Study on Variability and Its Components among Soybean Genotypes, Correlation and Effect of Yield Related Traits on Seed Yield.

Abstract:

During the *kharif* season of October 2023 to April 2024, sixteen different cultivars of soybean (*Glycine max* (L.) Merrill) were cultivated at AKS University in Satna using a Completely Randomized Block Design (CRBD). In order to determine variance, genetic variability, heritability, genetic progress, interrelationships, and the direct and indirect effects of various quantitative variables on seed yield, eleven quantitative traits were investigated. The experimental design revealed highly significant variations for all variables due to the treatments applied. The analysis of variance revealed significant variance in the genotypes for each character under investigation.   For the seed yield per plant (g), number of pods per plants, biological yield (gm), pod length (cm), number of primary branches per plants, and number of seed /pods, the highest GCV and PCV were noted. High genetic progress and high heritability were found for the seed index, number of pods per plant, number of branches per plant, and pod length (cm), suggesting that additive gene action may play a significant role in determining these traits. High genetic advancement and high heritability were found for the number of seed /pods, number of pods per plants, pod length (cm), and biological yield (gm). As per path analysis, increased seed yield per plant is essentially correlated with days to 50% flowering, days to maturity, number of pods per plants, pod length (cm), number of primary branches per plants, 100 seed weight (g), biological yield (gm), and harvest index. Therefore, these characters should be considered for yield improvement in chickpea breeding programme.

Keywords: Soybean, Variance, Variability, Heritability, Correlation and Path Coefficients

Introduction:

Soybean crop is highly valued as an oil seed and is considered one of the most important grain legumes globally. It is self-pollinated and characterized by its annual growth cycle. Stem, leaves, and pods of soybean are covered in soft hairs. Belonging to the order Fabales, family Fabaceae (Leguminaceae), and sub-family Faboideae (Papilionoideae), soybean is often hailed as a wonder crop. It is originally native to China, Japan, Korea and Russia (Singh et al. 2006) but it is introduced to India in 1968 from the U.S.A. The cultivated soybean, known as *Glycine max*

(L.) Merrill, with 2n=40 chromosomes and is a close relative of wild soybean *Glycine soja* (Singh et al. 2006).

It contains around 85% unsaturated fatty acids, including 55% polyunsaturated fatty acids (PUFA) containing two essential fatty acids (linoleic and linolenic acid) that are not produced by the human body (Balasubramaniyan and Palaniappan, 2003). The protein found in soybean is comparable to that of meat and fish. Despite its minimal input needs, Soybean remains a valuable commodity with a high market value (Gautam and Pant, 2004).

The flowers are hermaphrodite, complete, zygomorphic, perigynous, polypetalous, and white in color. The flower consists of 5 sepals, 5 petals, ten stamens that are diadelphous (9+1) in condition with a superior ovary. The germination of the seed is of the epigeal type (Ram and Singh. 2005). India ranks fourth in acreage and fifth in production of soybean in the world. According to the first advance estimates 2023-24, Government of India soyabean crop is estimated at 115.28 lakh tonnes as compared to 149.85 lakh tonnes in 2022-23. (Anonymous 2024). Soybean seed is least storable and is vulnerable to mechanical damage.

Understanding the relationship between yield and its various components is advantageous for plant breeders, as it can facilitate the selection of preferred traits (Jain et al. 2015). Character association studies based on correlation and path coefficient analysis provide the basis to identify the strength of association among various yield and its related attributes [Sakai and Suzuki (1964); Mahbub (2015)]. Path coefficient analysis, pioneered by Wright in 1921, is a significant technique for breaking down the correlation coefficient into direct and indirect impacts of variables on the dependent variable.

Material and methods:

The current study was carried out in the research farm of the Genetics and Plant Breeding department at AKS University, Sherganj, Satna, Madhya Pradesh, during the *kharif* season of 2023–24. Sixteen cultivars / varieties of soybean (*Glycine max* (L.) Merrill) germplasm, comprising native genotypes, were used in the experiment and were assessed using a completely randomized block design. There were 16 plots in each of the three equal blocks that made up the experimental field. Each plot was consisted of 5 rows of 2 meters length, following row to row spacing of 40 cm. and plant to plant spacing of 15 cm. Fertilizer dose was applied as per the

recommendation. Irrigation was given as and when required. Recommended cultural practices were applied to raise a good crop.

The 11 characters were studied viz. (D50%F) Days to 50 % flowering, (DM) Days to maturity, (PH) Plant height (cm), (NPPP) No of Pods per plant, (PL) Pod length (cm), (NSPP) No of Seed per pod, (NBPP) No of primary branches per plant, (TW) Test weight (1000 seed), (BY) Biological yield per plant (g), (HI) Harvest index (%), and (SYPP) Seed yield per plant (g). Five competitive plants were chosen at random from each plot to collect data for each of the twelve quantitative features. Plot-based measurements were made of these plants.

The process described by Panse and Sukhatme (1967) was followed in order to do the analysis of variance for the experiment's design. According to Burton and de Vane's (1953) formula, the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and environmental coefficient of variation (ECV) were computed. The formula proposed by Burton and de Vane (1953) was used to determine heritability in the wide sense (h2b). The Johnson et al., (1955) approach was used to calculate genetic progress.

As formula stated by Searle (1961), the basic relationships between various features at the genotypic and phenotypic levels were determined. Path coefficient analysis was performed using the (Dewey & Lu 1959) formula.

Result and discussion

1. Analysis of Variance (ANOVA):

The analysis of variance for the design of the experiment involving 16 soybean strains/varieties for the eleven quantitative characters. The design of the experiment indicated highly significant differences due to treatments for all the characters. The maximum variances due to treatment recorded for number of pods per plants (329.69). **Table 1** This indicates that the present sufficient variability for most of the characters among different genotypes and thus suggested a substantial scope of selection.

These results are corroborates with earlier results of wide range of variation in soybean was reported by Gohil *et al.* (2006); Jandong *et al.* (2020); Nayana and Fakrudin (2020); Rahaman *et al.* (2022); Sahoo *et al.* (2022); Saicharan *et al.* (2022); Chawan et al. (2023); Hızlı et al. (2023);

Ningwal *et al.* (2023); Vasanth et al. (2023); and Yirga and Sileshi (2023) indicating the presence of sufficient variability among the evaluated genotype for the traits under consideration.

2. Mean, Range and Variability Performance of Soybean Genotypes.

The mean performance of 16 genotypes of soybean were presented in Table 3 the genotypes showing very high performance in desirable direction for various characters listed in Table 2 can serve as suitable donors for improving the traits. As per recorded mean performance the varieties viz., NRC 131, RVS 18, JS 20-69, NRC 150, JS 20-116, NRC 138, and RVS 24 showing high seed yield per plant (g). So as per the data observed for these varieties are recommended for the cultivation in Satna district of M.P.

The GCV and PCV of 11 traits of chickpea were presented in Table 4 and Figure 1. The maximum genotypic coefficient variation was observed in seed yield per plant (g) (31.186), followed by number of pods per plants (29.045), biological yield (gm) (28.968), pod length (cm) (22.91), number of primary branches per plants (21.942), and number of seed /pods (20.639). This is an indicative of less amenability of these characters to environmental fluctuations and hence, greater emphasis should be given to these traits.

The high PCV were recorded for Seed yield per plant (g) (33.268), followed by Biological Yield (gm) (30.47), Number of pods per plants (30.384), Number of primary branches per plants (24.881), Pod length (cm) (24.046), and Number of Seed /pods (20.864). The magnitude of GCV and ranged from lowest days to 50% flowering (5.345) to highest seed yield per plant (g) (31.186) and magnitude of PCV ranged from lowest days to maturity (8.882) to highest seed yield per plant (g) (33.268).

The traits with high phenotypic coefficient of variation indicated more influence of environmental factors. Therefore, caution has to be exercised during the selection programme because the environmental variations are unpredictable in nature and may mislead the results. The PCV were higher than the GCV indication of lesser influence of environmental over these characters and effectiveness of selection based on phenotypic value for grain yield and yield contributing traits.

These results are accordance to results reported by Chawan et al. (2023) recorded highest GCV and PCV (%) for plant height (cm), number of pods plant-1, 100 seed weight (g), seed yield plant-1(g), etc. Hızlı et al. (2023) for days to 50% flowering, weight of fresh pods per plant (g), etc. Yirga and Sileshi (2023) recorded for days to 50% flowering, days to 95% pod maturity, plant height, number of pod per plant, etc. Ningwal *et al.* (2023) documented for biological yield per plant, numbers of pods per plant etc. Sahoo *et al.* (2022) recorded for seed yield per plant and dry matter weight per plant. Saicharan *et al.* (2022) recorded for the number of pods per plant, the number of pods per cluster, etc. Jandong *et al.* (2020) observed high value of PCV and GCV for plant height, number of leaves, number of pods and seed yield. Nayana and Fakrudin (2020), reported for number of clusters/plant, 100-seed weight, number of branches/plant, etc. Sonkamble *et al.* (2020) observed for 100 seed weight, seed yield and harvest index.

3. Heritability and Genetic Advance:

Heritability, h² (Broad Sense)%, GA @ 5%, and Genetic Advance as % of Mean 5% was estimated for all the characters and has been presented in Table: 4 and Figure 2.

High heritability estimates (h^2b) >80% were found for 100 seed weight (g) (97.90%), number of seed /pods (97.80%), days to maturity (92.50%), number of pods per plants (91.40%), pod length (cm) (90.80%), plant height (cm) (90.50%), biological yield (gm) (90.40%), and seed yield per plant (g) (87.90%) suggested that the characters are least influenced by the environmental factors and also indicates the dependency of phenotypic expression which reflect the genotypic ability of strains to transmit the gene to their progenies. However, moderate heritability (>40 % to <80%) observed for number of primary branches per plants (77.8090%), and harvest index (%) (61.2090%) and low Heritability (<40%) was observed for only one studied character viz., days to 50% flowering (16.00%).

The expected genetic advance in percent of mean @ 5% ranged from lowest days to 50% flowering (4.404%) to highest seed yield per plant (g) (60.225%). High estimate of expected genetic advance were found for seed yield per plant (g) (60.225%), followed by number of pods per plants (57.195%), biological yield (gm) (56.733%), pod length (cm) (44.964%), number of seed /pods (42.056%), and number of primary branches per plants (39.861%) at 5% level. However, moderate expected genetic advance in percent of mean @ 5% were recorded for plant

height (cm) (28.927%), 100 seed weight (g) (28.003%), and harvest index (24.296%). Low estimate of expected genetic advance as percent of mean were found for days to maturity (16.919) and days to 50% flowering (4.404%) at 5% level.

High heritability coupled with high genetic advance as percent of mean at 5% observed for number of seed /pods, number of pods per plants, pod length (cm), and biological yield (gm) indicating that these characters could be prominently governed by additive gene action. So the selection of these traits could be more effective for desired genetic improvement. Low heritability coupled with low genetic advance indicates that the trait is highly influenced by environmental effect and selection would be not effective.

Johnson *et al.* (1955) had pointed out that the heritability estimates along with genetic advance were more useful than heritability estimates alone in predicting the response to selection. These results are accordance to results reported by Joshi and Singh (2023) observed for number of clusters per plant followed by a number of pods per plants, pod length (cm), number of seed /pods and biological yield (gm). Vasanth et al. (2023) recorded the traits viz., plant height, number of branches per plant, number of pods per plant, etc. Hizli et al. (2023) recorded for forage yield, the number of nodes per plant, the weight of pods per plant, etc. Yirga and Sileshi (2023) were recorded for plant height, number of pod, number of seed, hundred seed weight and grain yield

4. Correlation and Path Coefficient Analysis:

In the present investigation correlation coefficient was worked out at genotypic and phenotypic levels for all the eleven quantitative traits and has been presented in Table 5.

Days to 50% flowering (0.406 and 0.2864), Days to Maturity (0.408 and 0.349), Number of pods per plants (0.34 and 0.314), Pod length (cm) (0.397 and 0.340), Number of primary branches per plants (0.598 and 0.483), 100 seed Weight (g) (-0.315 and -0.293), Biological Yield (gm) (0.950 and 0.891), and Harvest index (0.314 and 0.313) high positive/negative significant correlation with seed yield per plant (g) at both genotypic and phenotypic levels, respectively.

Grain yield of a crop is the result of interaction of a number of inter-related characters. Therefore, selection should be based on these component characters after assessing their

correlation with grain yield. Character association revealed the mutual relationship between two characters, and it is an important parameter for taking decision regarding the nature of selection to be followed for improvement in the crop under study.

Similar finding of positive and significantly correlation between seed yield per plant and for days to 50% flowering Mehra *et al.* (2020); Balla and Ibrahim (2017). For number of pods per clusters Ningwal *et al.* (2023); Mehra *et al.* (2020); Guleria *et al.* (2019); Balla and Ibrahim (2017); Chavan *et al.* (2016). For 100 seed weight (g) Rahaman *et al.* (2022); Mehra *et al.* (2020); Guleria *et al.* (2019); Balla and Ibrahim (2017); Chavan *et al.* (2016). And for biological yield (gm) Ningwal *et al.* (2023); Mehra *et al.* (2020); Balla and Ibrahim (2017).

The genotypic and phenotypic correlation coefficient of seed yield with the remaining characters under study were further partitioned into direct and indirect effects using path coefficient analysis at genotypic and phenotypic level are presented in Table 6 Figure 3 and Table 7 and Figure 4, respectively. The results of path coefficient analysis showed that the Path coefficient analysis revealed that number of seed /pods (2.5824 and 0.3036), 100 seed weight (g) (1.7606 and 0.0742), biological yield (gm) (1.2767 and 1.0261), number of pods per plants (0.9287 and 0.0212), and number of primary branches per plants (0.4098 and 0.2352) had the greatest positive direct effects on seed yield at both the genotypic and phenotypic levels, respectively. Conversely, plant height (cm) (-1.571 and -0.2461), and days to maturity (-0.4308 and -0.1798) showed a direct negative impact on seed production at the genotypic and phenotypic levels, respectively.

At the genotypic and phenotypic levels, the number of seed /pods, 100 seed weight (g), biological yield (gm), number of pods per plants, number of primary branches per plants, plant height (cm), and harvest index (%) showed the strongest direct influence on seed yield per plant, respectively. Hence, these characters may be considered as essential quantitative traits in soybean improvement programme and direct selection for these characters will be useful for crop improvement programme.

The early reports on genotypic level positive direct effect was recorded for biological yield (gm) Ghodrati *et al.* (2013). For harvest index Nagarajan *et al.* (2015); Ghodrati *et al.* (2013). For number of pods per clusters Ningwal *et al.* (2023); Berhanu *et al.* (2019). For

number of primary branches per plants Berhanu *et al.* (2019); Chavan *et al.* (2016); Laosuwan and Machikowa (2011); Kumar and Singh (2009). For days to maturity Ningwal *et al.* (2023); Rahaman *et al.* (2022); Balla and Ibrahim (2017); Chavan *et al.* (2016); Ghodrati *et al.* (2013).

Conclusion

The experiment's design revealed statistically significant variations for every character that was assessed. As per recorded mean performance the varieties viz., NRC 131, RVS 18, JS 20-69, NRC 150, JS 20-116, NRC 138, and RVS 24 showing high seed yield per plant (g). So as per the data observed for these varieties are recommended for the cultivation in Satna district of M.P. The traits viz., seed yield per plant (g), number of pods per plants, biological yield (gm), pod length (cm), number of primary branches per plants, and number of seed /pods showed the highest GCV and PCV. High genetic advancement and high heritability were found for the number of seed /pods, number of pods per plants, pod length (cm), and biological yield (gm). Increased seed yield per plant is essentially correlated with days to 50% flowering, days to maturity, number of pods per plants, pod length (cm), number of primary branches per plants, 100 seed weight (g), biological yield (gm), and harvest index. Therefore, these characters should be considered for yield improvement in chickpea breeding programme.

Table 1 Analysis of variance (mean sum of squares) for 11 quantitative characters in soybean.

S.No.	Traits	Replicate (df=2)	Treatments (df=15)	Error (df=30)
1	D50%F	103.84*	87.65	73.63
2	DM	3.77	204.76**	15.42
3	PH	74.74	164.96**	15.69
4	NPPP	46.68	329.69**	28.42
5	PL	0.51	1.87**	0.17
6	NSPP	0.37	1.32**	0.03
7	NBPP	12.07	3.83**	0.85
8	SW	3.74	10.41**	0.22
9	BY	1.12	307.09**	29.53
10	HI	38.12	160.04**	62.11
11	SYPP	9.32	50.49**	6.12

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

Table 2 Most desirable genotypes of soybean identified for 11 quantitative traits as per mean performance.

S.No.	Traits	Genotypes
1	D50%F	NRC-86, NRC 192, NRC 152, NRC 165, NRC 138, JS 20-116, NRC 157, and JS 20-34.
2	DM	NRC 127, NRC 192, NRC 152, NRC 150, JS 20-34, and NRC 165.
3	PH	NRC 165, RVS 24, NRC 86, NRC 94, RVS 18, NRC 127, and NRC 150.
4	NPPP	JS 20-69, NRC 157, RVS 18, NRC 86, RVS 24, JS 20-116, NRC 138, NRC 150, NRC 152.
5	PL	NRC 152, NRC 138, RVS 18, JS 20-116, NRC 131, RVS 24, and NRC 157.
6	NSPP	NRC 152, NRC 138, NRC 131, JS 20-34, NRC 94, RVS 18, JS 20-116, and JS 20-69.
7	NBPP	NRC 150, NRC 131, NRC 138, NRC 157, JS 20-69, NRC 127, NRC 94.
8	SW	NRC 86, NRC 136, RVS 24, NRC 157, NRC 150, NRC 165, and NRC 127.
9	BY	NRC 131, RVS 18, NRC 136, RVS 24, JS 20-69, and NRC 150.
10	HI	JS 20-116, NRC 138, NRC 127, NRC 150, JS 20-69, NRC 131, and NRC 165.
11	SYPP	NRC 131, RVS 18, JS 20-69, NRC 150, JS 20-116, NRC 138, and RVS 24.

Table 3 Mean performance of 11 quantitative characters of 16 soybean genotypes.

Genotypes	D50%F	DM	PH	NPPP	PL	NSPP	NBPP	SW	BY	HI	SYPP
NRC 165	36.62	89.48	36.13	21.11	3.43	2.48	4.10	14.48	23.67	40.14	9.45
NRC 127	57.69	74.02	44.63	24.64	3.43	2.70	5.15	14.48	21.79	43.23	9.41
JS 20-116	37.68	94.42	46.30	36.07	3.76	3.38	4.41	12.88	31.03	56.19	13.60
NRC 192	35.93	82.02	46.29	25.95	3.31	2.95	2.75	13.76	30.19	27.41	9.82
NRC 86	35.57	96.31	42.45	41.22	2.34	2.55	3.81	16.74	25.09	38.41	9.38
NRC 131	45.81	105.30	53.35	26.04	3.65	3.73	6.23	12.79	55.14	40.97	22.65
NRC 138	37.16	96.11	49.05	35.58	4.45	4.08	5.59	11.62	28.04	46.46	13.07
NRC 152	36.47	84.38	63.60	33.79	4.56	4.67	3.14	10.32	34.47	31.10	10.72
RVS 24	39.95	97.49	39.04	36.31	3.59	2.46	4.69	14.88	41.15	32.40	13.02
RVS 18	42.83	95.78	43.63	41.64	3.97	3.53	3.54	10.83	45.18	37.76	17.08
JS 20-69	40.01	94.00	49.60	60.80	2.36	3.36	5.23	10.94	40.52	41.14	16.69
NRC 94	41.34	106.09	43.09	29.43	2.53	3.58	5.07	12.97	17.99	34.42	6.19
NRC 157	38.36	98.52	52.53	50.86	3.54	2.64	5.32	14.82	34.03	33.23	11.35
NRC 150	42.24	88.72	44.96	34.43	3.47	2.60	6.32	14.55	34.70	41.77	14.44
NRC 136	41.13	96.87	62.40	30.91	2.58	2.57	4.67	15.93	44.84	29.42	12.98
JS 20-34	38.42	88.74	47.50	23.27	1.69	3.69	2.71	12.74	23.45	32.29	7.45

Table 4 Mean, Range, GCV, PCV, CV and CD 5% for 11 quantitative characters in soybean.

S.N.	Characters	Grand mean	Min	Max	GCV	PCV	CV	C.D. 5%	h²b%	GA 5%	GA as 5% of Mean
1	D50%F	40.45	35.57	57.69	5.345	13.363	11.21	2.32	16.00	1.782	4.404
2	DM	93.02	74.02	106.09	8.541	8.882	4.22	6.55	92.50	15.737	16.919
3	PH	47.78	36.13	63.60	14.762	15.518	8.29	6.61	90.50	13.823	28.927
4	NPPP	34.50	21.11	60.80	29.045	30.384	15.45	8.89	91.40	19.734	57.195
5	PL	3.29	1.69	4.56	22.91	24.046	12.65	0.69	90.80	1.479	44.964
6	NSPP	3.19	2.46	4.67	20.639	20.864	5.30	0.28	97.80	1.34	42.056
7	NBPP	4.55	2.71	6.32	21.942	24.881	10.32	1.54	77.80	1.812	39.861
8	SW	13.42	10.32	16.74	13.739	13.887	3.49	0.78	97.90	3.758	28.003
9	BY	33.20	17.99	55.14	28.968	30.47	16.37	9.06	90.40	18.838	56.733
10	HI	37.90	27.41	56.19	15.077	19.274	10.80	13.14	61.20	9.207	24.296
11	SYPP	12.33	6.19	22.65	31.186	33.268	10.06	4.13	87.90	7.427	60.225

Table 5 Genotypic and phenotypic correlation coefficient for 11 quantitative traits in soybean.

Traits		D50%F	DM	PH	NPPP	PL	NSPP	NBPP	SW	BY	HI	SYPP
D50%F	Gen	1.000	-0.844**	-0.220	-0.699**	0.057	-0.375**	0.660**	0.201	0.153	0.244	0.406**
	Phe	1.000	-0.379*	-0.042	-0.309*	0.032	-0.346*	0.420**	0.058	0.079	0.191	0.186
DM	Gen		1.000	0.032	0.322*	-0.157	0.096	0.505**	0.001	0.390**	0.095	0.408**
	Phe		1.000	0.021	0.285*	-0.120	0.087	0.383**	0.011	0.365*	0.042	0.349*
PH	Gen			1.000	0.154	0.147	0.481**	-0.023	-0.267	0.431**	-0.435**	0.227
	Phe			1.000	0.137	0.147	0.461**	0.010	-0.250	0.4192**	-0.272	0.229
NPPP	Gen				1.000	-0.031	0.001	0.260	-0.208	0.307*	0.159	0.34*
	Phe				1.000	-0.021	-0.009	0.221	-0.197	0.293*	0.119	0.314*
PL	Gen					1.000	0.338*	0.216	-0.380**	0.266	0.403**	0.397**
	Phe					1.000	0.327*	0.175	-0.369*	0.251	0.374**	0.340*
NSPP	Gen						1.000	-0.190	-0.871**	0.082	0.126	0.163
	Phe						1.000	-0.173	-0.859**	0.070	0.091	0.146
NBPP	Gen							1.000	0.138	0.347*	0.691**	0.598**
	Phe							1.000	0.131	0.279	0.437**	0.483**
SW	Gen								1.000	-0.187	-0.216	-0.315*
	Phe								1.000	-0.174	-0.165	-0.293*
BY	Gen									1.000	-0.107	0.950**
	Phe									1.000	-0.082	0.891**
HI	Gen										1.000	0.314*
	Phe										1.000	0.313*
SYPP	Gen											1.000
	Phe											1.000

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

Table 6 Direct and indirect effect for different characters on seed yield per plant at genotypic level in soybean.

Traits	D50%F	DM	PH	NPPP	PL	NSPP	NBPP	SW	BY	HI
D50%F	**0.2782**	-0.235	-0.0612	-0.1945	0.0158	-0.1044	0.4618	0.056	0.0425	0.0677
DM	0.364	**-0.4308**	-0.014	-0.1386	0.0677	-0.0412	-0.2178	-0.0002	-0.1681	-0.0408
PH	0.3454	-0.051	**-1.571**	-0.242	-0.2308	-0.7569	0.036	0.4199	-0.6779	0.6842
NPPP	-0.6494	0.2988	0.1431	**0.9287**	-0.029	0.0013	0.2411	-0.1934	0.2851	0.1475
PL	0.0163	-0.045	0.0421	-0.009	**0.2864**	0.0969	0.0618	-0.1088	0.0762	0.1156
NSPP	-0.9694	0.2467	1.2442	0.0035	0.8734	**2.5824**	-0.4897	-2.251	0.2122	0.3245
NBPP	0.6803	0.2071	-0.0094	0.1064	0.0884	-0.0777	**0.4098**	0.0564	0.1426	0.2833
SW	0.3545	0.0008	-0.4706	-0.3666	-0.669	-1.5346	0.2422	**1.7606**	-0.33	-0.3808
BY	0.1949	0.498	0.551	0.3919	0.3397	0.1049	0.4441	-0.2393	**1.2767**	-0.1362
HI	-0.2081	-0.081	0.3723	-0.1358	-0.3451	-0.1074	-0.591	0.1849	0.0912	**-0.8548**

Note: R Square = 1.1604, Residual Effect = SQRT(1- 1.1604), Diagonal & Bold = Direct path

Table 7 Direct and indirect effect for different characters on seed yield per plant at phenotypic level in soybean.

Traits	D50%F	DM	PH	NPPP	PL	NSPP	NBPP	SW	BY	HI
D50%F	**-0.0547**	0.0152	0.0023	0.0114	-0.0018	0.008	-0.023	-0.0032	-0.0043	-0.0105
DM	0.0501	**-0.1798**	-0.0038	-0.0513	0.0216	-0.0156	-0.0689	-0.002	-0.0657	-0.0076
PH	0.0102	-0.0052	**-0.2461**	-0.0336	-0.0361	-0.1135	-0.0024	0.0616	-0.1031	0.067
NPPP	-0.0044	0.006	0.0029	**0.0212**	-0.0004	-0.0002	0.0047	-0.0042	0.0062	0.0025
PL	-0.0027	0.01	-0.0122	0.0017	**-0.083**	-0.0272	-0.0145	0.0307	-0.0209	-0.0228
NSPP	-0.0442	0.0263	0.14	-0.0028	0.0994	**0.3036**	-0.0525	-0.2611	0.0213	0.0276
NBPP	0.0989	0.0901	0.0023	0.052	0.0412	-0.0407	**0.2352**	0.0308	0.0655	0.1028
SW	0.0043	0.0008	-0.0186	-0.0146	-0.0274	-0.0638	0.0097	**0.0742**	-0.0129	-0.0123
BY	0.0811	0.375	0.4301	0.3009	0.2582	0.0721	0.2857	-0.1787	**1.0261**	-0.0839
HI	0.0478	0.0105	-0.0681	0.0296	0.0686	0.0228	0.1093	-0.0414	-0.0205	**0.2501**

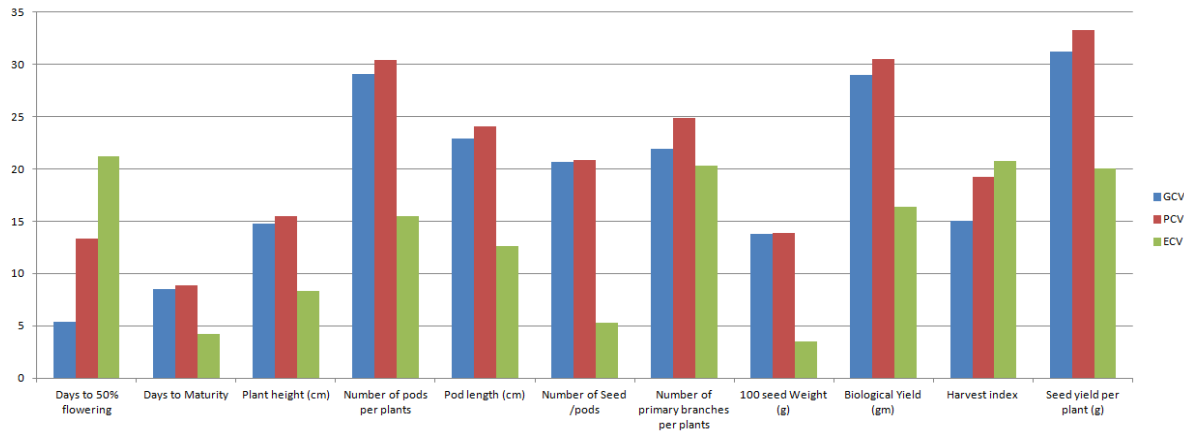Note: R Square = 0.9786, Residual Effect = 0.1462, Diagonal & Bold = Direct path

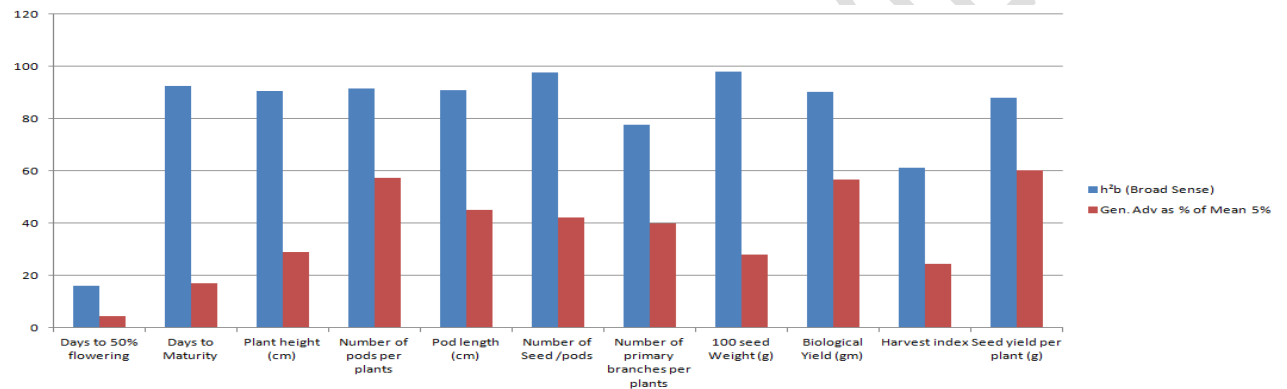Fig-1 Genotypic, Phenotypic, environmental coefficient of variances.

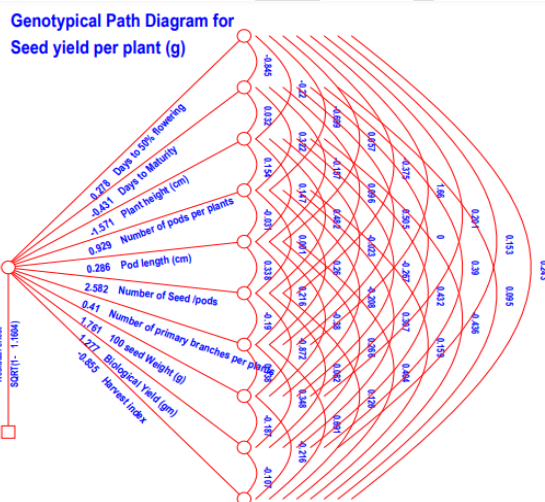Fig. 2 Heritability (%) in broad sense, Genetic advancement
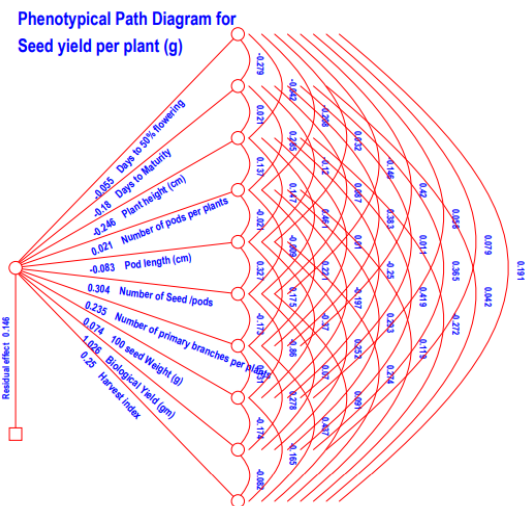

Fig. 3 Genotypic path diagram

Fig. 4 Phenotypic path diagram

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