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EXPLORING MEAN PERFORMANCE AND GENETIC VARIABILITY PARAMETERS IN CHICKPEA CULTIVARS (*CICER ARIETINUM*): INSIGHTS FOR ENHANCED CROP PRODUCTIVITY

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ABSTRACT

In the experimental setup, assessed 21 chickpea genotypes across 10 quantitative characters during the *rabi* season of 2020-21. Among the 20 evaluated varieties, a significant diversity in characters, especially seed yield, was observed, with AVT-2-G8 demonstrating exceptional performance. Additionally, genotypes like C-207 and C-1028 exhibited desirable attributes such as early flowering. High PCV values were evident in characters like secondary branches plant⁻¹, number of pods plant⁻¹, seed yield plant⁻¹, primary branches plant⁻¹, number of seeds plant⁻¹, plant height and 100-seed weight, while moderate PCV values were recorded for days to 50% pod setting and days to maturity. High GCV values were reported for secondary branches plant⁻¹, number of pods plant⁻¹, seed yield plant⁻¹, primary branches plant⁻¹, number of seeds plant⁻¹, plant height and 100-seed weight, with moderate GCV values for days to 50% flowering, days to 50% pod setting and days to maturity. The confluence of high heritability alongside notable Genetic Advance (% mean) was particularly evident for characters such as secondary branches plant⁻¹, followed by the number of pods plant⁻¹, number of seeds plant⁻¹, primary branches plant⁻¹, 100-seed weight, and seed yield plant⁻¹ and plant height.

Key words : Mean Performance, Genetic Variability, Chickpea Cultivars, *Cicer arietinum*.

Introduction

Chickpea, scientifically known as *Cicer arietinum*, belongs to the extensive legume family, Fabaceae, renowned for encompassing various vital plants such as beans, peas and peanuts. Esteemed as the third most crucial pulse globally, chickpea thrives in subtropical and warm-temperate regions. This annual plant, recognized for its characteristic yellow-brown, pea-like seeds is widely cultivated for its nutritional value and versatility in cuisines worldwide. Commonly referred to as garbanzo bean, Bengal gram, or chana, this crop is prized for its resilience to drought conditions and its ability to thrive without the need for nitrogen fertilizers. Its versatility

extends to its utilization both as an edible seed and in the production of flour, making it a staple ingredient globally. Chickpea (*Cicer arietinum* L.) stands as the leading pulse crop in India, spanning over 10.10 million hectares and yielding 11.57 million tonnes in the 2022-23 seasons (DES, 2023). Specifically, Uttar Pradesh boasts an area of 5.82 lakh hectares, production of 7.47 lakh tonnes, and a productivity of 1282 kg/ha during the same period (DES, 2023). The chickpea's average production remains low in the country, primarily due to the absence of high-yielding varieties resilient to diseases, pests and the intensive use of inputs. Addressing these challenges necessitates a thorough evaluation of the factors constraining chickpea growth and yield. Creating genetic

variability and selecting crucial characters are pivotal tasks for plant breeders to enhance yield and agronomic qualities. However, effective selection demands comprehensive knowledge of genetic variation among chickpea genotypes, the characters suitable for selection, and the influence of environmental factors on each trait. Understanding the nature and magnitude of variability and heritability in a population is indispensable for successful breeding programs, enabling breeders to select genotypes with desired characteristics effectively. Thus, understanding the heritability of agronomic characters is vital for improving crop yield effectively.

Materials and Methods

The current study, focused on chickpea was carried out at the Department of Genetics and Plant Breeding, SHUATS, Prayagraj, during the *rabi* season of 2020-21. The experimental setup comprised 21 distinct genotypes of chickpea (*Cicer arietinum* L.), alongside a standard check variety, Uday. Employing a randomized block design with three replications (RCBD), adhering to a spacing of 30 × 10 cm, and the genotypes were evaluated, ensuring robustness and reliability. Rigorous measures were taken to maintain consistent plant populations across treatments per replication. Comprehensive agricultural practices were meticulously followed, incorporating recommended protocols and essential prophylactic plant protection measures to ensure optimal crop development. Data pertaining to various parameters including days to 50% flowering, days to 50% pod setting, days to maturity, plant height (cm), number of primary and secondary branches plant⁻¹, number of pods plant⁻¹, number of seeds plant⁻¹, 100 seed weight (g), and seed yield plant⁻¹, were recorded from five randomly selected plants within each replication.

The analysis of variance for various characters was meticulously conducted utilizing the mean data, a method aligned with the principles outlined by Panse and Sukhatme (1961), enabling the precise delineation of variability attributed to diverse sources. To comprehensively gauge and quantify the genetic variability inherent among the different genotypes for the characters under scrutiny, a suite of genetic parameters was estimated. These included the genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), heritability (h²), genetic advance (GA) and genetic advance as a percentage of the mean (GAM). Broad-sense heritability was calculated according to the

formula elucidated by Hansan *et al.* (1956), while GA was derived using the methodology prescribed by Johnson *et al.* (1955). Phenotypic and genotypic coefficients of variation were computed employing the methodology pioneered by Burton and Devane (1953), adding a layer of robustness to the assessment of variability within the studied chickpea genotypes.

Results and Discussion

The analysis of variance conducted on 10 quantitative characters revealed significant discrepancies among the assessed genotypes, encompassing crucial characteristics such as seed yield plant⁻¹ (Table 1). This finding suggests promising avenues for genetic enhancement through selective breeding and hybridization, particularly targeting characters that exhibited notable variation among the tested genotypes. In addition to variance analysis, the evaluation of existing variability among genotypes involved computing the range and determining least significant differences. To gain insights into the heritability and potential for trait transmission, broad-sense heritability (Hanson *et al.*, 1956) and genetic advance as a percentage of the mean (following the method proposed by Johnson *et al.*, 1955) were calculated. These metrics contribute to a comprehensive understanding of the genetic underpinnings of the studied characters and inform strategies for effective crop improvement programs.

To comprehensively assess chickpea genotypes, Table 2 presents the mean performance of 20 varieties alongside the reference variety Uday across 10 key characters. Remarkable diversity in mean performance was evident across all characters studied. Notably, the entry AVT-2-G8 exhibited the highest seed yield plant⁻¹

Table 1 : Analysis of variance of yield and yield attributing characters in 21 chickpea genotypes.

S. no.	Character(s)	Mean sum of squares		
		Replication (df=02)	Treatments (df=20)	Error (df=40)
1	Days to 50% flowering	4.82	2324.3**	225.01
2	Days to 50% pod setting	1.45	160.01**	5.84
3	Days to maturity	4.76	206.90**	3.07
4	Plant height (cm)	26.00	197.75**	13.49
5	Primary branches plant ⁻¹	1.45	3.09**	0.48
6	Secondary branches plant ⁻¹	0.84	15.22**	0.90
7	Number of pods plant ⁻¹	20.71	407.41**	40.65
8	Number of seeds plant ⁻¹	91.92	511.92**	31.77
9	100 seed weight (g)	8.64	53.39**	3.54
10	Seed yield plant ⁻¹ (g)	2.04	14.87**	3.88

*, ** Significant at 5 % and 1% probability level, respectively.

(16.00 g) and demonstrated strong performance across all characters, mirroring the earliness characteristic of the standard check variety Uday. Among the top performers for seed yield plant⁻¹ were AVT-2-G8, C-223, CSJ-1089, C-210, C-1025, C-222 and CSJ-1093, all of which displayed noteworthy mean performance across multiple characters in addition to their high yield. Of these, C-223, securing the second position with a yield of 13.33 g, belonged to the highest mean performance group for characters such as 100-seed weight (g), primary branches plant⁻¹, and plant height (cm), while also exhibiting early maturity compared to the reference. Furthermore, beyond these highlighted genotypes, several others showcased exceptional mean performance for specific characters, making them potential donors for trait improvement through targeted breeding approaches, even if their seed yield was moderate or low.

In this regard, genotypes like C-207 and C-1028 were identified as desirable for early flowering, while C-137, C-207, C-138, ICC-2000 and AVT-2-G1 exhibited early 50% pod setting. Similarly, ICC-2000, C-138, C-21193, C-137, C-207 and AVT-2-G1 demonstrated early maturity. Genotypes such as C-137, C-21193, C-1012 and C-138 excelled in maintaining low plant height, while others like C-1028, C-207, C-137, C-205, AVT-2-G1, ICC-15561 and C-1023 exhibited a high number of primary branches plant⁻¹. Additionally, ICC-15561, C-137, C-1023, AVT-2-G1, C-205 and C-1028 showcased a higher number of secondary branches plant⁻¹. Moreover, C-1028, C-207, AVT-2-G1, ICC-15561 and C-1023 exhibited a higher number of pods plant⁻¹, while C-1028, AVT-2-G1, C-207, C-205, ICC-15561, C-1023 and C-137 displayed higher seed production plant⁻¹. Lastly, C-137, C-1028, C-207, and C-138 were notable for their 100-seed weight.

Genetic variability parameters, including PCV and GCV, offer insights into the extent of variation within populations, crucial for trait selection in breeding programs. Heritability measures the genetic component of trait expression, guiding decisions on trait heritance. GA and GAM assess the potential for trait improvement through selection, aiding in prioritizing characters and genotypes for breeding efforts. By quantifying both phenotypic and genotypic variation and estimating the genetic basis of characters, these parameters inform breeders on effective strategies to exploit variability and enhance desirable characters, ultimately contributing to the development of improved crop varieties with enhanced agronomic performance.

An in-depth analysis of Table 3 revealed a rich array of phenotypic variations among the utilized genotypes.

Notably, substantial estimates exceeding 20% of Phenotypic Coefficient of Variation (PCV) were recorded for various characters. Among these, secondary branches plant⁻¹ (39.94%), followed closely by the number of pods plant⁻¹ (35.69%), seed yield plant⁻¹ (33.60%), primary branches plant⁻¹ (32.56%), number of seeds plant⁻¹ (30.55%), plant height (28.69%) and 100-seed weight (22.52%) exhibited particularly high PCV values. Such pronounced PCV values suggest a significant influence of the prevailing environmental factors on these characters. Furthermore, moderate PCV values ranging between 10% and 20% were observed for days to 50% pod setting (18.64%) and days to maturity (18.62%). In contrast, characters such as days to 50% flowering displayed notably low PCV estimates, at a mere 1.97%. This comprehensive examination underscores the complex interplay between genotype and environmental conditions in shaping the observed phenotypic diversity. The earlier findings of Parameshwarappa *et al.* (2010), Tsehaye *et al.* (2020) and Sriraj and Gurjar (2022) also supported the present results.

In the realm of Genetic Coefficient of Variation (GCV), noteworthy findings emerged with estimates surpassing 20% for various characters. Specifically, significant GCV values were observed for secondary branches plant⁻¹ (38.74%), number of pods plant⁻¹ (33.86%), seed yield plant⁻¹ (30.40%), primary branches plant⁻¹ (29.87%), number of seeds plant⁻¹ (29.59%), plant height (24.58%) and 100-seed weight (21.76%). Conversely, moderate GCV values, falling within the range of 10% to 20%, were noted for days to 50% flowering (17.48%), days to 50% pod setting (15.46%) and days to maturity (15.23%). The findings by Singh *et al.* (2018) and Singh *et al.* (2020) lent support to the present study's outcomes. These results collectively suggest that, on the whole, Phenotypic Coefficient of Variation (PCV) tended to surpass GCV across all examined characters. However, an interesting deviation was observed in the case of days to 50% flowering, where GCV exceeded PCV, indicating a lesser influence of environmental factors among the genotypes. The prevalence of higher PCV values compared to GCV underscores the significant impact of environmental conditions on trait expression. Notably, characters such as secondary branches plant⁻¹, number of pods plant⁻¹, seed yield plant⁻¹, primary branches plant⁻¹, number of seeds plant⁻¹, plant height and 100-seed weight exhibited both high PCV and GCV, indicating a substantial genetic contribution to their variability under prevailing environmental influences.

Heritability serves as a metric to gauge the degree

Table 2 : *Per se* performance of 21 genotypes of chickpea for seed yield and its components characters.

S. no.	Genotypes	Days to 50% flowering	Days to 50% pod setting	Days to maturity	Plant height (cm)	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Number of pods plant ⁻¹	Number of seeds plant ⁻¹	100 seed weight (g)	Seed yield plant ⁻¹ (g)
1	C-205	90.33	104.33	135.33	65.27	3.27	5.60	26.47	51.53	13.33	7.47
2	C-223	87.00	95.00	127.67	58.94	5.33	7.33	48.67	61.00	22.91	13.33
3	C-135	82.33	112.67	141.33	52.13	2.33	3.80	20.07	29.80	15.33	7.07
4	C-1025	81.33	89.33	126.33	45.60	2.67	5.67	35.67	41.00	22.33	11.00
5	C-1012	82.67	109.33	141.67	48.27	2.40	3.13	24.47	32.73	17.67	9.00
6	C-137	80.33	90.67	126.33	45.38	3.33	8.33	27.67	41.00	26.83	9.00
7	ICC-15900	83.33	103.33	139.33	54.20	2.08	3.80	22.80	30.10	15.67	8.20
8	C-1023	89.00	106.33	138.33	78.19	2.67	6.53	32.07	45.93	16.00	8.07
9	C-210	83.33	94.33	127.33	49.96	3.67	5.67	32.67	45.67	25.09	11.00
10	CSJ-1089	86.67	117.67	135.67	52.87	3.13	5.47	23.60	28.73	16.33	12.27
11	C-222	82.67	94.00	142.33	48.43	4.67	5.67	41.00	51.00	24.17	11.00
12	AVT-2-G1	77.33	102.67	129.33	70.16	3.07	6.07	37.13	57.40	12.00	9.20
13	ICC-2000	83.33	102.33	118.67	53.27	1.67	3.67	16.47	22.87	13.67	7.67
14	AVT-2-G8	72.33	104.33	129.33	58.16	5.13	12.87	63.73	66.67	18.67	16.00
15	C-1028	72.33	97.00	142.33	51.33	4.33	5.53	51.33	63.13	23.33	7.62
16	ICC-15561	86.00	104.3	141.00	57.56	2.81	8.40	37.07	48.07	14.67	8.60
17	C-21193	77.33	105.67	121.00	47.80	2.27	4.13	23.60	27.93	16.67	9.13
18	CSJ-1093	81.00	104.00	145.33	55.40	2.67	5.13	29.33	38.93	18.33	10.07
19	C-207	62.67	94.67	128.33	55.47	3.47	4.40	41.27	52.80	22.20	8.83
20	C-138	79.33	109.67	118.67	50.53	2.00	2.80	22.00	26.33	19.33	7.27
21	UDAY	73.00	103.00	129.33	50.81	2.57	4.44	28.67	35.33	18.93	9.63
	CV	6.07	7.13	8.10	7.92	0.99	2.20	11.37	12.75	4.12	2.17
	SE	1.94	1.97	1.43	3.00	0.57	0.78	5.21	4.60	1.54	1.61
	CD at 5%	3.91	4.02	2.92	6.11	1.16	1.58	10.60	9.38	3.13	3.28

Table 3 : Estimate of grand mean, range, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense, genetic advance (GA) and genetic advance in per cent of mean (GAM) for different characters in chickpea genotypes.

S. no.	Character(s)	Grand Mean	Range	GCV (%)	PCV (%)	Hbs (%)	GA (%)	GAM (%)
1	Days to 50% flowering	81.13	62.67-90.33	17.48	1.97	65.20	12.20	15.04
2	Days to 50% pod setting	102.13	89.33-117.67	15.46	18.64	76.30	14.50	14.19
3	Days to maturity	132.62	118.67-145.33	15.23	18.62	58.50	16.85	12.71
4	Plant height (cm)	54.75	45.38-78.19	24.58	28.69	93.20	15.58	28.47
5	Primary branches plant ⁻¹	3.12	1.67-5.33	29.87	32.56	84.20	1.76	56.46
6	Secondary branches plant ⁻¹	5.64	2.80-12.87	38.74	39.94	94.10	4.37	77.41
7	Number of pods plant ⁻¹	32.65	16.47-63.73	33.86	35.69	90.00	21.61	66.18
8	Number of seeds plant ⁻¹	42.76	22.87-66.67	29.59	30.55	93.80	25.24	59.02
9	100 seed weight (g)	18.74	12.00-26.83	21.76	22.52	93.40	8.12	43.31
10	Seed yield plant ⁻¹ (g)	9.59	7.07-16.00	30.4	33.60	93.90	3.39	35.34

of trait transmission across generations. Notably, a predominance of high heritability estimates (>60%) was discerned across all examined characters, with the exception of days to maturity, which displayed a moderate level of heritability. Among the various characters assessed, secondary branches plant⁻¹ (94.10%) emerged as the most heritable, closely followed by seed yield plant⁻¹ (93.90%), number of seeds plant⁻¹ (93.80%), 100-seed weight (93.40%), and plant height (93.20%). These findings resonate with previous studies conducted by Tsehaye *et al.* (2020) and Mihoariya *et al.* (2023) affirming the robustness of the observed trends in heritability across different experimental contexts.

Johnson *et al.* (1955) advocate that both heritability and genetic advance, when considered together, offer a more comprehensive estimate compared to relying solely on heritability for predicting the effects of selection. Genetic Advance (GA) expressed as a percentage of the mean (% mean) yielded substantial values (>20%) for secondary branches plant⁻¹ (77.41%), number of pods plant⁻¹ (66.18%), number of seeds plant⁻¹ (59.02%), primary branches plant⁻¹ (56.46%), 100-seed weight (43.31%), seed yield plant⁻¹ (35.43%), and plant height (28.47%). Conversely, moderate GA (% mean) values ranging from 10% to 20% were noted for characters such as days to 50% flowering (15.04%), days to 50% pod setting (14.19%) and days to maturity (12.71%). These results echo those of previous studies conducted by Babbar *et al.* (2012), Arora *et al.* (2018), Munde *et al.* (2018) and Admas *et al.* (2021) reinforcing the consistency and reliability of the observed trends across different experimental contexts.

Hence, the conjunction of high heritability alongside notable Genetic Advance (% mean) was evident for

characters such as secondary branches plant⁻¹, followed by the number of pods plant⁻¹, number of seeds plant⁻¹, primary branches plant⁻¹, 100-seed weight, seed yield plant⁻¹ and plant height (Table 3). This alignment of elevated heritability and significant genetic advance for these characters echoes findings previously reported by Singh *et al.* (2021) and Singh *et al.* (2022). The outcomes of the current investigation underscore the efficacy of selection strategies for these particular characters, suggesting promising avenues for targeted breeding programs.

Conclusion

The current investigation, based on the mean performance of 20 chickpea varieties in comparison to Uday across 10 characters, reveals significant insights. AVT-2-G8 emerged as the top performer with the highest seed yield (16.00 g) and demonstrated overall robust performance similar to Uday. Other notable contenders for seed yield were C-223, CSJ-1089, C-210, C-1025, C-222 and CSJ-1093. Additionally, several genotypes showcased excellence in specific characters, highlighting their potential for targeted breeding endeavours. The presence of genetic variability stands as a pivotal criterion for crop enhancement endeavours. Drawing from the outcomes of this investigation, it is evident that a pronounced variability estimate was observed across all examined characters. Notably, for each trait under scrutiny, the Phenotypic Coefficient of Variation (PCV) exceeded the Genetic Coefficient of Variation (GCV), signifying the influential role of environmental factors in shaping the expression of these characters.

Furthermore, a compelling alignment of high heritability alongside notable Genetic Advance (% mean) was discerned for characters such as secondary branches

plant⁻¹, followed by the number of pods plant⁻¹, number of seeds plant⁻¹, primary branches plant⁻¹, 100-seed weight, and seed yield plant⁻¹ and plant height. This convergence of high heritability with substantial genetic advance suggests the potential for improvement through selection, as these characters are primarily governed by additive gene effects. Hence, it is imperative to interpret the anticipated genetic advance in light of both genetic variability and heritability when assessing the prospects for enhancement through selection processes. Such an integrated approach ensures a nuanced understanding of the breeding potential and aids in strategic decision-making towards crop improvement initiatives.

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