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## STUDIES ON GENETIC VARIABILITY, TRAIT ASSOCIATION, AND PATH ANALYSIS FOR SEED YIELD AND YIELD CONTRIBUTING TRAITS IN CHICKPEA (*CICER ARIETINUM* L.) MINI CORE GERMPLASM

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### ABSTRACT

Two hundred and eighty chickpea mini core germplasm including two checks (JG-11 and SA-1) were sown on 6<sup>th</sup> October, 2021 in Augmented Block Design (ABD) with one replication to evaluate variability parameters. Burton and De Vane provided the equation for the phenotypic and genotypic co-efficient of variability (PCV & GCV) (1953). Whereas, the equations for Broad sense heritability ( $h^2$ ) by Hanson (1956), genetic advance by Johnson (1955), correlation co-efficient equated by Singh and Chaudhary (1977), Path coefficients scale suggested by Lenka and Mishra, (1973). The software package INDOSTAT version 8.5 was used to analyse the statistical data. For every character under study, all genotypes showed high levels of variability. The characters with the peak values of phenotypic co-efficient of variation, and genotypic co-efficient of variation were seed yield/plant (44.56% and 37.18%) and 100 seed-weight (40.63% and 38.63%), indicating higher potential for selection to enhance these characters. For the characters viz., number of days to 50 percent flowering (86.59% and 23.12%), plant height (65.04% and 22.41%), 100 seed-weight (91.11% and 76.30%), and seed yield/plant (69.61% and 63.90%), high heritability ( $h^2$ ) along with high genetic advance as a percentage of mean (GAM) were observed, indicating that these traits are controlled by additive gene action. Out of five characters, seed yield/plant showed a significant and positive correlation with 100 seed-weight, indicating that selection pressure for this character will increase yield output in chickpea, according to correlation and path co-efficient analysis for seed yield/plant and its components. The findings suggested that in order to manipulate yield output in chickpea, greater attention should be placed on 100 seed weight.

**Keywords** : Chickpea, Correlation, Genetic advance, Heritability, Variability

### Introduction

Chickpea (*Cicer arietinum* L.), also known as Gram, Bengal gram, garbanzo bean, Chana, or Egyptian pea, is one of the first grain legumes domesticated by humans in the ancient world (Van der Maesen, 1984). It belongs to the sub-family *Papilionaceae* of the family *Leguminosae* (Bentham and Hooker, 1970). The chickpea is classified into two broad categories, first category comprises small, brown angular seeded *desi* type with high fiber content and cultivated in Southern Asia and Africa. Whereas, the second category comprises *Kabuli* a large seeded type with less fiber content and cultivated in the Mediterranean region (Cubero, 1975). Chickpea are massive storehouses of protein, vitamins, rich fiber, unsaturated fatty acid and  $\beta$ -carotene (Jukanti *et al.*, 2012). It has got exceptional importance in the Indian diet because it can be consumed in various ways. Chickpea split seeds are utilized in the form of chana dal, parched, fried, roasted and boiled as a snack food, sweet and condiments. The seeds are processed into besan flour, which is then used to make a variety of meals including pakora, laddu, etc.

Oxalic and malic acids found in the exudate from leaves have therapeutic significance and are used for gastrointestinal problems, stomach discomfort, blood cleansing, etc. The scurvy illness is prevented by the germination of the seeds.

Chickpea is a wintertime legume crop, India being a global leader in chickpea cultivation with a land area of 9.70 Mha, producing a yield of 11.90 MT, and a productivity of 1142 kg/ha (Anon, 2021). In India, Karnataka stands fifth in cultivation with 0.86 million ha producing a yield of 0.67 MT and productivity of 782 kg/ha (Anon, 2021). In Karnataka, Kalaburagi occupies first position in area, production and productivity followed by Bijapur, Bidar, Gadag and Dharwad districts. Even though the total chickpea production constitutes nearly 45.53% of total pulse production, still the demands are met by imports. So, there's a larger scope to increase both production and productivity by evaluating new germplasm. For plant breeders variability serves an important indices, because it provides a source of variance and a raw material for yield enhancement (Gaur *et al.*, 2020 and Verma *et al.*, 2018). Specifically, the level of genetic variability

present in breeding material has a significant impact on the quantity of advancement in crop improvement as a result of selection. Its expression is also influenced by the prevailing environmental conditions. Hence, to fulfil the growing demand for varietal improvement and increased productivity, it is critical to collect, analyse, and record all available variability in genotypes. Knowledge and experience of variability is a prerequisite for breeder in any crop upgrading programs. Both variability and heritability are crucial factors that can aid breeders at various phases of crop improvement. Seed yield is a dynamic variable that is affected by a variety of factors hence, it would be beneficial to intend enhanced genotypes by identifying vital characters and their interrelationships. As a result of this, selection based on yield component traits can result in a significant raise in yield. Correlation collective with path co-efficient analysis is the finest approach to determine inter-relationship among essential yield components. These strategies were engaged in breeding programme to take full advantage of the yield prospective of chickpeas in order to enhance efficiency and produce.

### Material and Methods

The experimental trail was carried out at Zonal Agricultural Research Station (ZARS), Kalaburagi, which is situated in North-Eastern Dry Zone (Zone-2) of Karnataka between latitude (N) 17° 36' and longitude (E) 76° 81' during Rabi 2020-21. Two hundred and eighty genotypes of chickpea were sown on 6<sup>th</sup> October, 2021 in a Augmented Block Design (ABD) with one replication. The germplasms were accommodated in 13 blocks, checks were repeated randomly in each block. Each entry was planted in one row of 4-meter length having a spacing of 0.3 m in between rows and a spacing of 0.1 m in between plants respectively. The data was noted for five polygenic traits *viz.*, days to 50 per cent flowering (No. of days), plant height (cm), days to maturity (No. of days), 100 seed weight (grams) and seed yield/plant (grams). Burton and De Vane (1953) provided the equation for the phenotypic and genotypic co-efficient of variability (PCV and GCV). Whereas, the equations for broad sense heritability ( $h^2$ ) by Hansen (1956), genetic advance by Johnson (1955), correlation co-efficient equated by Singh and Chaudhary (1977) and path coefficients scale suggested by Lenka and Mishra, (1973). The software package INDOSTAT version 8.5 was used to analyse the statistical data.

### Result and Discussion

Analysis of variance (ANOVA) is an important tool to quantify the variation present among the germplasm. The analysis (ANOVA) revealed the presence of significant variation among 280 genotypes including checks (JG-11 and SA-1) for the five polygenic traits (Table 1). The results show ample scope of incorporating the promising genotypes in the breeding programmes aimed for improving yield output and its contributing characters.

#### Estimation of variability parameters

An insight into the magnitude of variability that a crop possesses is of outmost importance as it provides the foundation for effective selection. Values of Phenotypic Co-efficient of Variability (PCV) were slightly greater than genotypic Co-efficient of Variability (GCV), according to estimates of PCV and GCV which denotes a slight influence

of environment factors on the trait expression (Table 2 and Fig. 1). Similar outcomes have already been noted by Nizama *et al.* (2013), Munde *et al.* (2018), Mayuribeian *et al.* (2019), Verma *et al.* (2020), Karthikeyan *et al.* (2022). These findings imply that selection can be efficient when phenotypic and genotypic values are equally likely. High per cent values of PCV and GCV were found for 100 seed-weight (40.63 and 38.63) and plant-level seed yield (44.56 and 37.18). The presence of significant variance for these characters under examination, as shown by the high value of GCV, allowed for character selection. It is not possible to determine the extent of heritable variation using only the genotypic co-efficient of variation. Thus, understanding a character's heritability assists plant breeders in forecasting the genetic advance for any polygenic trait and assisting in the necessary selection process. Burton (1952) proposed that the genotypic co-efficient of variation, combined with a heritability estimate, would provide the best insight for selection.

The traits that displayed highest heritability along with high Genetic Advance as percentage of Mean (GAM) were days to 50 percentage flowering (86.59 and 23.12), plant height (65.04 and 22.41), 100 seed-weight (91.11 and 76.30) and seed yield/plant (69.61 and 63.90). Johnson *et al.* (1955) proposed that the heritability ( $h^2$ ) along with high Genetic Advance as percentage of Mean (GAM) are more valuable than the heritability ( $h^2$ ) alone in forecasting efficient selection process. Characters with high heritability and GAM are little affected by the surrounding environment, and such traits are attributed to the predominance of additive gene action, and selection pressure could be profitably applied on these characters to improve yield outcome. These results are consistent with those of Roy *et al.* (2013), Banik *et al.* (2018), Barad and Javia (2018) Verma *et al.* (2020), Karthikeyan *et al.* (2022).

#### Association of seed yield/plant with the contributing characters

At phenotypic level, seed yield/plant displayed positive significant association with 100 seed-weight (0.6792) and significant negative association with days to 50 percent flowering (-0.2533) and days to maturity (-0.1224) (Table 3). It showed a positive and insignificant association with plant height (0.0907). The negative association of days to maturity with the seed yield/plant is important when the goal of plant breeder is to develop a short duration variety. At genotypic level, seed yield/plant had a highly significant and positive correlation with 100 seed-weight (0.7610) and plant height (0.1484). Whereas, it showed significant and negative correlation with the days to 50 percent flowering (-0.2575) and days to maturity (-0.2804). Shara *et al.* (2019) and Tengse *et al.* discovered a positive significant correlation between seed yield/plant and 100 seed-weight at both the genotypic and phenotypic levels.

#### Path coefficient analysis

The magnitude of direct effect on seed yield/per plant was explained according to the scale mentioned by Lenka and Mishra (1973). At phenotypic level, the character 100 seed-weight (0.6749) displayed a high degree of positive direct effect on seed yield/plant (Table 4 and Fig. 2), followed by days to maturity (0.0712). The high degree of positive direct effect of 100 seed weight on seed yield/plant indicated the true inter-relationship of this character which in

turn aid the plant breeder in enhancement of seed yield. The traits such as days to 50 per cent flowering (-0.1054) and plant height (-0.0431) were showed high magnitude of negative direct effects on seed yield/plant. The outcomes are in complement with the findings of Padmavathi *et al.* (2013), Samyuktha *et al.* (2017), Kumar *et al.* (2018). Kumar *et al.* (2019) noted positive direct association of 100 seed-weight and negative direct effect of days to 50 percent flowering on seed yield/plant. In contrast, Singh *et al.* (2017) observed positive direct contribution of days to maturity on seed yield/plant. Based on findings of the investigation we

could draw the conclusion that most desirable plant type in chickpea should possess higher 100 seed weight.

### Conclusion

The current study concluded that seed yield/plant and 100-seed weight exhibited a high degree of genetic advance expressed as a percentage of mean, along with high heritability ( $h^2$ ) values and greater genotypic and phenotypic co-efficient of variation. It advocates that additive gene action was at work for these characteristics. As a result, phenotypic selection for these traits would be the most effective.

**Table 1 :** Analysis of variance for seed yield/plant and its contributing traits of chickpea germplasm lines

Source of variation	df	Days to 50 per cent flowering	Days to maturity	Plant height	100 seed -weight	Seed yield/plant
Block (Ignoring treatments)	12	213.721***	634.293***	65.063*	34.769***	596.924***
Treatment (eliminating blocks)	281	44.416***	49.200**	57.907*	3.603*	42.164***
Checks	1	252.346***	133.885**	286.913**	1.858	63.711**
Checks + var vs var	280	43.673***	48.898**	57.089*	3.610*	42.087***
Block (Eliminating check + var.)	12	10.124	38.852*	14.012	2.485	2.514
Entries (Ignoring blocks)	281	53.110***	74.628***	60.087*	4.982**	67.548***
Varieties	279	50.038***	74.350***	53.940*	4.971**	67.758***
Check vs varieties	1	711.072***	93.032**	1548.416***	11.071**	12.808
Error	12	6.427	12.879	18.261	1.459	5.488

\* = Significant at P = 0.05, \*\* = Significant at P = 0.01, \*\*\* = Significant at P = 0.001 probability levels

**Table 2 :** Variability parameters for seed yield/plant and its contributing traits in 280 germplasm lines of chickpea

Sl. No.	Characters	Range		Mean	Co-efficient of variation (%)		$h^2$ bs (%)	GA (%)	GAM (%)
		Min	Max		GCV	PCV			
I	Days to 50 per cent flowering	34	79	53.40	12.06	12.96	86.59	12.35	23.12
II	Days to maturity	84	130	101.08	7.59	8.38	82.10	14.34	14.18
III	Plant height (cm)	24.66	66	43.10	13.35	16.62	65.04	9.68	22.41
IV	Seed yield/plant(g)	2	13.7	4.923	37.18	44.56	69.61	3.45	63.90
V	100 seed-weight (g)	4.8	56.8	19.94	38.63	40.63	91.11	15.18	76.30

Where,  $h^2$  bs (%) = heritability in broad sense

GCV (%) = Genotypic Co-efficient of variance

GA = Genetic advance

PCV (%) = Phenotypic Co-efficient of variance

GAM (%) = Genetic advance as percent mean

**Table 3 :** Estimation of phenotypic and genotypic correlation coefficients for yield and its contributing traits of chickpea germplasm lines

		DFF	DM	PH	100-SW	SY/PP
DFF	P	1	0.5318**	0.1127	-0.2681**	-0.2533**
	G	1	0.5704**	0.1147	-0.2749**	-0.2575**
DM	P		1	0.0338	-0.2017**	-0.1224*
	G		1	0.0643	-0.2482**	-0.2804**
PH	P			1	0.2230**	0.0907
	G			1	0.2531**	0.1484*
100-SW	P				1	0.6792**
	G				1	0.7610**

Where, DFF : Days to 50% flowering

100 SW : 100 seed-weight (g)

SY/PP : Seed yield/ plant (g)

DM : Days to maturity

PH : Plant height (cm)

**Table 4 :** Phenotypic direct and indirect effect of quantitative character on seed yield/plant

	DFF	DM	PH	100-SW	SY/PP
DFF	<b>-0.1054</b>	-0.0560	-0.0119	0.0282	-0.2533
DM	0.0379	<b>0.0712</b>	0.0024	-0.0144	-0.1224
PH	-0.0049	-0.0015	<b>-0.0431</b>	-0.0096	0.0979
100-SW	-0.1810	-0.1361	0.1505	<b>0.6749</b>	0.6792

**Phenotypic Residual Value=0.586**

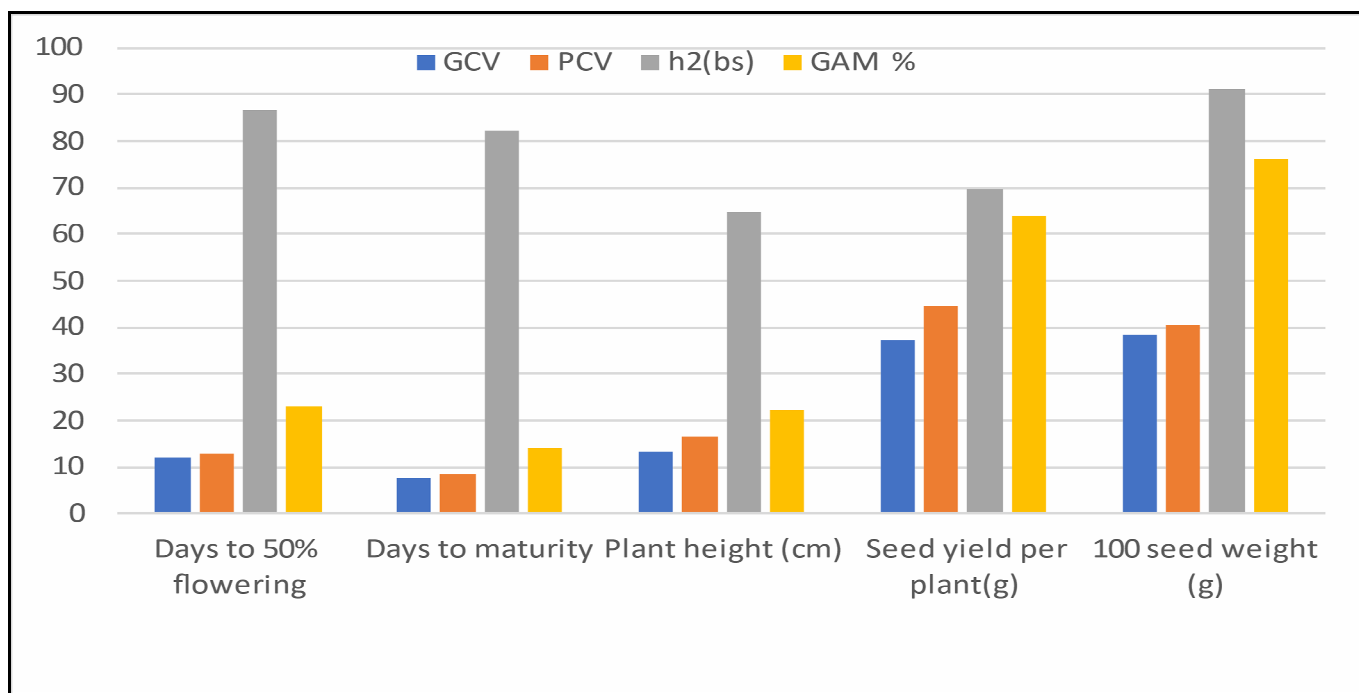
Where, DFF : Days to 50% flowering

100 SW : 100 seed-weight (g)

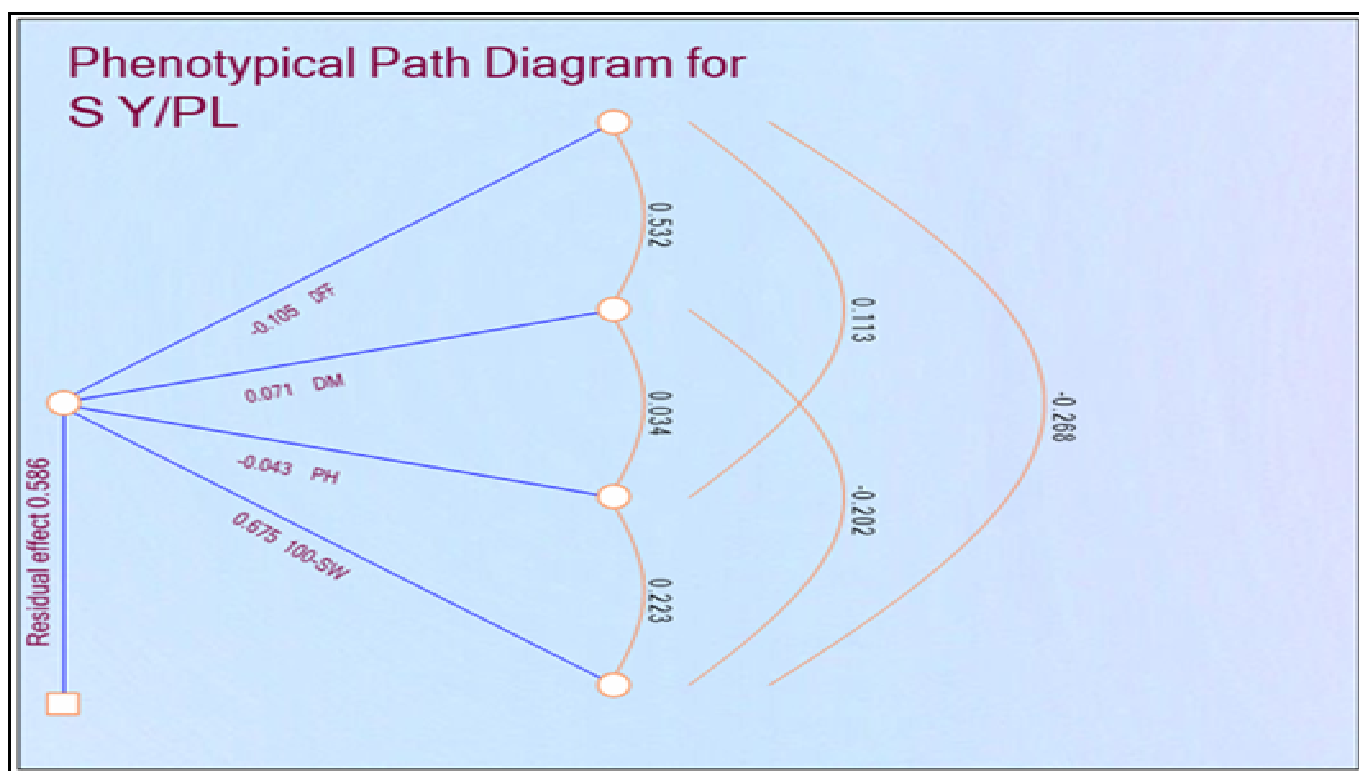
SY/PP: Seed yield/plant (g)

DM : Days to maturity

PH : Plant height (cm)



**Fig. 1:** Phenotypic co-efficient of variation (PCV), Genotypic coefficient of variation (GCV), Heritability, Genetic advance as percent of mean (GAM) estimate for traits in chickpea genotypes



**Fig. 2 :** Direct and indirect effects of quantitative characters on seed yield at phenotypic level

**References**

Anonymous (2021). Agriculture at glance, Directorate of Economic & Statistics, department of agriculture and cooperation, 105-108.

Banik, M., Deore, G.N. and Mhase, L.B. (2018). variability and heritability studies in chickpea. *Curr. J. App. Sci. Technol.*, 4(2):1-6.

Barad, S.H. and Javia, R.M. (2018). Estimation of genetic variability for *Kabuli* chickpea under timely and late sowing condition. *J. Pharmacogn. Phytochem.*, 7(4): 421-423.

Bentham, G. and Hooker, J.D. (1970). *Genera Plantarum*, London, Oxford and IBM publishing Co. Pvt. LTD., 3(2): 823

Burton, G.W. and Devane, E.H. (1953). Estimating of heritability in tall Fescue (*Festuca arundinaceae*) from a replicated clonal material. *Agron. J.*, 45: 478-482.

- Cubero, J.I. (1975). Morphology of Chickpea. In: The Chickpea, Saxena, M.C. and K.B. Singh (Eds.). CAB International, Wallingford, UK., 157-170.
- Gaur, P.M., Slinkard, A.E. and Rao, B.V. (2020). Genetic control and linkage relations of additional isozyme markers in chickpea. *Theor Appl Genet.*, 80: 648–656.
- Hanson, C.H., Robinson, H.F. and Comstock, R.E. (1956). Biometrical studies of yield in segregating populations of Korean Lespedeza. *Agron. J.*, 48: 268-272.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Genotypic and phenotypic co-rrrelation in soybeans and their implication in selection. *Agron. J.*, 47: 477-483.
- Jukanti, A.K., Gaur, P.M. and Gowda, C.L.L. (2012). Nutritional quality & health benefits of chickpea. *British J. Nutr.*, 108(1): 11-26.
- Karthikeyan, M., Pandey, S., Synrem, G., Sharma, P. and Singh, V. (2022). Genetic variability and co-relation studies for some polygenic traits in chickpea. *J. Pharm. Innov.*, 11(1): 1706-1709.
- Kumar, A., Kumar, A., Yadav, A.K., Nath, S. and Kumar, J.K. (2018). Co-rrrelation and path co-efficient analysis for various polygenic traits in chickpea. *J. Pharmacogn. Phytochem.*, 6(1): 2695-2699.
- Kumar, S., Suresh, B.G. and Lavanya, G.R. (2019). Genetic Variability, Co-relation and path co-efficient analysis in chickpea for yield and its component traits. *Int. J. Curr. Microbiol. App. Sci.*, 8(12): 2341-2352.
- Lenka, D. and Misra, B. (1973). Path Co-efficient Analysis of Yield in Rice Varieties. *Indian J. Agric. Sci.*, 43: 376-379.
- Mayuriben, R.T., Sunayan, R.P., Sunil, S.P., Arpan, J.N. and Harshad, N.P. (2019). Variability, heritability & genetic advance for polygenic traits in chickpea. *Int. J. Chem. Studies.*, 7(4): 1764-1767.
- Mohan, S. and Thiyagarajan, K. (2019). Genetic variability, Correlation and path co-efficient analysis in chickpea for yield & its component traits. *Int. J. Curr. Microbiol. App. Sci.*, 8(5): 1801-1808.
- Nizama, J.R., Patel, S.R. and Patel, A.I. (2013). Genetic variability and heritability among polygenic traits in chickpea under tropical region. *Asian Reson.*, 5(2): 45-48.
- Padmavathi, P.V., Murthy, S.S. and Rao, V.S. (2013). Correlation and path co-efficient analysis in kabuli chickpea. *Int. J. App. Bio. Pharma. Technol.*, 4: 107-110.
- Roy, A., Ghosh, S. and Kundagrami, S. (2013). Genetic approach and biometrical association of yield attributing traits in Chickpea. *Inter.J. Sci. Res.*, 5(7): 2208-2212.
- Samyuktha, S.M., Geethanjali, S. and Bapu, J.R. (2017). Genetic diversity & correlation studies in Chickpea based on morphological traits. *Electron.J. Plant Breed.*, 8(3): 874-884.
- Shara, J.H. (2019). Correlation and path co-efficient analysis for seed yield and its components in chickpea under rainfed condition. *Journal of Kerbala for Agricultural Sciences*. 2019;(6):1.
- Singh, R.K. and Chaudhary, B.D. (1977). Biometrical method in quantitative genetic analysis. Kalyani Publisher, Ludhiana, India.
- Tengse, S.M., Sarode, S.B., Deshmukh, S.S. and Shinde, A.V. (2022). Assessment of correlation and path analysis in chickpea (*Cicer arietinum* L.). *The Pharma Innovation*, 11(1): 184-188.
- Van der Maesen, L.J.G. (1984). Taxonomy, distribution and evolution of the chickpea and its wild relatives. In Genetic Resources and Their Exploitation-Chickpeas, Faba beans and Lentils, 95-104.
- Verma, J.P. and Yadav, J. (2018). Implication of microbial consortium on biomass and yield of chickpea under sustainable agriculture. *Environ. Eng. Manag. J.*, 17(3): 513-522
- Verma, S., Madala, N., Kumar Halavath, S., Suresh, B.G. and Lavanya, G.R. (2020). Evaluation of Chickpea Germplasm for yield and I attributing traits in eastern plain Zone of Uttar Pradesh. *Int. J. Curr. Microbiol. App. Sci.*, 9(10):1944-1956.