Original Research Article

Study of genetic variability and character association for yield and components traits in chickpea germplasm in Bundelkhand region (*Cicer arietinum* L.).

Abstract

Chickpea (*Cicer arietinum* L.) is a very important crop among the grain legume crops in India. It is grown in north India in the winter season on marginal and semi-marginal land as a commonly non-irrigated crop. Bundelkhand, a region in Uttar Pradesh, India, is notorious for its harsh climate, characterized by extreme heat and drought stress. Temperature fluctuate with highs reaching 50°C in summer and lows of 5°C in winter, exert substantial adverse effects on chickpea cultivation, impairing crop growth and yield and demand to have genetic resources used in breeding programs. The experiment aimed to characterise and evaluate 204 chickpea lines, including commercial varieties, to understand the magnitude of variability and the association of various yield parameters on the yield of chickpea based on 12 agro-morphological characters under Bundelkhand region. ANOVA shows that significant variation exists for most of the characteristics of chickpeas. Higher GCV and PCV were observed for plant population (GCV 24.92, PCV 31.22) followed by the number of secondary branches (GCV 21.61, PCV 26.55), number of pods per plant (GCV 12.92, PCV 18.47), seed yield per plant (GCV 11.39, PCV 21.98) and biological yield per plant (GCV 11.68, PCV 20.37), revealing that the environment plays a positive role in the expression of these characters. High heritability was found by 100 seed weight (96.41) followed by seed yield per plant (84.11) and number of pods per plant (66.26) and a high degree of genetic advance was found in the number of pods per plant (26.24) followed by biological and seed yield per plant (15.25 and 6.92). High heritability coupled with high genetic advance was found in seed yield per plant, followed by biological yield per plant, indicating selection could be rewarding in proper breeding programs. Correlation and path studies showed that biological yield per plant (r-0.91), number of pods per plant(r-0.680), number of secondary branches per plant (r-0.46), number of seeds per pod (r-0.32) and 100 seed weight (0.29) turned out to be the main components for seed yield per plant in chickpea, stipulating that these characters could be desirable selection parameter.

Introduction

Chickpea is a self-pollinated crop, and cross-pollination is a rare event with only 0-1 % of cross-pollination [1,2]. Chickpea (*Cicer arietinum*) is diploid species with 2n = 14, belongs to the Fabaceae family, and is considered the first most crucial pulse in the world is widely grown in many subtropical and warm temperate regions. It is usually grown as a rainfed cool-weather crop or as a dry climate crop in semi-arid regions.Chickpea (*Cicerarietinum*L.) is a highly nutritious crop containing 24% protein, 60-65% carbohydrate, 6% fat and also good source of many minerals and vitamins [3] and provides nutritious food for an expanding world population and will become increasingly important with climate change. The nutritional value of chickpea in terms of nutrition and body health has been recently emphasized frequently by nutritionists in health and food area in many countries. In Asia, chickpea is commonly used as dal, flour, salads, soups and stews, curry, and other meal products like channa while hummus is widely popular in many parts of the world, especially in the middle east and north Africa. The largest global producers of chickpea seed are India, Australia, and Myanmar, contributing approximately 78% of world production [4]. It is the food basket for the growing population in the country, which contains high protein. Bundelkhand region in Uttar Pradesh state of India is known for extreme heat and drought stress, which severely affect the growth, development, and yield of wheat crop. This region frequently experiences extreme temperature, usually 50°C during summer and 5°C in the winter season [5]. Agriculture in Bundelkhand is rainfed, diverse, complex, under-invested, risky and vulnerable. In addition, extreme weather conditions, like droughts, short-term rain and flooding in fields add to the uncertainties and seasonal migrations. The scarcity of water in the semi-arid region, with poor soil and low productivity further aggravates the problem of food security [6]. The knowledge of heritability and genetic advance is also essential to ascertain whether observed variability is heritable or non-heritable for the selection of component traits for yield improvement. Genetic characterization of the germplasm helpsto determine the relationship among the accessions and to estimate genetic diversity, which can be determined by using morphological parameters [7].

Materials and methods

A total of 204 chickpea accessions were obtained from the Division of Genetics, ICAR-IARI, New Delhi and ICRISAT, Patencheru, Hyderabad, along with released chickpea varieties. Four chickpea accessions, including two varieties, were taken as a check for this experiment **(Appendix I).** The field trial was conducted at the University Seed and Research Farm, D Block, RLBCAU, Jhansi (25.07˚ to 25.57˚ North latitude, 78.10˚ to 79.25˚ East longitudes and at an altitude of 284 meters above the mean sea level) in the Bundelkhand region of Uttar Pradesh during rabi 2019–20. The design of the experiment was a randomized complete augmented block design with a total of 5 homogenous blocks, and each block contained 44 test accessions, including 4 check accessions (ICC 1710, ICC 7867, RVG 203, and JAKI 9218), and replication and randomization of checks were done across the blocks.

Layout

The trial was conducted during Rabi 2019-20 in an augmented block design, where each entry was planted in 2 m rows with plant-to-plant spacing of 10 cm and row-to-row spacing of 60 cm. Approximately 20 seeds were planted in each row for each treatment. All normal agronomic practices were performed during the entire period of crop growth to ensure a good plant stand.

Data Sampling

To record the observations, five randomly chosen competitive plants were selected from a single row of each accession and the observation was recorded on a whole-row basis for DF and DM, whereas on the composite sample basis, SW and HI were also calculated. The observations were recorded as per the protection of plant varieties and farmers' rights authority (PPV & FRA) DUS guidelines (2007) for chickpea[8].

Statistical analysis

Statistical analyses of the data were carried out for both qualitative and quantitative traits, and frequency distribution was performed for each qualitative trait(s) using raw mean data. Analysis of variance (ANOVA)(s) for the quantitative character(s) was carried out according to the standard statistical procedure for Augmented Randomized Complete Block Design (Augmented Design II)[9]. Genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), broad sense heritability (h2) and genetic advance over a mean (GAM) in per cent were computed for quantitative traits by methods[10, 11] and [12] respectively and correlation and path coefficient analysis by using statistical software, Windostat ver. 8.0.

Phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) were computed according to the method suggested by [10]. These values were categorized as high (>20 %), moderate (10-20 %), and low (60 %).

Results and discussion

The analysis of Variance (ANOVA) for quantitative characters demonstrated that the set of chickpea germplasm accessions was statistically significantly different indicating that the experimental plant material had considerable genetic diversity. This suggests that there was an adequate amount of genetic variability in the experimental material for all 12 characters, viz. days to 50 per cent flowering, days to maturity, plant population, number of primary branches, number of secondary branches per pod per plant, number of seeds per pod, plant height,100 seed weight, and biological yield per plant. Seed yield per plant and harvest index evaluated in the current study. The variation due to blocks was found to be non-significant at both 0.005 and 0.001 levels of significance for all studied characters. The differences among the four checks were found to be highly significant for days to 50 % flowering, days to maturity, plant population, number of primary branches per plant, number of seeds per pod, plant height, 100 seed weight, biological yield per plant, and seed yield per plant, and significant for days to 50% flowering and number of secondary branches per plant respectively. For other characteristics, the numbers of pods per plant and harvest index were found to be non-significant. Similar results were also observed by [13,14].

Variability studies

The findings of GCV and PCV showed a large amount of variability in the available chickpea germplasm accessions for all characteristics (Table 2). The highest estimates of GCV (24.92%) and PCV (31.22%) were reported for plant populations, followed by the number of secondary branches per plant GCV, 21.61%; PCV, 26.55%). Similar results have been reported by [15, 16]. High estimates of PCV obtained in the number of pods per plant (24.36), followed

by harvest index (22.65), seed yield per plant (21.98), and biological yield per plant (20.31) showed that apparent variation is not only due to genetic factors but also by the environment, which significantly affects the expression of these characters. The moderate genotypic coefficient of variation found in seed yield per plant (18.68) followed by 100 seed weight (17.77), number of primary branches per plant (17.20), harvest index (14.34), plant height (13.71), number of pods per plant (12.92), and seed yield per plant (11.39) showed that a reasonable amount of genetic variation was present for most of the

Table 1 Analysis of variance for 12 quantitative characters of chickpea.

Source of variation	d.f	Days to 50% flowering (DF)	Days to maturity (DM)	Plant population(PP)	Number of primary branches per plant	Number of secondary branches per plant	Number of pods per plant	Number of seeds per pods	Plant height (cm)	100 seed weight (g)	Biological yield per plant (g)	Seed yield per plant (g)	Harvest index (%)
		Mean sum of square (MSS)											
Block	4	4.575000	5.075	3.125	.643	2.430	139.896	0.041	23.276	0.076	13.376	2.993	.000273
Entries	203	37.807**	20.374 *	9.617*	1.222*	28.39**	1349.21**	0.239**	94.007*	46.551**	360.41**	69.66**	0.005**
Check	3	59.40*	90.32 **	60.05**	6.70 **	30.39*	241.1	0.779**	428.21**	149.939**	379.879**	84.35**	0.004
Varieties	199	36.604**	19.409 *	8.48*	1.146	27.995**	1363.476**	0.231**	89.384*	44.622**	356.265**	69.32**	0.005**
Checks vs. Varieties	1	212.658**	2.49	84.046**	0.006	100.964**	1834.549*	0.017	11.636	120.115**	1126.392**	95.23**	0.008
Error	12	6.608	4.109	2.925	0.3199	4.759	124.703	0.0412	21.335	0.344	17.229	2.536	0.001

characters, and simultaneous estimates of PCV showed the effect of environment on the total variation. The small differences between GCV (13.71) and PCV (13.96) for plant height and 100 seed weight (GCV 17.77, PCV 19.87) showed that these characteristics were least influenced by the environment. These results were also supported by the findings[7, 13, 17].

The highest heritability in the broad sense was found for 100 seed weight (96.41 %), indicating the low effects of genotypic variance on total variance, and leading to a high heritable proportion (92 %) which shows the importance of additive gene action in the expression of this character. Other characteristics like seed yield per plant, biological yield per plant, and number of pods per plant, reported high heritability in a broad sense, with values of 84.11 %, 79.94 %, and 66.26%, respectively. A moderate broad-sense heritability value was observed for the number of secondary branches per plant (49.83 %), followed by days to 50 % flowering (49.00 %), number of seeds per pod (48.91 %), days to maturity (44. 00 %), harvest index (42.30 %), and plant height (40.2). A high genetic advance was reported for the number of pods per plant (26.24%), followed by biological yield per plant (15.26 %) and seed yield per plant (6.92 %) whereas the lowest was reported for the number of seeds per pod (0.53 %) revealed that selection may play a crucial role in improvement of characters with high genetic advance. Similar findings were recorded by[18][13] [19] [20][16].

Table 2 Estimates of variability parameters for 12 quantitative traits in chickpea

Characters	Range	Mean	Vp	Vg	PCV (%)	GCV (%)	Broad sense heritability (%)	Genetic Advance	Genetic Advance as % of mean
DF	68.1-96.6	85.75	12.85	6.24	4.17	2.90	49.70	3.59	4.17
DM	115.6-137.55	127.49	7.36	3.25	2.13	1.41	44.40	2.47	1.94
PP	4-19.5	9.2	4.00	1.08	31.22	24.92	26.88	1.11	12.17
NPB	1.075-9.5	3.38	0.50	0.18	24.36	17.20	36.06	0.53	15.64
NSB	2.73-33.035	15.11	9.48	4.73	26.55	21.61	49.83	3.16	25.01
NPPP	18.49-206.565	74.69	369.6	244.9	18.47	12.92	66.26	26.24	36.23
NS	0.88-3.03	1.51	0.08	0.04	10.79	6.87	48.91	0.29	18.61
PH	19.05-85.05	55.84	35.87	14.53	13.96	13.71	40.52	5.00	9.01
100 SW	10.11-41.139	22.36	9.59	9.24	19.87	17.77	96.41	6.15	27.73
BYPP	16.295-98.795	52.37	85.86	68.64	20.37	18.68	79.94	15.26	32.73
SYPP	7.485-41.26	19.06	15.96	13.42	21.98	11.39	84.11	6.92	35.29
HI	14.5-	0.37			22.05	14.34	42.30	0.65	19.21

	52.4								

Table 3. Correlation matrix of 12 different characters of chickpea

Correlation matrix	50% DTF	DTM	PP	NPB	NSB	NPPP	NSPP	PH	100SW	BYPP	SYPP
50% DTF	1	0.85***	0.024	0.060	-0.022	-0.061	0.11	-0.018	0.048	0.094	0.141
DTM		1	-0.071	-0.104	-0.104	-0.089	0.037	0.106	0.152	0.096	0.127
PP			1	0.21	0.018	0.014	0.14	-0.04	-0.22	0.022	0.01
NPB				1	0.494***	0.343*	0.182	0.083	-0.152	0.297*	0.33*
NSB					1	0.67***	0.062	0.08	-0.121	0.44**	0.46**
NPPP						1	0.087	0.222	-0.038	0.636***	0.69***
NSPP							1	-0.05	-0.18	0.19	0.315*
PH								1	0.234	0.33*	0.32*
100 SW									1	0.31*	0.29*
BYPP										1	0.91***
SYPP											1

50% DTF; days to 50 % flowering, DTM; days to 50 % maturity, PP ; plant population per plot, NPB; Number of primary branches per plant, NSB; number of secondary branches per plant, NPPP; number of pods per plant, NSPP; number of seeds per pod, PH; plant height, 100SW ; 100 seed weights, BYPP ; biological yield per plant, SYPP; seed yield per plant.

Table 4 **Direct and indirect effect on seed yield of 12 different characters of chickpea**

Character	50% DTF	DTM	PP	NPB	NSB	NPPP	NSPP	PH	100SW	BYPP
50% DTF	**0.0685**	0.0581	0.0016	0.0041	-0.0018	-0.0042	0.0071	-0.0006	0.0033	0.0064
DTM	-0.0006	**-0.0007**	-0.0000	-0.0000	0.0001	0.0001	0.0000	-0.0001	-0.0001	-0.0001
PP	-0.0003	0.0010	**-0.0147**	-0.0031	-0.0003	-0.0002	-0.0020	0.0006	0.0032	-0.0003
NPB	0.0022	-0.0014	0.0077	**0.0370**	0.0182	0.0127	0.0067	0.0031	-0.0056	0.0110
NSB	0.0006	0.0024	-0.0004	-0.0115	**-0.0232**	-0.0156	-0.0014	-0.0018	0.0028	-0.0102
NPPP	-0.0154	-0.0223	0.0034	0.0867	0.1695	**0.2530**	0.0220	0.0560	-0.0096	0.1609
NSPP	0.0185	0.0065	0.0249	0.0325	0.0111	0.0155	**0.1790**	-0.0090	-0.0327	0.0342
PH	-0.0002	0.0023	-0.0008	0.0018	0.0017	0.0048	-0.0011	**0.0217**	0.0051	0.0071
100 SW	0.0057	0.0181	-0.0259	-0.0182	-0.0144	-0.0045	-0.0219	0.0280	**0.1196**	0.0361
BYPP	0.0618	0.0628	0.0139	0.1957	0.2894	0.4191	0.1259	0.2173	0.1988	**0.6591**

Interrelationship studies

Character association refers to the degree of statistical relationship between different traits or characteristics of a crop. This is essential for crop improvement because it helps plant breeders identify which traits tend to co-occur or influence each other. Understanding character associations aids in the selection of key traits for simultaneous improvement, optimizing breeding strategies, and developing crop varieties with enhanced performance and adaptability. Character association studies revealed that seed yield per plant was highly influenced by independent characteristics, mainly biological yield per plant, number of pods per plant, number of secondary branches and 100 seed weight (Tables 3 and 4).

Highly significant positive correlations of seed yield per plant were found with biological yield per plant (0.9042), number of pods per plant (0.6807) and number of secondary branches per plant (0.4502) with number of primary branches per plant, number of seeds per pod, plant height, and 100 seed weight also showed significant correlations for seed yield per plant. Non-significant negative correlations were also found between days to 50% flowering and days to maturity with seed yield. The path analysis revealed the effect of each character on seed yield by using correlation coefficients and revealed that biological yield per plant had the highest direct effect (0.6591) on seed yield per plant, followed by the number of pods per plant (0.2530), number of seeds per pod(0.1790) and 100 seed weight (0.1196). The results of the correlation coefficient matched those reported by [7] and [14][21].

Interrelationship studies among quantitative characters in chickpea genotypes disclosed that characters such as biological yield per plant, number of pods per plant, number of secondary branches per plant, number of primary branches per plant, seeds per pod and 100 seed weight were the main components and affecting the seed yield per plant. To achieve maximum yield per plant the plant should have a greater number of pods per plant, secondary branches per plant, biological yield per plant, and 100 seed weights.

The correlation coefficients among these 10 quantitative characters with seed yield were divided into their direct and indirect effects by studying path coefficient analysis (Table 4). The highest

direct and indirect effect on seed yield per plant was exhibited by the biological yield per plant followed by the number of pods per plant and the number of seeds per pod, 100 seed weight indicating that these characteristics are major influencing factors on seed yield in chickpeas. Biological yield per plant, number of pods per plant, and number of seeds per pod, as well as 100 seed weight, show a high, moderate, and direct effect on seed yield per plant in chickpeas. Thus, these characteristics turned out to be the significant components of seed yield per plant. The high magnitude of biological yield was reported by [22] has also reported a high direct effect on seed yield.

The number of pods per plant exhibited a moderate direct influence on seed yield per plant and contributed indirectly through biological yield per plant and number of seeds per pod, establishing a significant and positive association with seed yield. Strong correlation and direct effects suggest that enhancing chickpea yield is achievable by improving these traits. Similarly, the high positive correlation of seeds per pod with most traits underscores its importance as a yield-contributing factor. These findings affirm the potential for yield enhancement by manipulating these attributes in the studied genotypes. Furthermore, seeds per pod and 100 seed weight displayed a moderate positive direct effect on seed yield per plant. While days to 50 per cent flowering, the number of primary branches per plant, and plant height exhibited a positive direct influence on seed yield, their effects were minimal. The positive and indirect impact of secondary branches per plant, mediated by biological yield per plant and number of pods per plant, suggests that selecting these traits in chickpea breeding programs can improve seed yield. However, negative indirect effects on most other traits indicate their limited potential for enhancing seed yield in chickpea. The similar finding for character association by [23, 14, 21, 24, 25].

Conclusions

The diverse and interconnected nature of chickpea accessions in this study underscores their potential as valuable parents for hybridization programs. Notably, these accessions exhibited a substantial degree of variability and association across the various traits examined. The prevalence of a higher phenotypic coefficient of variation (PCV) than the genotypic coefficient of variation (GCV) for all traits suggests the influence of environmental factors on trait expression. However, this environmental influence was relatively minor across the spectrum of traits, indicating relative stability. Among the traits, the mobility of traits such as the number of pods per plant, plant height, harvest index, seed yield per plant, and 100 seed weight was evident among chickpea accessions. To enhance seed yield, it is imperative to concentrate efforts on traits directly or indirectly, and the relationship between yield and yield-contributing traits through correlation and path coefficient analyses identified key factors. These traits exhibited significant positive associations and highly positive direct effects on seed yield per plant. In conclusion, our study not only highlights the genetic diversity and interplay of traits within chickpea accessions but also provides a clear direction for breeders. By prioritizing the enhancement of traits closely linked to seed yield, particularly the number of pods per plant, secondary branches, and biological yield per plant, we can chart a course toward achieving improved chickpea varieties with greater resilience and productivity.

References

[1] Saxena, M. C., & Singh, K. B. (1987). The chickpea [Cicer arietinum]. Commonwealth Agricultural Bureaux International. 1987.

[2] Smithson, J.B., J.A. Thompson & R.J. Summerfield, 1985. Chickpea (Cicer arietinum L.). In: R.J. Summerfield & E.H. Roberts (Eds), Grain Legume Crops. London, U.K.: Collins.

[3] Latham, M. C. (2002). Human nutrition in the developing world. Chinese Academy of Agricultural Sciences/Scientific and Technology Documentation Centre

[4] Food and Agriculture Organization (FAO). (2023). FAOSTAT Statistical Database of the United Nation Food and Agriculture Organization (FAO) statistical division. Rome.

[5] Kumar S, Kumar H, Gupta V, Kumar A, Singh CM, Kumar M, Singh AK, Panwar GS, Kumar S, Singh AK & Kumar R (2023) Capturing agro-morphological variability for tolerance to terminal heat and combined heat–drought stress in landraces and elite cultivar collection of wheat. Front. Plant Sci. 14:1136455. doi: 10.3389/fpls.2023.1136455

[6] Kumar, A., Singh, A., Arya, M., Bhanu, A.N., Jaiswal, A., Kumar, S. and Chaturvedi, S. K. 2023. Screening of chickpea (Cicer arietinum L.) germplasm accession against post-emergence herbicide imazethapyr. Journal of Food legumes, 36(2&3):136-142.

[7] Meena, V.K., Verma, P., Tak, Y. & Meena, D. (2021). Genetic Variability, Correlation and Path coefficient Studies in Chickpea (Cicer arietinum L.) Genotypes in South Eastern Rajasthan. Biological Forum – An International Journal, 13(3a): 93-98.

[8] Guidelines for the conduct of test for distinctiveness, uniformity and stability on chickpea (Cicerairetinum L.) (2007). Publ. by protection of plant varieties and farmer's rights authority (PRA & FRA). Reproduced from Plant Variety - J. of India

[9] Federer, W. T. (1961). Augmented designs with one-way elimination of heterogeneity. Biometrics, 17(3), 447-473.

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

[11] Robinson, H. F., Comstock, R. E., & Harvey, P. H. (1955). Genetic variances in open pollinated varieties of corn. Genetics, 40(1), 45.

[12] Johnson HW, Robinson HE & Comstock RE 1955. Estimate of genetic and environemental variability in soybean. Agron. J. 47: 314-318.

[13] Gautam, A., Panwar, R. K., Verma, S. K., Arora, A., Gaur, A. K., & Chauhan, C. (2021). Assessment of genetic variability parameters for yield and its components in chickpea (Cicer arietinum L.). In Biological Forum–An International Journal (Vol. 13, No. 2, pp. 651-655).

[14] Gediya, L. N., Patel, D. A., Kumar, S., Kumar, D., Parmar, D. J., & Patel, S. S. (2019). Phenotypic variability, path analysis and molecular diversity analysis in chickpea (Cicer arietinum L.). Vegetos, 32(2), 167–180.

[15] Dehal, I. B., Kalia, R., & Kumar, B. (2016). Genetic estimates and path coefficient analysis in chickpea (Cicer arietinum L.) under normal and late sown environments. Legume Research-An International Journal, 39(4), 510-516.

[16] Thakur, T. S., Johnson, P. L., & Nanda, H. C. (2015). Evaluation of desi chickpea (Cicer arietinum l.) genotypes for yield and yield contributing traits under rainfed rice-based cropping ecosystem of chhattisgarh. Journal of Food Legumes, 28(2), 21-26.

[17] Babbar, A., and Tiwari, A. (2018). Assessment of Genetic Variability & Yield Stability in Chickpea Genotypes under Diverse Environments. International Journal of Current Microbiology and Applied Sciences, 7(12), 3544–3554.

[18] Chaudhary, H., Jaiswal, J.P., Kumar, A. and Joshi S. 2022. Determination of genetic variability and diversity in bread wheat for yield and and yield contributing traits. International Journal of Plant and Soil Science, 34(19):16-23.

[19] Yadav, P., Tripathi, D. K., Khan, K. K., & Yadav, A. K. (2015). Dissection of genetic variability and heritability estimates in chickpea (Cicer arietinum L.) under late sown condition. Forage Research, 37(4): 1- 10.

[20] Aarif, M., Rastogi, N. K., Johnson, P. L., &Chandrakar, P. K. (2014). Genetic analysis of seed yield and its attributing traits in kabuli chickpea (*Cicer arietinum* L.). *Journal of Food Legumes*, 27(1), 24-27.

[21] Bhanu A. N., Singh M.N., Tharu R. & S.K. Saroj. (2017) Genetic variability, correlation and path coefficient analysis for quantitative traits in chickpea genotypes. Indian Journal

of Agricultural Research. 51(5):425-430.

[22] Agrawal, T., Kumar, A., Kumar, S., Kumar, A., Ranjan Kumar, R., Kumar, S., & Singh, P. K. (2018). Correlation and Path Coefficient Analysis for Grain Yield and Yield Components in Chickpea (*Cicer arietinum* L.) under Normal and Late Sown Conditions of Bihar, India. *International Journal of Current Microbiology and Applied Sciences*, 7(2), 1633– 1642.

[23] Thapa, R. S., Singh, T., Kumar, A., Kumar, H., & Pratap, D. (2022). Genetic divergence, variability and character association analysis in chickpea (Cicer arietinum L.) genotypes under normal and late sown conditions. *Electronic Journal of Plant Breeding*, *13*(2), 616-623.

[24] Jivani, J. V., Mehta, D. R., Vaddoria, M. A., & Raval, L. (2013). Correlation and path coefficient analysis in chickpea (Cicer arietinum L.). Electronic Journal of Plant Breeding, 4(2), 1167-1170.

[25] Kumar, A., Babu, G. S., & Lavanya, G. R. (2012). Character association and path analysis in early segregating population in chickpea (Cicer arietinum L.). Legume Research-An International Journal, 35(4), 337-340.