

# An Assessment of Genetic variability and association studies for yield and its components of soybean MAGIC population lines (*Glycine max* (L.) Merrill.)

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## ABSTRACT

In the present investigation, 565 soybean MAGIC population lines along with 6 checks were evaluated in augmented design in 5 blocks at Agricultural Research Station, Adilabad during *khariif*, 2019-20 to study genetic parameters, character association and the direct and indirect effects of the traits on seed yield. Based on range, all the traits exhibited huge amount of variability. In the present study, the estimate of PCV was higher than GCV indicating the important role of environment in the expression of the characters under study. The highest genotypic and phenotypic coefficient of variation observed for the traits number of branches per plant (PCV- 33.53 %, GCV-20.15 %), number of pods per plant ( PCV- 32.35 %, GCV-21.11 %), net plot yield( PCV- 36.36 %, GCV-27.27 %) and seed yield per plant (PCV- 31.67 %, GCV-22.30 %) which indicates selection can be applied on these traits to isolate more promising line. The broad sense heritability was lower to higher for all the traits ranged from days to 50% flowering (20.02%) to days to maturity (75.87 %) while high genetic advance was recorded in all traits under study except, days to 50% flowering (2.99 %) and days to maturity (9.47 %).Among all the characters, high heritability along with high genetic advance as percent of mean was observed for plant height and net yield indicating predominance of additive gene action and a limited role of environment in the expression of these traits. Hence, these traits are fixable in nature and selection on the basis of these traits would be effective. Correlation studies indicated that number of branches/plot, number of pods/plant, net yield/plot, 100 seed weight and number of nodes/plant had significant and positive correlation with seed yield/plant.

**Key words:** MAGIC population, Genetic variability, Correlation, Path analysis, Soybean

## Introduction

Soybean (*Glycine max* L.) is a major oil seed crop in terms of area, production and economic value in India. Currently, India is producing 13.15 million tonnes of soybean from an area of 11.67 Million hectares and the production share accounts 42% of country's total oilseeds production. The Telangana state is producing 0.25 million tonnes of soybean

from an area of 0.24 million hectares (Directorate of Economics and Statistics, 2017).

The knowledge of genetic variability existing within the various parameters contributing to yield is an important criterion for any crop improvement but, in highly self-pollinated crops like soybean narrow genetic base limited scope for selection. Genetic diversity provides an insight for selection of appropriate parents for combining new alleles for the trait

in a crop improvement programme (Rani *et al.*, 2016). For the effective selection of superior genotype to use in hybridization programme for the development of superior varieties, genetic variability is must (Prasad *et al.*, 2012). Hence, it is obligatory for a plant breeder to know the extent of association between yield and its various components, which will inevitably facilitate selection of desirable characteristics (Jain *et al.*, 2015). Huge amount of variability in the initial breeding material ensures better chances of producing new desired forms of a crop (Raturi *et al.*, 2014).

Correlation study provides a measure of association between characters and helps to identify important characters. Associations between many yield contributing characters can be evaluated by correlation analysis, which helps in the simultaneous selection for more than one character (Semahegn and Tesfaye, 2016).

Furthermore, Indian soybean cultivars have a very narrow genetic base due to the repetitive use of the same parents during hybridisation program (Bharadwaj *et al.*, 2002). Hence, A multi-way hybrid such as MAGIC (Multi-parent Advanced Generation Inter Cross) can contribute variability to the crop gene pool as these are highly variable and diverse source of germplasm which undergoes heavy genetic recombination events. Hence, the present study was carried out to assess genetic variability, association between seed yield its components in soybean MAGIC lines.

## Materials and Methods

Field study was conducted at Agricultural Research Station, Adilabad during *kharif*, 2019 with 565 soybean MAGIC population lines along with 6 checks to know the variability, character association and also to know the direct and indirect effects. Experiment was laid out in an augmented design with 5 blocks and the genotypes were planted with a spacing of 45 cm row to row and 5 cm plant to plant distance. All the recommended agronomical practices and plant protection measures were adopted to raise the healthy crop (Telangana Vyavasayam- Diksuchi, 2019). At maturity data was recorded on five randomly selected plants for plant height (cm), number of branches/plant, number of pods/plant, number of nodes/plant, seed yield/plant (g) and 100 seed weight (g), while data for 50 per cent flowering, days to maturity and net yield/plot was recorded

on plot basis. The mean of different characters were calculated on the basis of these individual data recorded for each character and subjected for statistical analysis.

The data were analyzed for augmented design (Federer, 1956), variability parameters were studied as per Panse and Sukhatme (1985), genetic parameters were computed according to Burton and Devane (1953) and Path coefficient analysis was done as per Dewey and Lu, 1959.

## Results and Discussion

Analysis of variance (Table 1) revealed significant difference among the genotypes for plant height, number of nodes/plant, days to maturity, net yield/plot, 100 seed weight and seed yield/plant indicating the existence of considerable genetic variation for these characters in the experimental material. Check vs test entry also revealed significant and wide variability for the characters mentioned indicating that the test entries were significantly different from checks. The estimates of range, mean, standard deviation, standard error, coefficient of variation, skewness and kurtosis are mentioned in Table 2. Considerable range of variation was observed in MAGIC lines for all the traits under study indicating enough scope for bringing about improvement in the desire direction. Coefficient of variation was highest for net yield/plot (35.99%) followed by number of branches/plant (33.35%) and number of pods/plant and seed yield/plant (31.64% and 31.63%, respectively). Lowest magnitude of CV was recorded for days to maturity (6.08%) followed by days to 50 % flowering (7.29%). Thus the variability facilitates selection which would bring the improvement in these characters. Similar findings were also reported by Akram *et al.*, (2016), Athoni and Basavaraja, (2012) in soybean. Phenological traits like days to 50% flowering and days to maturity showed low coefficient of variation which indicated that the breeders should go for source of high variability for these traits to make improvement.

The estimates depicting the genetic variability including mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ( $h^2$ ), and genetic advance % of mean (GAM) are presented in Table 3. The coefficient of variance *i.e.* GCV and PCV give information about the nature and magnitude of variation. It clarifies either the variation are due to genetic causes or en-

**Table 1.** ANOVA for yield and yield components of soybean in augmented design

<b>Treatment adjusted</b>										
Source of variation	d.f.	MSS								
		PLHT	NB	PO	DFF	NY	SW	DM	SY	NO
Block (ignoring Treatments)	4	551.31**	46.91**	2719.06**	83.19**	0.008**	35.50**	53.91**	57.52**	19.28**
Treatment (eliminating Blocks)	570	86.55**	4.42	195.82	8.92	0.002*	2.51**	42.92**	12.66*	5.23*
Checks	5	329.60**	3.57	689.67**	97.84**	0.002	2.41	365.63**	15.02	21.03**
Varieties+ Checks vs Varieties	565	84.40**	4.43	191.45	8.14	0.002*	2.51**	40.06**	12.64*	5.09*
Error	20	24.70	3.03	117.05	5.64	0.001	0.99	9.66	6.39	2.44
<b>Block adjusted</b>										
Source of variation	d.f.	MSS								
		PLHT	NB	PO	DFF	NY	SW	DM	SY	NO
Block (eliminating Treatments)	4	37.30	3.82	110.54	8.30	0.002	1.05	3.52	15.62	5.02
Treatment (ignoring Blocks)	570	90.16**	4.72	214.13	9.45	0.002*	2.75**	43.27**	12.96*	5.33*
Checks	5	329.60**	3.57	689.67**	97.84**	0.002	2.41	365.63**	15.02	21.03**
Varieties	564	87.90**	4.74	210.08	8.64	0.002*	2.74**	40.04**	12.63*	5.18*
Check vs. Variety	1	167.79*	1.46	123.22	23.76	0.025**	8.67**	256.14**	189.47**	11.21*
Error	20	24.70	3.03	117.05	5.64	0.001	0.99	9.66	6.39	2.44

\*\*Highly significant at P ≤0.01; \*Significant at P ≤0.05

PLHT- Plant height (cm); NB-Number of branches/plant; PO-Number of pods/plant; DFF-Days to 50% flowering; NY-Net yield/plot (kg); SW-100 seed weight (g); DM-Days to maturity; SY-Seed yield/plant, NO-Number of nodes/plant

vironmental causes.

The coefficient of phenotypic, genotypic and environmental variance was calculated for all the traits under study. The GCV was range from 4.27 % (Days to 50% flowering) to 27.27% (Net plot yield). Maximum GCV was observed for the net plot yield (27.27%) followed by the seed yield per plant (22.3 %). Whereas, the highest PCV was observed for net plot yield (36.36 %) followed by number of branches per plant (33.53 %). In general, estimate of PCV was higher than their GCV indicating the important role of environment in the expression of the characters. The highest genotypic and phenotypic coefficient of variation observed for the traits number of branches per plant (PCV- 33.53 %, GCV-20.15 %), number of pods per plant (PCV-32.35 %, GCV-21.11 %), net plot yield (PCV- 36.36 %, GCV-27.27 %) and seed yield per plant (PCV- 31.67 %, GCV-22.30 %). It indicates that selection can be applied on the traits to isolate more promising line. Similar trends of results were also reported by Akram *et al.*, (2016), Athoni and Basavaraja (2012) in soybean. The traits, days to 50% flowering and days to maturity showed low PCV and GCV which indicated that the breeders should go for source of high variability for these traits to make improvement.

In a population, observation is due to both factors, i.e. genetics and environmental, whereas genetic variability is the only heritable from generation to next generation so the heritability alone does not give an idea about the expected gain in the next generation, but it has to be considered in conjunction with the genetic advance. The traits those exhibit maximum heritability and high genetic advance as percentage of mean could be used as powerful tool in selection process such traits are controlled by the additive gene and less influenced by the environment (Panse and Sukhatme, 1995). The broad sense heritability was lower to higher for all the recorded traits. The traits, plant height (71.90 %), net plot yield (75.0%), 100 seed weight (63.86 %) and days to maturity (75.87 %) were ex-

pressed high heritability. Whereas, the remaining traits under study had moderate heritability except days to 50% flowering (20.02%). However, for efficient selection we cannot solely believe on heritability. The combination of high heritability with high genetic advance will provide a clear base on the reliability of that particular trait in the selection of variable genotypes. High genetic advance was re-

corded in all traits under study except, Days to 50% flowering (2.99 %) and days to maturity (9.47 %). These traits are highly reliable during selection process of the genotypes. Chandrawat *et al.*, (2017), Malek *et al.*, (2014) and Mishra *et al.*, (2015) have also calculated genotypic and phenotypic components of variance, heritability and genetic advance for different yield characters in soybean and have revealed

**Table 2.** Estimates of variability parameters for nine quantitative traits in soybean MAGIC population lines

Parameter	PLHT	NB	PO	DFF	NY	SW	DM	SY	NO
Mean	56.37	6.50	45.71	40.50	0.11	13.52	104.40	11.21	9.81
SE	0.39	0.09	0.61	0.12	0.002	0.07	0.27	0.15	0.10
Variance	87.61	4.69	209.12	8.73	0.00	2.72	40.35	12.58	5.17
SD	9.36	2.17	14.46	2.95	0.04	1.65	6.35	3.55	2.27
Range	23.20 to 91.00	1.20 to 12.80	18.30 to 88.40	30.80 to 45.00	0.03 to 0.27	9.01 to 19.38	81.00 to 114.00	3.33 to 25.57	4.60 to 14.60
CV(%)	16.60	33.35	31.64	7.29	35.99	12.20	6.08	31.63	23.16
Skewness	0.13	-0.26	0.09	-0.96	0.45	0.14	-1.30	0.33	-0.26
Kurtosis	1.26	-0.34	-0.67	-0.04	0.13	-0.27	1.61	-0.11	-0.62

Note: SE- Standard error; SD-Standard Deviation, CV (%) -Coefficient of variation

**Table 3.** Estimates of genetic parameters for quantitative traits in soybean MAGIC population lines

Trait	Mean	PCV (%)	GCV (%)	h <sup>2</sup> (broad sense- %)	Genetic Advance (% of Mean)
PLHT	56.37	16.62	13.94	71.90	24.60
NB	6.50	33.53	20.15	36.07	24.92
PO	45.71	21.11	44.28	44.28	28.89
DFF	40.50	7.26	4.27	20.02	2.99
NY	0.11	36.36	27.27	75.00	56.18
SW	13.52	12.27	9.76	63.86	16.15
DM	104.4	6.06	5.28	75.87	9.47
NO	9.81	23.24	16.92	52.89	25.32
SY	11.21	31.67	22.30	49.40	32.20

PLHT- Plant height (cm); NB-Number of branches/plant; PO-Number of pods/plant; DFF-Days to 50% flowering; NY-Net yield/plot (kg); SW-100 seed weight (g); DM-Days to maturity; NO-Number of nodes/plant; SY-Seed yield/plant

**Table 4.** Correlation coefficients for seed yield and yield component traits in soybean MAGIC population lines

Trait	PLHT	NB	PO	DFF	NY	SW	DM	NO	SY
PLHT	1.000	-0.080	0.050	-0.035	0.039	0.020	0.037	0.202**	0.046
NB		1.000	0.086*	-0.135**	0.097*	0.02	-0.132**	0.025	0.126**
PO			1.000	-0.096*	0.593**	0.038	-0.006	0.734**	0.582**
DFF				1.000	-0.092*	0.006	0.818**	-0.058	-0.114**
NY					1.000	0.136**	-0.021	0.493**	0.978**
SW						1.000	-0.051	0.104*	0.133**
DM							1.000	-0.008	-0.044
NO								1.000	0.480**
SY									1.000

Note: \*\*Highly significant at P≤0.01; \*Significant at P≤0.05

**Table 5.** Estimates of direct and indirect effects of different traits on seed yield in soybean MAGIC population lines

Trait	PLHT	NB	PO	DFF	NY	SW	DM	NO	Correlation with seed yield
PLHT	0.012	-0.002	0.000	0.000	0.038	0.000	-0.001	-0.002	0.046
NB	-0.001	0.028	0.001	0.001	0.095	0.000	0.002	0.000	0.126**
PO	0.001	0.002	0.009	0.001	0.577	0.000	0.000	-0.008	0.582**
DFF	0.000	-0.004	-0.001	-0.008	-0.089	0.000	-0.012	0.001	-0.114**
NY	0.000	0.003	0.005	0.001	0.973	0.000	0.000	-0.005	0.978**
SW	0.000	0.001	0.000	0.000	0.133	0.000	0.001	-0.001	0.133**
DM	0.000	-0.004	0.000	-0.007	-0.020	0.000	-0.014	0.000	-0.044
NO	0.002	0.001	0.006	0.000	0.480	0.000	0.000	-0.011	0.480**

\*\*Highly significant at  $P < 0.01$ ; \*Significant at  $P < 0.05$ , Bold diagonal values denote the direct effects, Residual are 0.43

that selection was effective for a population with broad genetic variability and character with high heritability.

Among all the characters, high heritability along with high genetic advance as percent of mean was observed for plant height and net yield indicating predominance of additive gene action and a limited role of environment in the expression of these traits. Hence, these traits are fixable in nature and selection on the basis of these traits would be effective. These results were in agreement with the findings of Ali *et al.* (2016). Traits like days to maturity and 100 seed weight exhibited high heritability with low-moderate genetic advance as percent of mean suggesting the combining or conditional role of additive and non-additive gene action in governing these traits and high heritability may have resulted from favorable influence of environmental factors. Thus, the selection of these traits may not be beneficial. Similar findings were reported by Gyanesh *et al.* (2016) for days to maturity.

In the present investigation, plant height, number of pods/plant, net yield/ plot and 100 seed weight had significant and positive correlation with number of nodes/plant (Table 4). Number of branches/plant showed significant and positive correlation with number of pods/plant and net yield/ plot. The traits, number of pods/plant and 100 seed weight exhibited significant and positive correlation with net yield/plot. Five quantitative characters viz., number of branches/plant, number of nodes/plant, number of pods/plant, net yield/ plot and 100 seed weight had significant and positive correlation with seed yield/plant and the selection based on these traits is expected to contribute towards yield en-

hancement. Shekar *et al.* (2018) reported similar results of significant and positive correlation between number of pods/plant and seed yield/plant. Days to 50% flowering showed significant and positive correlation with days to maturity and the same result was reported by Shekar *et al.* (2018). However, the seed yield/plant is significantly and negatively associated with days to 50 % flowering and days to maturity (Nutan and Gabriel, 2016; Sudhanshu *et al.*, 2015).

Seed yield is a complex character which is highly influenced by interaction of various component traits and the environment. Compartmentalization of correlation coefficients into direct and indirect effects revealed the true nature of associations observed among various characters (Table 5). The path coefficient analysis using phenotypic correlation coefficients among pair of characters depicting direct and indirect effects on seed yield/plant showed that net yield/plot had high and positive direct effects on seed yield/plant indicating this as the most important component character contributing to yield. However, number of branches/plant, plant height and number of pods/plant had low positive and direct effects on seed yield/plant. Low residual effects at phenotypic level indicated that most of the variation found in the dependent traits was well explained by the contributed traits studied. Mukesh and Kamendra (2009) reported primary branches/plant was found to have direct effect on seed yield. The characters with high positive correlation and high direct effects are amenable for selection. Hence, path analysis studies of present investigation revealed that number of branches/plant, number of pods/plant and net yield/plot were important yield

components with direct effects on improvement for seed yield.

## Conclusion

Based on present investigation, in the germplasm huge variation exist for the traits *viz.*, number of branches/plant, number of pods/plant, net plot yield and seed yield/plant and needs exploitation for development of high yielding varieties. In association studies, seed yield/ plant was significantly positively correlated with number of branches/plant, number of pods/plant and net yield/ plot with direct effect on seed yield/plant.

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## Conflict of interest

No interest of conflicts exists.

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