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Genetic Relationships and Principal Component Analysis in Elite Chickpea (*Cicer arietinum* L.) Genotypes for Seed Yield and Its Component Traits

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ABSTRACT

Background: Chickpea (*Cicer arietinum* L.) is the important *Rabi* season food legume crop ranked third after common bean and field pea. The degree and extent of trait variability, genetic relationship and genetic diversity in promising chickpea genotypes should be known for possible yield improvement. Realizing the importance of genetic relationships and genetic diversity in key economic traits, the present investigation envisaged to measure the genetic relationships in the yield component traits to make effective selection for yield improvement in chickpea breeding programme.

Methods: The experimental material comprised of 60 chickpea genotypes (both *Desi* and *Kabuli* types), grown in RBD with three replications at Pulses Section of Department of Genetics and Plant Breeding, CCSHAU, Hisar during *Rabi* 2014-15. The data on 11 quantitative traits was analysed for ANOVA, correlation coefficient, path coefficient, regression and principle component analysis.

Result: The present study has led the understanding of many inter-related traits involved in the genetic variation of chickpea seed yield. This would certainly provide guidelines for selection of parents as well as effective selection of promising chickpea genotypes, and also have paramount importance in formulating plant model for selection of segregating generations in chickpea breeding programmes for development of high yielding varieties.

Key words: Chickpea, Correlation, Path, PCA, Regression, Seed yield.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is the important *Rabi* season food legume crop ranked third after common bean- *Phaseolus vulgaris* L. and field pea- *Pisum sativum* L. (Aggarwal *et al*., 2015). Among pulses, chick-pea is one of the most important crops for human consumption (Kerem *et al*., 2007) and first grain legume to be domesticated by human (Nagaroje *et al*., 2016). It is a self-pollinated diploid plant (2n= 2x= 16), distinguished as *Desi* and *Kabuli* types based on seed types. The seed yield is an important economic trait in almost all crops, complex in nature and under polygenic control which manifests multiplicative interaction with its component traits and environments (Singh *et al*., 2014). The seed yield in chickpea is based on balance or overall net effects produced by various yield contributing traits and interactions with them. Therefore, direct selection for yield may not be effective since there may not be genes for yield per se. Hence, it is necessary to understand the traits interaction with each other as well as with environments to aid the selection process in chickpea breeding. In order to make the selection effective one has to put attention on the component traits, which contribute to yield in positive directions. The degree and extent of trait variability, relationship and genetic diversity in promising chickpea genotypes should be known for possible yield improvement (Upadhyaya *et al*., 2007a). The magnitude of genetic variability can determine the pace and quantum of genetic improvement through selection or hybridization followed by selection. Realizing the importance of genetic relationships and genetic diversity in important economic traits, the present investigation envisaged to measure the genetic relationships in yield component traits to make effective selection for yield improvement as well as parental selection in chickpea breeding programme.

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MATERIALS AND METHODS

The experimental material comprised of 60 chickpea genotypes (both *Desi* and *Kabuli* types) taken from chickpea germplasm maintained at Pulses Section of Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, India. Hisar is located at 29° 10′N latitude, 75° 46′E longitude and altitude of 215.2 m above mean sea level. These genotypes were grown in Randomized Block Design (RBD) with three replications keeping spacing 30 cm X 10 cm at Pulses Section of Department of Genetics

and Plant Breeding, CCS Haryana Agricultural University, Hisar during *Rabi* 2014-15. The data was observed on 11 quantitative traits *viz*., days to 50% flowering, days to maturity, number of secondary branches/plant, number of pods/plant, plant height (cm), number of seeds/pod, 100 seed weight (g), seed yield/plant (g), standard germination (%), seedling length (cm) and seedling vigour index-I. These traits were analyzed as per method suggested for ANOVA (Analysis of variance) by Gomez and Gomez (1984), correlation analysis by Al-Jibouri *et al.* (1958) and path analysis by Dewey and Lu (1959) using OPSTAT online software as well as regression analysis by Lush, 1940 and principal component analysis (PCA) by Kaiser, 1958 and Jeffers, 1967 using SPSS software 2.0.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA)

The MSS (mean sum of square) of ANOVA due to genotypes for various seed yield and its component traits were found highly significant which indicated the existence of substantial amount of genetic variability for all studied traits among 60 chickpea genotypes (Table 1). These ample variations in 11 quantitative traits could be utilized for improvement in seed yield through selection, heterosis and combination breeding in chickpea germplasm. Similar findings are reported by Peerzada *et al*., 2014 and Bala *et al*., 2015.

Correlation analysis

Correlation analysis measures the degree and direction of relationship between the traits which helps in understanding the nature and magnitude of association among yield and its component traits. In the present study, genotypic correlations exhibited higher than their corresponding phenotypic correlations indicated the highly heritable nature of traits (Table 2). The estimated genotypic and phenotypic correlations among seed yield and its component traits exhibited that the number of pods/ plant had shown positive and highly significant associations with plant height (0.271 and 0.202), 100 seed weight (0.393 and 0.368), seed yield/ plant (0.919 and 0.847), standard germination per cent (0.706 and 0.521), seedling length (0.497 and 0.374) and seedling vigour index-I (0.644 and 0.512) at both genotypic and phenotypic level, respectively (Table 2). Similarly another important yield component trait, number of secondary branches/plant exhibited positive and highly significant correlations with number of pods/ plant (0.289 and 0.234), seed yield/ plant (0.465 and 0.364), standard germination *per cent* (0.569 and 0.441) and seedling vigour index-I (0.366 and 0.288) at both genotypic and phenotypic level, respectively (Table 2).

Similarly, seed yield/ plant revealed positive and highly significant genotypic and phenotypic associations with number of secondary branches/ plant (0.465 and 0.364), number of pods/ plant (0.919 and 0.847), number of seeds/ pod (0.454 and 0.216), standard germination *per cent* (0.753 and 0.530), seedling length (0.325 and 0.281) and seedling vigour index-I (0.549 and 0.451), respectively and with 100 seed weight (0.184 and 0.173) showed only positive significant correlations at both genotypic and phenotypic levels, respectively (Table 2). The information on traits association on seed yield would be additional assistance to plant breeders in deciding the selection criteria and developing effective breeding strategy for evolving high yielding varieties. The strong positive correlation of seed yield with above mentioned traits have also been reported in chickpea by Malik *et al*., 2014; Bala *et al*., 2015 and Shafique *et al*., 2016.

Path analysis

Since correlation analysis is not alone sufficient to make a clear cut picture of association among traits therefore it become crucial to assess the real contribution of a trait towards seed yield. Path analysis makes a clear cut and more realistic picture of complex situation existing at correlation level among traits by measuring the direct and indirect effects of independent traits on dependent trait *via* other traits at genotypic correlation levels that was presented in Table 3, diagonal values indicating the direct effects whereas off-diagonal values as indirect effects. The positive direct effects on seed yield/ plant observed maximum by

Table 1: Analysis of variance (ANOVA) of chickpea genotypes for seed yield and its component traits.

Source of variation (SV)	Degree of freedom (df)	Mean sum of squares				
		Days to 50% flowering	Days to maturity	Number of secondary branches/ plant	Number of pods/plant	height Plant (cm)
Replication	2	0.290	16.940	0.120	0.650	4.820
Genotypes	59	59.400**	185.750**	6.430**	524.210**	86.230**
Error	118	1.910	2.630	0.650	19.230	13.960
Source of variation (SV)	Degree of freedom (df)	Mean sum of squares				
		Number of seeds/pod	100 seed weight (g)	Seed yield/plant (g)	Standard germination (%)	Seedling length (cm)	Seed vigour index-I
Replication	2	0.026	0.767	1.305	5.017	2.956	22911.18
Genotypes	59	0.036**	102.092**	40.681**	22.671**	6.615**	95750.93**
Error	118	0.014	0.449	1.543	3.621	0.880	9584.94

*Significant at p= 0.05, **Significant at p= 0.01.

Table 2: Genotypic (above diagonal) and phenotypic correlation coefficients (below diagonal) of seed yield and its component traits.

Traits	DF	DM	SB/P	Pd/P	PH (cm)	Ss/Pd	100SW (g)	SY/P (g)	SG (%)	SL (cm)	SVI-I
DF	**1.00**	0.771**	0.319**	-0.142	-0.197**	-0.135	-0.164*	-0.069	-0.222**	-0.284**	-0.295**
DM	0.713**	**1.00**	0.231**	-0.054	-0.065	-0.229**	-0.170*	0.003	-0.102	-0.301**	-0.252**
SB/P	0.259**	0.193**	**1.00**	0.289**	-0.293**	0.271**	-0.227**	0.465**	0.569**	0.179*	0.366**
Pd/P	-0.134	-0.056	0.234**	**1.00**	0.271**	0.284**	0.393**	0.919**	0.706**	0.497**	0.644**
PH (cm)	-0.148*	-0.049	-0.228**	0.202**	**1.00**	-0.303**	0.551**	0.141	-0.109	0.213**	0.096
Ss/Pd	-0.067	-0.151*	0.125	0.142	-0.094	**1.00**	-0.343**	0.454**	0.512**	0.391**	0.487**
100SW (g)	-0.161*	-0.163*	-0.183*	0.368**	0.438**	-0.194**	**1.00**	0.184*	0.157*	0.210**	0.212**
SY/P	-0.070	-0.007	0.364**	0.847**	0.121	0.216**	0.173*	**1.00**	0.753**	0.325**	0.549**
SG (%)	-0.167*	-0.069	0.441**	0.521**	-0.044	0.250**	0.122	0.530**	**1.00**	0.620**	0.856**
SL (cm)	-0.196**	-0.246**	0.115	0.374**	0.150*	0.170*	0.166*	0.281**	0.432**	**1.00**	0.936**
SVI-I	-0.222**	-0.210**	0.288**	0.512**	0.085	0.238**	0.176*	0.451**	0.778**	0.902**	**1.00**

* Significant at p= 0.05, ** Significant at p= 0.01.

Table 3: Direct (diagonal) and indirect effects (off-diagonal) of seed yield and its component traits among the 60 elite chickpea genotypes.

	DF	DM	SB/P	Pd/P	PH (cm)	Ss/Pd	100 SW (g)	SG (%)	SL (cm)	SVI-I	Correlation with seed yield/ plant
DF	**0.008**	-0.011	0.033	-0.112	-0.008	-0.004	0.019	-0.019	0.004	0.018	-0.071
DM	0.006	**-0.015**	0.025	-0.046	-0.003	-0.008	0.020	-0.008	0.006	0.017	-0.007
SB/P	0.002	-0.003	**0.129**	0.194	-0.013	0.007	0.022	0.051	-0.003	-0.023	0.364
Pd/P	-0.001	0.001	0.030	**0.831**	0.011	0.008	-0.044	0.060	-0.008	-0.041	0.847
PH (cm)	-0.001	0.001	-0.029	0.168	**0.056**	-0.005	-0.053	-0.005	-0.003	-0.007	0.121
Ss/Pd	-0.001	0.002	0.016	0.118	-0.005	**0.056**	0.023	0.029	-0.004	-0.019	0.216
100 SW (g)	-0.001	0.002	-0.024	0.306	0.025	-0.011	**-0.121**	0.014	-0.004	-0.014	0.173
SG (%)	-0.001	0.001	0.057	0.433	-0.002	0.014	-0.015	**0.116**	-0.010	-0.062	0.530
SL (cm)	-0.002	0.004	0.015	0.311	0.008	0.010	-0.020	0.050	**-0.023**	-0.072	0.281
SVI-I	-0.002	0.003	0.037	0.425	0.005	0.013	-0.012	0.090	-0.020	**-0.080**	0.460

DF-Days to 50 *per cent* flowering, DM- Days to maturity, SB/P- Number of secondary branches/ plant, Pd/P- Number of pods/ plant, PH (cm)- Plant height (cm), Ss/Pd- Number of seeds/ pod, 100SW (g)-100 seed weight (g), SY/P- Seed yield/ plant (g), SG (%)- Standard germination (%), SL (cm)- Seedling length (cm), SVI-I- Seed vigour Index-I.

Table 4: Summary of Stepwise multiple regression analysis for seed yield and its component traits.

Steps	Entered variables	b_i	R^2 value	Adjusted R^2	SE	t value
1	Number of pods/ plant (X_1)	0.864	0.830	0.826	1.604	14.499**
2	Number of secondary branches/ plant (X_2)	0.154	0.852	0.844	1.517	13.845**
	Intercept = -0.389		Suggested model: Y = -0.389 + 0.864 (X_1) + 0.154 (X_2).			

** Significant at 1% level of significance, b_i = regression coefficient, R^2 = coefficient of determination.

number of pods/ plant (0.831) followed by number of secondary branches/ plant (0.129), standard germination *per cent* (0.116), plant height (0.056), number of seeds/ pod (0.056) and days to 50 % flowering (0.008), while negative direct effects by 100 seed weight (-0.121) after that seedling vigour index-I (-0.080), seedling length (-0.023) and days to maturity (-0.015) on seed yield/ plant (Table 3).

The positive indirect effects on seed yield/ plant via number of pods/ plant had shown by days to maturity (0.001), number of secondary branches/ plant (0.030), plant height (0.011), number of seeds/ pod (0.008) and standard germination *per cent* (0.060). Similarly traits such as days to maturity (0.002), number of secondary branches/ plant (0.016), number of pods/ plant (0.168), 100 seed weight (0.023) and standard germination *per cent* (0.029) had positive indirect effects on seed yield/ plant via number of seeds/ pod. The positive indirect effects on seed yield/ plant via 100 seed weight displayed by days to maturity (0.002), number of pods/ plant (0.306), plant height (0.025) and standard germination *per cent* (0.014). A residual effect on dependent variable measures the error and unexplained variance by other possible independent variables. The residual effects observed in present study were 0.23 for genotypic path coefficient analysis which is too low. These findings are in accordance with Yucel *et al*., 2010; Kumar and Lavanya, 2012 and Mushtaq *et al*., 2013. Correlation and path analysis together helps in effective selection of important economic traits for yield improvement in chickpea. The highly significant positive correlation and direct positive effects on seed yield/ plant exhibited by number of pods/ plant, number of secondary branches/ plant, number of seeds/ pod and standard germination *per cent* which could be used for selection of promising chickpea genotypes.

Stepwise multiple regression analysis

In stepwise multiple regression analysis, seed yield/ plant considered a dependent variable, while other traits as independent variables. The results of stepwise multiple regression analysis was shown in Table 4. Firstly, number of pods/ plant entered in the model which explained 82.60% of variations subsequently by number of secondary branches/ plant in the model, explained 84.40% cumulative variations. The findings are in accordance with Zali *et al*., 2011. The multiple regression analysis together with correlation and path analysis had identified the most important economic traits *viz*., number of pods/ plant and number of secondary branches/ plant which could be used for effective selection of promising chickpea genotypes in future chickpea breeding programme.

Table 5: Total variability explained by principal components among 60 diverse chickpea genotypes.

Principal components	Eigen values	Variability (%)	Cumulative variability (%)
1	3.94	35.78	35.78
2	2.15	19.54	55.32
3	1.64	14.88	70.20
4	1.07	9.72	79.92

Principal component analysis (PCA)

PCA is a well-known method of dimension reduction technique used to reduce a large set of variables into a small set that still contains most of the information of the large set (Massay, 1965 and Jolliffie, 1986). It helps in identification and ranking of genotypes and important economic traits contributing in genetic diversity for developing superior hybrid in chickpea. In present investigation, PCA was performed for yield and its contributing traits in chickpea in which principal components greater than one Eigen value were selected for interpretation (Kaiser, 1958 and Jeffers, 1967). Out of eleven, only 4 PCs (PC 1, PC 2, PC 3 & PC 4) exhibited greater than 1.0 Eigen value *viz*., 3.94, 2.15, 1.64 and 1.07, respectively and explained 79.92% (35.78%, 19.54%, 14.88% and 9.72%, respectively) variability of the total variation among the 60 chickpea genotype (Table 5). Among them PC 1 accounted for maximum proportion of total variability (35.78%) in yield contributing traits and progressively lesser and lesser amount of variation in remaining components.

Further, principal factor analysis carried out with Rotation method (Kaiser, 1985) to derive a clear picture of interaction among yield component traits in terms of common factor accounts for remaining variance (including error) with respective to principal factors (correlation values > ±0.5). PC 1 was mostly correlated to yield contributing traits *viz*., number of pods/ plant, seed yield/ plant, number of seeds/ pod and standard germination *per cent*, whereas, PC 2 dominated by seed and seedling traits *viz*., standard germination (%), seedling length (cm) and seedling vigour index-I and PC 3 explained by phenological traits *viz*., days to 50% flowering and days to maturity (Table 6). The main variables of PC 4 were plant height (cm) and 100 seed weight (g). Thus, PC 1 and PC 4 had shown maximum variation related to seed yield and its component traits simultaneously

Table 6: Factor loading of traits with respect to different principal factor (Varimax rotation).

Yield component traits	PF-1	PF-2	PF-3	PF-4
Days to 50% flowering	-0.060	-0.148	0.869	-0.123
Days to maturity	0.027	-0.188	0.869	-0.028
Number of secondary branches/ plant	0.329	0.422	0.493	-0.347
Number of pods/ plant	0.853	0.297	-0.003	0.304
Plant height (cm)	0.034	0.020	-0.089	0.838
Number of seeds/ pod	0.530	-0.099	-0.445	-0.453
100 seed weight (g)	0.179	0.080	-0.096	0.814
Seed yield/ plant (g)	0.918	0.219	0.070	0.094
Standard germination (%)	0.639	0.637	-0.008	-0.083
Seedling Length (cm)	0.075	0.884	-0.186	0.136
Seedling Vigour Index-I	0.368	0.894	-0.152	0.066

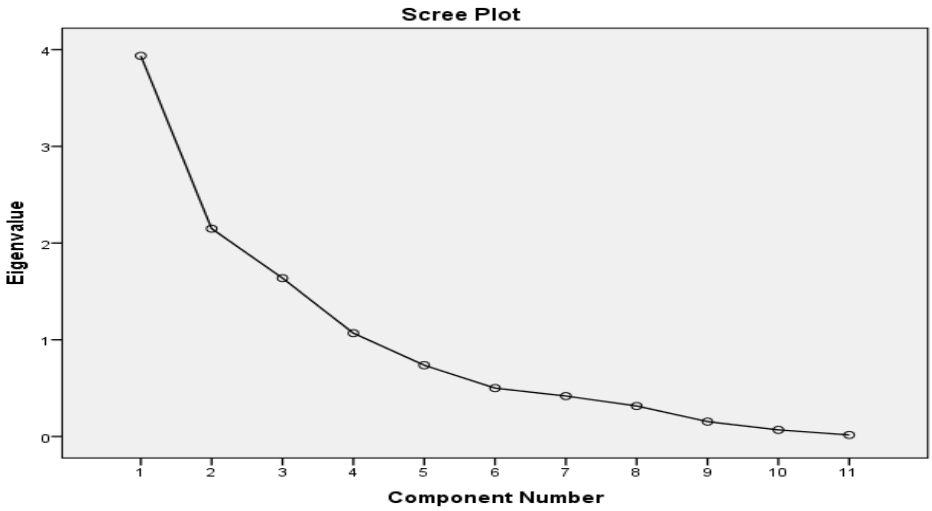


Fig 1: Scree plot constructed based on thirteen principal components and their Eigen values.

shown to significantly positive associations with seed yield by correlation and path analysis which could be used for selection of promising chickpea genotypes to bring out rapid improvement in yield. Screen plot explain the percentage of variation associated with each principal component obtained by drawing a graph between Eigen value and principal components (Fig 1). The results are in support with the reports of Rekha *et al.,* 2013, Amrita *et al.,* 2014 and Mahendra *et al.,* 2015.

CONCLUSION

The present study has led the understanding of many inter-related traits involved in the genetic variation of seed yield. This would certainly provide guidelines in the selection of parents, effective selection of promising chickpea genotypes and also have paramount importance in formulating plant model in selection of segregating generations. The positive correlation and direct effects on seed yield/plant exhibited by number of pods/ plant, number of secondary branches/ plant, number of seeds/ pod and standard germination per cent. Simultaneously, these traits were exhibited principal cause of variations among 60 elite chickpea genotypes by multiple regression analysis and PCA. Therefore, these traits especially number of pods/ plant and number of secondary branches/ plant could be considered as the best selection criteria in chickpea breeding programmes for the development of high yielding varieties.

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