Study of genetic variability parameters for yield and its components under normal and late sown conditions in chickpea (*Cicer arietinum* L.)

ABSTRACT

An investigation consisted of 50 chickpea genotypes including 4 checks viz., JG64, ICC10685, ICC4567 and NBeG47 was conducted during the rabi season of year 2022-23 at Seed Research and Technology centre, Rajendranagar, Telangana. The objective of the study was to estimate magnitude of different parameters of genetic variability for yield and its attributes. The observations were recorded for thirteen different yield and its contributing characters and the results obtained indicated that in general the phenotypic coefficient of variance was found to be higher as compared to genotypic coefficient of variance for all studied traits. High heritability along with high genetic advance (% mean) was obtained for characters like number of seeds per plant, number of filled pods per plant, seed yield per plant, number of pods per plant, number of primary branches, 100 seed weight, number of secondary branches, and plant height at normal sown conditions, which determines the presence of additive gene action for these characters and in late sown conditions the characters like number of seeds per plant, number of filled pods per plant, seed yield per plant, number of pods per plant, number of primary branches, 100 seed weight, number of secondary branches, and plant height and harvest index had shown high heritability along with high genetic advance. So, it determines the presence of additive gene action for these characters. So, that selection for these characters is beneficial in the breeding programmes.

Keywords: *Chickpea, Variability, Heritability, PCV, GCV, Genetic Advance*.

1.INTRODUCTION

"The chickpea (*Cicer arietinum* L.) is an annual legume of the family Fabaceae, subfamily Faboideae. Its numerous varieties are known as gram or Bengal gram, chana, garbanzo or garbanzo bean, or Egyptian pea. It is a cool-season pulse crop" [1]. "Despite the fact that it is a diploid (2n=2x =16) and primarily self-pollinated crop, cross-pollination by insects does occur on occasion" [2]. "It has spread across more than 50 countries, with Asia accounting for 89.7 percent of the total, Africa accounting for 4.3 percent, America accounting for 2.9 percent, Oceania accounting for 2.6 percent, and Europe accounting for 0.4 percent" [3]. "In India, It is grown mainly as a rainfed crop. India accounts for a substantial share of the world's chickpea area (70 per cent) and production (67 per cent), and continues to be a major producer along with other countries viz., Myanmar, Ethiopia, Turkey, and Pakistan" [4]. "Madhya Pradesh (M.P), Maharashtra, Rajasthan, Uttar Pradesh (U.P), Andhra Pradesh (A.P), Karnataka, Chhattisgarh, Bihar, and Jharkhand are the states that produce the majority of the chickpeas, responsible for > 95 % of the total production. However, chickpea area, production, and productivity have risen significantly in recent years" [3]. "The main concern for India is the decreasing area from 9.27 mha in 1961 to 8.39 mha in 2016. From 1961 to 2019, there has been a significant increase in production by 1.56 million tonnes" [5]. "There is urgent need for development of selection criteria and action towards improving yield levels of chickpea

Genetic variability is important indices for plant breeders because it provides a source of variation as well as raw material for yield enhancement" [6,7]. "The selection of yield contributing characters is important for crop improvement and the selection of such characters depends mainly on heritable variation as well as the heritability of the trait concerned". [25]

"The collecting of superior alleles into a single population is referred to as an effective and economical crop improvement technique. Genetic variability in a population can be divided into heritable and nonheritable variations using genetic parameters such as variance, genotypic coefficient of variation, heritability, and genetic advance, which serve as a foundation for selecting some outstanding genotypes from the existing ones. The selection of parents is influenced not only by desirable agronomic qualities, yield components, and the level of variability, but also by the heritability of yield contributing factors. The environment in which selection is made is also important because heritability and genetic advance vary with the change in environment. Any crop development plan requires breeders to have knowledge and expertise with variability. Variability and heritability are both essential factors that might help breeders at various stages of crop development.. The effectiveness of the breeding programme would depend on the magnitude of variability and heritability in early-generation populations for important economic traits" [8]. "The heritability estimate in combination with the genetic advance, is required to predict the specific impact from the selection of the most appropriate individuals for a given situation" [9]. Therefore, the current study conducted and analysed using potential genotypes to estimate variability, heritability, and genetic advance for yield and yield contributing traits in chickpea.

2. MATERIALS AND METHODS

Experimental Material and Field Trial.

The experimental material for this study consists of 50 chickpea genotypes including four checks, namely JG64, ICC10685, ICC4567 and NBeG47. Considering each genotype as one treatment, the experiment was laid out in RBD with Three replications during rabi season of year 2022-23 at Seed Research and Technology centre, Rajendranagar, which is geographically located at $17^0$19'52.6"N latitude and $78^0$24'35.6"E longitude and falls under Southern Telangana agro-climatic zone.

Each accession was planted in a single 4 meter long row with a row to row distance of 30 cm and plant to plant distance of 10 - 15 cm. The standard package of practices for chickpea cultivation was followed.

Observed traits and sampling measurements: The observations were recorded for 13 parameters on 5 plants randomly selected from a single row of each chickpea genotypes for yield and its attributes (Table 1). The observation was recorded on whole row basis for DFF, DPI and DM. The mean values from each observation for each replication were used for statistical analysis.

Table 1: Observations recorded for yield and yield contributing trait

Sr.No	Characters
1	Days to 50% flowering
2	Days to pod initiation
3	Days to maturity
4	Plant height (cm)
5	Number of primary branches
6	Number of secondary branches
7	Number of pods per plant
8	Number of filled pods per plant
9	Number of seeds per pod
10	Number of seeds per plant
11	Seed yield per plant
12	100 seed weight
13	Harvest index

Statistical analysis:

The phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) were calculated according to the method suggested by Burton et al [10]. These values were categorized as high (>20 %), moderate (10-20 %) and low (<10%) as indicated by Sivasubramanian and Menon et al., [11]. Heritability (h^2_{bs}) was estimated for each character as suggested by Hanson et al.,[12].The heritability was categorized as high (>60%), moderate (30-60%) and low (<30%) as given by Robinson *et al*.,[13]. For each character, genetic advance (GA) was estimated by method given by Johnson et al.,[9]. Genetic advance as % of mean (GA % mean) was classified as high (>20%), moderate (10-20%) and low (<10%) as classified by johnson et al.,[9].

3. Results and Discussion

Analysis of variance on 50 chickpea genotypes under normal and late sown conditions:

Analysis of variance (ANOVA) for the normal and late sown conditions involving a set of 50 chickpea genotypes for 13 quantitative characters namely days to 50% flowering, days to pod Initiation, days to Maturity, plant height, number of primary branches, number of secondary branches, pods per plant, filled pods per plant, number of seeds per plant, number of seeds per pod, seed yield per plant, 100 seed weight, and harvest index revealed that the mean sum of squares due to replications was non-significant for all the traits except no of seeds per pod and mean sum of squares due to genotypes were found to be highly significant for all the characters indicating the presence of high diversity among the 50 chickpea genotypes in both normal and late sown conditions.

3.2 Estimation of genetic variability parameters:

Phenotypic coefficient of variance (PCV):

The phenotypic coefficient of variance (PCV) for 13 traits are listed in Table 4 and 5 and these characters are classified in to high, moderate, and low PCV values. The high values of PCV were observed for the characters like no. of seeds per plant (41.53) followed by no. of filled pods per plant (38.3), seed yield per plant (37.71), no. of pods per plant (35.2), and no. of primary branches (22.15) under normal sown conditions. But at late sown conditions high values of PCV were exhibited for the characters like no. of seeds per plant (41.51) followed by no. of filled pods per plant (40.27), seed yield per plant (39.17) and no. of pods per plant (37.89). For these studied characters presence of high PCV indicated the influence of prevailing environmental conditions. Under late sown conditions moderate values of PCV observed for no. of primary branches (19.81), no. of secondary branches (19.5), 100 seed weight (16.87), harvest index (16.2), and plant height (12.08). Under normal sown conditions low values of PCV observed for the character days to maturity (5.14), days to pod initiation (7.09), no. of seeds per pod (8.41), days to 50% flowering (9.64) and low values of PCV under late sown conditions exhibited by days to maturity (5.3), no. of seeds per pod (6.72), days to panicle initiation (8.3), and days to 50% flowering (8.85).

Genotypic coefficient of variance (GCV):

The high values of GCV were observed for the characters like no. of seeds per plant (36.5) followed by no. of filled pods per plant (33.6), seed yield per plant (32.1), and no. of pods per plant (30.63) under normal sown conditions. But at late sown conditions high values of GCV were exhibited for the characters like no. of seeds per plant (37.65) followed by no. of filled pods per plant (36.23), seed yield per plant (35.3) and no. of pods per plant (33.9). Moderate values of GCV were observed for 100 seed weight (16.89), no. of secondary branches (15.9), plant height (11.34), no. of primary branches (10.37) and harvest index (10.03) under normal sown conditions. Under late sown conditions moderate values of GCV observed for no. of secondary branches (17.9), 100 seed weight (16.77), no. of primary branches (16.74), harvest index (13.84), and plant height (11.72). Under normal sown conditions low values of GCV observed for the character days to maturity (4.53), no. of seeds per pod (6.32), days to pod initiation (6.80), days to 50% flowering (8.17) and low values of GCV under late sown conditions exhibited by no. of seeds per pod (4.67), days to maturity (4.91), days to pod initiation (7.53), and days to 50% flowering (8.33). Similar results for GCV and PCV were obtained by Gautam et al., [14], Arora et al., [15]. Kishor et al ., [16], Pandey et al., [17] and Zali et al., [18]., for characters DFF, DM, no of primary branches, plant height, no of pods per plant, seed yield per plant, and Kishor et al., [16] and Zali et al., [18] for DFF, DM, PH, no of primary branches, number of pods per plant ,number of seeds per plant, seed yield per plant and 100 seed weight and Arora et al., [15] for harvest index.

The phenotypic coefficient of variance (PCV) is greater than the genotypic coefficient of variance (GCV) for all the 13 characters under study at both normal and late sown conditions. Both the high values of

GCV and PCV for the characters are very important in the breeding programmes to select the superior genotypes.

Broad sense heritability (h^2):

Broad sense heritability for 13 characters under normal and late sown conditions is given in table 4 and 5 For all the characters broad sense heritability ranges from 71% to 92% under normal conditions and under late sown conditions it ranges from 48% to 98%. Under normal sown conditions, high levels of heritability (broad sense) seen in the characters like days to pod initiation (92%), plant height (92%), 100 seed weight (92%), days to maturity (77%), no. of seeds per plant (77%), no. of primary branches (76%), no. of filled pods per plant (76%), no. of pods per plant (75%), seed yield per plant (72%), harvest index (72%), days to 50% flowering (71%), and no. of secondary branches (71%). But at late sown conditions, high levels of heritability seen in the characters like 100 seed weight (98%), plant height (94%), days to 50% flowering (88%), days to maturity (85%), no. of secondary branches (84%), days to pod initiation (82%), no. of seeds per plant (82%), seed yield per plant (81%), no. of pods per plant (80%), no. of filled pods per plant (80%), harvest index (73%), and no. of primary branches (71%). Moderate level of heritability exhibited by no. of seeds per pod at both normal and late sown conditions. At normal sown conditions no. of seeds per pod has shown (56%) of heritability and at late sown conditions it has shown (48%) of heritability. Similar results for heritability were obtained by Gautam et al., [14], Kishor et al., [16] (2018) and Puri et al., [19] (2013) for PH, number of pods per plant seed yield per plant and 100 seed weight. Mushtaq et al., [20] (2013) for DPI , PH and 100 seed weight. Kumar et al., [21] (2019) for DM, PH, number of primary branches, and 100 seed weight. Kishor et al., [16] (2018) obtained similar results for DM.

Genetic advance:

Genetic advance values for 13 characters under normal and late sown conditions at 5% selection intensity (k=2.06) is presented in table 4 and 5 and all the 13 characters showed different values for genetic advance parameter. At normal sown conditions the trait no. of seeds per plant exhibited (43.36) value followed by no. of pods per plant (37.01), no. of filled pods per plant (36.08), plant height (10.46), harvest index (10.03), seed yield per plant (10), 100 seed weight (9.37), days to maturity (7.26), days to pod initiation (6.45), days to 50% flowering (5.89), no. of secondary branches (4.81), no. of primary branches (1.08), and no. of seeds pod (0.10). under late sown conditions the trait no. of seeds per plant exhibited (39.23) value followed by no. of pods per plant (35.74), no. of filled pods per plant (33.76), harvest index (12.43), plant height (10.62), seed yield per plant (9.21), 100 seed weight (8.85), days to maturity (7.29), days to pod initiation (6.66), days to 50% flowering (6.30), no. of secondary branches (5.8), no. of primary branches (0.91), and no. of seeds pod (0.07).

Table 2 Analysis of variance for 13 characters in 50 chick pea genotypes under normal conditions

	Mean sum of squares													
SOV	**d.f.**	**DFF**	**DPI**	**DM**	**PH**	**PB**	**SB**	**Pods PP**	**Filled Pods PP**	**Seeds PP**	**Seeds per pod**	**Seed yield PP**	**100 SW**	**HI**
REP	2	13.760	2.427	6.540	5.967	0.209	0.467	418.502	206.156	511.978	0.019 **	30.742	3.541	37.779
GEN	49	38.656 ***	32.884 ***	52.656 ***	85.752 ***	1.211 ***	25.863 ***	1416.065 ***	1329.677 ***	1890.150 ***	0.018 ***	109.109 ***	68.394 ***	110.568 ***
Error	98	4.467	0.923	4.615	2.218	0.113	3.012	136.739	121.515	168.633	0.004	12.067	1.674	12.380
Total	149	15.836	11.454	20.440	29.739	0.475	10.493	561.239	519.966	739.378	0.009	44.231	23.640	45.011
General Mean		41.300	47.953	88.300	46.493	3.123	17.277	67.411	59.555	65.575	1.094	17.671	27.933	56.981
CV%		5.118	2.004	2.433	3.203	10.753	10.045	17.347	18.509	19.803	5.610	19.659	4.631	6.175

SOV = source of variation, d.f. = Degree of freedom, REP= Replication, GEN = Genotypes, CV%= Co-efficient of variation, DFF=Days to 50% flowering, DPI=Days to pod Initiation, DM= Days to Maturity, PH= Plant Height, PB= no. of Primary Branches, SB= No. of Secondary Branches, Pods PP= Pods per plant, Filled pods PP= Filled pods per plant, Seeds PP= Seeds per plant, Seeds per pod= Seeds per pod, Seed yield PP= Seed yield per plant, 100 SW= 100 Seed weight, HI= Harvest Index.

Table 3 Analysis of variance for 13 characters in 50 chick pea genotypes under late sown conditions

	Mean sum of squares													
SOV	**d.f.**	**DFF**	**DPI**	**DM**	**PH**	**PB**	**SB**	**Pods PP**	**Filled Pods PP**	**Seeds PP**	**Seeds per pod**	**Seed yield PP**	**100 SW**	**HI**
REP	2	4.020	8.027	4.047	4.058	0.059	5.033	283.975	237.881	280.122	0.010 *	17.467	0.502	6.030
GEN	49	33.061 ***	40.798 ***	46.373 ***	86.597 ***	0.947 ***	29.999 ***	1220.971 ***	1074.517 ***	1421.311 ***	0.011 ***	79.684 ***	56.365 ***	168.309 ***
Error	98	1.367	2.714	2.448	1.758	0.112	1.761	93.433	78.312	95.139	0.003	5.693	0.224	18.470
Total	149	11.826	15.309	16.915	29.689	0.386	11.091	466.791	408.065	533.746	0.006	30.184	18.690	67.579
General Mean		39.000	47.293	77.893	45.369	3.151	17.097	57.172	50.297	55.727	1.111	14.061	25.793	51.054
CV%		2.998	3.483	2.009	2.922	10.603	7.763	16.907	17.594	17.503	5.039	16.969	1.836	8.418

SOV = source of variation, d.f. = Degree of freedom, REP= Replication, GEN = Genotypes, CV%= Co-efficient of variation, DFF=Days to 50% flowering, DPI=Days to pod Initiation, DM= Days to Maturity, PH= Plant Height, PB= no. of Primary Branches, SB= No. of Secondary Branches, Pods PP= Pods per plant, Filled pods PP= Filled pods per plant, Seeds PP= Seeds per plant, Seeds per pod= Seeds per pod, Seed yield PP= Seed yield per plant, 100 SW= 100 Seed weight, HI= Harvest Index.

Table 4 Estimation of genetic variability for 13 characters of chick pea genotypes under normal sown conditions

S. No	CHARACTERS	MEAN	RANGE MIN	RANGE MAX	ECV (%)	GCV (%)	PCV (%)	h^2 bs (%)	Genetic advance	Genetic advance as % of mean
1	**DFF**	41.3	34.0	52.0	5.11	8.17	9.64	71	5.89	14.27
2	**DPI**	47.9	43	60	2.0	6.80	7.09	92	6.45	13.45
3	**DM**	88.3	80	103	2.43	4.53	5.14	77	7.26	8.22
4	**PH**	46.49	35.6	61.0	3.20	11.34	11.79	92	10.46	22.5
5	**PB**	3.12	2.0	5.6	10.75	10.37	22.15	76	1.08	34.9
6	**SB**	17.2	9.6	27.0	10.04	15.9	18.8	71	4.81	27.8
7	**Pods PP**	67.4	22.6	136.8	17.34	30.63	35.20	75	37.01	54.91
8	**Filled Pods PP**	59.4	19.8	128.8	18.4	33.6	38.3	76	36.08	60.66
9	**Seeds PP**	65.5	20	162.4	19.8	36.5	41.53	77	43.36	66.1
10	**Seeds per pod**	1.09	1	1.44	5.56	6.32	8.41	56	0.10	9.79
11	**Seed yield PP**	17.67	4.1	35.7	19.65	32.1	37.71	72	10	56.59
12	**100 SW**	27.9	13.5	42.7	4.63	16.89	17.51	92	9.37	33.5
13	**HI**	56.9	28.7	72	6.17	10.03	11.7	72	10.03	17.61

ECV= Environment co-efficient of variance, **GCV**= Genotypic co-efficient of variance, **PCV**= Phenotypic co-efficient of variance, **DFF**= Days to 50% flowering, **DPI**=Days to pod Initiation, **DM**= Days to Maturity, **PH**= Plant Height, **PB**= no. of Primary Branches, **SB**= No. of Secondary Branches, **Pods PP**= Pods per plant, **Filled pods PP**= Filled pods per plant, **Seeds PP**= Seeds per plant, **Seeds per pod**= Seeds per pod, **Seed yield PP**= Seed yield per plant, **100 SW**= 100 Seed weight, **HI**= Harvest Index.

Table 5 Estimation of genetic variability for 13 characters of chick pea genotypes under late sown conditions

S. No	CHARACTERS	MEAN	RANGE MIN	RANGE MAX	ECV (%)	GCV (%)	PCV (%)	h^2 bs (%)	Genetic advance	Genetic advance as % of mean
1	**DFF**	39	32	48	2.99	8.33	8.85	88	6.30	16.15
2	**DPI**	47.2	40.0	57	3.48	7.53	8.3	82	6.66	14.08
3	**DM**	77.8	71	90	2.0	4.91	5.30	85	7.29	9.36
4	**PH**	45.3	35.6	63.2	2.92	11.72	12.08	94	10.62	23.42
5	**PB**	3.15	2.0	5.2	10.6	16.74	19.81	71	0.91	29.13
6	**SB**	17.08	9.4	28.8	7.76	17.9	19.5	84	5.8	33.95
7	**Pods PP**	57.17	18.6	120	16.9	33.9	37.89	80	35.74	62.51
8	**Filled Pods PP**	50.29	18.4	113.1	17.59	36.23	40.27	80	33.76	67.13
9	**Seeds PP**	55.7	21.90	128.60	17.48	37.65	41.51	82	39.23	70.36
10	**Seeds per pod**	1.11	1.0	1.42	4.81	4.67	6.72	48	0.07	6.68
11	**Seed yield PP**	14.06	3.95	29.8	16.96	35.3	39.17	81	9.21	65.5
12	**100 SW**	25.79	13.5	35.6	1.83	16.77	16.87	98	8.85	34.34
13	**HI**	51.05	22.03	68.79	8.41	13.84	16.20	73	12.43	24.36

ECV= Environment co-efficient of variance, **GCV**= Genotypic co-efficient of variance, **PCV**= Phenotypic co-efficient of variance, **DFF**= Days to 50% flowering, **DPI**=Days to pod Initiation, **DM**= Days to Maturity, **PH**= Plant Height, **PB**= No. of Primary Branches, **SB**= No. of Secondary Branches, **Pods PP**= Pods per plant, **Filled pods PP**= Filled pods per plant, **Seeds PP**= Seeds per plant, **Seeds per pod**= Seeds per pod, **Seed yield PP**= Seed yield per plant, **100 SW**= 100 Seed weight, **HI**= Harvest Index.

Genetic advance expressed as percentage of mean (GAM %):

For all the thirteen characters genetic advance as percentage of mean (GAM%) at normal and late sown conditions are presented in table 4 and 5. The trait no. of seeds per plant (66.1%) exhibited highest GAM % value followed by no. of filled pods per plant (66.66%), seed yield per plant (56.59%), no. of pods per plant (54.91%), no. of primary branches (34.9%), 100 seed weight (33.5%), no. of secondary branches (27.8%) and plant height (22.5%) at normal sown conditions. At late sown conditions high levels of GAM % values exhibited by no. of seeds per plant (70.36%), followed by no. of filled pods per plant (67.13%), seed yield per plant (65.5%), no. of pods per plant (62.51%), 100 seed weight (34.34%), no. of secondary branches (33.95%), no. of primary branches (29.13%), harvest index (24.36%), and plant height (23.42%). Moderate values of GAM % values are observed for harvest index (17.61%), days to 50% flowering (14.27%), and days to pod initiation (13.45%) at normal sown conditions. But at late sown conditions the characters like days to 50% flowering (16.15%), and days to pod initiation (14.08%) had shown moderate values of GAM %. Low values were observed for days to maturity (8.22%), and no. of seeds per pod (9.79%) at normal sown conditions. But at late sown conditions, the characters like days to maturity (9.36%), and no. of seeds per pod (6.68%) had shown low level of GAM%.

The characters like no. of seeds per plant, no. of filled pods per plant, seed yield per plant, no. of pods per plant, no. of primary branches, 100 seed weight, no. of secondary branches, and plant height had shown High heritability along with high genetic advance as percent mean GAM (%) at normal sown conditions, which determines the presence of additive gene action for these characters. So, the selection for these characters is beneficial in the breeding programmes and in late sown conditions the characters like no. of seeds per plant, no. of filled pods per plant, seed yield per plant, no. of pods per plant, no. of primary branches, 100 seed weight, no. of secondary branches, and plant height and harvest index had shown high heritability along with high genetic advance. So, it determines the presence of additive gene action for these characters. So, that selection for these characters is beneficial in the breeding programmes. The high heritability coupled with high genetic advance for these traits was also reported earlier by Goutam et al., [14] and Singh et al., [22] , Mohammad et al., [23] , Kishor et al., [16] . and high heritability along with high genetic advance for no of pods per plant , seed yield per plant and 100 seed weight were reported by Arora et al., [19], Puri et al., [2] and Babbar et al., [24].

It may be inferred from research on morphological variability that the characters no. of seeds per plant, no. of filled pods per plant, seed yield per plant, and no. of pods per plant at both normal and late sown conditions had showed high PCV, GCV, heritability, and genetic advance as a percent mean. So, it is demonstrating that the inheritance of these traits is mostly due to additive gene activity and these characters are important in breeding programmes.

4. CONCLUSION

The presence of genetic variability is considered important criteria for crop improvement. Based on the findings of this study, it is concluded that a high variability estimates was observed for all studied traits. For all studied characters, the PCV was larger than GCV, showing that the environment had an impact on expression of these characters. High heritability coupled with high GA (% mean) was observed for PH, PB, SB, Filled pods per plant , number of pods per plant, number of seeds per plant ,100 seed weight, and seed yield per plant. The high heritability coupled with high genetic advance indicated that these characters can be improved upon by selection since they were under control of additive gene effect. Therefore, it is important to interpret expected genetic advance in relation to both genetic variability and heritability for deciding the possibilities of improvement through selection.

Acknowledgement:

We are grateful to our beloved PJTSAU, for providing support financially, Seed Research and Technology Centre, and Institute of Biotechnology, Hyderabad for providing lab facilities and ICRISAT, Patancheru, for providing germplasm lines.

REFERENCES :

[1] Zwart, R. S., Thudi, M., Channale, S., Manchikatla, P. K., Varshney, R. K., & Thompson, J. P. (2019). Resistance to plant-parasitic nematodes in chickpea: current status and future perspectives. Frontiers in plant science, 10: 1-14.

[2] Ahmad, F., Gaur, P. M., & Croser, J. (2005). Chickpea (*Cicer arietinum L*.). In: Genetic resources, chromosome engineering, and crop improvement- grain legumes, 1: 187-217.

[3] Dixit, G. P., Srivastava, A. K., & Singh, N. P. (2019). Marching towards self-sufficiency in chickpea. Curr. Sci., 116(2): 239-42.

[4] Food & Agriculture Organization (FAO). (2019). FAOSTAT Statistical Database of the United Nation Food and Agriculture Organization (FAO) statistical division. Rome.

[5] Merga, B., & Alemu, N. (2019). Integrated weed management in chickpea (*Cicer arietinum* L.). Cogent Food & Agriculture, 5(1): 1-18.

[6] Gaur, A. K., Verma, S. K., & Panwar, R. K. (2020). Estimation of genetic variability and character association for development of selection criteria in pigeonpea [*Cajanus cajan* (L.) Millspaugh]. IJCS, 8(2): 391-394.

[7] Verma, S. K., Bisht, C., Gaur, A. K., & Chandra, D. (2018). Study on Some Genetic Parameters for Yield and Related Traits in Pigeonpea [*Cajanus cajan* (L.) Millspaugh] Genotypes. Chem. Sci. Rev. Lett., 7(25): 70-76.

[8] Pal, D., Verma, S. K., Panwar, R. K., Arora, A., & Gaur, A. (2018). Correlation and path analysis studies in advance lines of pigeonpea [*Cajanus cajan* (L.) Millspaugh] under different environments. International Journal of Current Microbiology and Applied Sciences, 7(4): 378-389.

[9] Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Genotypic and phenotypic correlations in soybeans and their implications in selection. Agronomy journal, 47(10): 477-483.

[10] Burton, G. W., & De Vane, E. H. (1953). Estimations of heritability in tall festca (*Festuca arundinacea*) from replicated clonal materials. Agronomy Journal, 45: 487-488.

[11] Sivasubramanian, S., & Menon, M. (1973). Heterosis and inbreeding depression in rice. Madras Agric. J., 60(7): 1139-1140.

[12] Hanson, C. H., Robinson, H. F., & Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza 1. Agronomy journal, 48(6): 268- 272.

[13] Robinson, H. F., Comstock, R. E., & Harvey, P. H. (1949). Estimates of heritability and the degree of dominance in corn. Agronomy journal.

[14] Gautam, A., Panwar, R.K., Verma, S.K., Arora, A., Gaur, A.K. and Chauhan, C. (2021). Assessment of Genetic Variability Parameters for Yield and its Components in Chickpea (Cicer arietinum L.). *Biological Forum* – An International Journal, 13(2): 651-655.

[15] Arora, Arora, R.N. and Kumar, K., 2018. Genetic variability studies for yield contributing traits in Kabuli chickpea (Cicer arietinum L.). Journal of Pharmacognosy and Phytochemistry, *7*(2), pp.2675-2677.

[16] Kishor, L., Swarup, I., Nehra, A., Kirar, G. and Jeeterwal, R. C., 2018 Genetic variability,heritability and genetic advance analysis in chickpea (*Cicer arietinum* L.), Int. J. Pure App. Biosci.6(4): 141-144.

[17] Pandey, A., Gupta, S. , Kumar, A., Thongbam, P. D. and Pattanayak, A. 2013. Genetic divergence, path coefficient and cluster analysis of chickpea (Cicer arietinum) cultivars, in the mid-altitudes of Meghalaya. Indian Journal of Agricultural Sciences. **83 (12):** 1300–1304.

[18] Zali, H., Farshadfar**,** E. and Sabaghpour**,** S.H. 2010. Genetic variability and interrelationships among agronomic traits in chickpea (*Cicer arietinum* L.) genotypes. Crop Breeding Journal*.* **1(2)**: 127-132.

[19] Puri, M. K., Johnson, P. L. and Sharma, R. N. 2013. Study of variability, diversity and association analysis of chickpea (*Cicer arietinum* L.) Germplasm under normal and late sown condition of chhattisgarh state. Trends in Biosciences*.* **6 (6):** 723-731.

[20] Mushtaq, M. A., Bajwa, M. M., and Saleem, M. 2013. Estimation of genetic variability and pathanalysis of grain yield and its components in chickpea (*Cicer arietinum* L.) International Journal of Scientific and Engineering Research 4(1): 2229-5518.

[21] Kumar, S., Suresh, B.G., Kumar, A and Lavanya, G.R. 2019. Genetic variability in chickpea (*Cicer arietinum* L.) under heat stress condition. Current Journal of Applied Science and Technology*.* 38(6): 1-10.

[22] Singh, B., Kumar, V., & Mishra, S. P. (2021). Genetic variability, path analysis and relationship among quantitative traits in chickpea (*Cicer arietinum* L.) genotypes. The pharma innovation journal, 10(5): 1564-1568.

[23] Mohammed, A., Tesso, B., Ojiewo, C. and Ahmed, S., 2019. Assessment of Genetic Variability and Heritability of Agronomic Traits of Ethiopian Chickpea (*Cicer arietinum* L.) Landraces. Black Sea Journal of Agriculture, *2*(1), pp.10-15.

[24] Babbar, A., Prakash, V., Prakash ,T. and Iquabal, M.A. 2012. Genetic variability of chickpea (*Cicer arietinum* L.) under late sown condition. Legume Research. **35(1)**: 1-7.

[25] Gautam A, Panwar RK, Verma SK, Arora A, Gaur AK, Chauhan C. Assessment of genetic variability parameters for yield and its components in chickpea (Cicer arietinum L.). InBiological Forum–An International Journal 2021 (Vol. 13, No. 2, pp. 651-655).