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Correlation, heritability and genetic advance analysis in chickpea genotypes under Plain gangatic region

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Abstract

The experimental materials consisting of seeds of 30 genotypes along with three check varieties (Pant G-186, Udai and BG-372) of chickpea were used for experimentation under Randomized Block Design (RBD) at Genetics and Plant Breeding Farm, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (UP). The observations on the following traits was recorded as per guidelines. Days to 50% flowering, Days to maturity, Number of primary branches/plant, Number of secondary branches/plant, Plant height (cm), Number of pods/plant, Number of seeds/pod, Harvest index, Biological yield per plant (g), 100-seed weight (g), Seed yield/plant (g). The data were recorded on eleven characters to estimate mean, range, and least significant differences, correlations. The seed yield per plant showed highly significant and positive correlation with number of seeds per pod (0.459), number of Pods per plant (0.748), Biological yield (0.902) and Harvest index (0.732). The correlation coefficient of seed yield per plant with remaining nine characters was registered non-significant. Among the thirty chickpea genotypes Bidhan Chola 1, GCP 105, GNG 2207, GNG 38, GNG 312, GNG 0703, GNG 0820, GNG 1001 and GNG 1013 and GNG 1969 also possessed high mean performance for most of the seed qualitative and quantitative traits. The genotypes mentioned above and some other genotypes having high mean performance for characters may be used as donor parents in hybridization programme for improving the characters for which they showed high mean performance.

Keywords: Biological, correlation, material, significance

Introduction

Chickpea (*Cicer arietinum* L.) is the most important *Rabi* season self-pollinated, diploid ($2n=2x=16$) pulse crop. It belongs to the family *Fabaceae* and sub family *Papilionaceae*. Mostly two types of chickpea are with domain and cultivate *Kabuli* is grown in temperate regions while the *Desi* type is in the semi-arid tropics, having extensive geographical distribution. Chickpea is the 3rd pulse crop, 5th food legume and 15th grain crop of the world among various grain legumes. Chickpea is known by different names in various countries such as Gram, Chana, Bengal gram, garbanzo bean, Indian pea, cerci bean etc. Chickpea is predominantly consumed as a pulse, dry chickpea is also used in preparing a variety of snack foods, sweets and condiments and green fresh chick peas are commonly consumed as a vegetable. It has several potential health benefits and, in combination with other pulses and cereals, it could have beneficial effects on some of the important human diseases like cardiovascular disease, diabetes, digestive diseases and some cancers. Overall, chickpea is an important pulse crop with a diverse array of potential nutritional and health benefits (Jukantil *et al.*, 2012) [20] among the pulses, chickpea has wide adaptability and low input requirement crop. Beside its main use as dal, the tender green seeds are used as a vegetable, crushed dry seed as animal feed, green leaves as green leafy vegetable and also as fodder etc. Chickpea is grown in India, Bangladesh, Iran, Nepal, Pakistan, Syria, and Turkey. Pulses are wonderful gifts of the nature.

They have unique ability of biological nitrogen fixation, deep root system, mobilization of insoluble soil nutrients and bringing qualitative changes in soil physical properties and restore soil fertility. Pulses can arrest the declining trained in productivity of cereal based cropping systems. Inclusion of pulses in intensive cereal based cropping system acts as a component of integrated nutrient supply. Therefore, pulses have emerged as available option to improve soil health, conserve the natural resources and sustain the agricultural productivity. Pulses are grown in semi-arid region of India since time immemorial. They are cheap and excellent source of dietary protein, minerals, vitamins and crude fiber and also a source of feed and fodder for animals.

Pulses are considered as health food and offer nutritional security to millions of population suffering with protein malnutrition especially in south Asia and Africa. Some of the short duration pulses have shown great promise for crop intensification in irrigated areas. The alleviatory effects of pulses on the yield of subsequent crops have long been realized and documented.

The cultivated species, *C. arietinum* cannot colonize successfully without human intervention. The wild species (*C. reticulatum* and *C. bijugum*) occur in weedy habitats (fallow or disturbed habitats, roadsides, cultivated fields of wheat and other places not touched by man or cattle), mountain slopes among rubble (*C. pungenis* and *C. yamashitae*), on forest soils, in broad-leaf. Chickpea (*C. arietinum* L.) belongs to the family Fabaceae, within the tribe Cicerae. It is a self-pollinated, diploid, annual grain legume crop. The global production of chickpea is nearly 11million tonnes and India is the major producer accounting for 64% of the total chickpea production (Anonymous, 2012) [5]. It is a major source of high quality protein in human diet and also provides high quality crop residues for animal feed. Genetic variation among trait is important for breeding and on selecting Desirable types. On the other hand, an analysis of the correlation between seed yield and yield component is essential in determining selection criteria. However path coefficient analysis helps to determine the direct effect of trait and their indirect effect on other trait.

The success of any crop breeding programme depends on the nature and amount of variability and existing with germplasm collection. Germplasm serves as valuable natural reservoir in providing needed attributes for developing successful variety. The germplasm resources will be little value unless these are properly evaluated, because evaluation provides an estimate of its potential value. In order to launch a sound breeding strategy, it is essential to have an idea of the nature and magnitude of variability, heritability and genetic advance in respect to breeding materials at hand. The choice of genetically diverse potential parents for use in hybridization programme is based on the hypothesis that crosses involving divergent parents offer greater possibility of obtaining desirable segregants in the segregating generation. Several workers have emphasized need of parental diversity in optimum magnitude to obtain superior genotypes in the segregating generations (Gupta *et al.* 2003) [14].

Materials and Methods

The field experiment under present investigation was conducted during Rabi 2019-20 at the Student's Instructional Farm and lab experiments were conducted in Seed Testing Laboratory, Seed Technology Section, N. D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U. P.). Geographically Narendra Nagar situated between 26.47 0N latitude, 82.12 0E longitude and at an altitude of 113 meters above the mean sea level. The climate of district Faizabad is semi-arid with hot summer and cold winter. Nearly 80 percent of total rainfall is received during the monsoon (only upto September) with a few showers in the winter. The soil type of experimental site was sandy loam, low in organic carbon, nitrogen, phosphorus and rich in potash. The experiment was conducted in Randomized Block Design (RBD) with three replications. Each plot consisted of four rows of 4 m length with the inter and intra row spacing of 30 cm and 10 cm, respectively. To avoid the border effect

experimental plot was surrounded on all side by non experimental rows. Recommended cultural practices were followed to raise the crop. Five plants from each treatment were selected randomly for data recording. Observations on the following characteristics were recorded on the basis of five plants randomly selected and tagged from each row except for days to 50% flowering and days to maturity, which were recorded on the plot basis. Laboratory observation were recorded as per ISTA rules. The field components and seed quality observation are Number of primary branches per plant, Number of secondary branches per plant, Plant height (cm), Number of pods per plant, Number of seeds per pod, Harvest index, Biological yield per plant (g), 100-seed weight (g) and Seed yield per plant (g) etc.

Results and Discussion

The analysis of variance for the Randomized Block Design (RBD) accommodating 30 chickpea accessions and 3 checks (Pant G -186, Udai and BG-372) was done for each of the 11 characters. The Analysis of variance is presented in Table 1. The analysis of variance revealed that mean squares due to treatments were highly significant for all the characters. The assessment of existing variability in the germplasm collections was done by computing range and least significant differences. The heritability in broad sense (Hanson *et al.*, 1956) [15] and genetic advance in percent of mean (Johnson *et al.*, 1955) [19] were calculated for understanding the transmissibility of characters. The natures of association among different characters were studied by using correlations coefficient (Searle, 1961) [37] and path coefficient analysis (Dewey and Lu, 1959) [13]. The estimates of phenotypic (PCV) and genotypic (GCV) coefficient of variation for all the twelve yield contributing traits and seed quality parameters of chickpea genotypes and presented in Table 3. The high estimates (>15%) of phenotypic (PCV) and genotypic (GCV) coefficients of variation were recorded in case of seed yield per plant (PCV=41.39%, GCV=39.22%) followed by 100-seed weight (PCV=25.66%, GCV=24.59%), seeds per pod (PCV=21.43%, GCV=32.25%) and while primary branches per plant (PCV=11.16%, GCV=8.38%) and pods per plant (PCV=33.57%, GCV=32.25%) showed high PCV along with moderate GCV. Moderates estimates (<15% ->10%) of PCV and GCV were noted for secondary branches per plant (PCV=36.01%, GCV=35.65) and plant height (PCV=14.57%, GCV=13.95%) whereas, the low estimates (<10%) of phenotypic and genotypic coefficients variation were observed for biological yield (PCV=30.26%, GCV=28.11%), harvest index (PCV=19.01%, GCV=16.77), days to 50% flowering (PCV=7.30%, GCV=6.84%), and days to maturity (PCV=3.41, GCV=3.11%). (Chavan *et al.*, 1995, Jahagirdar *et al.*, 1995, Mishra *et al.*, 1998, Tripathi, 1998, Kumar *et al.*, 1999, Suryawanshi *et al.*, 1999, Wahid and Ahmad, 1999, Jeena and Arora, 2000, Kumar *et al.*, 2001, Ali *et al.*, 2002, Khan *et al.*, 2006, Singh, 2007, Lokere *et al.*, 2007, Ojha *et al.*, 2010) [11, 17, 26, 43, 23, 41, 43, 45, 22, 2, 21, 38, 25, 46]. Heritability in broad sense and genetic advance in percent of mean for all the 11 yield contributing traits were estimated and findings are given in Table 2. The magnitude of heritability in broad sense varied between 30.48% in case of harvest index to 92% for plant height. The high estimates of broad sense heritability (> 75%) were noted for Biological yield (86%), 100-seed weight (92.5%), seed yield per plant (90%) primary branches per plant (56%), seeds per pod (77.51%) and days to maturity (83%) and days to 50% flowering (76.50%). Moderates

estimates of heritability (> 65 < 75%) were observed for while primary branches per plant showed low estimate of heritability (56.675).

The genetic advance in percent of mean ranged from 5.82% for germination to 76.57% for seed yield per plant. The very high estimates of genetic advance (>30%) were registered for secondary branches per plant (72.71) pods per plant (63.86%) seed yield per plant (76.57%) followed by 100- seed weight (48.54%) and Biological yield (53.78%), Harvest index (30.48) while the high estimates of genetic advance (<20%) were recorded for plant height(27.50%), and no of seed per pod (26.47%). The moderate estimates of genetic advance (<20% to >10%) were observed for days to 50% flowering (13.21%), number of primary branches per plant (12.96%) The low estimates of genetic advance (<10%) days to maturity (5.82%). (Mathuraj *et al.*, 2001, Sreelakshmi *et al.*, 2010, Dar *et al.*, 2012, Hasan *et al.*, 2013, Amel A. *et al.*, 2015, Kumar *et al.*, 2015) [29, 40, 12, 16, 47, 24].

Correlation coefficient was worked out at phenotypic and genotypic levels for different yield contributing characters and seed quality parameters in Chickpea (*Cicer arietinum* L.) genotypes are presented in Table 3. and 4., respectively. In general, the values of genotypic correlation coefficient were similar in sign or nature but slightly higher than phenotypic ones in magnitude for most of the characters. Some of the characters had non-significant and negative correlation coefficient either at genotypic or phenotypic level. Seed yield per plant exhibit ted highly significant and negative correlation with days to 50% flowering (-0.038) and where as pods per plant (0.748) characters showed significant and positive correlation with this traits. The correlation coefficients of seed yield per plant with remaining nine characters were non-significant. 100-seed weight possessed significant and positive correlation with primary branches per plant (0.078), plant height (-0.061) and secondary branches per plant (-0.069) besides remaining character *viz.* days to 50% flowering, days to maturity, pods per plant, seeds per plant, biological yield, harvest index and seed yield per plant

were found non-significant. Pods per plant indicated highly significant and positive correlation with secondary branches per plant (0.305) where as the remaining traits were possessed non-significant correlation with above mentioned trait. Significant and positive correlation of secondary branches per plant was noted with primary branches per plant (0.249) and plant height (0.042), while the rest of all the characters exhibited non-significant correlation with this character. Days to maturity exhibited highly significant and positive correlation with days to 50% flowering (0.875), whereas remaining traits were possessed non- significant association with this character. On the other hand biological yield, harvest index, seeds per pod, primary branches per plant and plant height were expressed non-significant association with all the attributes. (Ali and Tahir, 1999, Kumar *et al.*, 1999, Raval and Dobariya, 2003, Muhammad *et al.*, 2003, Muhammad *et al.*, 2004, Raout *et al.*, 2004, Renukadevi and Subbalakshmi 2006, Rao 2005, Lokere *et al.*, 2007, Bhawani *et al.*, 2008, Thakur and Sirohi, 2009, Sreelakshmi *et al.*, 2010, Ojha *et al.*, 2011, Qurban *et al.*, 2011 and Aycicek and Babagil, 2013) [3, 23, 35, 28, 27, 34, 36, 33, 25, 9, 42, 40, 30, 32, 7].

Table 1: Analysis of variance for eleven characters

S. No.	Characters	Source of variation		
		Replications	Treatments	Error
	d.f.	2	32	64
1.	Days to 50% flowering	28.798**	61.732**	2.725
2.	Days to maturity	7.394	48.797**	3.154
3.	Plant height	13.721*	94.853**	2.810
4.	Primary branch	0.059	0.064**	0.013
5.	Secondary branch	0.195	14.326**	0.096
6.	Pods/plant	17.496**	396.685**	10.747
7.	Seeds/pod	0.051	0.213	0.039
8.	Biological/plant	26.139**	176.269**	8.881
9.	Harvest index	26.151**	98.949**	8.584
10.	100 seed wt	3.300	59.728**	1.718
11.	Yield/plant	8.891*	37.215**	1.358

Table 2: Coefficient of variation, heritability and genetic advance for eleven characters in chickpea

	Days to 50% flowering	Days to maturity	Plant height	Primary branch	Secondary branch	Pods/plant	Seeds/pod	Biologic al/plant	Harvest index	100 seed wt	Yield/plant
h ²	0.88	0.83	0.92	0.56	0.98	0.92	0.60	0.86	0.78	0.92	0.90
GCV	6.84	3.11	13.95	8.38	35.65	32.25	16.60	28.11	16.77	24.59	39.22
PCV	7.30	3.41	14.57	11.16	36.01	33.57	21.43	30.26	19.01	25.66	41.39
CV	2.55	1.41	4.22	7.37	5.06	9.32	13.56	11.21	8.95	7.33	13.22
GA	8.56	7.31	10.92	0.20	4.44	22.45	0.38	14.29	9.97	8.68	6.75
GA % M	13.21	5.82	27.50	12.96	72.71	63.82	26.47	53.78	30.48	48.54	76.57
Range Min	56.00	113.67	29.73	1.27	3.43	14.27	1.07	12.15	17.95	12.10	3.30
Range Max	71.67	132.67	54.57	1.87	14.60	56.73	2.07	44.50	48.52	26.49	18.38
General Mean	64.84	125.58	39.71	1.55	6.11	35.17	1.45	26.57	32.72	17.88	8.81

Table 3: Genotypic correlation

Days to 50% flowering	Days to maturity	Plant height	Primary branch	Secondary branch	Pods/plant	Seeds/pod	Biological/ plant	Harvest index	100 seed wt	Yield/plant
1	0.875**	0.217*	0.212*	0.191	0.011	0.056	-0.118	0.070	-0.053	-0.038
	1	0.194*	0.173*	0.331*	0.084	-0.013	-0.102	0.126	-0.032	-0.004
		1	-0.146	0.042	0.359*	0.537**	0.447**	0.416**	-0.061	0.529**
			1	0.249*	0.127	-0.112	0.092	0.053	0.078	0.125
				1	0.305*	-0.103	0.086	0.196*	-0.069	0.125
					1	0.328*	0.875**	0.266	-0.377*	0.748**
						1	0.454**	0.309*	-0.458**	0.459**
							1	0.324*	-0.123	0.902**
								1	0.495**	0.732**
									1	0.164

Table 4: Phenotypic Correlation

Days to 50% flowering	Days to maturity	Plant height	Primary branch	Secondary branch	Pods/plant	Seeds/pod	Biological/plant	Harvest index	100 seed wt	Yield/plant
1	0.773	0.169	0.133	0.177	0.006	0.011	-0.090	0.042	-0.059	-0.045
	1	0.176	0.100	0.316	0.062	-0.027	-0.074	0.101	-0.013	-0.003
		1	-0.135	0.044	0.324	0.445	0.414	0.334	-0.066	0.496
			1	0.193	0.105	-0.101	0.037	0.021	0.039	0.043
				1	0.293	-0.075	0.080	0.174	-0.072	0.116
					1	0.198	0.778	0.224	-0.360	0.684
						1	0.350	0.372	-0.417	0.480
							1	0.262	-0.114	0.813
								1	0.404	0.699
									1	0.149

Conclusion

In conclusion, the seed yield per plant showed highly significant and positive correlation with number of seeds per pod (0.459**), number of Pods per plant (0.748**), Biological yield (0.902**) and Harvest index (0.732**). The correlation coefficient of seed yield per plant with remaining nine characters was registered non-significant. The estimate of heritability with high genetic advance in percent of mean was observed for number of primary branches per plant, number of seeds per pod, 100- seed weight, plant height and number of seeds per plant. The characters, mentioned above, having high values of heritability and genetic advance in percent of mean emerged as ideal traits for improvement through selection. Wide spectrum of variation was observed for seed characters of thirty chickpea genotypes. High magnitudes of genotypic and phenotypic coefficients of variation were observed for number of seeds per pod and number of primary branches per plant, indicating thereby, and substantial scope for improvement in this character after hybridization and subsequent selection. The moderate estimate of GCV and PCV were observed for 100-seedweight, plant height, secondary branches per plant and number of seeds per pods one or both parameters, which suggested possibility of obtaining reasonable improvement through selection. The presence of correspondence between the phenotypic and genotypic variances for all the characters indicating stable expression of the quality attributes and absence of high environmental influence.

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