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GENETIC VARIABILITY STUDY IN READY TO ROAST GENOTYPES OF DESI CHICKPEA (*CICER ARIETINUM* L.)

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ABSTRACT

The study evaluated genetic variability in seed yield across 16 chickpea genotypes (12 ready to roast genotypes and four commercial checks viz., JG 11, A-1, SA-1 and GULAK) during Rabi 2023-24 at three locations (Bidar, Kalaburagi and Raichur) in Karnataka. Experiment was conducted in a Randomized Block Design, the experiment followed recommended agronomic practices for the region Significant genetic variation was observed, particularly in traits like swelling and hydration capacity, which displayed high genotypic and phenotypic co-efficient of variation, indicating strong genetic variability with minimal environmental influence. High heritability and genetic advance were noted for traits like test weight and iron content, suggesting they are influenced by additive genetic factors.

Keywords**:** Genetic variability, genetic co-efficient of variation, phenotypic co-efficient of variation, broad sense heritability, genetic advance,

Introduction

Chickpea (*Cicer arietinum* L.) is a self-pollinating, annual diploid species with a genome size of 738 Mb. Known by various names such as gram and garbanzo, it belongs to the fabaceae family and has two main types: Kabuli and Desi. India leads the world in chickpea area (9.59 million hectares) and production (11.04 million tonnes), with Karnataka contributing significantly 0.638 million hectares and 0.386 million tonnes (Anon 2023-24). Chickpeas are a staple food across all regions of India, enjoyed in both rural and urban areas.

The success of crop improvement relies on genetic variability, heritability and genetic advance in relation to yield and its attributes. High genotypic and phenotypic co-efficient of variation indicate substantial variability, making traits with high heritability and genetic advance valuable for enhancing yield. Seed yield, being a polygenic trait, is influenced by various genetic and environmental factors, complicating direct cultivar selection.

Material and Methods

In the present study 16 chickpea genotypes (12 genotypes and four commercial checks) were sown during *Rabi* 2023-24 across three locations *viz.*, Zonal Agricultural Research Station (ZARS), Kalaburagi, MARS, PG research block, UAS Raichur and Agriculture Research Station, Janwada, Bidar. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was sown in four rows of four meters in length with a spacing of 30 cm between rows and 10 cm between plants. Data were recorded on phenological traits *viz* days to 50 per cent flowering, days to maturity; yield attributing traits namely plant height, number of branches per plant, number of pods per plant, test weight, seed yield; and quality traits *viz*., hydration capacity, swelling capacity, cooking time, moisture content, crude protein content, carbohydrate content, crude fat content, zinc content and iron content; qualitative traits like seed ribbing, seed shape and seed testa texture, roasting traits like expansion index and puffing index. Observations were recorded on five randomly selected plants per entry per replication for all the characters under study except for test weight, seed yield, seed ribbing, seed shape, seed testa texture, moisture content, expansion index, puffing index, crude protein content, iron content, zinc content, carbohydrate content, crude fat content, zinc content, hydration capacity, swelling capacity and cooking time which were recorded on a whole plot basis. The average values of the random sample of the respective character used for analysis. while genotypic co-efficient of variance (GCV) and phenotypic co-efficient of variance (PCV) were computed for each character as per the method suggested by Burton and Devane (1953). Heritability (%), while genetic advance as a per cent of mean was estimated by using the formula of Johnson *et al.* (1955).

Table 1 : List of 16 chickpea genotypes used for study**.**

Sl. No.	Genotype	Pedigree
1	ICCV-191256	ICC-4958/ICCV-00108//ICCV-93954/ICCV-94954///ICCV10/ICCV-97105//ICCV-93952/ICCV-96970
2	ICCV-191156	ICC-4958/ICCV-93954//ICCV-96970/ICCV-97105///ICCV-10/ICCV-93952//ICCV-94954/ICCV-00108
3	RG-2016-134	ICCV 03112 x ICCV10
4	ICCV-191151	ICC-4958/ICCV-10//ICCV-93952/ICCV-93954
5	ICCV-191251	ICC-4958/ICCV-10//ICCV 93952/ICCV 93954
6	ICCV-191255	ICC-4958/ICCV-10//ICCV-93952/ICCV-93954
7	ICCV-191161	ICC-4958/ICCV-10//ICCV-93952/ICCV-93954///ICCV-94954/ICCV-96970//ICCV-97105/ICCV-00108
8	ICCV-191253	ICC-4958/ICCV-97105//ICCV-10/ICCV-00108
9	ICCV-88202	PRR-1///H-208/T-3//26-2-B-BP-BP-BP-4P-1P-1P-1P-BP
10	ICCV-191159	ICC-4958/ICCV-97105//ICCV-10/ICCV-00108///ICCV-93952/ICCV-94954//ICCV-93954/ICCV-96970
11	ICCV-191126	JG 11///JG 11//Harigantars/JG 11
12	ICCV-191155	ICC-4958/ICCV-00108//ICCV-93954/ICCV-94954///ICCV-10/ICCV-97105//ICCV-93952/ICCV-96970
13	JG-11 (NC for yield)	ICCV-93954
14	SA-1 (RC for yield)	Annigeri-1 × WR-315
15	A-1 (LC for ready to roast/Parching)	Selection from land race
16	Gulak (Check Parching/ready to roast)	(N-59 × D-8) 1-88-88A

Results and Discussion

Studies on Genetic Variability Components

Genotypic and phenotypic co-efficient of variance

To develop high-yielding genotypes, it is crucial to understand the existing variability and the degree of association between yield-contributing traits, as well as their relative impact on yield. The variability observed is influenced by both genetic and environmental factors.

The genetic variability study conducted for seed yield and its attributing traits revealed that the PCV value ranged from 2.51 per cent for days to maturity to 28 per cent for swelling capacity percentage. Similarly, GCV values ranged from 1.27 per cent for days to maturity to 27.05 per cent for swelling capacity percentage is presented in Table 2. The narrow difference between the GCV and PCV indicates the major portion of phenotypic variation is due its genetic constitution.

A higher magnitude of GCV and PCV values were recorded for number of pods per plant, seed yield per plant, hydration capacity and swelling capacity. These results reveals that the traits mentioned above exhibit significant genetic variability indicating the potential for genetic improvement through a selection of these traits.

The results were on par with the studies of Hagos *et al.* (2018) for number of pods per plant; Dar *et al.* (2020) for seed yield per plant; Johnson *et al.* (2018) for hydration capacity and Tripathi *et al.* (2012) for swelling capacity.

The investigation recorded a moderate to low GCV as well as PCV values were observed for plant height, number of branches per plant, test weight, seed yield, expansion index, puffing index, fat content, iron content, zinc content, days to 50 per cent flowering, days to maturity, cooking time, moisture content, protein content and carbohydrate content suggesting minimal genetic variability within these traits for selection.

These findings were in accordance with the results of earlier workers Deshmukh *et al.* (2024) for plant height; Ali *et al.* (2010) for number of branches per plant; Tamatam and Pandey (2024) for test weight; Rathod *et al.* (2020) for seed yield; Misra *et al.* (2020) for iron content; Grewal *et al.* (2020) for zinc content and Jayalakshmi and Trivikrama Reddy (2018) for protein content.

Heritability and genetic advance

According to Johnson *et al.* (1955), broad sense heritability combined with genetic advance is crucial for predicting the success of selecting the best individuals. Therefore, it is vital to assess both heritability and genetic advance to improve the effectiveness of selection.

The broad sense heritability values varied from 25.60 per cent to 94.8 per cent for day to maturity and test weight respectively while GAM values were between 1.32 per cent to 53.83 per cent for days to maturity and swelling capacity respectively is presented in Table 2.

Estimates of higher broad sense heritability coupled with high genetic advance as per cent of mean (GAM) were observed for test weight, hydration capacity, swelling capacity and iron content indicating that these traits are governed by additive gene action and direct selection for the higher phenotypic value of this trait will be effective.

The results were on par with the studies of Karthikeyan *et al.* (2022) for test weight; Prasanthi *et al.* (2023) for hydration capacity; Johnson *et al.* (2018) for swelling capacity and Saha *et al.* (2018) for iron content.

Days to 50 per cent flowering, cooking time, expansion index, puffing index, moisture content, protein content and fat content exhibited high broad sense heritability but a moderate GAM value while carbohydrate content recorded a low GAM value revealing the prevalence of both additive and non-additive gene actions. Improvement of these traits could be achieved through simple selection, progeny selection or modified selection methods that focus on fixing additive gene effects rather than solely relying on selection.

These findings were in accordance with the results of earlier workers Bicer and Sarkar (2004) for days to 50 per cent flowering; Prasanthi *et al.* (2023) for cooking time and Padmavathi *et al.* (2013) for protein content.

Table 2 : Estimation of mean and genetic variability parameters in chickpea for Raichur, Kalaburagi and Bidar locations

Sl. No.	**Characters**		**Range**		**Coefficient of variation**		**h^2 (%) (Broad sense)**	**GAM**
		Mean	**Minimum**	**Maximum**	**PCV (%)**	**GCV (%)**		
1	Days to 50 per cent flowering	42.11	38.55	46.55	7.51	6.15	67.00	10.36
2	Days to maturity	92.56	90.22	95.22	2.51	1.27	25.60	1.32
3	Plant height(cm)	41.94	37.37	47.99	11.68	7.80	44.60	10.74
4	Number of branches per plant	2.41	1.84	2.79	17.05	8.81	26.70	9.36
5	Number of pods per plant	30.37	25.59	37.10	20.34	7.38	13.10	5.51
6	Seed yield per plant (g)	6.92	5.25	9.99	25.85	13.46	27.10	14.43
7	Test weight(g)	21.57	13.82	29.26	19.46	18.94	94.80	37.99
8	Seed yield (kg/ha)	1416.76	1003.21	1663.54	14.01	9.31	44.10	12.73
9	Hydration capacity (g/seed)	0.244	0.11	0.34	24.30	23.49	93.50	46.78

10	Swelling capacity (ml/seed)	0.50	0.17	0.76	28.00	27.05	93.30	53.83
11	Cooking time (minutes)	28.71	24.77	32.55	8.80	7.87	80.00	14.51
12	Expansion index (%)	180.02	152.63	215.13	12.72	10.96	74.20	19.48
13	Puffing index (%)	201.54	168.50	235.69	12.15	10.66	77.10	19.30
14	Moisture content (%)	14.60	13.15	15.87	6.35	5.60	79.90	10.18
15	Protein content (%)	20.33	18.33	22.71	6.09	5.45	80.20	10.06
16	Fat content (%)	4.95	3.78	5.65	11.04	10.17	84.90	19.30
17	Carbohydrate content (%)	57.56	55.97	60.29	2.65	2.21	71.40	3.90
18	Iron content (ppm)	180.83	143.33	216.67	13.46	12.45	85.60	23.73
19	Zinc content (ppm)	48.04	40.66	52.66	11.83	7.52	40.40	9.86

Conclusion

The study reveals significant genetic variation across various traits, highlighting differences in phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). Traits like swelling and hydration capacity show high GCV and PCV, indicating strong genetic variability with minimal environmental influence, making them suitable for selection. High heritability and genetic advance in traits like test weight, iron content and swelling capacity suggest they are largely influenced by additive genetic factors, facilitating selective breeding.

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