Study on the performance of Chickpea (*Cicer arietinum* L.) genotypes for seed yield and its component traits at Kanpur agroclimatic condition

Aneeta Yadav, Syed Mohd Quatadah, Rishikesh Kumar Pal, Jitendra Kumar & Vinay Joseph Silas

Faculty of Agricultural Sciences and Allied Industries, Rama University, Kanpur-209217.

Corresponding Author email: syedquatadah.fas@ramauniversity.ac.in

Abstract

The present study was conducted to evaluate genetic variability, yield performance, physiological traits, and interrelationships among twenty-eight chickpea genotypes along with three checks (BGD 72, GNG 663, and Birsa Chana-3) under both timely and late sowing conditions in chickpea (*Cicer arietinum* L.). Analysis of variance indicated significant differences among genotypes for most yield and yield-related traits, reflecting ample genetic variability for effective selection.

Under timely sown conditions, higher seed yield per plant (12.99 g) and per plot (793.06 g) were linked with an increased number of pods per plant (58.27), more secondary branches (6.20), and higher 100-seed weight (22.40 g). In contrast, late sowing led to a considerable reduction in yield per plant (10.86 g) and per plot (409.24 g), mainly due to a decline in pods per plant, as well as primary and secondary branches under heat stress conditions. Among all traits, the number of pods per plant was identified as the most influential contributor to yield across environments. Estimates of genetic parameters revealed that phenotypic coefficient of variation (PCV) was slightly higher than genotypic coefficient of variation (GCV) for most traits, suggesting moderate environmental influence but a predominance of genetic control. High heritability coupled with high genetic advance was observed for 100-seed weight, proline content, protein content, specific leaf area (SLA), and specific leaf weight (SLW) under both environments, indicating the role of additive gene action and the effectiveness of direct selection. Under late sowing conditions, traits such as number of pods per plant and yield per plot exhibited higher heritability and genetic advance, implying better selection efficiency under stress conditions.

Physiological traits including proline content, chlorophyll content, and relative water content showed high heritability along with high genetic advance, suggesting their usefulness as reliable selection criteria for heat tolerance. Genotypic correlation analysis further revealed strong positive associations of seed yield with plant height, number of primary branches, seeds per plant, and 100-seed weight under both sowing conditions.

Overall, the findings suggest that simultaneous selection for higher pod number, increased seed weight, and improved physiological adaptability can aid in developing high-yielding, heat-tolerant, and stable chickpea genotypes suitable for changing climatic conditions.

Key Words: *Chickpea, Genetic variability, Correlation, Heritability, Seed Yield*

Introduction:

Chickpea (*Cicer arietinum* L.), commonly referred to as Bengal gram or chana, is a self-pollinated, diploid (2n = 2x = 16) grain legume of considerable nutritional and agronomic significance. It is an annual species with a genome size of approximately 738 Mb (Varshney *et al.*, 2013). Globally, chickpea ranks as the second most important pulse crop and plays a vital role in ensuring food and nutritional security, particularly in semi-arid tropics and warm temperate regions. India is the leading producer and consumer, contributing nearly two-thirds of the world's total chickpea production. The crop is highly valued for its rich protein content, essential minerals, and its capacity to enhance soil fertility through symbiotic nitrogen fixation with Rhizobium, thereby supporting sustainable cropping systems. In India, chickpea is cultivated over an area of about 10.47 million hectares, with an annual production of approximately 12.27 million tonnes and an average productivity of 1,172 kg ha^{-1} (Tripathi *et al.*, 2025; Asati *et al.*, 2022; Sahu *et al.,* 2020a, 2020b), underscoring its substantial contribution to national pulse production and food security.

Despite its importance, chickpea productivity remains below its potential, primarily due to constraints such as a narrow genetic base, erratic climatic conditions, and terminal heat and moisture stress, particularly under late-sown environments. Recent climatic variability has intensified the occurrence of high-temperature stress during the reproductive phase, adversely affecting flowering, pod formation, seed filling, and ultimately yield. Therefore, the identification of genetically diverse, high-yielding, and climate-resilient genotypes adapted to varying sowing conditions is imperative for achieving stable productivity.

Genetic variability constitutes the cornerstone of any crop improvement program. The availability of sufficient variability in breeding material facilitates effective selection and genetic gain. Estimation of genetic parameters, including phenotypic and genotypic coefficients of variation, heritability, and genetic advance, provides insight into the magnitude of variability and the nature of gene action governing key agronomic traits. Moreover, seed yield in chickpea is a complex quantitative trait influenced by multiple component characters (Kumar *et al.,* 2023).

Hence, understanding interrelationships among traits through correlation and path coefficient analysis is essential for identifying characters that exert direct and indirect effects on yield, thereby aiding in the formulation of efficient selection strategies under diverse environmental conditions.

Given the critical influence of sowing time on crop performance, the evaluation of genotypes under both timely and late-sown conditions is essential to assess their adaptability and stability. Late sowing often subjects the crop to terminal heat stress, significantly impacting growth and yield attributes. Therefore, a comparative assessment under contrasting sowing environments is necessary to identify genotypes with superior performance and stable trait associations. In this context, the present study aims to assess genetic variability, analyze trait associations, and identify promising genotypes along with key yield-contributing traits for their potential use in breeding programs targeting the development of high-yielding and climate-resilient chickpea cultivars.

Materials and methods:

The present investigation was carried out to assess the magnitude of genetic variability and character association in Twenty-eight diverse chickpea genotypes collected from different research institute. The experimental material was evaluated in three different replications under two different cropping environments All the recommended optimal agronomic practices have been performed to raise the good crop and data have been recorded for the traits viz., days to 50% flowering (DFF), days to maturity (DTM), plant height (PHT), number of primary (NPB) and secondary branches per plant (NSB), pods per plant (NPP), 100-seed weight (HSW), yield per plant (Y/Plant), yield per plot (Y/Plot), and wilt incidence (%) by selecting 5 randomly selected competitive plants from each replication. Data have been compiled and subjected to statistical analysis to extract the valuable information.

Result and Discussion:

The analysis of variance revealed significant differences among the genotypes for most of the studied traits, particularly plant height, number of primary and secondary branches, number of pods per plant, 100-seed weight, and yield parameters under both timely and late sown conditions. The mean performance of twenty-eight chickpea genotypes along with three checks (BGD 72, GNG 663, and Birsa Chana-3) demonstrated considerable variation for yield and its contributing traits, indicating the presence of substantial genetic variability and scope for selection (Babbar et al., 2018).

Under timely sown conditions, higher mean seed yield per plant (12.99 g) and per plot

(793.06 g) were primarily associated with a greater number of pods per plant (58.27), increased number of secondary branches (6.20), and higher 100-seed weight (22.40 g). In contrast, late sowing resulted in a marked reduction in yield per plant (10.86 g) and per plot (409.24 g), largely due to a significant decline in the number of pods per plant (38.25) and secondary branches (4.41). A reduction in primary branches (from 4.15 to 2.66) further contributed to decreased pod formation under heat stress conditions, corroborating earlier findings (Jha et al., 2022). Among all the traits, number of pods per plant (range: 45.4–77.9 under timely and 22.9–57.9 under late sown conditions) emerged as the most critical direct contributor to yield, as its reduction closely paralleled the decline in seed yield. Seed yield per plant (9.6–16.1 g under timely and 8.2–13.2 g under late sowing) also exhibited strong dependence on 100-seed weight (17.2–29.8 g and 16.4–28.2 g, respectively), indicating that both sink size (pod number) and seed weight play pivotal roles in determining productivity (Karim *et al.,* 2022). Secondary branches further supported yield by contributing to higher pod numbers. Overall, the results highlight number of pods per plant, secondary branches, and 100-seed weight as the principal yield-determining traits under both environments (Jha et al., 2015). Genotypes capable of maintaining higher pod number and seed weight under late sown conditions may be considered promising for heat stress tolerance and yield stability.

Genetic parameter analysis under both timely and late sown conditions revealed substantial variability for yield, physiological, and quality traits, indicating strong potential for genetic improvement. In general, phenotypic coefficient of variation (PCV) values were slightly higher than genotypic coefficient of variation (GCV) for most traits, suggesting moderate environmental influence; however, the relatively narrow differences between PCV and GCV for several characters indicate a predominance of genetic control. Under late sown conditions, higher GCV and PCV values were observed for number of pods per plant (GCV: 22.76%), yield per plot (18.06%), relative water content (RWC: 15.69%), and physiological traits such as proline content (43.1%) and chlorophyll content (29.14%), reflecting enhanced variability under heat stress (Kaur *et al.,* 2019).

Notably, 100-seed weight exhibited very high heritability under both environments (94.5% under timely and 95% under late sown conditions), coupled with high genetic advance as percent of mean (27.44% and 29.26%), indicating the predominance of additive gene action and the effectiveness of direct phenotypic selection. Similarly, proline content, protein content, specific leaf area (SLA), and specific leaf weight (SLW) recorded very high heritability (>93%) along with high genetic advance, suggesting stable inheritance and their suitability for selection under stress conditions (Kinjal H. et al., 2022). Number of pods per plant exhibited moderate heritability under timely conditions (36.14%) but high heritability under late sowing (83.06%), along with very high genetic advance (42.73%), identifying it as a key yield-contributing trait under heat stress. Yield per plot also showed moderate to high heritability (30.22% under timely and 53.9% under late sowing) with improved genetic advance under stress (27.31%), indicating enhanced selection efficiency in late sown environments.

Plant height and number of secondary branches exhibited moderate heritability with appreciable genetic advance, suggesting partial involvement of additive gene effects. Physiological traits such as proline content, chlorophyll content, RWC, SLA, and SLW showed high heritability coupled with high genetic advance under late sown conditions, indicating their potential as reliable selection indices for heat tolerance (Kumar *et al.*, 2020). The predominance of additive gene action for these traits suggests that they can be effectively improved through direct selection. Overall, the findings indicate that selection for number of pods per plant, 100-seed weight, yield per plot, proline content, chlorophyll content, protein content, SLA, and SLW would be highly effective for improving yield and stability under heat stress. Traits with high heritability and genetic advance can be improved through simple selection, whereas those with moderate heritability may require hybridization followed by selection. Incorporating physiological traits such as proline content, RWC, and chlorophyll content as screening tools can further enhance the efficiency of breeding programs aimed at developing heat-tolerant and stable genotypes.

Genotypic correlation analysis under both normal and late sown conditions revealed several significant associations among yield and its component traits. Days to flowering exhibited a strong positive correlation with days to maturity under both normal (0.380**) and late sown (0.344**) conditions, indicating synchronized phenological development. It also showed a significant positive association with seed yield per plant under both environments (0.453** under normal and 0.342** under late sown conditions), suggesting its importance in yield determination (Jivani et al., 2013). Plant height showed a strong positive correlation with seed yield per plot under normal conditions (0.453**) and maintained significance under late sowing (0.289*). Additionally, plant height was positively correlated with number of primary branches under both conditions.

Number of primary branches exhibited a strong positive association with number of secondary branches under both normal (0.404**) and late sown (0.444**) conditions. Under late sowing, it also showed a strong correlation with seed yield per plant (0.463**), emphasizing its importance under stress conditions. Number of seeds per plant was positively and significantly correlated with seed yield per plant under both environments (0.298** under normal and 0.277** under late sown conditions), confirming its role as a key yield component (Hagos et al., 2018). Similarly, 100-seed weight exhibited a significant positive association with seed yield per plant under both normal (0.345**) and late sown (0.256*) conditions. Wilt percentage showed a positive correlation with seed yield per plot under both environments, which may reflect environmental or population-level influences rather than a direct causal relationship (Kaur et al., 2019).

In conclusion, the study underscores the importance of key yield components such as number of pods per plant, seed weight, and branching traits, along with physiological attributes, in determining yield under both normal and heat stress conditions. The integration of these traits in selection strategies will facilitate the development of high-yielding, heat-tolerant, and stable chickpea genotypes suited to changing climatic conditions.

Conclusion

In conclusion, the study demonstrated substantial genetic variability among twenty-eight chickpea genotypes of Cicer arietinum evaluated under timely and late sown conditions, with clear identification of key yield-determining traits. Number of pods per plant emerged as the most decisive character, showing wide variation (45.4–77.9 in timely; 22.9–57.9 in late) and high heritability under late sowing (83.06%) with high genetic advance (42.73%), directly paralleling seed yield per plant (9.6–16.1 g in timely; 8.2–13.2 g in late). Hundred seed weight also proved highly stable and reliable, recording very high heritability (94.5% in timely and 95% in late) with substantial genetic advance (27.44% and 29.26%) and significant positive correlation with seed yield (0.345** in normal; 0.256* in late). Number of primary branches (correlation with yield under late: 0.463**) and secondary branches (mean 6.20 in timely; 4.41 in late) significantly supported pod formation and yield stability under heat stress. Physiological traits such as proline content (GCV 43.1%), chlorophyll content (29.14%), and RWC (15.69%) exhibited high heritability (>93%) and strong genetic advance, indicating their usefulness as selection indices for heat tolerance. Overall, integrating high pod number, superior seed weight, strong branching ability, and stable physiological resilience will be most effective for developing high-yielding, heat-tolerant and stable chickpea cultivars suited to changing climatic conditions.

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Table-4.2: Mean of different characters in twenty-eight genotypes of chickpea (Cicer arietinum L.) under normal condition and rainout shelter.

Genotypes	DFF		DM		PH (cm)		NPB		NSB		NPP		HSW (g)		Y/Plant (g)		Y/Plot (g)	
	N	**L**	**N**	**L**	**N**	**L**	**N**	**L**	**N**	**L**	**N**	**L**	**N**	**L**	**N**	**L**	**N**	**L**
RUG-1	80	79	123.3	121.3	52.3	57	4.7	2.6	6.7	3.3	55.5	36.1	20.8	19	12.3	11.3	808	438
RUG-2	82.7	83	117	116	70.9	53.9	3.5	2.9	7.7	3.4	59.3	34.1	26.5	25.3	15	10.8	928.7	537.3
RUG-3	77	77.7	121	120	50.7	54.8	4.8	3	6.1	4.1	53	41.2	19.8	18.4	13.4	11.7	821.9	519
RUG-4	76.7	75	125.3	125	51.9	55.7	4.5	2.7	6	4.1	48.6	41.9	20.7	21	9.7	10.1	626.7	337.3
RUG-5	81.7	80.7	117	118	51.7	52.8	3.8	2.7	6.2	4.4	58.6	36.1	17.6	17.8	12	12	701.2	467
RUG-6	75.7	75.3	123	118.7	40.3	54.8	4.4	2.1	6.7	3.7	59.1	42.5	21.4	19.5	12.8	9.7	827.1	447.3
RUG-7	77	76.3	114.3	117	51	48.3	4.5	2.3	6.9	5	60.7	33.6	20.1	20	13.3	10.8	800.8	520.7
RUG-8	79.3	80	126.3	124	62.6	51.1	3.5	1.7	4.8	3.4	54.4	23.3	23.1	22.7	12.7	12.8	912	351.3
RUG-9	76	78	131.7	130.3	53.8	56.8	4.3	2.6	8.1	4.7	54.4	41.5	21.6	21.1	14.3	11.1	806.5	382.7
RUG-10	75.3	74.3	131	118.3	47.3	50.1	2.7	2.9	7.2	5.7	67.1	48.2	21.4	22.8	16.1	10.3	907.7	525.7
RUG-11	81.7	82	120	121	51.9	48.2	4.1	2.5	7.5	5.2	58	35.6	23.3	22.5	15.6	8.4	925.3	248.7
RUG-12	75.3	75	117.7	120	37.1	47.4	4	2.7	7.1	6.1	52.5	41.1	24.7	24.1	13.7	10.5	884.3	357.7
RUG-13	77	77	119.3	115.3	50.8	54.9	3	2.5	6.9	3.7	61.4	22.9	24.8	22.4	13.1	8.2	860.4	351
RUG-14	75	75.3	126.7	120.3	47.6	54.6	4.7	3.1	6.4	4.5	74.3	27.4	21.5	20.4	11.8	8.7	760.7	274
RUG-15	85	85	135.7	133	46.5	55.4	4.9	1.9	6.5	4.3	77.9	43.1	18.9	19.1	13	10.1	735.1	370
RUG-16	83	76	130	127.7	52.1	58.7	4.3	3.1	5.5	4.1	45.4	42	28.1	27.4	11.8	9.8	622.3	360.7
RUG-17	78	76.7	124	125	48.5	50.1	4.7	2.5	6	4.4	57.5	57.9	26.6	25	12.5	10.2	684.1	373.3
RUG-18	80.3	80.7	131.3	129.7	64.9	64.8	4.9	2.5	5.7	4.3	55.2	38.6	19.6	17.9	11.6	10	557.8	360.3
RUG-19	79.3	80	117.7	121	50.6	54.1	4.7	2.3	5.7	4.3	60.6	27.2	21.4	19.9	12.6	13.2	651.9	492.7
RUG-20	84	83.3	126.3	123	49	56.8	3.9	2.9	6.1	4.3	58.8	50.6	29.8	28.2	13.3	12.4	912.4	442
RUG-21	75.7	74.7	125	115	42.1	49.9	4.7	3.3	5.5	5.1	52.8	26.1	24.3	22.6	9.9	10.3	631.3	275.7
RUG-22	83.7	83.7	115	126.3	48.6	62.4	3.4	2.7	3.9	4.2	60.4	32.5	20.5	16.4	9.6	12.2	701	447.3
RUG-23	79	77	120	120.3	53.3	67.5	3.6	3.5	6	4.8	59.3	41.8	26.9	26.1	12.6	12.2	711.6	449

RUG-24	81.7	81.3	122	122.7	39.7	48.7	3.8	2.6	5.2	3.9	50.2	33	20.5	16.9	13.8	9.9	797.5	338.7
RUG-25	79.3	78.3	120	126	41.7	45.4	3.9	1.8	4.5	3.8	51.3	26.9	21.3	19.5	12.1	9.9	941.8	348.7
BGD 72 (NC)	82.7	83	116.3	122	47.6	48.5	4.3	3.4	6.9	4.6	66.3	53.7	22.1	21.5	15.9	12.4	856.7	555.7
GNG 663 (NC)	76	76	130.3	133.7	35.5	61	4.2	2.9	5.5	5	57.3	46.9	17.2	17.5	13.7	12.7	932.7	418.7
BirsaChana-3(LC)	78.3	79	117.7	121.7	41.9	55	4.3	3	6.3	5.1	61.8	45.2	22.8	22.2	15.5	12.4	898.2	470.3
Lowest	75	74.3	114.3	115	35.5	45.4	2.7	1.7	3.9	3.3	45.4	22.9	17.2	16.4	9.6	8.2	557.8	248.7
Highest	85	85	135.7	133.7	70.9	67.5	4.9	3.5	8.1	6.1	77.9	57.9	29.8	28.2	16.1	13.2	941.8	555.7
Mean	79.15	78.69	123.04	122.58	49.35	54.24	4.15	2.66	6.2	4.41	58.27	38.25	22.4	21.33	12.99	10.86	793.06	409.24
CV%	1	1.04	1.24	1.09	11.86	8.17	15.29	14.03	15.05	16.57	12.85	13.84	3.32	3.36	15.58	15.06	16.96	16.72
SEm (±)	0.46	0.47	0.88	0.77	3.38	2.56	0.37	0.22	0.54	0.42	4.32	3.06	0.43	0.41	1.17	0.94	77.65	39.5
CD at 5%	1.3	1.34	2.5	2.19	9.58	7.25	1.04	0.61	1.53	1.2	12.25	8.67	1.22	1.17	3.31	2.68	220.17	112
CD at 1%	1.73	1.78	3.32	2.92	12.76	9.66	1.38	0.81	2.03	1.59	16.32	11.54	1.62	1.56	4.41	3.57	293.21	149.15
p-value (t-test)	0.57		0.75		0.009		0		0		0		0.2		0		0	

Table-4.4: Genetic parameters of twenty eight genotypes for different characters under normal condition and rainout shelter

Characters	**GCV**		**PCV**		**h² (Broad Sense)**		**Genetic advance**		**GAM (5%)**	
	N	**L**	**N**	**L**	**N**	**L**	**N**	**L**	**N**	**L**
DFF	2.85	3.97	5.32	4.1	28.66	93.6	2.48	6.22	3.14	7.91
DM	3.55	4.04	6.41	4.18	30.73	93.2	4.99	9.84	4.06	8.03
PH	14.34	8.66	18.61	11.9	55.04	52.9	10.62	7.03	21.53	12.97
NPB	10.82	14.65	18.73	20.28	33.4	52.1	0.53	0.58	12.87	21.78
NSB	12.96	11.86	19.86	20.38	42.6	33.9	1.08	0.63	17.41	14.22
NPP	9.55	22.76	15.96	24.97	36.14	83.06	6.92	16.33	11.88	42.73
HSW (g)	13.71	14.57	14.1	14.95	94.5	95	6.15	6.24	27.44	29.26
Y/Plant (g)	9.55	9.18	18.28	17.63	27.3	27.1	1.34	1.07	10.28	9.85
Y/Plot (g)	10.43	18.06	19.91	24.61	30.22	53.9	96.57	111.77	12.18	27.31
Wilt %	18.33	13.08	26.5	22.47	47.8	33.9	1.08	3.26	26.11	15.69

Proline content (µmol/g)	40.99	43.1	41.38	43.6	98.1	97.7	6.13	10.77	83.62	87.77
Chlorophyll content (mg/g)	10.45	29.14	11.45	29.52	83.3	97.41	0.51	1.04	19.65	59.24
Protein content (%)	17.91	27.36	18.51	27.96	93.6	95.7	4.28	10.12	35.71	55.15
SLA (cm^2/g)	19.23	24.83	19.29	24.86	99.4	99.8	77.58	63.56	39.5	51.09
RWC (%)	4.14	15.69	5.69	15.82	52.9	98.4	3.96	14.53	6.21	32.05
SLW (mg/cm^2)	24.36	22.46	24.45	22.51	99.2	99.6	2.66	3.91	50	46.17

Table-4.5: Genotypic Correlation for different characters in twenty eight genotypes of chickpea (*Cicer arietinum* L.) under natural condition and rainout shelter.

Characters		DF	DM	PH	NPB	NSB	NSP	HSW	Y/ Plant (g)	Y/ Plot (g)	Wilt %
DFF	**N**	1	0.380**	0.207	-0.077	-0.232	0.230	0.165	0.453**	0.267*	-0.087
	L	1	0.344**	0.089	-0.201	-0.227	-0.178	-0.151	0.342**	0.344**	-0.054
DM	**N**		1	0.165	0.210	0.050	-0.035	-0.081	0.256*	0.279*	-0.025
	L		1	0.144	-0.225	-0.039	-0.209	-0.252*	0.326**	0.276**	0.154
PH	**N**			1	0.308**	0.260*	0.142	0.112	0.324**	0.453**	-0.008
	L			1	0.365**	0.274*	-0.061	-0.019	0.278*	0.289*	0.039
NPB	**N**				1	0.404**	-0.039	0.258*	0.289*	0.266*	0.169
	L				1	0.444**	-0.233	0.262*	0.463**	0.254**	-0.132
NSB	**N**					1	0.040	0.116	0.345**	-0.244*	0.098
	L					1	0.012	0.236*	0.452**	-0.279*	0.094
NSP	**N**						1	-0.034	0.298**	0.299*	0.203
	L						1	-0.303**	0.277**	0.344**	0.182
HSW	**N**							1	0.345**	0.255*	-0.340**
	L							1	0.256*	0.367**	-0.298**
	N								1	0.267*	-0.233*

Y/ Plant (g)	**L**								1	0.277*	-0.297**
Y/ Plot (g)	**N**									1	0.461**
	L									1	0.355**
Wilt %	**N**										1
	L										1