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## Genotypic and phenotypic correlation studies among the eleven characters of 27 genotypes Mung bean (*Vigna radiata* L. Wilczek)

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### Abstract

Pulses in India have long been considered as only source of poor man's protein. India is the largest importer, producer and consumer of pulses (Jitendra *et al.*, 2011). India accounts for 33% of the world area and 22% of the world production of pulses (Amarender, 2009). Pulses production in India 18.34 million tonne (ICAR 2013-14). Combining ability analysis is frequently employed to identify the desirable parents for inclusion in hybridization programme The genotypes K-851, Sublobata-02, IPM-2-3 were found, on evaluation as superior with respect to yield along with a number of yield components as well as and protein content and with respect to earliness in IPM2-3. These genotypes can be employed to develop early maturing protein rich high yielding lines. Seed yield plant<sup>-1</sup> had shown significant positive correlation with pod width and positive correlation with number of pods plant<sup>-1</sup> which also exerted positive direct effect on yield except protein content and these characters may be used as criteria for selection for simultaneous improvement in yield.

**Keywords:** Phenotypic correlation studies among, eleven characters of 27 genotypes Mung bean

### Introduction

Mung bean (*Vigna radiata* L. Wilczek) is a pulse species of the pan-tropical region (kumar *et al.*, 2004)<sup>[3]</sup>. But (Tomooka *et al.*, 1992)<sup>[4]</sup>, considered it as native to Asia and widely cultivated in Africa, Asia and Latin America. They also examined the variations of seed proteins in Mung bean landraces from Asia, and proposed it as diverse region for Mung bean. According to their study, the region of protein type diversity is found in West Asia (Afghanistan-Iran-Iraq area) rather than in India. Judging from the geographical distribution of protein types, Mung bean might have spread mainly to the east by two routes, one route is from India to Southeast Asia strains consisting of a few protein types with prominent protein type were disseminated by this route and another dissemination pathway may have been the route known as the Silk Road. By this route, protein type 7 and 8 strains spread from West Asia or India to China and Taiwan via the Silk Road, not by the route from Southeast Asia. A large proportion of alleles of higher productivity have been lost in the present populations of Mung bean due to overriding role of natural selection even long after the crop domestication (Jain, 2004)<sup>[5]</sup>. The interrelationship of quantitative traits with yield determines the efficiency of selection in breeding programmes. It indicates the intensity and degree of association between different character pairs. To improve Mung bean for both yield and yield components, an understanding of their association among themselves is necessary. Variability and correlation studies help in selection of reliable yield components for efficient yield improvement (Vijayalaxmi *et al.*, 2000)<sup>[6]</sup>. The use of diverse germplasm as a significant factor contributing to high yield and quality characteristics had been also stressed by (Gopalakrishnan and Dwivedi, 2008)<sup>[20]</sup>. Heritability in conjunction with genetic advance is more useful than heritability alone in the prediction of resultant effect of selecting the best individual (Singh *et al.*, 2010)<sup>[7]</sup>. Correlation analysis provides information on inter-relationship of important plant characters and hence, leads to a directional model of selection providing scope for direct and or indirect improvement in grain yield (khan *et al.*, 2004)<sup>[8]</sup>. The correlation values decide only the nature and degree of association existing between pairs of characters.

### Materials and methods

The field experiment was conducted at Jaguli instructional farm Bidhan Chandra Krishi Viswavidyalaya, Nadia district, West Bengal during 27 genotypes were sown in the 1<sup>st</sup> of

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March 2014. The farm is located at 22.93° (N), latitude, 88.53° (E) longitude and at 9.75m. Above main sea level. Five plants were selected at random from each entry in each replication for recording data. For estimation of protein by Lowry's Method, 27 genotypes and 21 genotypes of Mung bean from each genotype was pipette in different test tube separately. In this method, the blue colour developed by the reduction of the phosphomolybdic-phosphotungstic components in the Folin-Ciocalteu's reagent by the amino acids tyrosine and tryptophan present in the protein plus the colour developed by the biuret reaction of the protein with alkaline cupric tartrate are measured in the Lowry's Method at 660nm with the help of spectrophotometer. Reagents used in this method are phosphate buffer (pH 8.0) for extraction protein and bovine serum albumin (BSA) for working standard. Preparation of different buffer solutions with their composition are listed below. Reagent A: 2% sodium carbonate in 0.1(N) sodium hydroxide. 0.4g sodium hydroxide pellet was dissolved in 100ml distilled water to prepare 0.1(N) sodium hydroxide solution. 2g sodium carbonate was added and dissolved in 0.1(N) sodium hydroxide solution. Reagent B: 0.5% copper sulphate (CuSO<sub>4</sub> 5H<sub>2</sub>O) in 1% potassium sodium tartrate. 0.5% copper sulphate was dissolved in 100ml distilled water. Then 1g potassium sodium tartrate was added and dissolved completely. Reagent C: alkaline copper solution: Mixture of 50ml of reagent A and 1ml of Reagent B. Reagent D: Folin and Ciocalteu's Phenol Reagent 1(N).

### Result and Discussion

Analysis of variance (table 1) for different characters studied in present investigation revealed significant differences among genotypes for all the eleven characters which provides enough scope for significant improvement on the traits through selection. Khairnar *et al.*, (2003) [19], Siddique *et al.*, (2006) [21], Rao *et al.*, (2006) [22], also observed high magnitude in genetic variability for yield and many component traits. Plant height is an important growth index of plant. WBM-314 was the shortest genotype (38.7) and Hum-12 as tallest genotype (72.25), Marginal difference between PCV and GCV was recorded and so the character may be less influenced by the environment and selection on the basis of phenotypic value could provide worthwhile step to improve the character, Presence of high heritability (99.88%) coupled with high genetic advance over percent of mean indicated the character being predominantly controlled by additive gene action. The mean data revealed that Basanti as the early flowering genotype and TARM -02 as late flowering genotype. The PCV value (4.057) was higher than the GCV value (3.404), and the character might be assumed to be influenced by environment. Presence of moderate heritability (70.93%) with low genetic advance over percent of mean indicated that this trait was governed mostly by non-additive gene action. The maximum number of days taken for maturity

was by PS-16 (83.5) could be consider as a late maturing genotype and IPM-2-3 as early genotype which matured by (72.5). The difference between PCV and GCV value were recorded small and the character less influenced by the environment. Presence of high heritability (99.38) with low genetic advance over percent of mean indicated that the character was influenced predominantly by non-additive gene action. IPM -2-3 showed more number of branches plant<sup>-1</sup> (5.58) and Bireswar and Pantmung-5 showed least number of branches plant<sup>-1</sup> by (2.34). The PCV value (29.859) higher than GCV value (27.717) which suggested substantial environmental effect was prevailed on controlling the character. High heritability (98.29%) and high genetic advance as observed for the character suggested mainly the influence of additive gene action in expression of the character. K-851 contributing least number of seeds pod<sup>-1</sup> with (7.85) and TM-99-50 had maximum number of seeds pod<sup>-1</sup> by (13.5). The PCV (9.624) was marginally higher than the GCV (9.583) indicating least influence of environment on the character. Presence of high heritability (98.92%) and average genetic advance over percent of mean indicated the influence of both additive and non-additive gene action on the expression of the character. Among the genotypes, PDM-54 had the shortest pod length with mean of (6.35) and TM-99-30 showed the longest length by (8.75). The PCV (31.2) is higher than GCV value (23.671) which tells us that the character might be influenced by the environment. With the presence of high heritability (89.85%) and high genetic advance over percent of mean tells us that the character was also predominantly influenced by additive gene action. Genotype with highest pod width was found to be in Kopergaon (0.52) and lowest pod width in Sublobata-02 (0.30). The PCV (48.612) was found to be marginally higher than the GCV which implied that the character might also be least influenced by the environment. The character was suggested to be controlled by non-additive gene action as it had high heritability and low genetic advance. The maximum number of pods plant<sup>-1</sup> was observed in TM-99-37 (28.63) and the least was found in Pusa vishal (13.20). High PCV value (13.2) was found to be marginally higher than GCV value (12.421) which indicated least environmental influence on the character. Presence of high heritability (99.56%) coupled with high genetic advance indicated the character was predominantly controlled by additive gene action. The maximum 100 seed weight was observed in IPM-2-3 (5.81) and minimum TM-99-21 (2.51). The PCV value (18.129) was higher than GCV value (17.64) which indicated environment influence on the character. Presence of high heritability (99.24%) coupled with high genetic advance over percent of mean suggested that the character was influenced predominantly by additive gene action. TM-99-21 was found to be poor in protein content (18.15) while the genotype Pantmung-5 was found to be high in protein content (25.45). The PCV value (23.879) was found higher than the GCV value (23.568) indicating

the likely influence of the environment on the characters. With the presence of high heritability (97.411) and low genetic advance indicated that the character was influenced predominantly by non-additive gene action. Seed yield plant<sup>-1</sup> among the genotype varies from 3.29g to 14.3g and genotype with lowest yield was TM-99-30 (3.25) and highest yield was K-851 (14.75) respectively. The PCV value (17.276) differed least from GCV (16.982) which indicated absence of environment influence on the character. With the presence of high heritability (96.623) and very high genetic advance over percent of mean indicated the character mainly influenced by additive gene action.

From the above results it could be suggested that the genotypes differed significantly for all the studied characters as was observed by Roychowdhury *et al.*, (2012) [11]. PCV was found to be marginally higher than GCV for most of the characters, the difference for characters like number of days to 50% flowering, number of branches plant<sup>-1</sup> and pod length showed wider differences between GCV and PCV which might be due to higher environmental influence on these characters. Jonson *et al.*, (1955) [23], suggested that heritability along with genetic gain were most useful in predicting the selection of best individual. In the present experiment higher genetic advance was observed in plant height, number of branches plant<sup>-1</sup>, number of pods plant<sup>-1</sup>, 100 seed weight, protein content, pod width, pod length and seed yield plant and the characters are predominantly influenced by additive genes. On the other hand the characters such as number of days for 50% flowering and number of days to maturity had shown lower genetic advance which suggested that the clusters of characters are governed predominantly by non-additive gene action. Those characters which were highly influenced by additive gene effect would be highly responsive to phenotypic selection and following simple breeding method Mung bean could be improved for these important characters such as plant height, number of branches plant<sup>-1</sup>, number of pods plant<sup>-1</sup>, 100 seed weight, protein content, pod width, pod length and seed yield plant<sup>-1</sup>.

Ullah Zaid *et al.*, (2012) [24], observed the high heritability for pod length (99%), Lavanya *et al.*, (2010) [25], observed high significant correlation was recorded for pods plant<sup>-1</sup> and harvest index at both genotypic and phenotypic levels with seed yield plant<sup>-1</sup>, plant height, and primary branch plant<sup>-1</sup>, clusters branch<sup>-1</sup> and days to maturity had direct positive effect on seed yield. The genotypic and phenotypic correlation coefficients among eleven characters are presented in table 4. Correlation studies among the eleven characters indicated different degree of association between characters at genotypic and phenotypic levels. Both positive and negative correlation was found between different pairs of characters. The correlation coefficient at genotypic level was in general higher than their phenotypic correlations. Plant height also showed significant positive correlation with number of pods plant<sup>-1</sup> and protein content at both the phenotypic and genotypic levels.

Days to maturity showed positive significant correlation at both the phenotypic and genotypic levels with protein content. Number of pods plant<sup>-1</sup> showed significant positive correlation with 100 seed weight, protein content and seed yield plant<sup>-1</sup> at the genotypic and phenotypic levels. Pod width showed significant positive correlation at both the phenotypic and genotypic level with the character seed yield plant<sup>-1</sup>. The character pod length showed positive significant correlation with Number of pods plant<sup>-1</sup> but only at the genotypic level. Days to 50% flowering showed significant negative correlation with Days to maturity at both the phenotypic and genotypic levels. Number of branches plant<sup>-1</sup> showed significant negative correlation with number of seeds pod<sup>-1</sup> at both the phenotypic and genotypic levels. Days to maturity showed significant negative correlation with seed weight plant<sup>-1</sup> (100 seeds) at both the phenotypic and genotypic levels. Pod width showed significant negative correlation with Protein content at both the phenotypic and genotypic levels. Number of pods plant<sup>-1</sup> showed significant negative correlation with Seed weight plant<sup>-1</sup> (100 seeds) at both the phenotypic and genotypic levels. Protein content showed significant negative correlation with seed yield plant<sup>-1</sup> both the phenotypic and genotypic levels.

The correlation is a measure of the degree of which variables vary together or a measure of intensity of association (Steel and Torrie, 1980) [12].

**Path Coefficient Analysis**

The direct and indirect effects of different characters on the yield plant<sup>-1</sup> are presented in table 5. The direct and indirect contribution of yield attributing characters on yield following path analysis was worked out in phenotypic as well as genotypic levels. Residual effect was low (0.46820) indicating the number of characters chosen for the study were sufficient for yield determination in Mung bean. Path coefficient analysis revealed that among the studied characters six characters out of eleven viz plant height, number of seeds pod<sup>-1</sup>, pod width, number of pods plant<sup>-1</sup> and Seed weight (100 seeds) had positive direct effect on yield. Protein content showed negative direct effect on yield. Pod width imparted the highest direct effect on yield per plant followed by Number of pods plant<sup>-1</sup>, number of seeds per pod, plant height, seed weight (100 seeds). Pod width had significantly positive relation with yield per plant. Therefore direct selection through this trait would be effective to improve yield potential of a genotype. Though Plant height, days to 50% flowering, number of branches plant<sup>-1</sup>, number of seeds pod<sup>-1</sup> and number of pods plant<sup>-1</sup> had positive direct effect on yield but showed non-significant correlation with yield. Four characters out of eleven viz. number of days to maturity, pod length and seed weight and protein content showed negative direct effect on yield. On the basis of path analysis studied Pod width found to be the most important attributable components for yield improvement.

**Table 1: Anova**

S. No	Characters	Source of variation			
		RMS	TMS	EMS	CD
1	Plant Height	0.019	18.996**	0.005	0.0103
2	Days To 50% Flowering	1.338	7.014**	1.219	2.51114
3	Days To Maturity	0.022	10.696**	0.033	0.06798
4	No. Of Branches Plant <sup>-1</sup>	0.296	1.435**	0.107	0.22042
5	No. Of Seeds Pod <sup>-1</sup>	0.005	2.31**	0.01	0.0206
6	Pod Length	0.000	0.036**	0.01	0.0206
7	Pod Width	0.012	49.701**	0.008	0.01648
8	No. Of Pods Plant <sup>-1</sup>	0.022	2.168**	0.009	0.01854
9	Seed Weight (100 Seeds)	0.098	0.982**	0.027	0.05562
10	Protein Content	0.267	33.732**	0.442	0.91052
11	Seed Yield Plant <sup>-1</sup>	0.074	4.895**	0.084	0.17304

**Table 2:** Mean of eleven characters of twenty seven genotypes in Mung bean (*Vigna radiata* L. Wilczek)

S. No	Genotypes	Plant height	Days to 50% flowering	Days to maturity	No. of branches plant <sup>-1</sup>	No. of seeds pod <sup>-1</sup>	Pod length	Pod width	No. of pods plant <sup>-1</sup>	Seed weight (100 seeds)	Protein content	Seed yield
1.	Basanti	58.4	54.5	77.5	2.43	12.65	7.95	0.42	21.00	2.66	23.16	4.16
2.	Bireswar	48.9	48.8	74.5	4.22	8.25	6.75	0.37	21.35	2.97	19.15	7.60
3.	Hum-12	72.5	52.5	73.5	4.54	12.45	8.35	0.40	15.90	4.66	19.02	9.22
4.	Ps-16	46.5	49.5	83.5	3.45	10.35	8.55	0.42	16.05	3.58	20.05	7.12
5.	Tm-99-50	52.6	48.0	75.5	3.66	13.5	7.95	0.41	15.00	2.28	22.01	5.27
6.	Wbm-314	38.7	47.0	78.5	2.87	8.25	6.75	0.38	27.25	3.87	22.32	9.96
7.	Ipm-2-3	45.2	48.0	72.5	5.08	9.75	6.84	0.35	25.45	5.81	19.92	10.47
8.	K-851	62.3	47.9	74.5	4.29	7.85	7.24	0.39	20.10	3.94	21.99	14.75
9.	Koperagon	50.2	51.0	77.5	4.11	10.35	8.65	0.52	17.05	2.86	24.88	7.38
10.	Malda-95-13	70.7	52.3	78.5	3.32	8.65	7.95	0.41	21.45	3.65	19.85	7.45
11.	Meha	44.5	49.0	77.5	3.63	8.75	6.75	0.36	17.10	3.12	20.27	8.62
12.	Midnapur local	54.2	48.5	78.5	2.85	9.75	8.35	0.39	16.50	4.23	19.34	5.00
13.	Pantmung-5	64.0	48.5	79.5	2.34	8.75	7.35	0.47	19.65	3.58	25.45	5.32
14.	Pdm-54	55.4	47.5	78.5	2.57	7.95	6.35	0.36	16.95	3.15	23.16	4.30
15.	Pusa vishal	56.0	47.5	79.5	3.11	9.75	8.55	0.37	13.20	4.47	19.92	5.76
16.	Samrat	45.5	49.5	80.5	3.44	11.25	6.75	0.43	18.00	2.33	20.35	4.76
17.	Sonali	43.9	50.0	81.5	2.57	12.65	7.85	0.42	24.20	3.70	22.01	4.92
18.	Sublobata-02	41.2	51.5	79.5	2.69	8.25	6.85	0.30	25.45	3.68	23.44	10.47
19.	Sublobata-14	53.3	53.5	78.5	2.82	12.45	7.05	0.31	24.20	4.95	18.04	9.96
20.	Tarm-02	59.1	51.5	73.5	3.33	9.75	8.55	0.32	17.65	4.05	19.15	6.24
21.	Tm-99-21	62.2	48.6	79.5	5.58	7.95	8.25	0.35	18.50	2.51	18.15	5.95
22.	Tm-99-30	45.5	47.5	77.5	2.56	5.65	8.75	0.41	17.10	3.86	21.59	3.25
23.	Tm-99-37	58.6	48.5	78.5	4.25	10.35	7.95	0.51	28.63	3.66	19.92	9.70
24.	Wbm 04-05	46.9	49.5	82.5	3.89	11.25	6.75	0.32	21.35	2.99	22.32	7.48
25.	Wbm-220	42.6	50.0	80.5	4.51	15.25	8.35	0.35	21.00	2.66	19.68	4.68
26.	Wbm-4131	59.3	51.5	81.5	3.36	11.25	8.55	0.38	16.50	3.26	20.05	7.34
27.	Wbm-611-3	53.3	48.5	77.5	4.58	12.65	7.95	0.46	17.05	3.70	23.44	6.68
28.	Grand mean	51.824	49.845	79.560	3.899	11.191	7.493	0.487	18.765	3.917	21.311	7.133
29.	C.d.	0.820	1.726	0.890	0.469	1.157	0.862	0.016	0.596	0.154	0.692	0.39
30.	SE(m)	0.402	0.910	0.465	0.234	0.254	0.414	0.008	0.248	0.072	0.366	0.133
31.	C.v.	0.604	1.826	0.834	0.496	0.459	3.821	0.000	1.494	2.579	1.73	2.789

**Table 3:** Mean, range and other genetic characters of Mung bean

S. No	Character	Range		Mean	SED	Variances			CV	GCV	PCV	ECV	H2	GA	GA % mean
		Min	Max			PV	GV	EV							
1	Plant height	38.7	72.5	51.824	0.402	9.500911	9.495381	0.00553	0.869449	20.609	20.615	0.497337	99.943	6.346	42.443
2	Days to 50% flowering	47.0	54.5	49.845	0.910	4.1158	2.897499	1.218301	0.129984	3.404	4.057	2.207268	70.393	2.942	5.883
3	Days to maturity	72.5	83.5	79.560	0.465	5.363755	5.331055	0.0327	0.646631	2.939	2.948	0.23018	99.389	4.742	6.036
4	No. of branches plant <sup>-1</sup>	2.34	5.58	3.899	0.234	0.771153	0.664481	0.106672	1.972118	27.717	29.859	11.1053	86.164	1.559	53
5	No. of seeds pod <sup>-1</sup>	7.85	13.5	11.191	0.254	1.159976	1.150114	0.009862	0.482531	9.583	9.624	0.887405	99.137	2.2	19.655
6	Pod length	6.35	8.75	7.493	0.414	0.023087	0.013289	0.009798	167.1458	23.671	31.2	20.32545	57.557	0.18	36.994
7	Pod width	0.30	0.52	0.487	0.008	24.85667	24.84849	0.008181	1.277301	48.604	48.612	0.881889	99.969	10.267	100.109
8	No. of pods plant <sup>-1</sup>	13.20	28.63	18.765	0.248	1.088963	1.079556	0.009407	0.812911	12.421	12.475	1.159476	99.143	2.131	25.478
9	Seed weight (100 seeds)	2.51	5.81	3.917	0.072	0.50426	0.477424	0.026836	1.838141	17.64	18.129	4.182229	94.683	1.385	35.36
10	Protein content	18.15	25.45	21.311	0.366	17.08742	16.64523	0.442195	0.38126	23.568	23.879	3.841356	97.411	8.295	47.917
11	Seed yield plant <sup>-1</sup>	3.25	14.75	7.133	0.133	2.489507	2.405496	0.084011	1.456258	16.982	17.276	3.173618	96.623	3.141	34.387

**Table 4:** Genotypic and Phenotypic Correlation among the Elven Characters of Mung bean (*Vigna radiata* L. Wilczek)

S. No	Characters		Plant height	Days to 50% flowering	Days to maturity	No. of branches plant <sup>-1</sup>	No. of seeds pod <sup>-1</sup>	Pod length	Pod width	No. of pods plant <sup>-1</sup>	Seed weight (100 seeds)	Protein content	Seed yield plant <sup>-1</sup>
1	Plant height	G		0.226	-0.022	0.046	0.061	0.005	0.01	0.307*	-0.194	0.319*	0.188
		P		0.188	-0.021	0.041	0.06	0.007	0.01	0.306*	-0.19	0.315*	0.186
2	Days to 50% flowering	G			-0.486**	-0.221	-0.006	-0.096	-0.088	-0.199	0.201	0.1	0.046
		P			-0.409**	-0.167	0.001	-0.113	-0.074	-0.177	0.164	0.08	0.036
3	Days to maturity	G				-0.143	0.223	0.152	0.175	0.073	-0.333*	0.276*	-0.145
		P				-0.137	0.221	0.109	0.174	0.075	-0.327*	0.270*	-0.141
4	No. of branches plant <sup>-1</sup>	G					-0.504**	-0.419**	0.024	0.231	-0.21	-0.201	0.083
		P					-0.456**	-0.231	0.021	0.217	-0.205	-0.186	0.074
5	No. of seeds pod <sup>-1</sup>	G						0.124	-0.072	-0.13	-0.056	0.145	0.131
		P						0.091	-0.072	-0.126	-0.059	0.144	0.125
6	Pod length	G							0.18	0.313*	0.255	-0.266	-0.179
		P							0.134	0.247	0.147	-0.186	-0.132
7	Pod width	G								0.127	-0.023	-0.325*	0.418**
		P								0.126	-0.021	-0.320*	0.410**
8	No. of pods plant <sup>-1</sup>	G									-0.392**	-0.102	0.239
		P									-0.392**	-0.099	0.232
9	Seed weight (100 seeds)	G										-0.18	-0.097
		P										-0.172	-0.091
10	Protein content	G											-0.269*
		P											-0.288*

\*significant at 5% level, \*\*significant at 1% level

**Table 5:** Path Coefficient Analysis at Genotypic Level of 11 Elven Characters in (*Vigna radiata* L. Wilczek)

S. No	Characters	Plant height	Days to 50% flowering	Days to maturity	No. of branches plant <sup>-1</sup>	No. of seeds pod <sup>-1</sup>	Pod length	Pod width	No. of pods plant <sup>-1</sup>	Seed weight (100 seeds)	Protein content	Seed yield
1	Plant height	0.197	-0.008	0.002	-0.011	0.015	-0.003	0.004	0.138	-0.032	-0.113	0.188
2	Days to 50% flowering	0.045	-0.036	0.048	0.055	-0.001	0.063	-0.035	-0.089	0.033	-0.035	0.046
3	Days to maturity	-0.004	0.018	-0.099	0.035	0.054	-0.099	0.070	0.033	-0.055	-0.097	-0.145
4	No. of branches plant <sup>-1</sup>	0.009	0.008	0.014	-0.248	-0.123	0.273	0.010	0.104	-0.035	0.071	0.083
5	No. of seeds pod <sup>-1</sup>	0.012	0.000	-0.022	0.125	0.243	-0.080	-0.029	-0.058	-0.009	-0.051	0.131
6	Pod length	0.001	0.003	-0.015	0.104	0.030	-0.651	0.072	0.140	0.042	0.094	-0.179
7	Pod width	0.002	0.003	-0.017	-0.006	-0.017	-0.117	0.402	0.057	-0.004	0.115	0.418**
8	No. of pods plant <sup>-1</sup>	0.061	0.007	-0.007	-0.057	-0.032	-0.204	0.051	0.449	-0.065	0.036	0.239
9	Seed weight (100 seeds)	-0.038	-0.007	0.033	0.052	-0.014	-0.166	-0.009	-0.176	0.165	0.064	-0.097
10	Protein content	0.063	-0.004	-0.027	0.050	0.035	0.173	-0.131	-0.046	-0.030	-0.354	-0.269*

Residual effect: 0.46820

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