Genetic Variability and Association Analysis in Chickpea (*Cicer arietinum* L.) for Seed Yield Characters

ABSTRACT:

The present experiment was conducted at field experimentation centre of the Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad to evaluate genetic variability, correlation and path analysis in twenty six chickpea genotypes for twelve quantitative traits during Rabi, 2019-2020. The analysis of variance showed significant differences among the genotypes for all the characters under the study, indicating a high degree of genetic variability present in the experimental material. The values of PCV were found higher than GCV for all the traits studied representing environmental factors influencing the characters. High PCV and GCV were observed for biological yield per plant indicates large extent of genetic variability for these traits in the material. High heritability were recorded by plant height, days to 50% flowering, harvest index, biological yield per plant, hundred seed weight, seed yield per plant and number of pods per plant. High heritability coupled with high genetic advance as percent of mean was observed for the traits, viz., biological yield per plant, seed index, harvest index, number of pods per plant, seed yield per plant and plant height indicated that these characters were predominantly governed by additive gene effects. So, direct selection of these characters by simple selection method would be effective due to accumulation of more additive genes leading to further improvement of chickpea genotypes. Grain yield per plant showed positive significant genotypic and phenotypic correlations with number of seeds per plant, number of pods per plant, biological yield per plant, number of primary branches per plant, number of secondary branches per plant as well as plant height. At phenotypic level, biological yield per plant and number of seeds per plant had high positive direct effect on grain yield per plant had given the maximum contribution on yield per plant. So significance should be given to these characters throughout the selection for yield improvement in chickpea.

Key words: Chickpea, Phenotypic coefficient of variation, Genotypic coefficient of variation, Heritability and Genetic advance, Correlation and Path coefficient.

1. INTRODUCTION:

Pulses are an essential group of food crops that hold a unique position in the world of agriculture due to their high protein content. Pulses are an imperative part of the Indian diet, provided that roughly 30% of the daily protein ingestion.

Chickpea (*Cicer arietinum* L.), a foremost winter pulse crop in India, contributes appreciably to the pulse economy. This crop is vital part of our daily nourishment because it is an admirable source of protein, adapts well to farming techniques, and can resist drought. It generates 126 kg of protein per hectare on average, building it the most protein-rich legume after groundnut and soybean.

Chickpea is identified by a variety of names in India, counting Chana, Gram, Bengalgram, Chani, Chhole, Chola, Harbara, Boot, Sanagalu, Kadalai, and Kadala.

Chickpea (*Cicer arietinum* L.) is an autogamous crop with 2n = 2x = 16 chromosomes and a genome size of 732 megabytes that belongs to the fabaceae family. Southwest Asia and the Mediterranean were predictable as primary centres of diversity by Vavilov (1926), while Ethiopia was designated as a secondary centre of diversity.

Pakistan, Mexico, Turkey, Canada, Iran, Australia, Tanzania, Ethiopia, Spain, and Burma are all chief producers of chickpea. Madhya Pradesh, Uttar Pradesh, Rajasthan, Maharashtra, Andhra Pradesh, Telangana, and Karnataka are the key chickpea-growing states in our nation, and they mainly cultivate in rainfed circumstances.

Chickpea is principally grown in India through the *rabi* season, on the other hand there has recently been substantiation of chickpea production extending from Northern India's cool season to the warm climates of Central and Southern India (Kuldeep *et al*., 2015).

Chickpeas are a high-protein crop that can be used to supplement cereal-based diets. Chickpeas are high in both protein and carbohydrates. Chickpea protein is higher than that of pigeonpea, blackgram, and greengram legumes (Kaur and Singh, 2005).

Chickpea seeds enclose 23% protein, 64% total carbohydrates (47% starch, 6% soluble sugar), 5% fat, 6% crude fibre, and 2% ash on average, as well as micronutrients such as phosphorus (340 mg/100 g), calcium (160 mg/100 g), magnesium (140 mg/100 g), iron (5 mg/100 g), zinc (4.1 mg/100 g) (Jukanti *et al*., 2012). Cereals and pulses correspond to a huge part of billions of people's diets throughout the World, chickpeas are being targeted in many nations to assist combat malnutrition to some extent.

The degree to which yield and yield-related traits are inherited from generation to generation and the extent of genetic variability enclosed in the breeding material are the most essential factors in crop development. Estimates of genotypic and phenotypic coefficients are requisite to comprehend the force of the environment on various traits.

Heritability and genetic advance expressed as a percent of the mean is a useful tool in the selection programme for determining the extent to which various characters can be improved by selection. The identification of high-yielding chickpea genotypes aids breeders in identifying donors for future breeding programmes.

Yield is a complicated attribute that is determined by a number of factors. It would be beneficial to intend enhanced genotypes by identifying vital characters and their interrelationships. As a result, selection based on yield component traits can result in a significant raise in yield.

Correlation collective with path coefficient analysis is the finest approach to measure the inter-relationship among essential yield components. These strategies were engaged in the breeding programme to take full advantage of the yield prospective of chickpeas in order to enhance efficiency and produce high-yielding improved varieties. The mutual association between the variables is known as correlation, and it contributes in establishing the most efficient procedures for genotype selection. Breeding strategies would be quite effective when there is a positive correlation among major yield components, but selecting becomes awfully difficult when there is a negative association. Due to mutual termination of component characters, estimates of correlation coefficients alone might be ambiguous. As a result, in the study of yield contributing characters, correlation analysis combined with path analysis is a more effective tool. Path coefficient analysis is a helpful technique for unravelling the direct and indirect effects of the causal components on the complex component in the correlation coefficient.

2. MATERIALS AND METHODS:

The current research consists of twenty six genotypes of chickpea in Rabi 2019-2020 at experimentation centre of Genetics and Plant Breeding, SHUATS, Prayagraj. The experiment was laid in randomized complete block design with three replications during Rabi 2019-2020 with inclusion of the suggested packages and practices required for a vigorous crop. Data for twelve quantitative characters were recorded *viz*., days to 50% flowering, days to 50% pod setting, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of days to maturity, number of pods per plant, number of seeds per plant, seed index (gm), biological yield per plant (gm), harvest index (gm) and seed yield per plant (gm). Days to 50% flowering, days to 50% pod setting, number of days to maturity were accounted on a plot basis and plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per plant, seed index (gm), harvest index (gm), biological yield per plant (gm) and seed yield per plant (gm) were predictable from random sample of five plants in each plot. Data were subjected to statistical analysis to work out genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV), heritability, genetic advance and genetic advance as percent mean as per standard methods. Standard statistical manner was used for the analysis of variance, genotypic coefficient of variation and phenotypic coefficient of variation (Burton, 1952), heritability (Burton and Devane, 1953) and genetic advance (Johnson *et al*., 1955). The genotypic and phenotypic correlation coefficients were computed using genotypic and phenotypic variances and co-variances (Ai Jibouri *et al*., 1958). The path coefficient analysis was made according to the technique suggested by Dewey and Lu (1959).

3. RESULTS AND DISCUSSION:

The analysis of variance revealed significant differences between the genotypes for all the characters under the study (Table 1). Hence, it indicated substantial amount of genetic variability among twenty six chickpea genotypes.

3.1 Estimation of genetic parameters:

Assessment of genetic parameters, correlation and path coefficient analysis helps to examine, important characters throughout the selection for improving yield of chickpea. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance (GA) and genetic advance as percent of mean GA (%), for all the yield contributing traits are shown in Table 2.

PCV was higher than the corresponding GCV for all the characters indicative of that there was an influence of the environment. Highest GCV and PCV were recorded for biological yield per plant (26.833 and 32.118) and moderate GCV and PCV were observed for number of pods per plant (14.277, 18.306), seed index (14.128, 17.061), harvest index (13.186, 15.457), seed yield per plant (12.427, 15.735), number of seeds per plant (11.651, 15.100), number of primary branches per plant (11.621, 16.712) and plant height (10.316, 10.942). High to moderate estimates of GCV and PCV suggesting ample variability among these characters and thus offer scope for genetic enhancement through effective selection. Similar findings have been reported by Thakur and Sirohi (2008), Shweta and Yadav (2013), Kishore *et al*. (2018) and Tsehaye *et al*. (2020).

The estimates of genotypic coefficient of variation reveal the overall amount of genotypic variability present in the material. However, the proportion of this genotypic variability which is transmitted from parents to offspring is reflected by heritability. Lush (1947) gave the theory of broad sense heritability. It determines the usefulness with which we can use the genotypic variability in a breeding programme. The range of heritability was proposed by Johnson *et al*., (1955). The estimates of heritability from the current examination are presented in Table 2.

The traits considered moderate to high heritability ranging from 45.7% to 88.9%. Among the traits studied the highest heritability was recorded by plant height (88.900), days to 50% flowering (83.000), harvest index (72.800), biological yield per plant (69.800), seed index (68.600), seed yield per plant (62.400) and number of pods per plant (60.800). The high heritability values of the traits considered in this study exposed that they were less predisposed by the environment, allowing for successful selection of traits based on phenotypic appearance using a simple selection method and representing the potential for genetic progress. Similar findings have been reported by Ali *et al*. (2008), Borate *et al*. (2010), Khan *et al*. (2011), Gaikwad *et al*. (2011), Babbar *et el*. (2012), Akanksha *et al*. (2016) and Yucel *et al*. (2020).

Heritability assessment provides information on the degree of the inheritance of traits from parents to offspring, whereas genetic advance is helpful in determining the real gain expected beneath selection.

In the present study, high heritability coupled with moderate genetic advance were observed for biological yield per plant (69.800, 10.672) and plant height (88.900, 10.482) indicative of that these traits were inclined by both additive and dominance gene effects. Hence, cautious selection may direct towards progress of these traits in chickpea.

The evaluation of genetic advance as percent mean helps to comprehend the type of gene action concerned in the appearance of a trait. It is classified by Johnson *et al*., (1955). The estimates of genetic advance as percent of mean for present study, which are presented in Table 2.

High heritability along with high genetic advance as percent of mean estimated the highest for biological yield per plant (69.800, 46.179), seed index (68.600, 24.102), harvest index (72.800, 23.172), number of pods per plant (60.800, 22.938), seed yield per plant (62.400, 20.219) and plant height (88.900, 20.035) demonstrating that these traits are most likely under the control of additive gene action and hence these traits can be predetermined by appropriate selection. Similar findings have been reported by Vaghela *et al*. (2009), Parameshwarappa *et al*. (2012), Jakhar *et al*. (2016), Srivastava *et al*. (2017), Chopdar *et al*. (2017), Thakur *et al*. (2018), Arora *et al*. (2018), Mohammed *et al*. (2019) and Anusha *et al*. (2020).

So direct selection of these characters based on phenotypic expression by simple selection process would be efficient due to addition of more additive genes leading to further enlargement. Similar findings have been reported by Shivashish *et al*. (2020).

3.2 Estimation of correlation coefficient among the traits:

Associations among yield and yield contributing characters were studied during analysis of correlation between them. Phenotypic and genotypic correlation coefficients between the studied characters of 26 chickpea genotypes are presented in Table 3. Correlation analysis among the yield and its causative traits shown that the genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients representing the association was mainly due to genetic factor (Bhattacharyya *et al*., 2007). The phenotypic correlation coefficients in some cases were higher than their genotypic correlation, which indicates the suppressing effect of the environment that can modify the expression of characters at the phenotypic level.

Grain yield per plant showed positive significant genotypic and phenotypic correlation with number of seeds per plant (0.985**, 0.833**), number of pods per plant (0.983**, 0.781**), biological yield per plant (0.830**, 0.687**), number of primary branches per plant (0.812**, 0.633**), number of secondary branches per plant (0.719**, 0.533**) and plant height (0.596**, 0.515**).

Days to 50% flowering exhibited positive significant genotypic and phenotypic correlation with days to 50% pod setting (0.977**, 0.892**), number of pods per plant (0.345**, 0.261*) and number of seeds per plant (0.330**, 0.242*) and primary branches per plant (0.346** at genotypic level), biological yield per plant (0.291** at genotypic level).

Days to 50% pod setting showed significant positive correlation with number of pods per plant (0.399**), number of seeds per plant (0.353**), biological yield per plant (0.229*) and number of primary branches per plant (0.271*) at genotypic level only. At phenotypic level, days to 50% pod setting exhibited non significant positive correlation for all the characters except seed index (-0.037), harvest index (-0.009) and number of secondary branches per plant (-0.006) showed non significant negative correlations.

Plant height registered significant and positive association with number of pods per plant (0.580**, 0.437**), number of seeds per plant (0.535**, 0.452**) and biological yield per plant (0.389**, 0.324**) at both genotypic and phenotypic level but number of primary branches per plant (0.237*), number of secondary branches per plant (0.237*) at genotypic level only.

Number of primary branches per plant showed positive significant association with number of pods per plant (0.880**, 0.681**), number of secondary branches per plant (0.846**, 0.757**), biological yield per plant (0.839**, 0.516**) and number of seeds per plant (0.788**, 0.615**) at both genotypic and phenotypic levels. It had significant negative correlation with harvest index (-0.503**, -0.238*) at both genotypic and phenotypic level but seed index (-0.232*) at genotypic level only.

Number of secondary branches per plant revealed positive significant correlation with number of pods per plant (0.660**, 0.529**), biological yield per plant (0.660**, 0.466**) and number of seeds per plant (0.544**, 0.399**) at both genotypic and phenotypic levels where as it showed significant negative correlation with harvest index (-0.526**, -0.305**) at both genotypic and phenotypic level but seed index (-0.334**), number of days to maturity (-0.305**) at genotypic level only.

Number of days to maturity showed significant positive correlation with harvest index (0.281*) while significant negative correlation with biological yield per plant (-0.253*) at genotypic level only.

Number of pods per plant exhibited significant positive correlation with number of seeds per plant (0.959**, 0.832**) and biological yield per plant (0.823**, 0.571**) whereas, it showed significant negative correlation with harvest index (-0.486**, -0.239*).

Number of seeds per plant registered significant positive correlation with biological yield per plant (0.864**, 0.644**) whereas significant negative correlation with harvest index (-0.504**, -0.264*) at both genotypic and phenotypic levels.

Seed index showed non significant positive association at both genotypic and phenotypic level for biological yield per plant (0.026, 0.080). It showed significant negative correlation at genotypic level for harvest index (-0.241*) and non significant negative correlation at phenotypic level for harvest index (-0.195).

Biological yield per plant had significant negative correlation with harvest index (-0.872**, -0.669**) at both genotypic and phenotypic levels.

Correlation study exposed that grain yield per plant exhibited significant and positive correlations with number of seeds per plant, number of pods per plant, biological yield per plant, number of primary branches per plant, number of secondary branches per plant and plant height at both genotypic and phenotypic levels respectively (Table 3). Similar results were reported by Babbar *et al*. (2005), Meena *et al*. (2006), Babbar *et al*. (2012), Gul *et al*.(2013), Kuldeep *et al*. (2014), Vartika singh *et al*. (2017), Astereki *et al*. (2017) and Manasa *et al*. (2019).

3.3 Estimation of Path coefficient analysis:

Path coefficient investigation is one of the reliable statistical techniques in quantifying the interdependence of traits and the degree of control of independent characters either directly or indirectly on seed yield (Mushtaq *et al*., 2013). The idea of direct and indirect influence of yield contributing characters on the final end product yield in any crop is of chief importance in selecting high yielding germplam. The direct and indirect effects of twelve characters were presented in Table 4. The path analysis showed that the utmost positive direct effects contributing to seed yield was registered by biological yield per plant (0.432), number of seeds per plant (0.419) followed by harvest index (0.285), number of secondary branches per plant (0.188), plant height (0.142), number of pods per plant (0.127), days to maturity (0.040) and seed index (0.029) which implies direct that direct selection for these characters would progress the seed yield per plant. Similar findings were reported by Renukadevi and Subbalakshmi (2006), Naveed *et al*. (2012), Dehal *et al*. (2016), Tadesse *et al*. (2016), Tiwari *et al*. (2016) and Agarwal *et al*. (2018).

Biological yield per plant showed positive indirect effect *via* number of seeds per plant (0.279), number of pods per plant (0.247), number of primary branches per plant (0.223), number of secondary branches per plant (0.202), plant height (0.14), days to 50% flowering (0.094), days to 50% pod setting (0.045) and seed index (0.035). Whereas, negative indirect effect *via* harvest index (-0.289) days to maturity (-0.072).

Contribution of number of seeds per plant through number of pods per plant (0.349), biological yield per plant (0.27), number of primary branches per plant (0.258), plant height (0.189), number of secondary branches per plant (0.168), days to 50% flowering (0.101) and days to 50% pod setting (0.07) and negative indirect effect through harvest index (-0.111) days to maturity (-0.013), seed index (-0.008).

From the path study the characters biological yield per plant and number of seeds per plant exhibited high positive direct effects on seed yield per plant. Both these characters exhibited significant and positive association with seed yield per plant.

4. CONCLUSION

In the present study, genetic variability, correlation and path analysis revealed that biological yield per plant, number of seeds per plant, number of pods per plant, number of primary branches per plant, number of secondary branches per plant, harvest index, seed index and plant height contribute higher seed yield per plant. Therefore, to improve the yield potential in chickpea the importance should be given to the selection based on these characters.

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Table 1. Analysis of variance for different characters in chickpea

S. No.	**Characters/traits**	**Mean Sum of Squares**		
		Replication (df =02)	**Treatments (df = 25)**	**Error**

				(df = 50)
01	Days to 50% Flowering	2.71	33.74**	2.15
02	Days to 50% pod setting	0.17	29.23**	3.95
03	Plant height	3.83	91.04**	3.64
04	Number of primary branches/plant	0.20	0.84**	0.22
05	Number of secondary branches/plant	0.22	0.89**	0.25
06	Days to maturity	10.76	10.08**	1.93
07	Number of pods per plant	193.59	125.13**	22.11
08	Number of seeds per plant	134.59	135.93**	25.11
09	Seed index	12.26	34.24**	4.54
10	Biological yield per plant	16.80	132.00**	16.64
11	Harvest index	7.63	87.10**	9.66
12	Seed yield per plant	1.82	4.23**	0.71

** indicates 1% level of significance

Table 2. Estimation of genetic parameters for twelve characters in chickpea genotypes

Traits	**GCV**	**PCV**	**h^2 (Broad Sense)**	**GA**	**GAM**
Days to 50% flowering	4.900	5.377	83.000	6.092	9.199
Days to 50% pods setting	3.218	3.899	68.100	4.935	5.470
Plant height	10.316	10.942	88.900	10.482	20.035

Number of primary branches per plant	11.621	16.712	48.300	0.652	16.645
Number of secondary branches per plant	9.092	13.449	45.700	0.644	12.663
Number of days to maturity	1.382	1.807	58.400	2.595	2.176
Number of pods per plant	14.277	18.306	60.800	9.414	22.938
Number of seeds per plant	11.651	15.100	59.500	9.660	18.519
100 seed weight	14.128	17.061	68.600	5.368	24.102
Biological yield per plant	26.833	32.118	69.800	10.672	46.179
Harvest index	13.186	15.457	72.800	8.928	23.172
Seed yield per plant	12.427	15.735	62.400	1.762	20.219

PCV: Phenotypic Coefficient of Variation, GCV: Genotypic Coefficient of Variation, h^2*: heritability (Broad sense), GA: Genetic Advance, GAM: Genetic Advance as Percent of Mean*

Table 3. Genotypic and phenotypic correlation coefficient for yield and yield contributing traits in twenty six chickpea genotypes

Traits	r	DFF	D50%P	PH	PB/ P	SB/ P	DM	Pods/ P	Seeds/ P	SI	BY/ P	HI	SYPP
DF50%	G	1.000	0.977**	0.034	0.346**	0.170	-0.143	0.345**	0.330**	0.001	0.291**	-0.179	0.192
	P	1.000	0.8920 **	0.054	0.172	0.087	-0.071	0.2610 *	0.2422 *	0.004	0.218	-0.086	0.135
DP50%	G		1.000	0.016	0.271*	-0.017	0.089	0.399**	0.353**	-0.013	0.229*	-0.080	0.196
	P		1.000	0.076	0.084	-0.006	0.112	0.218	0.166	-0.037	0.103	-0.009	0.068
PH	G			1.000	0.253*	0.237*	0.114	0.580**	0.535**	0.046	0.389**	-0.208	0.596**
	P			1.000	0.202	0.189	0.113	0.4372 **	0.4522 **	0.047	0.3242 **	-0.153	0.515**
NPBP	G				1.000	0.846**	-0.106	0.880**	0.788**	-0.232*	0.839**	-0.503**	0.812**
	P				1.000	0.7572 **	-0.051	0.6810 **	0.6155 **	-0.117	0.5169 **	-0.2382 *	0.633**
NSBP	G					1.000	-0.305**	0.660**	0.544**	-0.334**	0.660**	-0.526**	0.719**
	P					1.000	-0.136	0.5295 **	0.3999 **	-0.207	0.4669 **	-0.3057 **	0.533**
DM	G						1.000	0.082	-0.087	-0.082	-0.253*	0.281*	-0.095
	P						1.000	0.101	-0.031	-0.026	-0.165	0.205	0.019
NPP	G							1.000	0.959**	-0.165	0.823**	-0.486**	0.983**
	P							1.000	0.8327 **	-0.121	0.5718 **	-0.2392 *	0.781**
NSP	G								1.000	-0.081	0.864**	-0.504**	0.985**
	P								1.000	-0.019	0.6444 **	-0.2643 *	0.833**
SI	G									1.000	0.026	-0.241*	-0.107
	P									1.000	0.080	-0.195	-0.045
BYP	G										1.000	-0.872**	0.830**
	P										1.000	-0.6693 **	0.687**
HI	G											1.000	-0.490**
	P											1.000	-0.212
SYP	G												1.000
	P												1.000

, Significant at $P<0.05$, $P<0.01$, respectively. DF50%: Days to 50% flowering, DP50%: Days to 50% pod setting, PH: Plant height, NPBP: Number of primary branches per plant, NSBP: Number of secondary branches per plant, DM: Days to maturity, NPP: Number of pods per plant, NSP: Number of seeds per plant, SI: Seed index, BYP: Biological yield per plant, HI: Harvest index, SYP: Seed yield per plant*

Table 4. Direct (diagonal) and indirect (off diagonal) effects of 12 traits on grain yield in chickpea evaluated during *Rabi* 2019-2020

Traits	**DF50%**	**DP50%**	**PH**	**NPBP**	**NSBP**	**DM**	**NPP**	**NSP**	**SI**	**BY/P**	**HI**	**SYP**
DF50%	-0.063	-0.056	-0.003	-0.011	-0.005	0.004	-0.016	-0.015	0.000	-0.014	0.005	0.135
DP50%	-0.024	-0.027	-0.002	-0.002	0.000	-0.003	-0.006	-0.005	0.001	-0.003	0.000	0.068
PH	0.008	0.011	0.142	0.029	0.027	0.016	0.062	0.064	0.007	0.046	-0.022	0.515**
NPBP	-0.003	-0.002	-0.004	-0.020	-0.015	0.001	-0.014	-0.012	0.002	-0.010	0.005	0.633**
NSBP	0.016	-0.001	0.036	0.142	0.188	-0.026	0.100	0.075	-0.039	0.088	-0.058	0.533**
DM	-0.003	0.005	0.005	-0.002	-0.006	0.040	0.004	-0.001	-0.001	-0.007	0.008	0.019
NPP	0.033	0.028	0.056	0.086	0.067	0.013	0.127	0.106	-0.015	0.073	-0.030	0.781**
NSP	0.101	0.070	0.189	0.258	0.168	-0.013	0.349	0.419	-0.008	0.270	-0.111	0.833**
SI	0.000	-0.001	0.001	-0.003	-0.006	-0.001	-0.004	-0.001	0.029	0.002	-0.006	-0.045
BYP	0.094	0.045	0.140	0.223	0.202	-0.072	0.247	0.279	0.035	0.432	-0.289	0.687**
HI	-0.024	-0.003	-0.044	-0.068	-0.087	0.058	-0.068	-0.075	-0.056	-0.191	0.285	-0.212

*Residual effect: 0.407. ** Significant at P<0.01, respectively. DF50%: Days to 50% flowering, DP50%: Days to 50% pod setting, PH: Plant height, NPBP: Number of primary branches per plant, NSBP: Number of secondary branches per plant, DM: Days to maturity, NPP: Number of pods per plant, NSP: Number of seeds per plant, SI: Seed index, BYP: Biological yield per plant, HI: Harvest index, SYP: Seed yield per plant*