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Unveiling genetic associations for enhanced grain yield in soybean [*Glycine max* (L.) Merr.] Germplasm

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Abstract
An experiment entitled "Unveiling Genetic Associations for Enhanced Grain Yield in Soybean [*Glycine max* (L.) Merr.] Germplasm" was carried out during Kharif 2023-24 at the research farm experimental farm of the College of Agriculture, Badnapur. Vasantrao Naik Marathwada Krishi Vidyapeeth Parbhani (M.S). The experiment was laid out in Randomized Block Design (RBD) with 38 genotypes and two replications to estimate the association between grain yield and yield contributing characters. In this experiment, genotypic correlation coefficients were higher than the phenotypic correlation coefficients. According to correlation results, grain yield per plant was significantly and positively correlated with Number of pod per cluster, Number of pod per plant, 100 seed weight, Harvest index, Number of seed per pod at both genotypic and phenotypic levels.

Keywords: Correlation, genotypic, phenotypic, Soybean

Introduction
Soybean (*Glycine max* (L.) Merrill) is a self-pollinated crop which belongs to the family leguminaceae and sub-family pap tribe phaseolae and genus glycine. Genus Glycine comprises of 1200 species. The plant is normally diploid with 2n=40 chromosomes. The genus Glycine is divided into two sub genera, Glycine and Soja. The sub genus Glycine includes 16 perennial species and the sub genus Soja (Moench) includes the cultivated soybean, *G. max* (L.) Merril (2n=40) and the two annual species, Glycine soja Siebold and Zucc. The cultivated species, G. max, hybridizes easily with its wild annual relative and most probable progenitor G. soja while with the perennial relatives it has low crossability rate (Singh and Hymowitz, 1999) [7].
Cultivated soybean is an erect, bushy herbaceous annual that can grow up to 1.5 meters (m) tall Footnote 10. Soybean varieties are adapted to a range of geographic and climatic regions Footnote 11. The main growth habits (also referred to as stem types) of soybean are: determinate, semi-determinate and indeterminate. Determinate varieties, characterized by vegetative growth that is nearly complete when the plant starts flowering

Materials and Methods
The present investigation was conducted during the Kharif season of 2023 at the experimental farm of the College of Agriculture, VNMKV Parbhani, Maharashtra. The experimental material consisted of thirty-eight genotypes of soybean along with two checks, MAUS 612 and MAUS 158. The evaluation of different genotypes was performed in two replications using a Randomized Block Design (RBD). Each genotype was sown in one row of 3 m length with spacing of 45 cm between rows and 5 cm between plants. Recommended agronomical and plant protection practices were implemented to ensure successful crop cultivation. Observations were recorded for five randomly selected plants from each replication for 10 characters, including days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per cluster, number of pods per plant, 100-seed weight (g), seed yield per plant (g), number of seeds per pod, and harvest index (%). Appropriate variances and covariances were used for calculate phenotypic and genotypic correlation coefficients (Johnson et al., 1955) [3].

Results and Discussion

Genotypic correlation provides insight into the extent to which two traits are controlled by the same set of genes or share a common physiological basis for their expression. If the genotypic correlation is positive, selection for improvement in one trait will automatically result in improvement in the other, and vice versa. Understanding the relationship between grain yield and its components is essential, as selecting for one component trait may induce a simultaneous change in another. Therefore, a rational approach to yield improvement requires information on character associations. While genotypic correlation coefficients were generally higher than their corresponding phenotypic correlation coefficients for most traits, in some cases, the phenotypic correlation coefficients were higher than the genotypic ones. This discrepancy can be attributed to environmental influences. The values of genotypic and phenotypic correlations are shown in Table 1.

The character seed yield per plant show negative non-significant association with plant height (rg=-0.177, rp=-0.173) at both genotypic and phenotypic levels, while, this traits show positive non- significant association with number of branches per plant (rg = 0.016,rp =0.008) at both genotypic and phenotypic levels, whereas the character seed yield per plant show positive significant with number of pod per plant (rg = 0.770 rp =0.721), number of pod per cluster (rg = 0.917 rp=0.920), 100 seed weight (rg = 0.359 rp=0.340), harvest index (rg=0.753, rp=0.651), number of seed pod (rg=0.537, rp=0.513) at both the level.The character seed yield per plant show negative significant with days to 50 per cent flowering (rg=-0.417,rp=- 0.392), days to maturity (rg=-0.345,rp=- 0.318) at genotypic and phenotypic level.

The character days to 50 per cent flowering had positive and significant association with days to maturity (rg= 0.47, rp=0.42) at both genotypic and phenotypic levels. The character days to 50 per cent flowering had negative significant association with number of pod per cluster (rg=0.28, rP=0.26), seed yield per plant (rg=-0.04, rP=-0.05) , number of seed per pod (rg=0.28, rP=0.26), harvest index (rg=-0.04, rP=-0.05) at both levels. The character days to 50 per cent flowering was positive non-significant at genotypic level and phenotypic level with), plant height (rg= 0.14, rP=0.13), no of branches (rg=0.18, rP=0.16). (Bhuva et al. 2020) [2].

The character plant height is negativelye significant with number of branches per plant at genotypic and phenotypic levels (rG=-0.28 rp=-0.27), The character Plant height was negatively non-significant with number of pod per cluster (rg=-0.14, rP=-0.14), number of pod per plant (rg= -0.169, rP= -0.166), 100 seed weight (rg= -0.048, rP= -0.043), number of seed per pod (rg=-0.018, rP=-0.014), seed yield per plant (rg=-0.177, rP=-0.173) at both level. The character plant height is negatively significant with harvest index (rg=-0.23) at genotypic and negatively non significant (rP=-0.208) at phenotypic level.

The character days to maturity had significant and positive correlation with plant height (rg=0.33, rp=0.32) at both level. The character association of days to maturity had negatively non-significant with number of branches (rg=-0.106 rp=-0.104), 100 seed weight (rg=-0.177 rp=-0.144), harvest index (rg=-0.146 rp=-0.119), number of seed per pod (rg=-0.18, rp=-0.17) at both levels. The character association of days to maturity had negatively significant with number of pod per cluster (rg=-0.294 rp=-0.267), number of pod per plant (rg=-0.234 rp=-0.231), seed yield per plant (rg=-0.345 rp=-0.318) at both level. (Khan N.A 2022) [5].

Number of branches per plant was positive and non-significantly correlated with seed yeild per plant (rg=0.016, rp=0.061), number of pod per plant (rG=0.089, rP=0.076), 100 seed weight (rg=0.142, rp=0.145), harvest index (rg=0.68, rp=0.055), at genotypic and phenotypic level. Number of branches per plant was negative and non-significantly correlated with number of pod per cluster (rG=-0.054, rP=-0.061) at genotypic and phenotypic level. Number of branches per plant was negative and significantly correlated with number of seed per pod (rG=-0.235, rP=-0.235) at genotypic and phenotypic level. Showkat *et al*, (2010) [6].

A positive and significant correlation of number of pods per cluster was correlated with no of pod per plant (rg=0.703, rp=0.703), 100 seed weight (rg=0.254, rp=0.238), harvest index (rg=0.750, rp=0.645), number of seed per pod (rg=0.522, rp=0.499), seed yield per plant (rg=0.917, rp=0.920) at both levels.

The character number of pods per plant had significant and positive correlation with number of harvest index (rg=0.484, rp=0.366), 100 seed yield per plant (rg=0.770, rp=0.721). The character number of pods per plant had positive and non significant with number of seed per pod (rg=0.099 rp=0.082) at genotypic levels and phenotypic level . The character number of pods per plant had negative non-significantly correlated with 100 seed weight (rg=0.089, rp=0.094) at both the level. (Bhuva et al, 2020) [2].

The character 100 seed weight had positive significant correlation with harvest index (rg=0.297, rp=0.267), seed yield per plant (rg=0.359, rp=0.340) at genotypic and phenotypic level. The character 100 seed weight had positive non significant correlation with number of seed per pod (rg=0.193, rp=0.169) at both the level. (Arshad et al)

The character harvest index had showed positive and significant association with seed yield per plant (rg=0.753, rp=0.651) and number of seed per pod (rg=0.489, rp=0.408) at genotypic level and phenotypic level Similar result were reported by Vinod Kumar et al

The character harvest index had showed positive and significant association with seed yield per plant (rg=0.537, rp=0.513) at genotypic level and phenotypic level same work reported by K.K Chandel (2017) [4].

Table 1: Estimates of genotypic (G) and phenotypic (P) correlations for yield and yield contributing traits in soybean.

Sr. No.	Name of the Character		Days to 50 per cent flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pod per cluster	No. of pods per plant (g)	100 seed weight (g)	Harvest Index (%)	No. of seed per pod	Seed yield per plant (g)
1	Days to 50 per cent flowering	r_g	1.000	0.471*	0.147^{NS}	0.189^{NS}	-0.280*	-0.205^{NS}	-0.179^{NS}	-0.322**	-0.350**	-0.417**
		r_p	1.000	0.428**	0.131^{NS}	-0.164^{NS}	-0.265*	-0.159^{NS}	-0.173^{NS}	-0.231*	-0.333**	-0.392**
2	Days to maturity	r_g		1.000	0.332**	-0.106^{NS}	-0.294**	-0.238*	-0.177^{NS}	-0.146^{NS}	-0.180^{NS}	-0.345**
		r_p		1.000	0.332**	-0.104^{NS}	-0.267*	-0.231*	-0.144^{NS}	-0.119^{NS}	-0.170^{NS}	-0.318**
3	Plant height (cm)	r_g			1.000	-0.282*	-0.145^{NS}	-0.169^{NS}	-0.048^{NS}	-0.231*	-0.018^{NS}	-0.177^{NS}
		r_p			1.000	-0.279*	-0.141^{NS}	-0.166^{NS}	-0.043^{NS}	-0.208*	-0.014^{NS}	-0.173^{NS}
4	No. of branches per plant	r_g				1.000	-0.054^{NS}	0.089^{NS}	0.142^{NS}	0.068^{NS}	-0.236*	0.016^{NS}
		r_p				1.000	-0.061^{NS}	0.076^{NS}	0.145^{NS}	0.055^{NS}	-0.235*	0.008^{NS}
5	No. of pod per cluster	r_g					1.000	0.753**	0.254*	0.750**	0.522**	0.917**
		r_p					1.000	0.703**	0.238*	0.645**	0.499**	0.920**
6	No. of pods per plant	r_g						1.000	-0.089^{NS}	-0.484**	0.099^{NS}	0.770**
		r_p						1.000	-0.094^{NS}	-0.366**	0.082^{NS}	0.721*
7	100 seed weight (g)	r_g							1.000	0.297**	0.193^{NS}	0.359**
		r_p							1.000	0.267**	0.169^{NS}	0.340**
8	Harvest index (%)	r_g								1.000	0.489**	0.753**
		r_p								1.000	0.408**	0.651**
9	Number of seed per pod (g)	r_g									1.000	0.537 **
		r_p									1.000	0.513 **
10	Seed yield per plant (g)	r_g										1.000
		r_p										1.000

* Indicates significance at 5 per cent level,
** Indicates significance at 1 per cent level

Conclusion

Grain yield per plant had highly positive and significant correlation with Number of pod per cluste, Number of pod per plant, 100 seed weight, Harvest index, Number of seed per pod at both genotypic and phenotypic levels. It would be inferred that yield is function of these traits and selection for high yield would be effective through selection of these characters.

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