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Correlation and path analysis for different traits in Soybean [*Glycine max* (L.) Merrill] genotypes favorable under foothill conditions of Nagaland

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Abstract
Fourteen quantitative characters were studied across 20 soybean genotypes. The results of the analysis of variance showed that the genotype-related mean sum of square was significant for all the attributes. Biological yield per plant, number of pods per cluster, number of primary branches per plant, number of clusters per plant, number of pods per plant, days to 50% flowering, plant height, and days to maturity all were significantly and positively associated with seed yield per plant. In addition these traits also had significant and positive inter-correlation among themselves. Genotypic path analysis indicated that direct relationships between the number of pods per cluster, number of pods per plant, and the number of days to maturity will probably increase seed yield per plant.

Introduction
Globally, most significant seed legume *viz.* soybean [*Glycine max* (L.) Merrill] provides around two-thirds of the world's protein concentrates for livestock feeding and 25% of the world's edible oil. It is also an essential component of formulated feeds for poultry and fish. In addition to making a large contribution to the production of edible oil, it brings in an adequate amount of foreign exchange for the nation. In terms of global soybean cultivated area, India ranks fourth. However, in terms of total production, India is ranked fifth globally after the United States, Brazil, Argentina, and China. India's contribution to global soybean output is barely 4%, which highlights its far lower productivity levels than the global average and is a key cause for concern.

Only heritable populations with observed population variability can be selected successfully. Plant breeders must determine the type of variation present in the germplasm because majority of the traits affecting yield are polygenic. Due to the complexity and degree of environmental dependence or influence of these quantitative features, direct selection for yield is ineffective. Improvement will be hampered by a significant genotype-environment interaction if selection relies solely on yield.

Thus, selection based on yield component characters can effectively boost yield. The main objective of correlation studies is to determine the acceptability of multiple characters for indirect selection because selection on any one characteristic may have unfavorable changes in other associated traits. (Singh, 1999) [26]. The correlation coefficient must be split into direct and indirect effects using path coefficient analysis since multiple traits can have an effect on a single trait. Correlation and path analysis can thus be combined to help understand the causes and effects of different character pairings more thoroughly.

Materials and Methods
The study was conducted at the School of Agricultural Sciences and Rural Development (SASRD), Medziphema Campus, Nagaland, experimental farm (Genetics and Plant Breeding) during the kharif season (rain fed) for two consecutive years, 2017 and 2018. Experimental material of the investigation comprised of 20 genotypes.

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RBD, or randomized block design, was used for the experiment. Each accession was planted in four rows of one meter each, spaced 50 cm apart from one another (row to row) and 10 cm apart plant to plant distance.

Statistical analysis

The Randomised Block Design (RBD), which was chosen, was replicated three times. The data for separate characteristics were statistically tested for significance using pooled analysis of variance and coefficients of variance obtained using the formulas provided by Lush (1940) [18] and Chaudhary and Prasad (1968) [6]. Simple correlation coefficients between two characters were calculated at the genotypic and phenotypic levels using the formula provided by Al-Jibouri et al. (1958) [2] as well as Panse and Sukhatme (1967) [22]. By using the path coefficient method recommended by Wright (1921) [30] and Dewey and Lu (1959) [10], both direct and indirect effects at genotypic and phenotypic levels were calculated considering grain yield per plant as the dependent variable.

Results and Discussion

The data were collected on 14 different characters viz., days to 50 percent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, pod length (cm), 100 seed weight (g), oil%, biological yield per plant (g), harvest index (%) and seed yield per plant (g). The analysis of variance revealed highly significant differences (p≤0.01) among genotypes.

The genotypic correlation coefficients were typically higher in magnitude for the majority of the character pairs analyzed in the current analysis when compared to the values of the phenotypic correlation coefficients, showing a significant inherent association among the characters under review; while expression of their association is dimmed by the influence of the environment. This may be because of the genotypes' relative stability, given that the majority of genotypes underwent certain level of selection Johnson et al. (1955) [16]. These outcomes support the conclusions reached by Singh et al. (2000) [27], Sultana et al. (2005) [17] and Malik et al. (2007) [19].

To assess the relationship between two traits, the correlation coefficient at the phenotypic and genotypic levels was constructed for all potential combinations between yield components (table 1). In the present study 82 associations were significant out of 91. Among them 45 associations were found positive and significant (p≤0.01) and thirty five associations were found to be negative and significantly associated. However nine were found to be non-significant.

Seed yield per plant exhibited significant and positive association with days to 50 percent flowering (results are in agreement with Malik et al. 2007 and Patil et al. 2011) [19, 23] days to maturity (Patil et al. 2011 and Baraskar et al. 2015) [23, 3], plant height (Dubey et al. 2015 and Tigga 2021) [12, 29], number of primary branches per plant (Dubey et al. 2015 and Akkamahadevi and Basavaraja, 2017) [1, 12], number of clusters per plant (Neelima et al. 2017 supported the findings) [21], number of pods per cluster (Chandel et al. 2014) [5], number of pods per plant (Dubey et al. 2015; Neelima et al. 2017 and Tigga, 2021 reported similar association) [12, 21, 29] and biological yield per plant (Baraskar et al. 2015 and Dubey et al. 2015) [3, 12] exhibited highly significant and positive correlation with seed yield at the both genotypic and phenotypic level. As a result of these findings, it can be inferred that selecting any one of the aforementioned traits will simultaneously improve the other traits and, as a result, increase seed yield because the traits have a positive association among themselves and have practical applications. Number of pods per cluster, followed by number of pods per plant, pod length days to maturity, and 100 seed weight, exhibited the highest positive direct effect in path coefficient analysis at the genotypic level when seed yield per plant was taken into account as the dependent character (table 2). Similar result has been reported for number of pods per plant by Gohil et al. (2003) [14]; Datta et al. (2005) [8]; Kumar et al. (2005) [17]; Gaikwad et al. (2007) [13]; Malik et al. (2007) [19]; Baraskar et al. (2015) [3]; Jain et al. (2015) [15]; Silva et al. (2015) [25] and Dubey et al. (2018) [11]. The findings were in agreement with Bhuva et al. (2020) [4] for number of pods per plant, pod length and days to maturity. Baraskar et al. (2015) [3] supported the results for number of pods per cluster whereas Akkamahadevi and Basavaraja (2017) [1] corroborate for 100 seed weight.

However, negative direct effect was contributed by days to 50 percent flowering (Bhuva et al. 2020) [4], number of clusters per plant, harvest index (Narne et al. 2002) [20], plant height (Shrivastava et al. (2001) [24]; Chavan et al. (2016) [7] and Bhuva et al. 2020) [4], number of primary branches per plant (Baraskar et al. 2015) [3], oil%, and negligible values of number of seeds per pod (Baraskar et al. 2015) [3] and biological yield per plant (Narne et al. 2002) [20].

Table 1: Correlation between seed yield and its contributing traits in soybean both at Genotypic and phenotypic level

Characters		DFF	DM	PH	NPB/P	NC/P	NPo/C	NPo/P	NS/Po	PoL	HSW	Oil %	BY/P	HI	SY/P
DFF	G	1.00	0.97**	0.84**	0.74**	0.56**	0.45**	0.84**	0.25**	-0.52**	-0.82**	-0.74**	0.57**	-0.83**	0.37**
	P	1.00	0.95**	0.78**	0.51**	0.48**	0.36**	0.71**	0.19*	-0.49**	-0.78**	-0.69**	0.45**	-0.55**	0.28**
DM	G		1.00	0.85**	0.74**	0.53**	0.37**	0.81**	0.26**	-0.55**	-0.84**	-0.79**	0.48**	-0.91**	0.26**
	P		1.00	0.79**	0.52**	0.45**	0.29**	0.70**	0.21*	-0.51**	-0.81**	-0.74**	0.37**	-0.57**	0.20*
PH	G			1.00	0.69**	0.43**	0.36**	0.81**	0.24**	-0.59**	-0.81**	-0.86**	0.47**	-0.73**	0.33**
	P			1.00	0.52**	0.36**	0.30**	0.69**	0.13NS	-0.53**	-0.73**	-0.75**	0.40**	-0.50**	0.31**
NPB/P	G				1.00	0.73**	0.76**	0.90**	0.07NS	-0.64**	-0.70**	-0.59**	0.80**	-0.58**	0.71**
	P				1.00	0.54**	0.56**	0.59**	0.02 NS	-0.48**	-0.48**	-0.39**	0.54**	-0.40**	0.53**
NC/P	G					1.00	0.73**	0.84**	-0.02NS	-0.40**	-0.50**	-0.54**	0.74**	-0.42**	0.67**
	P					1.00	0.61**	0.82**	0.01 NS	-0.31**	-0.44**	-0.44**	0.68**	-0.16 NS	0.64**
NPo/C	G						1.00	0.69**	-0.19*	-0.70**	-0.41**	-0.26**	0.65**	-0.05NS	0.73**
	P						1.00	0.52**	-0.11 NS	-0.53**	-0.32**	-0.18*	0.50**	0.00 NS	0.57**
NPo/P	G							1.00	0.13NS	-0.64**	-0.82**	-0.82**	0.73**	-0.69**	0.62**
	P							1.00	0.16 NS	-0.47**	-0.71**	-0.68**	0.74**	-0.20*	0.67**
NS/Po	G								1.00	0.07NS	-0.35**	-0.34**	-0.13NS	-0.22*	-0.25**

	P	1.00	0.10 NS	-0.28**	-0.24**	0.07 NS	0.13 NS	0.01 NS
PoL	G		1.00	0.75**	0.58**	-0.18*	0.24**	-0.20*
	P		1.00	0.69**	0.50**	-0.08 NS	0.24**	-0.08 NS
HSW	G			1.00	0.85**	-0.30**	0.78**	-0.12NS
	P			1.00	0.77**	-0.24**	0.47**	-0.08 NS
Oil %	G				1.00	-0.30**	0.70**	-0.13NS
	P				1.00	-0.21*	0.42**	-0.09 NS
BY/P	G					1.00	-0.46**	0.95**
	P					1.00	-0.04 NS	0.94**
HI	G						1.00	-0.14NS
	P						1.00	0.15 NS

* and ** Significant at 5% and 1% probability level

Table 2: Direct (diagonal) and Indirect (above and below diagonal) path effects on seed yield in soybean through different characters both at genotypic and phenotypic level

Characters		DFF	DM	PH	NPB/P	NC/P	NPo/C	NPo/P	NS/Po	PoL	HSW	Oil %	BY/P	HI	G and P Correlation (SY/P)
DFF	G	-2.04	1.22	-0.16	-0.51	-1.09	1.41	1.56	-0.01	-0.89	-0.50	0.56	-0.01	0.83	0.37
	P	0.07	-0.16	0.09	0.07	-0.04	0.03	0.29	0.00	0.03	-0.29	-0.05	0.30	-0.06	0.28
DM	G	-1.98	1.25	-0.16	-0.51	-1.01	1.14	1.50	-0.01	-0.93	-0.51	0.60	-0.01	0.90	0.26
	P	0.07	-0.17	0.09	0.07	-0.04	0.02	0.28	0.00	0.03	-0.30	-0.05	0.24	-0.06	0.20
PH	G	-1.72	1.06	-0.19	-0.48	-0.84	1.12	1.51	-0.01	-1.01	-0.49	0.65	-0.01	0.73	0.33
	P	0.05	-0.13	0.11	0.07	-0.03	0.03	0.28	0.00	0.03	-0.27	-0.05	0.27	-0.05	0.31
NPB/P	G	-1.50	0.93	-0.13	-0.69	-1.40	2.36	1.67	0.00	-1.09	-0.43	0.45	-0.01	0.58	0.71
	P	0.04	-0.09	0.06	0.13	-0.04	0.05	0.24	0.00	0.03	-0.18	-0.03	0.36	-0.04	0.53
NC/P	G	-1.15	0.66	-0.08	-0.51	-1.92	2.28	1.56	0.00	-0.68	-0.30	0.41	-0.01	0.42	0.67
	P	0.03	-0.08	0.04	0.07	-0.08	0.05	0.33	0.00	0.02	-0.16	-0.03	0.45	-0.02	0.64
NPo/C	G	-0.92	0.46	-0.07	-0.52	-1.40	3.12	1.28	0.01	-1.20	-0.25	0.19	-0.01	0.05	0.73
	P	0.02	-0.05	0.03	0.07	-0.05	0.09	0.21	0.00	0.03	-0.12	-0.01	0.33	0.00	0.57
NPo/P	G	-1.71	1.01	-0.16	-0.62	-1.61	2.14	1.86	0.00	-1.09	-0.50	0.62	-0.01	0.69	0.62
	P	0.05	-0.12	0.08	0.08	-0.07	0.04	0.41	0.00	0.03	-0.26	-0.05	0.49	-0.02	0.67
NS/Po	G	-0.51	0.33	-0.05	-0.05	0.03	-0.59	0.23	-0.03	0.12	-0.21	0.25	0.00	0.22	-0.25
	P	0.01	-0.03	0.01	0.00	0.00	-0.01	0.07	0.02	-0.01	-0.10	-0.02	0.04	0.01	0.01
PoL	G	1.07	-0.68	0.11	0.44	0.76	-2.20	-1.18	0.00	1.71	0.46	-0.44	0.00	-0.24	-0.20
	P	-0.03	0.08	-0.06	-0.06	0.03	-0.05	-0.19	0.00	-0.06	0.25	0.04	-0.05	0.02	-0.08
HSW	G	1.67	-1.05	0.16	0.49	0.96	-1.29	-1.53	0.01	1.27	0.61	-0.65	0.00	-0.77	-0.12
	P	-0.05	0.14	-0.08	-0.06	0.04	-0.03	-0.29	-0.01	-0.04	0.37	0.05	-0.16	0.05	-0.08
Oil %	G	1.52	-0.99	0.17	0.41	1.03	-0.80	-1.53	0.01	0.98	0.52	-0.76	0.00	-0.70	-0.13
	P	-0.05	0.12	-0.08	-0.05	0.04	-0.02	-0.28	-0.01	-0.03	0.28	0.07	-0.14	0.04	-0.09
BY/P	G	-1.17	0.61	-0.09	-0.56	-1.42	2.04	1.37	0.00	-0.30	-0.18	0.23	-0.01	0.45	0.95
	P	0.03	-0.06	0.04	0.07	-0.06	0.04	0.30	0.00	0.00	-0.09	-0.01	0.66	0.00	0.94
HI	G	1.70	-1.13	0.14	0.40	0.82	-0.16	-1.28	0.01	0.42	0.47	-0.53	0.01	-1.00	-0.14
	P	-0.04	0.10	-0.05	-0.05	0.01	0.00	-0.08	0.00	-0.01	0.17	0.03	-0.03	0.10	0.15
Residual effect	G	0.227	P	0.180											

G = Genotypic, P = phenotypic

Conclusion
A thorough examination of the genotypic positive correlation analysis between seed yield/plant and characters like days to maturity, number of pods per cluster, and number of pods per plant revealed the true relationship between them, and direct selection for these traits will be fruitful for yield improvement. The residual effect (0.227) was of moderate significance, indicating that additional variables exist that influence yield in addition to the traits under study.

References
1. Akkamahadevi S, Basavaraja, GT. Genetic variability and character association among vegetable soybean genotypes for yield and components traits. Journal of Farm Sciences. 2017;30(3):315-319.
2. Al-jibouri A, Miller PA, Robinson HF. Genotype and environmental Variation and correlation in an upland cotton crop of the interspecific origin. Agronomy Journal. 1958;50:626-636.
3. Baraskar VV, Vachhani JH, Kachhadia VH, Patel MB, Barad HR. Correlation and path analysis for seed yield in soybean [*Glycine max* (L.) Merrill]. Electronic Journal of Plant Breeding.2015;6(2):570-573.
4. Bhuva RB, Babariya CA, Movaliya HM, Gadhiya JA, Balar VS. Correlation and Path Analysis for Seed Yield in Soybean [*Glycine max* (L.) Merrill]. Indian Journal of Pure and Applied Bioscience. 2020;8(4):375-380.
5. Chandel KK, Patel NB, Patel JB. Correlation coefficients and path analysis in soybean (*Glycine max* L. Merrill). AGRES-International e-Journal. 2014;3(1):25-31.
6. Chaudhary LB, Prasad B. Genetic variation and heritability of quantitative characters in Indian mustard (*Brassica juncea*). Indian Journal of Agricultural Science. 1968;124(1):48-55.
7. Chavan BH, Dahat DV, Rajput HJ, Deshmukh MP, Diwane SL. Correlation and path analysis in soybean. International Multidisciplinary Research Journal. 2016;2(9):1-5.
8. Datta AK, Hossain MA, Rahman L. Genetic parameters, inter-relationship and path coefficient analysis in soybean

[*Glycine max* (L.) Merrill]. Journal of Bangladesh Agricultural University. 2005;3(2):225-230.

9. Datta AK, Hossain MA, Rahman L. Genetic parameters, inter-relationship and path coefficient analysis in soybean [*Glycine max* (L.) Merrill]. Journal of Bangladesh Agricultural University. 2005;3(2):225-230.

10. Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheat, grass, seed production. Agronomy Journal. 1959;47:477-483.

11. Dubey N, Avinashe HA, Shrivasthava AN. Genetic parameters and character association studies of soybean genotypes in Madhya Pradesh region. Annals of Biology. 2018;34(2):207-211.

12. Dubey N, Shrivasthava AN, Avinashe HA, Jaiwar S. Genetic variability, correlation and path analysis for yield and yield contributing characters in soybean (*Glycine max* L.). Electronic Journal of Plant Breeding. 2015;6(1):318-325.

13. Gaikwad SR, Bangar ND, Chavan BH. Correlation and path coefficient analysis in soybean. Journal of Maharashtra Agricultural Universities. 2007;32(2):276-277.

14. Gohil VN, Pandya HM, Mehta DR. Genetic association and path analysis for seed yield, its components and quality attributes in soybean. Gujarat Agricultural University Research Journal. 2003;28(1-20):9-11.

15. Jain S, Srivastava SC, Sing SK, Indapurkar YM, Singh BK. Studies on genetic variability character association and path analysis for yield and its contributing traits in soybean (*Glycine max* (L.) Merrill). Legume Research. 2015;38 (2):182-184.

16. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47(2):314-318.

17. Kumar AP, Ramana MV, Sultana R, Rao AS. Character association and path analysis in soybean. The Andhra Agicultural Journal. 2005;52(1-2): 48-51.

18. Lush JL. Inter size correlation and regression of offspring on dams as a method of estimating heritability of characters. Proceedings of American Society of Animal Production. 1940;33:293-301.

19. Malik MFA, Muhammad A, Qureshi AS, Abdul G. Assessment of genetic variability, correlation and path analyses for yield and its components in soybean. Pakistan Journal of Botany. 2007;39(2):405-413.

20. Narne, Aher P, Dahat V, Aher AR. Selection of protein rich genotypes in soybean. Crop Research. 2002;24(1):106-112.

21. Neelima G, Mehtre SP, Narkhede GW. Correlation coefficient and path analysis studies in soybean (*Glycine max* (L.) Merrill.) Multilogic in Science. 2017;7(23):96-99.

22. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. ICAR, New Delhi; c1967.

23. Patil SS, Naik MR, Patil PP, Shinde DA Genetic variability, correlation and path analysis in soybean. Legume Research. 2011;34(1):36-40.

24. Shrivastava MK, Shukla RS, Singh CB. Genetic divergence in soybean. JNKVV Research Journal publication. 2001;34(1-2):25-28.

25. Silva AF, Sediyama T, Silva FCS, Bezerra ARG, Ferreira LV. Correlation and path analysis of soybean yield components. International Journal of Plant, Animal and Environmental Sciences. 2015;5(1):177-17.

26. Singh I. Genetic variability and correlation studies in soybean [*Glycine max* (L.) Merrill]. Journal of Oilseeds Research. 1999;16:118-120.

27. Singh K, Singh S, Kler DS. Correlation and regression studies among various growth and yield parameters of soybean [*Glycine max* (L.) Merrill] under Punjab conditions. Crop Research. 2000;19:287-297.

28. Sultana S, Rahman L, Habib SH. Genetic variability, correlation and path analysis in soybean (*Glycine max* (L.) Merrill). International Journal of Sustainable Agricultural Technology. 2005;1(5):16-20.

29. Tigga A. Genetic variability and diversity analysis for yield and its contributing characters in soybean (*Glycine max* (L.) Merrill). M.Sc. Thesis, Indira Gandhi Krishi Vishwavidyalaya, Raipur; c2021.

30. Wright S. Correlation and causation. Journal of Agricultural Research. 1921;20:557-587.