low productivity of soybean in India (1.15 t/ha) in comparison to world average (2.71 t/ha) and leading soybean growing countries viz. Brazil (3.42 t/ha) and USA (3.40 t/ha) is the major cause of concern (FAOSTAT 2023). Narrow

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genetic base of breeding populations has often been thought to be the culprit of poor genetic gains in soybean. For broadening the genetic base of breeding populations, breeders look for maximizing the genetic variance initially by selection of diverse parents and then by appropriate breeding method for generation advance that could help to obtain desired genetic gains for yield and component traits (KHOSLA *et al.* 2022). Inspite of this fact, most of the plant breeders routinely use populations derived from bi-parental crosses for development of varieties. Most of the varieties in self-pollinated crops like soybean are based on single crosses involving two parents. More complex crosses having multiple crosses for breeding self-pollinated crops were recommended earlier (JENSEN 1970) but these were not used much in soybean varietal development. Even in bi-parental crosses, a cross between high yielding parents is more likely to produce desirable progeny than a cross between high and low yielding parents (SCHOENER and FEHR, 1979; FASOULA and BOERMA, 2005). As a result, a pronounced reduction of genetic variation in newly generated cultivars is being observed (GIZLICE *et al.,* 1994; 1996; HYTEN *et al.,* 2006). To maintain high genetic variability, populations derived from complex crosses may be used to develop varieties. The approach to define the usefulness or the genetic worth of a set of genetic materials or a cross has been described (BERNARDO 2010; ALLIER *et al,* 2019) but the concept has been largely applied in cross pollinated crops like maize (TABANAO and BERNARDO, 2005).

In order to harness the productivity potential of novel materials, it is important to understand the magnitude and nature of genetic variability and association of various agro-morphological traits with grain yield. Genetic parameters help to understand the gene action, identification of components of genetic variances and finally facilitate the selection of a desirable breeding method. The genotypic and phenotypic variance influences the heritability estimates. The heritability and genetic advance are important selection parameters and more helpful in predicting the genetic gain under effective selection (BISNE *et al.,* 2009). Heritability is more accurate if it is equipped with genetic advance to determine the selection value.

In earlier studies in soybean, the genetic variability parameters *viz.* phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (H_{bs}) and genetic advance as a percentage of mean (GAPM) were exploited for grain yield and component traits to understand the extent of genetic variability, although the usefulness criterion as described by TABANAO and BERNARDO (2005) was not used.

In the present study, comparison of lines derived from bi-parental and multi-parental crosses in soybean was used to work out the worthiness of complex crosses with respect to maintain high genetic variability and heritability in the segregating progenies.

MATERIAL AND METHODS

Seven soybean crosses as given in Table 1 were used in this study. Three crosses were multi-parental crosses with five, four and three different parents whereas four crosses were bi-parental crosses. Each cross had at least one parent which is a released high yielding variety adapted to local conditions. Lines SL 525, SL 744, SL 682, SL 783, SL 794 and SL 871 are the high yielding varieties of soybean and AGS 328 and AGS 752 are vegetable soybean lines from AVRDC Taiwan, IC 391477 is an indigenous collection obtained from NBPGR, New Delhi, India and Lsb 23 is early maturing photo-insensitive variety from Southern India. During *kharif*

2016 and *kharif* 2017, the F_7 and F_8 progenies obtained from all the seven crosses were evaluated in separate experiments with three replications in each trial. Each experiment was grown in a randomized block design with three replications each. Each entry was grown in a single row of 4 m length with a row and plant spacing of 45 cm and 5 cm, respectively. The weed control was done through pre-emergence application of Stomp 30EC (Pendimethalin) @ 1600ml per acre and Parimaze 10SL (Imazethpyr) @ 300ml per acre at 20 days after sowing. Recommended fertilizer application i.e. 12.5 kg nitrogen and 32 kg phosphorous per acre was applied to raise the crop. Observations on metric traits *viz.,* plant height (cm), number of branches per plant, number of pods per plant, seeds per pod, 100-seed weight (g), harvest index (%) and seed yield per plant (g) were recorded on five random competitive plants from each treatment, whereas observations on days to flowering and maturity were recorded on plot basis.

Table 1. Number of lines studied in different crosses.

Cross No.	Cross	Number of lines studied
1	(SL 525 x AGS 328) x {(SL 744 x SL 682) x AGS 752}	31
2	SL 525 x {(AGS 328 x SL 682) x AGS 752}	35
3	SL 744 x (SL 525 x AGS 328)	39
4	SL 525 x IC 391477	47
5	SL 525 x Lsb 23	43
6	SL 783 x SL 871	36
7	SL 755 x SL 794	43

The data were analysed by MVM program for ANOVA and year x cross interaction. Heritability and Genetic advance in percent of mean (GA_{PM}) were estimated using the formula suggested by JOHNSON *et al.* (1955), HANSON *et al.* (1956). The genetic worth or usefulness (U) of each population was then estimated based on the mean and genetic advances according to (TABANAO and BERNARDO 2005, BERNADO 2010) as:

U = μ + G_A, Where, U is the genetic usefulness of a population, μ is the mean of the population and G_A is the expected genetic advance.

RESULTS AND DISCUSSION

Genetic variability is the pre-requisites for genetic improvement in a systematic breeding programme. Analysis of variance (Table 2) revealed that the treatments differ significantly for almost all the traits in all the crosses except number of branches per plant. ANOVA for the crosses pooled over years (Table 3) revealed that the crosses vary significantly for all the traits studied.

The broad sense heritability (H_{bs}), genetic advance (GA) and genetic advance as per cent of mean (GA_{PM}) were calculated for different traits in all the crosses (Table 4). The coefficients of variation depict total variability present in the population whereas, the estimate for proportion of genetic variability which is transmitted from parents to off springs is reflected by heritability. Traits with heritability more than 49 per cent are considered high (CARGNELUTTI FILHO *et al.,* 2009). Heritability estimates of all the traits varied in different crosses. Plant height

showed high heritability in cross 2 (86.8%) followed by cross 1 (76.7%) and it was lowest in cross 3 (46.5%). Branches per plant also followed the same pattern. Pods per plant also had high heritability in cross 2 (87.2%) and cross 1 (82.7%) followed by cross 4 (80.8%) and was lowest in cross 7 (69.3%). Heritability estimates varied widely for 100-seed weight ranging from high in cross 2 (80.0%) and cross 6 (71.7%) to lowest value in cross 3 (39.7%). For biomass per plant, high heritability was observed in all the crosses with highest value in cross 5 (88.2%) and lowest in cross 3 (70.1%). Days to 50% flowering also had high heritability values in all the crosses ranging from 71.0% (cross 5) to 86.1% (cross 4). Days to maturity had low to medium heritability in different crosses. Cross 2 being an exception for this trait that had the lowest heritability value (23.3%) and cross 1 having the highest heritability (66.9%). Heritability for seeds per pod varied from moderate to high heritability estimates with cross 7 having the lowest value (30.6%) and cross 6 with the highest heritability estimate of 73.7%. Yield per plant also had high heritability values in all the crosses. Cross 1 had the highest heritability value (83.5%) for seed yield closely followed by cross 4 (82.7%). Similar findings were reported by BANGAR *et al.,* (2003), KARNWAL and SINGH, (2009) for plant height, branches, and seed yield, RAMANA *et al.,* (2000), KARAD *et al.,* (2005), MALIK *et al.,* (2006), THAKUR *et al.,* (2024) for days to flowering and maturity, THORAT *et al.,* (1999), IQBAL *et al.,* (2003) for 100 seed weight, SIROHI *et al.,* (2006), GHODRATI *et al.,* (2013) for number of pods per plant and DUBEY *et al.* (2015) for biomass per plant.

Table 2. Mean square values for different traits in seven crosses pooled over two years.

Trait*	Cross1	Cross2	Cross3	Cross4	Cross5	Cross6	Cross7
PH 30 (cm)	19.1**	26.0**	13.7**	6.5**	7.2**	17.5**	11.8**
PH maturity (cm)	148.0**	372.2**	69.5**	48.4**	60.9**	94.7**	115.4**
Branches	2.3**	6.1**	0.8	1.2	1.1	1.1	0.9
Pods/plant	543.8**	1374.4**	515.7**	722.9**	553.2**	515.5**	304.3**
100-SW (g)	2.4**	5.6**	2.0**	2.5**	1.4	3.0**	1.7*
Biomass (g)	2121.3**	2333.7**	997.5**	2427.8**	1947.0**	1613.1**	1461.2**
DF	17.9**	7.5**	12.1**	13.9**	6.7**	16.4**	7.9**
DM	12.2**	4.9**	10.7**	5.8**	4.2**	7.0**	4.6**
Seeds/pods	7.0**	8.6**	9.2**	11.6**	5.9**	12.0**	6.6**
Yield (g/plant)	30.3**	36.1**	29.8**	51.5**	36.9**	33.3**	24.8**

*PH 30: Plant height (cm) 30 days after sowing; PH maturity: Plant height (cm) at maturity; Branches: number of branches per plant; pods/plant: number of pods per plant; 100-SW: 100 seed weight (g); biomass: biomass per plant (g) at maturity; DF: days to flowering; DM: days to maturity; seeds/pod: number of seeds per pod; yield: seed yield per plant (g)

Table 3. Mean square values for different traits obtained from the comparison of seven crosses for two years

Source of variation	df	Mean squares				
		PH 30 (cm)	PH maturity (cm)	Branches	Pods/plant	100-SW (g)
Year	1	1355.6[**]	37.5[**]	6.6[**]	9009.4[**]	63.4[**]
Cross	6	24.3[**]	89.5[**]	3.1[**]	723.5[**]	2.5[**]
Year x Cross	6	11.4[**]	23.6[**]	0.6[**]	218.7[**]	0.4[**]
Error	26	1.1	4.0	0.1	5.7	0.1

Source of variation	Df	Mean squares				
		Biomass (g)	DF	DM	Seeds/pods	Yield (g/plant)
Year	1	26933.3[**]	40.5[**]	43.0[**]	3.2[**]	471.0[**]
Cross	6	554.1[**]	6.5[**]	3.0[**]	3.5[**]	16.8[**]
Year x Cross	6	178.4[**]	0.6[**]	1.1[**]	0.6[**]	4.5[**]
Error	26	16.2	0.1	0.1	0.1	0.4

PH 30: Plant height (cm) 30 days after sowing; PH maturity: Plant height (cm) at maturity; Branches: number of branches per plant; pods/plant: number of pods per plant; 100-SW: 100 seed weight (g); biomass: biomass per plant (g) at maturity; DF: days to flowering; DM: days to maturity; seeds/pod: number of seeds per pod; yield: seed yield per plant (g)

Genetic advance as per cent of mean (GA$_{PM}$) for plant height at maturity varied from 8.09 in cross 5 to 27.6 in cross 2. For number of branches, pods per plant and 100-seed weight, cross 2 had highest GA$_{PM}$ of 38.8, 49.1 and 22.3, respectively, that was much higher than those in the other crosses. GA$_{PM}$ for biomass per plant was highest in cross 1 (41.4) followed by cross 4 (40.4). Days to flowering and days to maturity had low GA$_{PM}$ values in all the crosses with highest values in cross 1 for both the traits. GA$_{PM}$ for seeds per pod ranged from 4.9 (cross 7) to 13.9 (cross 6). GA$_{PM}$ for yield was high in all the crosses ranging from 34.5 to 46.0%. Highest GA$_{PM}$ was observed in cross 1 followed by cross 4. Lowest value was observed in cross 7. Traits like pods per plant, biomass per plant, days to flowering and yield per plant had high heritability as well as high genetic advance whereas 100-seed weight had high heritability and moderate genetic advance. High heritability along with high genetic advance was earlier reported for pods per plant (GOHIL *et al.,* 2006, BARUAH *et al.,* 2014), biomass per plant (DUBEY *et al.,* 2015) and seed yield per plant (SRIRANJANI *et al.,* 2007; RENI and RAO, 2013; MALEK *et al.,* 2014). High heritability combined with high genetic advance could be an indication of additive gene action and selection based on these parameters would be more reliable. The high heritability along with high genetic advance for grain yield per plant, number of pods per plant, plant height and biomass per plant indicate the role of additive genes, therefore, the selection of these characters will be effective (AKRAM *et al.*, 2011, SALMAN *et al*., 2021).

Table 4. Heritability (broad sense), genetic advance (per cent of mean) and genetic usefulness of various traits in different crosses

Trait	Genetic Parameter	Cross1	Cross2	Cross3	Cross4	Cross5	Cross6	Cross7
PH30	H_{bs}	51.12	74.78	57.16	47.33	40.08	67.62	59.85
	GA_{PM}	9.90	16.03	9.98	6.65	5.79	12.54	8.60
	U	35.92	35.98	32.80	28.5	30.2	34.1	36.13
PH maturity	H_{bs}	76.71	86.84	46.49	50.29	59.3	47.99	60.11
	GA_{PM}	17.45	27.60	8.47	8.09	9.92	9.66	12.13
	U	81.28	96.44	73.67	67.99	71.49	78.04	82.87
Branches	H_{bs}	65.39	77.97	30.59	58.53	49.14	51.39	44.35
	GA_{PM}	20.94	38.81	8.55	18.93	14.35	16.19	14.33
	U	7.84	8.84	5.77	5.73	5.87	5.6	5.01
Pods/plant	H_{bs}	82.71	87.24	75.77	80.85	75.92	78.94	69.26
	GA_{PM}	34.22	49.08	31.92	32.11	25.32	31.52	24.91
	U	95.65	122.16	92.36	113.87	114.73	95.94	80.80
100-SW	H_{bs}	57.47	80.00	39.67	67.68	65.99	71.7	57.85
	GA_{PM}	11.02	22.29	7.65	15.24	11.3	15.97	9.96
	GU	12.62	13.26	12.05	10.9	10.43	11.89	11.83
Biomass	H_{bs}	85.81	79.76	70.10	87.67	88.18	85.01	87.41
	GA_{PM}	41.43	36.94	24.78	40.36	34.7	33.65	34.23
	U	168.64	182.67	148.19	186.51	187.17	169.99	162.81
DF	H_{bs}	83.45	77.63	82.33	86.13	71.02	79.66	78.52
	GA_{PM}	7.87	4.77	6.36	7.07	4.2	6.95	4.83
	U	52.14	54.82	53.34	52.77	55.52	55.25	55.78
DM	H_{bs}	66.94	23.28	58.07	53.79	43.96	55.16	48.09
	GA_{PM}	2.41	0.68	2.05	1.44	1.06	1.61	1.18
	U	127.46	128.54	127.18	126.77	127.34	126.77	127.98
Seeds/pod	H_{bs}	40.69	59.95	49.44	57.51	41.41	73.69	30.58
	GA_{PM}	6.85	10.16	9.04	10.85	6.21	13.95	4.95
	U	2.57	2.65	2.65	2.82	2.63	2.73	2.71
Seed yield	H_{bs}	83.54	78.28	79.40	82.71	78.18	75.86	76.27
	GA_{PM}	45.96	39.94	37.69	44.72	36.07	39.86	34.54
	U	18.42	21.20	20.29	24.3	23.05	19.93	19.20

PH 30: Plant height (cm) 30 days after sowing; PH maturity: Plant height (cm) at maturity; Branches: number of branches per plant; pods/plant: number of pods per plant; 100-SW: 100 seed weight (g); biomass: biomass per plant (g) at maturity; DF: days to flowering; DM: days to maturity; seeds/pod: number of seeds per pod; Seed yield: seed yield per plant (g)

Genetic usefulness criteria will help in finding crosses having high levels of variability as well as high mean performance for various traits. Usefulness criteria have been applied to bi-parental populations with full sib progeny to predict population performance in early

generations. The advantage of genetic usefulness is that is provides the overall value of a population in terms of its mean performance and total variance (TABANAO and BERNARDO, 2005, BERNADO, 2010, ALLIER *et al.,* 2019). For pods per plant, cross 2 had the highest genetic usefulness (122.16) followed by cross 5 (114.73) and cross 4 (113.87). For 100-seed weight also, cross 2 had the highest usefulness (13.26) followed by cross 1 (12.62) and cross 3 (12.05). For total biomass and seed yield per plant, cross 4 (186.51 and 24.30, respectively) and cross 5 (187.17 and 23.05, respectively) had high usefulness. These were closely followed by cross 2 (182.67 and 21.20, respectively) in both the traits. Cross 4 also had highest usefulness for seeds per pod (2.82). For days to flowering and days to maturity, as the earliness is the desired character, so we deducted genetic advance from the mean to calculate usefulness. Cross 1 (52.14) had the lowest value of usefulness for days to flowering while cross 4 (126.77) and cross 6 (126.77) had lowest usefulness for days to maturity. The results of usefulness criteria were consistent with that from variance components and genetic advance. This suggested that the concept of genetic usefulness may be used to evaluate the genetic worth of breeding materials that are not necessarily derived from a two-parent cross.

In general, low estimates of heritability and genetic advance were observed in all the bi-parental crosses. Highest heritability estimates for traits like plant height, number of branches per plant, number of pods per plant and 100-seed weight were observed in cross 2 whereas, cross 1 had highest heritability for days to maturity and grain yield per plant. Similar trends were observed for genetic advance. Out of ten traits studied, cross 3 had lowest estimates for heritability and genetic advance in four traits viz. height at maturity, number of branches per plant, 100-seed weight and biomass per plant. Vegetable type soybean lines viz. AGS 328 and AGS 752 used in the multi-parental crosses were highly susceptible to yellow mosaic disease (YMD) and Ludhiana is a hot spot for YMD (KHOSLA *et al*., 2021), Multi-parental crosses (Crosses 1 and 2) due to diverse parental lines used in mating resulted in wider variability in advanced generation, although due to presence of YMD susceptible progenies, average yield in multi-parental crosses would be lower than bi-parental crosses. This was evident from comparatively low usefulness indices for seed yield per plant, biomass and seeds per pod in multi-parental crosses.

The crosses with high heritability, genetic advance along with high genetic usefulness for important traits, would respond well to future selection, resulting in selection of superior lines for yield related traits from these crosses. When we are handling multiple populations, a combination of the means and genetic advance is more reliable in choosing the best sets of materials to advance in the breeding program (TABANAO and BERNARDO, 2005, BERNADO, 2010). The use of these genetic parameters is helpful in predicting the genetic worth of different breeding populations and therefore helps in utilizing resources for advanced testing on lines from populations with high genetic usefulness. The findings in the present study were consistent with the past studies which used similar genetic parameters to evaluate the effectiveness of population response to selection (OMOIGUI *et al.,* 2006; MANGGOEL, 2012; NWOSU *et al.,* 2013; ONGOM *et al.,* 2021).With homozygous lines and the opportunity for replicated testing at later generations as is the case in the present study, there is improved prediction accuracy of genetic usefulness.

CONCLUSION

Selection and combination of parents to develop new crosses is a crucial step in plant breeding. To warrant maximum selection progress, a new cross should provide a large progeny variance. Study of various genetic parameters to estimate genetic variability present in various crosses in the present study revealed that multi parental crosses possess highest variability in terms of heritability and genetic advance for different traits. Low genetic usefulness for yield in multi-parental crosses highlighted the importance of selection of parents in mating system. While selecting diverse parents, care should be taken to consider susceptibility of parental lines to various biotic and abiotic factors responsible for yield losses.

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GENETIČKA KORIST OD VIŠE-RODITELJSKIH UKRŠTANJA U ODNOSU NA DVORODITELJSKA UKRŠTANJA KOD SOJE

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Izvod

Napredne oplemenjivačke linije iz sedam različitih ukrštanja procenjene su randomizovanim blok dizajnom tokom Karif 2016. i 2017. godine radi proučavanja genetskih parametara. Visoka heritabilnost u širem smislu (Hbs) i genetski napredak kao procenat srednje vrednosti (GAPM) primećeni su za prinos semena po biljci, biomasu po biljci i broj mahuna po biljci, što prikazuje aditivno dejstvo gena, pa bi selekcija zasnovana na ovim osobinama bila pouzdanija. Višeroditeljska ukrštanja su generalno imala veće procene heritabilnosti i genetskog napretka u poređenju sa dvoroditeljskim ukrštanjima. Genetička korist (U) za osobine koje doprinose prinosu, kao što su mahune po biljci, težina 100 semena, bila je veća kod ukrštanja 2, dok su dvoroditeljska ukrštanja imala visoku genetsku korist za prinos semena i biološki prinos po biljci. Osetljivost roditeljskih linija mogla je dovesti do niže genetske koristi kod višeroditeljskih ukrštanja. Izbor raznovrsnih roditelja koji će se koristiti u programu oplemenjivanja treba sprovesti uzimajući u obzir podložnost roditeljskih linija različitim biotskim i abiotskim faktorima odgovornim za gubitak prinosa.