Exploiting Indigenous Collections for efficient Utilization of Chickpea (*Cicer arietinum* L.) Genotypes for Crop Improvement based on Agro-Morphological Traits

Dilip Panwar[1], Anshuman Singh[1] and Pramod Kumar Sharma[2]*
[1]Department of Genetics and Plant Breeding,
Rani Lakshmi Bai Central Agricultural University, Jhansi (Uttar Pradesh), India.
[2]Department of Soil Science,
Rani Lakshmi Bai Central Agricultural University, Jhansi (Uttar Pradesh), India.

(Corresponding author: Dilip Panwar*)

ABSTRACT: Agro-morphological traits are stable across various biotic and abiotic stresses owing to oligogenic nature. Hence, for efficient identification and purification at varietal or genotypic level and even in seed production these traits may serve as morphological markers. During a period of *Rabi* 2020-21 a total of 44 elite chickpea genotypes were experimented in randomized block design (RBD) with three replicates for assessing the genetic variability among 16 agro-morphological traits. ANOVA revealed that seed yield per plant and its contributing traits had significant differences among all the genotypes. Significant differences were observed for days to 50% flowering (days) (Range: 75 to 93; Mean: 82), Seed yield per plant (g/plant) (Range: 4.6 to 20.36; Mean: 10.19), 100 seed weight (g) (Range: 13.23 to 36.06; Mean: 22.14. High heritability with high genetic advance observed for trait 100 seed weight followed by number of secondary branches per plant, biological yield per plant and seed yield per plant. These traits may serve as markers for varietal selection to enhance seed yield of chickpea. Similarly, these putative characters could be recommended for further breeding and selection of genetic materials for developing suitable chickpea genotypes. Correlation analysis exhibited that seed yield per plant had strong positive and significant association with biological yield per plant followed by number of secondary branches per plant and 100 seed weight. Path analysis indicated that biological yield per plant followed by days to 50% flowering, number of secondary branches and 100 seed weight had positive direct effect on seed yield. Genotypic variation found in germplasm collection can be exploited through efficient selection and hybridization among identified genotypes for future crop improvement program of chickpea.

Keywords: ANOVA, Chickpea, heritability, Correlation, Path analysis.

INTRODUCTION

Worldwide, pulses have been extensively used as prime protein meal as vegan diet. Legumes are procuring desirable demand, perception, and intercontinental marketability as the "futuristic and upgraded" health giving nutriment source due to their gluten-free quality, low-fat source of protein, magnificent dietary fibre, less glycemic index with ample amount of essential minerals required for the healthy human body. Among various grain legumes grown, Chickpea (*Cicer arietinum* L.) is one of the most demanding and superior leguminous crops in most of the Indian states referred to as "King of Pulses". Chickpea is an autogamous flowering plant with a genomic dimension of 738 Mbp having a true diploid chromosomal makeup of 2n = 2x = 16. (Varshney *et al*., 2013). In India, chickpea occupied the highest ever production of 13.75million tonnes covering an area of 10.91 million hectares with a productivity of 12.61 qt/ha (Anonymous, 2022).

Practically, a genotype has a DUS variation among the traits that are useful in the varietal identification and selection during crop improvement program for plant breeder. Hence, for maintaining the varietal purity, stable diagnostic qualitative traits and plant phenotypic appearance with good stand are utmost essential. (Lalitha, 2007). The different vital species or generating breeding populations detains immense quantity of here dietary genetic variability at genotypic level ensuing, greater probability to obtain a vast degree of environmentally stable individuals having more resistance potential towards different biotic and abiotic stresses. To attain further breakthroughs for improving yield and stability in future crop varieties, new traits of interest must be incorporated into the cultivated background of chickpea (Singh *et al*., 2022). For this detailed information on genetic variability in indigenous germplasm collection and varieties is required to be generated besides genetic parameters. Assessing genetic variability among elite breeding lines and estimating genetic parameters helps in

pinpointing characters for practicing selection from advance segregating generations.

MATERIALS AND METHODS

An experiment with forty-four chickpea (*Cicer arietinum* L.) indigenous collections developed under ambit of All India Coordinated Research Project (AICRP) (Table 1) was laid out in randomized block design (RBD) with three replicates under well-irrigated condition at research farm of the Rani Lakshmi Bai Central Agricultural University (RLBCAU), Jhansi (U.P.) during *Rabi* 2020-21. Each replication, planted with 4 m row with four rows per plot in each treatment followed by row to row spacing of 30 cm and plant to plant spacing of 10 cm under well irrigated condition. In present study observations were taken for morphological traits *viz*; stem anthocyanin pigmentation, plant growth habit, colour of foliage, flower colour, stripes on standard, leaflet size (mm), peduncle length (mm),pod length (mm) and flower number per peduncle, seed colour, seed size, seed shape, seed testa texture, seed ribbing and seed type as well as data were recorded on five randomly chosen competitive plants from each genotype in each

replication for quantitative traits *viz*; plant height (cm), primary branches per plant, secondary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g), while data on days taken to 50 % flowering and days taken to maturity were recorded on plot basis.

Observed data on quantitative traits were subjected to analysis of variance (ANOVA) as per standard statistical procedure suggested by (Panse and Sukhatme 1985) and estimation of genetic parameters *viz*; Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton and Devane (1953). Similarly, heritability (h^2_{bs}%) and genetic advance (GA) were computed as per Robinson *et al.* (1949) and Johnson *et al.* (1955). Correlation coefficients were computed at genotypic, phenotypic and environmental levels suggested by Miller *et al.* (1958).The direct and indirect effects of the yield contributing traits were estimated by path co-efficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

Table 1: List of chickpea genotypes used for present study.

Sr. No.	Genotypes	Pedigree	Developed at centres
1.	GL-16063	GPF 2 x [PBG 1 x (ICCV 96030 x C. *pinnatifidum 188)* x ICCV 96030]	Ludhiana, Punjab
2.	BRC 9-14	SAKI 19516 x GNG 1958	Dholi, Bihar
3.	GNG 2462	GNG1958 x BG1064	Sriganganagar, Rajasthan
4.	GJG 1707	GJG 0107 x GJG 0207	Junagadh, Gujarat
5.	BG 4010	JG 11 / BG 1098	IARI, New Delhi
6.	PG 227	M 35 (selection from MAGIC cross involving 8 parents)	Pantnagar, Uttarakhand
7.	NBeG 690	ICCV 03112 x JAKI 9218	Nandyal, Andhra Pradesh
8.	IPC 2015-12	IPC 2009-50 x IPC 2007-88	IIPR, Kanpur, Uttar Pradesh
9.	NBeG 698	ICCV 03112 x JAKI 9218	Nandyal, Andhra Pradesh
10.	ADBG 487	ICC4958 TM x JAKI9218	Adilabad, Telangana
11.	RVSSG 79	JG 11 x JSC52	Sehore, Madhya Pradesh
12.	RKG 19-1	JAKI 9218 x ICCV 00108	Kota, Rajasthan
13.	DC 18-1107	ICC 4958 TM/JG 130	Dholi, Bihar
14.	BAUG 106	JG 11 x ICC 4958	Ranchi, Jharkhand
15.	PG 237	M 47 (Selection from MAGIC cross involving 8 parents)	Pantnagar, Uttarakhand
16.	GJG 1708	GJG 0727 x GCP 101	Junagadh, Gujarat
17.	JG 2019-155-118	ICCV 05530 x ICCV 88510	Jabalpur, Madhya Pradesh
18.	Phule G 171103	(JG 11 x ICC 4552) x (ICCC 37 x ICC 5683)	Rahuri, Maharashtra
19.	H 13-36	PDG84-16 x H04-31	Hisar, Haryana
20.	RLBG 6	JG 14/ICCV 96836	Jhansi, Uttar Pradesh
21.	DC 18-1104	Genesis 836/JAKI 9218	Dholi, Bihar
22.	DBGC 1	BGD256 x WR315	CER Patna, Bihar
23.	Phule G 171105	(ICC 4958 x ICCV 97105) x (ICCV 10 x ICCV 00108)	Rahuri,Madhya Pradesh
24.	BG 4011	F1[F1(ICC4958 x ICCV10) x F1(Pusa372 x Pusa 256)] x F1(Pusa 547 x JAKI 9218)	IARI, New Delhi
25.	H 12-22	HC1 x (HC1 x ICCV96030)	Hisar, Haryana
26.	IPC 2016-107	IPC 2009-50 x IPC 2007-88	IIPR Kanpur, Uttar Pradesh
27.	NDG 18-2	MPJGK6 x BG 2058) x BGD 112	Faizabad, Uttar Pradesh
28.	RSGD 1071	RSG-931 x JG-11	Jaipur, Rajasthan
29.	BDNG 2017-44	Digvijay x ICC 4533	Badnapur, Maharashtra
30.	RSGD 1057	JG-11 x RSG 973	Jaipur, Rajasthan
31.	GL 17020	ICCX 04147 x ICCX 040126	Ludhiana, Punjab
32.	BDNG 2017-49	BDNG 804 x BDNG 797	Badnapur, Maharashtra

33.	BUC-1	Genesis 836 x JAKI 9218	Banda, Uttar Pradesh
34.	IPCD 2016-44	IPC 2008-57 x WR 315	IIPR Dharwad, Karnataka
35.	RKG 19-2	ICCV-14103 x BGD 72	Kota, Rajasthan
36.	NDG 18-9	(MPJGK 6 x BG 2058) x BGD 112	Faizabad, Uttar Pradesh
37.	GNG 2477	GNG 1581 x ICC1 2951	Sriganganagar, Rajasthan
38.	AKG 1506	JAKI 9218 x AKG 46	Akola, Maharashtra
39.	RVSSG 81	JAKI 9218 x JSC 52	Sehore, Madhya Pradesh
40.	GCP 101	GCP 2 x ICCV 2	Junagadh, Gujarat
41.	RVG 202	(JAKI 9226 x DCP 20) x JG 412	Sehore, Madhya Pradesh
42.	JG 315	Selection from WR 315	Jabalpur, Madhya Pradesh
43.	JG 16	ICCV 4 x ICCV 10	Sehore, Madhya Pradesh
44.	Phule G 0405	Digvijay x WCG 2002-2	Rahuri, Maharashtra

RESULTS AND DISCUSSIONS

Based on variation observed in agro-morphological traits genotypes was identify each one of them through descriptors (Table 2) Among all the 44 chickpea (*Cicer arietinum* L.) genotypes anthocyanin pigmentation was present in 43 (Desi) genotypes and absent only in one (Kabuli) genotype. In plant growth habit almost 40 genotypes had semi-erect type, 2 genotypes showed erect type and 2 genotypes showed spreading type of canopy structure. Based on intensity of green foliage colour, all genotypes were divided into three groups *viz.*, 37 genotypes examined dark green, 4 genotypes showed light green and 3 genotypes had greenish purple type of foliage shade. Based on flower petal colour; only one genotype had white and remaining all the 43 genotypes showed pink flowers. In terms of leaflet size 30 genotypes recorded small (<10 mm) and 14 genotypes had medium (10-15 mm) size of leaflets. Similar findings were supported by Honnappa *et al.* (2018).

In terms of peduncle length 3 genotypes had medium (5 -10 mm) and remains all 41 genotypes showed long (>10 mm) type of peduncle length. The study of pod size revealed four types of chickpea in that only one genotype had small (<15 mm), 6 genotypes showed medium (15 -20 mm) and remaining 37 genotypes showed large (>20 mm) pod size. With regards to the number of flowers per peduncle two types of chickpea were found *viz.*, almost 42 genotypes found with single flower and only 2 genotypes recorded twin flowers per peduncle. Genotypes were examined for the stripes on standard petal of the flower, the stripes were present in 43 genotypes except one kabuli genotype. Great variation was observed in terms of seed colour; one genotype seed had creamy beige, one with green seed, one with yellow seed, two with dark brown seed and majority of 39 genotypes had brown colour of seed.

According to seed size (100 SW), 4 categories were formed *viz.*, 18 genotypes recorded very small (<20 gm) seed size,9 genotypes had small (20-25 gm) seeds, 16 genotypes measured medium sized (26-35 gm) seeds and only one genotype revealed large (36-45 gm) type of seed size. For seed shape trait, one genotype with pea shaped, 18 genotypes found with owl shaped and 25 genotypes had angular seed shape. The availability of novel transgressive variations among the seed shape will be useful trait for the future chickpea breeding programme. Three groups were made based on seed testa texture; 10 genotypes showed rough texture, 28 genotypes observed smooth and 6 genotypes showed tuberculated testa texture. For seed ribbing 11 genotypes found with ribbing and absent in about 33 genotypes. Gediya *et al.* (2018).

Table 2: Characterization of chickpea genotypes based on DUS traits.

Sr. No.	Characters	Number of genotypes	Frequency (%)
1.	**Stem: Anthocyanin pigmentation**		
	Present	43	98%
	Absent	1	2%
2.	**Plant: Growth habit**		
	Erect	2	4%
	Semi erect	40	91%
	Spreading	2	5%
3.	**Plant: Colour of foliage**		
	Dark green	37	84%
	Light green	4	9%
	Greenish purple	3	7%
4.	**Plant: Height**		
	Tall	7	16%
	Medium	37	84%
5.	**Flower: Colour**		
	White	1	2%
	Pink	43	98%
6.	**Flower: Stripe on standard**		
	Absent	1	2%
	Present	43	98%

7.	**Leaflet: Size**		
	Small	30	68%
	Medium	14	32%
8.	**Peduncle: Size**		
	Medium	3	7%
	Long	41	93%
9.	**Pod: Size**		
	Small	1	2%
	Medium	6	14%
	Large	37	84%
10.	**Flower: Number per peduncle**		
	Single	42	95%
	Twin	2	5%
11.	**Seed: Colour**		
	Creamy beige	1	2%
	Green	1	2%
	Yellow	1	2%
	Dark brown	2	5%
	Brown	39	89%
12.	**Seed: Size**		
	Very small	18	41%
	Small	9	20%
	Medium	16	37%
	Large	1	2%
13.	**Seed: Shape**		
	Pea	1	2%
	Owl	18	41%
	Angular	25	57%
14.	**Seed: Testa texture**		
	Rough	10	23%
	Smooth	28	63%
	Tuberculated	6	14%
15.	**Seed: Ribbing**		
	Absent	33	75%
	Present	11	25%
16.	**Seed: Type**		
	Desi	43	98%
	Kabuli	1	2%

The analysis of variance (Table 3) was done for agronomic traits and mean sum of squares value for traits showed highly significant ($p<0.005$) differences which denoting the presence of ample genetic variability among the experimental material that can be further exploited for efficient utilization of chickpea genotypes for crop improvement. Thus, the experiment findings of the current investigation are in conformity with the results reported by Zerfu *et al.* (2021).

Mean of DF was 82 days which ranged from 75 to 93 days (Table 4). Maturity days ranged from 123 to 146 days with the mean of 135 days. Plant height trait was classified into two classes, 7 genotype having tall and 37 genotype having medium plant height which possessed a mean of 57.62 cm ranging from 49.16 to 81.83 cm. Primary branches and secondary branches also emphasized on yield, had a mean of 4.31 and 16.68, respectively. Highest variation exist in trait number of pods per plant (PPP) was ranged from 31 to 110.33 with a mean of 69.61. Genotype JG 16 showed high number of pods per plant (110.33). Weight of 100 seeds ranged from 13.23 to 36.06 g with mean of 22.14 g and highest 100 SW recoded in genotype RVSSG 79 (36.07 g). SYP was recorded highest in Phule G 0405 (20.36 g) ranging from 4.6 to 20.36 g with the mean of 10.19 g. Leaflet size ranged from 6.22 to 13.33 cm with mean of 9.17 cm, similarly peduncle length was ranged from 9.42 to 22.21 cm with mean of 13.31 cm and pod length varied between 13.1 to 28.66 cm with an average of 23.27 cm. Biological yield ranged from 7.4 to 29.6 g with mean of 16.17 g.

Table 3: ANOVA table for different 14 agro-morphological traits.

Source of Variation	Replication	Treatment	Error
Degree of freedom	2	43	86
DF	2.54	42.15**	17.18
DM	105.28	90.19**	37.31
PH	158.56**	154.25**	17.29
LS	0.15	6.08**	0.12
PEDL	3.68	25.73**	3.19
PODL	16.99	26.79**	7.7
PB	0.52	1.46**	0.2
SB	0.75	65.62**	0.28
PPP	175.52	1040.90**	104.23
100SW	0.46	80.11**	0.18
NSP	0.07	0.13**	0.03
BYP	4.46	61.56**	1.61
SYP	5.85*	24.73**	1.34
HI	0.004	0.004**	0.002

** and * represent 1% and 5% level of significance, respectively

DF- Days to 50% flowering, DM- Days to maturity, PH- plant height (cm), LS- leaflet size (mm), PEDL- peduncle length (mm), PODL- pod length (mm), PB- Number of primary branches, SB- Number of secondary branches, PPP- Number of pods per plant, 100 SW- weight of 100 seeds, NSP- Number of seeds per pods, BYP- Biological yield per plant (g), SYP- Seed yield per plant (g), HI- Harvest index

Table 4: Estimation of mean performance and range of chickpea genotypes.

Characters	Range	Mean	CV(%)
DF (days)	75-93	82	5.07
DM (days)	123-146	135	4.52
PH (cm)	49.16-81.83	57.62	7.21
LS (mm)	6.22-13.33	9.17	3.87
PEDL (mm)	9.42-22.21	13.13	13.6
PODL (mm)	13.1-28.66	23.27	11.92
PB	3.22-6.22	4.31	10.5
SB	6.33-28.66	16.68	3.17
PPP	31-110.33	69.61	14.66
100SW (g)	13.23-36.06	22.14	1.93
NSP	1-2	1.29	13.81
BYP (g)	7.4-29.6	16.17	7.84
SYP (g)	4.6-20.36	10.19	11.35

Phenotypic coefficients of variability (PCV) varied from 5.48 to 29.65% (Table 5, Fig. 1). The highest phenotypic coefficient of variability was observed for seed yield per plant (29.65%) followed by number of pods per plant (29.31%), biological yield per plant (28.72%) Zerfu *et al.* (2021); Banik *et al.* (2018). Low estimates for PCV were obtained for days to maturity (5.48%) and days to flowering (6.18%), indicating a scarcity of variability in the population. Similar results were showed by Honnappa *et al.* (2018). The highest genotypic coefficient of variability (GCV) was with number of secondary branches (27.97%) followed by biological yield per plant (27.63%), seed yield per plant (27.39%). Similarly low estimates for GCV were also found for days to maturity (3.11%) and days to flowering (3.53%) indicate that the environment has a small influence on the expression of this trait. The same results were found by Zerfu *et al.* (2021); Banik *et al.*(2018).

Phenotypic and genotypic variance provides information about variability present in material whereas the heritable portion of this genetic variability was confirmed by the indication of heritability estimates. In present investigation broad-sense heritability (h^2_{bs}) ranged from 24.93% to 97.31% (Table 5). Higher heritability (%) coupled with high genetic advance as % of the mean (GAM) was recorded (Fig. 1) for 100 seed weight (97.31, 47.18) followed by number of secondary branches (95.72, 57.26), leaflet size (94.01, 30.67), biological yield per plant (92.53, 54.76) and seed yield per plant (85.32, 52.12) respectively. The same findings were confirmed by Jain *et al.* (2020); Anusha *et al.* (2020). High heritability estimate reveals the effective selection for the above traits in crop improvement whereas less environmental effects were involved in the traits (Maniee *et al.*, 2009). Moderate estimates of heritability were found for number of seeds per pods (51.01), pod length (45.21) followed by days to 50% flowering (32.62) and days to maturity (32.07). Same results were in agreement with Dehal *et al.* (2016); Desai *et al.* (2015).

Table 5: Estimation of genetic variability parameters of chickpea genotypes.

Characters	Vp	Vg	PCV(%)	GCV(%)	h^2_{bs}(%)	GA	GAM(%)
DF (days)	25.51	8.32	6.18	3.53	32.62	3.39	4.15
DM (days)	54.94	17.62	5.48	3.11	32.07	4.89	3.62
PH (cm)	62.95	45.65	13.76	11.72	72.52	11.85	20.56
LS (mm)	2.11	1.98	15.83	15.35	94.01	2.81	30.67
PEDL (mm)	10.7	7.51	24.91	20.86	70.17	4.37	36.01
PODL (mm)	14.06	6.36	16.11	10.83	45.21	3.49	15.01
PB	0.62	0.41	18.31	14.99	67.06	1.09	25.29
SB	22.06	21.78	28.15	27.97	95.72	9.55	57.26
PPP	416.45	312.22	29.31	25.38	74.97	31.51	45.27
100 SW (g)	26.82	26.64	23.3	23.3	97.31	10.46	47.18
NSP	0.06	0.03	19.73	14.09	51.01	0.26	20.73
BYP (g)	21.59	19.98	28.72	27.63	92.53	8.85	54.76
SYP (g)	9.14	7.79	29.65	27.39	85.32	5.31	52.12
HI	0.002	0.007	8.59	4.29	24.93	0.02	4.41

Genetic advance as % of the mean (GAM) (Table 5) was found to be high *i.e.,* above 20% for all the traits except days to maturity (3.62), days to 50% flowering (4.15), harvest index (4.41) and pod length (15.01). Higher estimates of heritability coupled with good genetic advance as % of the mean denotes a very good indication for nature of inheritance and effectiveness of selection for a particular trait. (Johnson *et al.*, 1955). In the present investigation, the yield attributing traits *viz*; seed yield per plant, number of secondary branches and 100-seed weight revealed higher estimates of GCV, heritability and GAM showing that these characters are govern by the additive gene action and are suitable for the phenotypic selection in crop improvement. In contrast, moderate heritability with low genetic advance observed for days to 50% flowering (32.62, 4.15) and days to maturity (32.07, 3.62), while harvest index showed low heritability with low genetic advance (24.93, 4.41) respectively. The low estimate of genetic advance is supported with the results of Kumar *et al.* (2019).
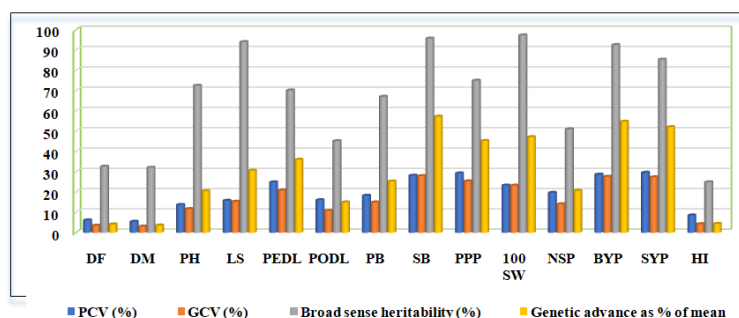
Fig. 1. Performance of different genetic parameters in chickpea genotypes.

The estimates of genotypic coefficients of correlation among the yield and its contributing attributes are shown in Table 6. The table reveals that seed yield per plant was highly significant and positively correlated with biological yield per plant (0.973**), number of secondary branches per plant (0.539**), 100 seed weight (0.393**) denoting that these characters might be useful for effective selection of crop yielding accessions from a pool of genotypes in chickpea and hence these traits helpful for bringing improvement in seed yield (Zerfu *et al.,* 2021; Philanim 2020; Hama, 2019). The 100 seed weight had significant positive correlation with leaflet size (0.368*), pod length (0.323*), biological yield per plant (0.402*) and seed yield per plant (0.393**). This correlation of 100 seed weight and biological yield per plant, as well as seed yield, indicate that 100 seed weight could be used as a selection parameter for chickpea breeding.

The path analysis was done to find out the relative contribution of seed yield and its contributing factors. In this genotypic correlation coefficient was splits into direct and indirect effects by various yield contributing traits are presented in Table 7. The path analysis studies find out the effect of each character on seed yield by using correlation coefficients and revealed that biological yield per plant (0.924), days to 50% flowering (0.109), number of secondary branches (0.093), 100 seed weight (0.080), number of pods per plant (0.047), number of seeds per pods (0.034) and harvest index (0.025) had the greatest positive direct and indirect effect on seed yield per plant suggesting that these traits significantly contributing into seed yield. High magnitude of biological yield with grain yield was supported by Agrawal *et al.* (2018) has also reported a high direct effect on seed yield. Jivani *et al.* (2013); Tadesse *et al.* (2016). In this investigation plant height showed

positive indirect effect with seed yield via number of pods per plant and number of primary branches. These results were agreed with the findings of Bhanu *et al.* (2017); Noor *et al.* (2003).

Based on results, it can be concluded that the key traits responsible for the variation of seed yield in chickpea is biological yield per plant and number of secondary branches. Correlation and path analysis suggests the nature and extent of association between different traits contributing to yield and causes of association can be better understood which helps in formulation of selection criteria for improvement of yield.

Table 6: Correlation among the agro-morphological in chickpea genotypes.

Traits	DF	DM	PH	LS	PEDL	PODL	PB	SB	PPP	100 SW	NSP	BYP	HI	SYP
DF	1.000	0.304*	-0.158	-0.026	-0.218	0.067	0.050	0.081	0.165	-0.266	0.029	0.052	0.206	0.087
DM		1.000	-0.206	-0.250	-0.429**	0.002	0.023	0.150	0.038	-0.056	0.053	-0.074	0.079	-0.016
PH			1.000	-0.080	0.094	0.211	-0.252	-0.063	-0.211	0.270	0.123	0.146	0.026	0.086
LS				1.000	0.171	0.023	-0.108	-0.068	-0.064	0.368*	0.025	0.073	-0.145	0.077
PEDL					1.000	-0.185	0.082	-0.082	0.154	0.028	-0.071	0.078	0.156	0.018
PODL						1.000	-0.172	0.009	-0.373*	0.323*	0.021	0.047	-0.237	-0.004
PB							1.000	0.030	0.372*	-0.279	0.116	-0.077	0.083	-0.105
SB								1.000	0.208	0.241	-0.320*	0.474**	0.086	0.539**
PPP									1.000	-0.235	0.050	0.126	0.147	0.138
100SW										1.000	-0.065	0.402**	-0.135	0.393**
NSP											1.000	-0.172	0.130	-0.184
BYP												1.000	0.027	0.973**
HI													1.000	0.061
SYP	* and ** correlation is significant at the 0.05 and 0.01 level.													1.000

Table 7: Path matrix; direct and indirect effects of yield components on seed yield.

Traits	DF	DM	PH	LS	PEDL	PODL	PB	SB	PPP	100SW	NSP	BYP	HI
DF	**0.109**	-0.062	0.014	0.001	0.018	-0.020	-0.016	0.010	-0.015	-0.039	0.001	0.080	0.006
DM	0.057	**-0.098**	0.027	0.022	0.050	-0.010	-0.001	0.027	-0.002	-0.007	0.003	-0.089	0.005
PH	-0.027	0.029	**-0.057**	0.003	-0.007	-0.025	0.017	-0.007	0.004	0.023	0.004	0.137	-0.008
LS	-0.004	0.031	0.005	**-0.038**	-0.012	-0.012	0.007	-0.006	0.001	0.030	0.004	0.069	0.002
PEDL	-0.019	0.057	-0.005	-0.007	**-0.069**	0.023	-0.004	-0.008	-0.003	0.002	-0.002	0.062	-0.009
PODL	0.012	-0.024	-0.030	-0.009	0.018	**-0.085**	0.013	0.001	0.008	0.031	-0.001	0.069	-0.007
PB	0.010	-0.002	0.017	0.004	-0.005	0.030	**-0.058**	0.014	-0.007	-0.024	0.003	-0.087	-0.006
SB	0.012	-0.019	0.004	0.003	0.006	-0.011	-0.007	**0.093**	-0.004	0.019	-0.008	0.444	0.007
PPP	0.026	-0.029	0.015	0.002	-0.029	0.042	-0.041	0.020	**0.047**	-0.038	0.002	0.120	0.001
100SW	-0.038	0.008	-0.016	-0.014	-0.012	-0.033	0.018	0.023	0.004	**0.080**	-0.002	0.377	-0.002
NSP	0.017	-0.012	-0.011	-0.001	0.020	0.017	-0.009	-0.035	-0.002	-0.006	**0.034**	-0.195	-0.001
BYP	0.009	0.009	-0.009	-0.015	-0.005	-0.006	0.005	0.045	-0.002	0.033	-0.005	**0.924**	-0.010
HI	0.025	-0.020	0.019	-0.003	0.024	0.022	0.013	0.026	-0.001	-0.007	0.001	-0.063	**0.025**

CONCLUSIONS

In present study genetic variability was observed to exploit the more variable agro- morphological trait which might be useful in making the superior genotypes against the biotic and abiotic stresses in the hybridization programme. The chickpea breeding lines used in the study showed vast amount of genetic variability among morphologicaltraits. In view of these traits *viz*; seed size, seed testa texture, seed shape and plant height had great frequency of variability in phenotypic appearance among genotypes. Similarly, in agronomic traits *viz*; number of pods per plant, number of seed per pod, seed yield per plant and pod length were showed more genetic variability. In a view to achieve advancement in the seed yield attention should be given on those traits which are directly or indirectly govern the yield component. For that, to find out the relationship among the yield and yield contributing traits correlation and path analysis were done. In results, traits like biological yield per plant, number of secondary branches per plant and 100 seed weight recorded strong positive correlation as well as high positive direct effects with seed yield per plant. Hence, these traits might be useful as selectable marker in the yield improvement of the chickpea genotypes.

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