Research Note

Genetic variability, correlation and path analysis for yield and yield contributing characters in soybean (*Glycine max* L.)

Nidhi Dubey*, A. N. Shrivasthava, H. A. Avinashe and Samidha Jaiwar
Department of Plant Breeding and Genetics
Jawaharlal Nehru Krishi Vishwavidyalaya, College of Agriculture, Jabalpur (M.P)
*Email: nddubeynidhidubey7@gmail.com

Abstract
The genetic variability studies carried out on 50 soybean genotypes indicated that the estimate of phenotypic coefficient of variation were greater than those of the genotypic coefficient of variation for all the traits studied. The close proximity between PCV & GCV values for most of the characters indicated less influence of environment on the expression of the characters under study. Considering heritability, most of the characters showed high values. High heritability coupled with high genetic advance as per cent of mean were recorded for biological yield plant[-1], harvest index, number of seeds plant[-1], seed yield plant[-1] and number of pods plant[-1] indicating the scope of improvement through direct selection. Correlation analysis revealed that number of pods node[-1], number of seeds plant[-1], biological yield plant[-1], number of nodes plant[-1] and harvest index were positively and significantly associated with seed yield plant[-1]. Path analysis revealed that number of pods node[-1] had the high positive direct effect on seed yield plant[-1] followed by number of nodes plant[-1], number of seed yield plant[-1], biological yield plant[-1] and harvest index. Traits *viz.,* number of pods plant[-1], days to 50% flowering, days to maturity had negative direct effect on seed yield plant[-1]. Most of the other traits had indirect effect via number of branches plant[-1], number of pods plant[-1] and 100-seed weight. Hence, these characters should be given more weightage in selection programme of high yielding soybean genotypes.

Soybean [*Glycine max* (L.) Merrill] is a major oil seed crop in the world and is called as a golden bean or miracle bean because of its versatile nutritional qualities having 20% oil and 38 to 43 % protein, which has biological value as meat and fish protein and rich in amino acids like lysine and tryptophan (Quayam *et al.,* 1985).In India, cultivation of soybean has reached about 12.03 million hectare, with the total production of about 12.98 million tones and average productivity of about 1079 kg/ha in 2013-2014(Anonymous, 2013). There is a substantial scope to increase both area and productivity of soybean in India. Genetic variability is the basic requirement for crop improvement as this provides wider scope for selection. Thus, effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in material and extent to which it is heritable. Selection for seed yield, which is a polygenic trait, often leads to changes in other characters. Therefore, the knowledge of relationship between seed yield and other characters is desirable to choose the appropriate selection during breeding programme. Correlation studies enable the breeder to study the strength of relationship between various characters as well as the magnitude and direction of changes expected during selection. Path coefficient analysis measures the direct and indirect effect of one variable upon another and permits the separation of the correlation coefficient into direct and indirect components (Dewey and Lu, 1959). Hence, the present study is conducted to estimate heritability and genetic advance of genotypes for yield and yield related traits and to measure the extent of direct and indirect causes of association among traits through path coefficient analysis nin soybean.

The present investigation was carried out at Seed Breeding Farm, Department of Genetics and Plant Breeding, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P) during *rabi* 2013-14.The experimental material consisted of 50soybean genotypes. These genotypes were sown in Randomized Block Design (RBD) with three replications. Each genotype was grown in two rows of four meter length. Row to row and plant to plant distance was maintained at 60 cm and 5 cm respectively. All the recommended package of practices were followed during the course of experimentation to grow a normal crop. Five individual plants from each genotype were randomly selected and tagged from each replication for data recording. Data was recorded on whole plot basis for days to 50% flowering and days to maturity whereas for plant height, number of branches plant[-1], number of nodes plant[-1], number of pods plant[-1], number of pods node[-1], number of seeds plant[-1], number of seeds pod[-1], 100-seed weight, biological yield plant[-1], harvest index, seed yield plant[-1] from individual tagged plant. The mean performance of each genotype was subjected for statistical analysis. The statistical analysis was done by the method given by Panse and Sukhatme (1954).Correlation coefficient and path coefficient was worked out as method suggested by Al-Jibouri *et al.* (1958) and Dewey and Lu (1959), respectively.

The analysis of variance (Table 1) revealed that the treatments were highly significant for all the characters. This suggested that the genotypes selected were genetically variable and considerable amount of variability existed among them. Similar findings were reported by Reni and Rao (2013).

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed in the experimental material for all the characters studied (Table 2). The PCV was higher than GCV for all the characters indicating that the visible variation in the expression of traits was not only due to varying influence of environment. High PCV was observed for harvest index(41.56), followed by biological yield plant[-1] (34.49), seed yield plant[-1] (33.15), number of seeds plant[-1] (32.97), number of branches plant[-1] (32.25), number of pods plant[-1] (27.48), number of seeds pod[-1] (26.97), number of pod node[-1] (21.07) and plant height (20.14). High GCV was observed for harvest index (37.99), followed by biological yield plant[-1] (34.45), seed yield plant[-1] (28.78), number of seeds plant[-1] (28.73), number of pods plant[-1] (24.53), number of branches plant[-1] (23.66) and number of seeds pod[-1](20.62). These results are in conformity with the finding of Osekita and Ajayi (2013) who observed high PCV and GCV for seed yield plant[-1] and number of seeds plant[-1].

These values alone are not helpful in determining the heritable portion of variation. The proportion of genetic variability which is transmitted from parents to all springs is reflected by heritability (Lush, 1949). The estimates of heritability varied from 53.75% for 100-seed weight to 99.81% for biological yield plant[-1]. Among all the characters biological yield plant[-1](99.81%) recorded highest estimates followed by days to maturity (98.14%), days to 50% flowering (96.87%), harvest index (83.56%), number of pods plant[-1] (79.69%), plant height (79.46%), number of nodes plant[-1] (76.35%), number of seeds plant[-1] (75.89%) and seed yield plant[-1] (75.39%). Okonkwo and Idahosa (2013) reported high heritability estimates for days to maturity, days to 50% flowering. While in present study, low heritability was also reported for number of seeds pod[-1] (58.47%), number of pods node[-1] (55.88%), number of branches plant[-1] (53.84%) and 100-seed weight (53.75%). Similar findings were reported by Osekita and Ajayi (2013) for number of branches plant[-1] and 100-seed weight. Genetic advance as per cent of mean was recorded maximum for harvest index (71.55) followed by biological yield plant[-1] (70.91), number of seeds plant[-1] (51.55), seed yield plant[-1] (51.49) and number of pods plant[-1] (45.11). In general, biological yield plant[-1], harvest index, number of seeds plant[-1], seed yield plant[-1] and number of pods plant[-1]revealed high heritability with high genetic advance. The estimates of high heritability (broad sense) and high genetic advance indicate that improvement in these traits could be possible by direct selection. High heritability coupled with moderate genetic advance was observed for plant height, number of nodes plant[-1] and days to 50% flowering indicating presence of G x E interaction. This indicated that simple selection may not be rewarding for these traits. The present findings corroborate the earlier report of Okonkwo and Idahosa (2013) and Bhat and Basavaraja (2011).

Correlation coefficient analysis (Table 3) measure natural relation between 13 various plant characters and determine the component characters on which selection can be used for genetic improvement in yield. The correlation coefficient estimated positive and significant genotypic and phenotypic correlation in number of seeds plant[-1] (0.934, 0.905), number of pods node[-1] (0.743, 0.558), number of pods plant[-1] (0.712, 0.624), biological yield plant[-1] (0.474, 0.414), number of nodes plant[-1] (0.455, 0.363), number of branches plant[-1] (0.422, 0.286), number of seeds pod[-1] (0.396, 0.420), harvest index (0.269, 0.402) and plant height (0.281, 0.244) with seed yield plant[-1]. Similar findings were reported by Ghodrati*et al.* (2013) that harvest index and number of pods plant[-1] showed positive association with seed yield plant[-1]. Thus selection for higher yield on the basis of above characters would be reliable.

When characters having direct bearing on yield are selected, their association with other character are to be considered simultaneously as they will indirectly affect the yield. Days to 50% flowering implied positive significant correlation at both levels with plant height (0.813, 0.709), days to maturity (0.798, 0.774), number of branches plant[-1] (0.750, 0.542), number of nodes plant[-1] (0.730, 0.632), biological yield plant[-1] (0.684, 0.673), number of pods plant[-1] (0.568, 0.490), number of pods node[-1] (0.338, 0.235) and number of seeds plant[-1] (0.278, 0.241) while negatively associated with harvest index (-0.706, -0.629), number of seeds pod-1 (-0.461, -0.332) and 100-seed weight (-0.411, -0.296).Days to maturity had positive and significant correlation with plant height (0.677, 0.600), biological yield plant[-1] (0.607, 0.601), number of branches plant[-1] (0.591, 0.418), number of nodes plant[-1] (0.477, 0.414), number of pods plant[-1] (0.388, 0.343) at both genotypic and phenotypic level, whereas number of pods node[-1] (0.281) recorded significant and positive correlation at genotypic level. While it had significant and negative correlation with harvest index (-0.809, -0.740), number of seeds pod[-1] (-0.646, -0.500) at both genotypic and phenotypic level and 100-seed weight (-0.233) at the genotypic level. Plant height showed positive significant association with number of nodes plant[-1] (0.834, 0.726), biological yield plant[-1](0.791, 0.707), number of branches plant[-1](0.796, 0.581), number of pods plant[-1] (0.667, 0.581), number of

seeds plant[-1] (0.348, 0.303) and number of pods node[-1] (0.377, 0.263) whereas negative significant association with harvest index (-0.667, -0.515) and number of seeds pod[-1] (-0.445, -0.314) at both genotypic and phenotypic level. Number of branches plant[-1] hadpositive and significant correlation with number of nodes plant[-1] (0.817, 0.634), biological yield plant[-1] (0.778, 0.571), number of pods plant[-1] (0.695, 0.576), number of pods node[-1] (0.421, 0.301) and number of seeds plant[-1] (0.396, 0.260) while negative and significant correlation with number of seeds pod[-1] (-0.409, -0.338) at both genotypic and phenotypic level whereas with harvest index (-0.526) at genotypic level alone. Number of nodes plant[-1] was positively correlated with number of pods plant[-1] (0.847, 0.678), biological yield plant[-1](0.668, 0.585), number of seeds plant[-1] (0.526, 0.409) at both genotypic and phenotypic level and number of pods node[-1] (0.528) at genotypic level, whereas it had negative and significant correlation with harvest index (-0.448, -0.342), number of seeds pod[-1] (-0.427, -0.291) at both the levels, while with 100 seed weight(-0.255) at the genotypic level alone. Number of pods plant[-1] showed positive association with number of pods node[-1] (0.893, 0.837), number of seeds plant[-1](0.779, 0.663) and biological yield plant[-1] (0.697, 0.625) whereas negative association with number of seeds pod[-1](-0.253, -0.300) at both genotypic and phenotypic level and significant and negative correlation with harvest index (-0.256) and 100-seed weight (-0.251) at genotypic level. Number of pods node[-1] showed positive correlation with number of seeds plant[-1] (0.782, 0.576), biological yield plant[-1](0.551, 0.414) at both genotypic and phenotypic level. Number of seeds plant[-1] showed significant and positive association at both genotypic and phenotypic level with biological yield plant[-1](0.473, 0.412), number of seeds pod[-1](0.387, 0.484) and at the genotypic level with harvest index (0.327) ,while negative association with 100 seed weight (-0.234) at phenotypic level. Number of seeds pod[-1] was positively correlated with harvest index (0.745, 0.652) while negatively correlated with biological yield plant[-1] (-0.275, -0.212)at both genotypic and phenotypic level. Hundred seed weight showed positive significant correlation with harvest index (0.245, 0.214). Biological yield plant[-1] showed negative significant association with harvest index (-0.655, -0.597) at both genotypic and phenotypic level. These results showed close resemblance with the report of Siahbidi et al. (2013).

Path coefficient analysis is more useful for partitioning of direct and indirect causes of correlation and also enables to compare the component factors on the basis of their relative contributors. The path coefficient analysis in Table 4 revealed that highest positive direct effects was noted for number of pods node[-1] (2.2310) followed by number of nodes plant[-1] (1.7681), number of seeds plant[-1](0.7695), number of branches plant[-1](0.3596), biological yield plant[-1] (0.3376) and harvest index (0.2795)on the dependent character i.e., seed yield plant[-1]. Similar results were reported by Arshad et al. (2014) who observed highest contribution towards seed yield plant[-1] with number of branches plant[-1]. Therefore, these characters should be considered as main components for selection in a breeding program for higher seed yield. It was also observed that the highest negative direct effect was exerted by number of pods plant[-1] (-3.6087) followed by days to 50% flowering (-0.3293) and days to maturity (-0.0989). Arshad et al. (2014) reported that days to 50% flowering and days to maturity have direct but negative effects on seed yield plant[-1].

Days to 50% flowering had moderate positive indirect effect via harvest index (0.2325).Moderate indirect effect of number of branches plant[-1] was positive via number of nodes plant[-1] (0.2941), plant height (0.2865), biological yield plant[-1] (0.2799), days to 50% flowering (0.2698), number of pods plant[-1] (0.2500) and days to maturity (0.2126). Number of nodes plant[-1] exhibited high positive indirect effect via number of pods plant[-1](1.4983), plant height (1.4751), number of branches plant[-1] (1.4460), days to 50% flowering (1.2908), biological yield plant[-1](1.1815), number of pods node[-1](0.9338), number of seeds plant[-1] (0.9309) and days to maturity (0.8440).Number of pods plant[-1] had high positive indirect effect via harvest index (0.9264), number of seeds pod[-1](0.9152) and 100-seed weight (0.9069); number of pods node[-1] had high positive indirect effect via number of pods plant[-1](1.9924), number of seeds plant[-1](1.7463), biological yield plant[-1](1.2309), number of nodes plant[-1](1.1783), number of branches plant[-1](0.9405), plant height (0.8415), days to 50% flowering (0.7551) and days to maturity (0.6278). Number of seeds plant[-1] imposed high indirect effect via number of pods node[-1] (0.6024), number of pods plant[-1](0.5996), number of nodes plant[-1](0.4052), biological yield plant[-1](0.3646) and number of branches plant[-1](0.3053).Biological yield plant[-1] had moderate positive indirect effect via plant height (0.2670), number of branches plant[-1](0.2628), number of pods plant[-1](0.2354), days to 50% flowering (0.2311), number of nodes plant[-1](0.2256) and days to maturity (0.2051).Harvest index imposed moderate positive indirect effect via number of seeds pod[-1](0.2084).These results are in conformity with the findings of Abady et al. (2013).The residual effect (0.0316) on seed yield plant[-1] was negligible, which suggest that most of the yield component was included in the study.

Hence it can be concluded that in soybean, traits like number of pods node[-1], number of seeds plant[-1], harvest index and biological yield plant[-1] showed positive correlation with yield as well as they have direct effect on yield. Hence these traits can be used as selection indices in soybean to bring about the improvement in yield.

References

Abady, S., Merkeb, F. and Dilnesaw, Z. 2013. Heritability and path-coefficient analysis in soybean (*Glycine Max* (L).Merrill) genotypes at Pawe, North -Western Ethiopia.*J. Environmental Sci. and Water Resour.,* 2(**8**): 270-276.

Al-Ji-Bouri., Muller,H. A. and Robinson, H.F.1958. Genetic and environmental variance and variances in upland cotton cross of inter specific origin. *Agron. J.,*50:633-636.

Anonymous, 2013. The Soybean Processors Association of India, 33rd Annual General Meeting of SOPA, pp. 1-2.

Arshad, W., Zees an, M., Khan, M .I., Ali, S., Hussain, M. and Rahman, S. 2014. Character association and causal effect analysis for yield and yield components among early maturing genotypes of soybean (*Glycine max* (L.) Merrill). *J. Renewable Agriculture.,* 2(**1**):1-4.

Bhatt, S. and Basavaraja, G. T. 2011.Genetic variability and correlation studies in segregating generation of soybean (*Glycine max* (L.) Merrill). *Crop Improve.,* 38(**1**):77-87.

Dewey D.R. and Lu K.H. 1959. A correlation and path coefficient analysis of components of crested wheatgrass seed production. *Agron. J.,* 51: 515-518.

Ghodrati, G. R., Sekhavat, R., Mahmoodinezhadedezfully, S. H.and Gholami, A. 2013. Evaluation of correlations and path analysis of components seed yield in soybean.*International J. Agriculture.,* 3(**4**):795-800.

Lush J.L. 1949. Heritability of quantitative characters in farm animals. *Herbicides*, 35:356-357.

Okonkwo, F.A.and Idahosa, D.O. 2013. Heritability and correlation studies of yield characters in some soybean (*Glycine Max* L.) varieties in Ekpoma.*American J. Res. Comm.:* 2325-4076.

Osekita, O. S. and Ajayi, A. T. 2013.Character expression and selection differential for yield and its components in soybean (*Glycine max* (L.) Merrill). *Academia J. Agri. Res.,* 1(**9**):167-171.

Panse, V. G. and Sukhatme, P. V. 1954.*Statasticals methods for Agricultural Workers,*ICAR, New Delhi, pp. 54-57.

Quayam, A., Rao, M. S. S. and Violet Kerketta 1985. Soybean: A miracle oil seed crop-its prospects and constraints in Bihar plateau. In:*Proc. Oil Seed Production Constraints and Opportunities,*pp: 219-232.

Reni, Y. P. and Rao, Y. K. 2013.Genetic variability in soybean (*Glycine max* (L.) Merrill). *International J. Plant, Animal and Environment Sci.,* 3(**4**): 2231-4490.

Siahbidi, M. M.,Hoseinzadeh, J.,Aboughadareh, A. P., Bazdar, A.,Beasty, H. and Rad, H.N. 2013. Character association and path analysis of soybean genotypes under water deficit stress. *International J. Biosci.,* 3(**10**):126-132.

Table 1. Analysis of variance for various yield contributing characters in soybean

Characters	Mean Sum of Squares		
	Replication (do=2)	Treatments (do=49)	Error (do=98)
Days to 50% flowering	0.060	103.852**	1.107
Days to maturity	0.046	246.487**	1.550
Plant height(cm)	18.391	150.232**	11.917
Number of branches plant^{-1}	0.677	3.936**	0.874
Number of nodes plant^{-1}	0.781	6.445**	0.603
Number of pods plant^{-1}	143.836	754.511**	59.080
Number of pods node^{-1}	0.888	3.642**	0.759
Number of seeds plant^{-1}	122.775	1942.256**	185.978
Number of seeds pod^{-1}	0.089	0.304**	0.058
100 seed weight(g)	0.010	4.666**	1.040
Biological yield plant^{-1}(g)	0.196	501.771**	0.323
Harvest index	6.808	429.396**	26.420
Seed yield plant^{-1}(g)	1.067	30.307**	2.974

*, ** significant at 5% and 1% levels, respectively

Table 2.Estimates of variability, heritability and genetic advance as per cent of mean in soybean

Characters	Range		Mean	Coefficient of variation (%)		Heritability (%)	Genetic Advance	GA as per cent of mean
	Min	Max		PCV	GCV			
Days to 50% flowering	51.00	78.00	64.50	8.93	8.79	96.87	11.86	17.83
Days to maturity	101.00	142.00	121.50	7.13	7.07	98.14	18.43	14.43
Plant height(cm)	21.86	53.13	37.49	20.14	17.96	79.46	12.46	32.98
Number of branches plant^{-1}	1.66	6.66	4.16	32.25	23.66	53.84	1.52	35.77
Number of nodes plant^{-1}	6.06	13.33	9.69	16.11	14.08	76.35	2.51	25.34
Number of pods plant^{-1}	23.80	96.73	60.26	27.48	24.53	79.69	27.99	45.11
Number of pods node^{-1}	3.91	8.60	6.25	21.07	15.75	55.88	1.50	24.25
Number of seeds plant^{-1}	42.67	145.42	94.04	32.97	28.73	75.89	43.42	51.55
Number of seeds pod^{-1}	0.70	2.19	1.44	26.97	20.62	58.47	0.45	32.48
100 seed weight(g)	9.66	15.63	12.64	11.93	8.75	53.75	1.66	13.21
Biological yield plant^{-1}(g)	9.42	60.21	34.81	34.49	34.45	99.81	26.60	70.91
Harvest index	13.21	61.26	37.23	41.56	37.99	83.56	21.82	71.55
Seed yield plant^{-1}(g)	4.66	16.46	10.56	33.15	28.78	75.39	5.39	51.49

Table 3.Genotypic (G) and phenotypic (P) coefficient of correlation among different character in soybean genotypes

Characters		DTM	PH	NBP	NNP	NPP	NPN	NSP	NSPo	100SW	BYP	HI	SYP
DTF	G	0.798**	0.813**	0.750**	0.730**	0.568**	0.338**	0.278**	-0.461**	-0.411**	0.684**	-0.706**	0.146
	P	0.774**	0.709**	0.542**	0.632**	0.490**	0.235*	0.241*	-0.332**	-0.296**	0.673**	-0.629**	0.130
DTM	G		0.677**	0.591**	0.477**	0.388**	0.281**	0.017	-0.646**	-0.233*	0.607**	-0.809**	-0.049
	P		0.600**	0.418**	0.414**	0.343**	0.204	0.004	-0.500**	-0.166	0.601**	-0.740**	-0.050
PH	G			0.796**	0.834**	0.667**	0.377**	0.348**	-0.445**	-0.221	0.791**	-0.667**	0.281**
	P			0.581**	0.726**	0.581**	0.263*	0.303**	-0.314**	-0.161	0.707**	-0.515**	0.244*
NBP	G				0.817**	0.695**	0.421**	0.396**	-0.409**	0.021	0.778**	-0.526**	0.422**
	P				0.634**	0.576**	0.301**	0.260*	-0.338**	0.033	0.571**	-0.332	0.286**
NNP	G					0.847**	0.528**	0.526**	-0.427**	-0.255*	0.668**	-0.448**	0.455**
	P					0.678**	0.180	0.409**	-0.291**	-0.155	0.585**	-0.342**	0.363**
NPP	G						0.893**	0.779**	-0.253*	-0.251*	0.697**	-0.256*	0.712**
	P						0.837**	0.663**	-0.300**	-0.138	0.625**	-0.155	0.624**
NPN	G							0.782**	-0.103	-0.179	0.551**	-0.081	0.743**
	P							0.576**	-0.214*	-0.076	0.414**	0.003	0.558**
NSP	G								0.387**	-0.194	0.473**	0.218	0.934**
	P								0.484**	-0.234*	0.412**	0.327**	0.905**
NSPo	G									0.102	-0.275**	0.745**	0.396**
	P									-0.124	-0.212*	0.652**	0.420**
100SW	G										-0.071	0.245*	0.160
	P										-0.047	0.214*	0.180
BYP	G											-0.655**	0.474**
	P											-0.597**	0.414**
HI	G												0.269**
	P												0.402**

*,** significant at 5% and 1% level of significance.

DTF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height, NBP: Number of branches plant[-1], NNP: Number of nodes plant[-1], NPP: Number of pods plant[-1], NPN: Number of pods node[-1], NSP: Number of seeds plant[-1], NSPo: Number of seeds pod[-1], 100SW: 100-seed weight, BYP: Biological yield plant[-1], HI: Harvest index, SYP: Seed yield plant[-1].

Table 4. Path coefficient showing direct (diagonal) and indirect effect (off diagonal) of different characters on seed yield plant^{-1} in soybean

Trait	DTF	DTM	PH	NBP	NNP	NPP	NPN	NSP	NSPo	100SW	BYP	HI	SYP
DTF	**-0.3293**	-0.2628	-0.2679	-0.2471	-0.2404	-0.1872	-0.1115	-0.0917	0.1519	0.1354	-0.2255	0.2325	0.1469
DTM	-0.0789	**-0.0989**	-0.0670	-0.0585	-0.0472	-0.0384	-0.0278	-0.0017	0.0639	0.0231	-0.0600	0.0800	-0.0492
PH	0.0779	0.0649	**0.0958**	0.0763	0.0799	0.0639	0.0361	0.0334	-0.0426	-0.0212	0.0758	-0.0640	0.2812**
NBP	0.2698	0.2126	0.2865	**0.3596**	0.2941	0.2500	0.1516	0.1427	-0.1472	0.0077	0.2799	-0.1894	0.4221**
NNP	1.2908	0.8440	1.4751	1.4460	**1.7681**	1.4983	0.9338	0.9309	-0.7550	-0.4518	1.1815	-0.7926	0.4554**
NPP	-2.0510	-1.4011	-2.4083	-2.508	-3.0579	**-3.6087**	-3.2227	-2.8116	0.9152	0.9069	-2.5164	0.9264	0.7126**
NPN	0.7551	0.6278	0.8415	0.9405	1.1783	1.9924	**2.2310**	1.7463	-0.2315	-0.3992	1.2309	-0.1811	0.7431**
NSP	0.2142	0.0135	0.2682	0.3053	0.4052	0.5996	0.6024	**0.7695**	0.2984	-0.1500	0.3646	0.1679	0.9346**
NSPo	-0.0096	-0.0135	-0.0093	-0.0086	-0.0089	-0.0053	-0.0022	0.0081	**0.0209**	0.0021	-0.0058	0.0156	0.3960**
100SW	-0.0258	-0.0146	-0.0139	0.0013	-0.0160	-0.0157	-0.0112	-0.0122	0.0064	**0.0626**	-0.0045	0.0154	0.1600
BYP	0.2311	0.2051	0.2670	0.2628	0.2256	0.2354	0.1863	0.1600	-0.0929	-0.0242	**0.3376**	-0.2212	0.4749**
HI	-0.1973	-0.2262	-0.1866	-0.1472	-0.1253	-0.0717	-0.0227	0.0610	0.2084	0.0685	-0.1831	**0.2795**	0.2690**

Residual effect = 0.0316

*,** significant at 5% and 1% level of significance.

DTF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height, NBP: Number of branches plant^{-1}, NNP: Number of nodes plant^{-1}, NPP: Number of pods plant^{-1}, NPN: Number of pods node^{-1}, NSP: Number of seeds plant^{-1}, NSPo: Number of seeds pod^{-1}, 100SW: 100-seed weight, BYP: Biological yield plant^{-1}, HI: Harvest index, SYP: Seed yield plant^{-1}.