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Assessment of genetic variability in chickpea (*Cicer arietinum* L.)

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Abstract
The present investigation conducted to evaluate forty-four diverse chickpea genotypes to estimate genetic variability, heritability and genetic advance, correlation coefficient, path analysis during *Rabi* season, 2023-2024. Results showed that there were highly significant differences among genotypes for all the traits. On combined analysis of all genotypes it was found that estimations for all the characters genotypic coefficients of variation (GCV) were lower than those for their phenotypic coefficients of variation (PCV. Highest value of GCV and PCV for the seed yield per plant, number of primary branches and secondary branches showed high degree of variability for those two traits. Heritability is a good indicator of character transmission from parents to offspring (Falconer, 1981). The current study showed high heritability for the majority of characteristics in chickpea. High estimate of genetic advance as percent of mean was seen in seed yield per plant, followed by 100 seed weight, harvest index, number of secondary branches and number of pods per plant. Seed yield per plant exhibited positive and significant correlation with, Pods per plant, seed per pod, number of primary branches, number of secondary branches, 100 seed weight and harvest index at genotypic and phenotypic level. The results of a path coefficient analysis reported that the 100 seed weight and harvest index had the most favourable direct effects on yield. The Mahalanobis D^2 cluster analysis categorized the forty four genotypes into seven distinct clusters, indicating genetic diversity in genotypes. Cluster III and VI exhibited particularly high inter cluster distances. Results confirms that genotypes NDG 22-10, Phule G 1521-12-2, BG 4047, Phule Vikram in cluster IV performing better traits.

Keywords: Genetic variability, Heritability, Genetic advance, Correlation coefficients, Path coefficient

1. Introduction

Chickpea (*Cicer arietinum* L.) is one of the oldest and most widely cultivated legumes in the world. Belonging to the Fabaceae (Leguminosae) family, it is a cool-season, self-pollinated, diploid (2n = 2x = 16) pulse crop primarily grown in tropical and subtropical climates. Commonly known as Gram, Bengal gram, Chana (in Hindi), and Harbhara (in Marathi), it plays a significant role in global food systems.

Legumes, represent the third-largest family of angiosperms. They include a diverse range of food crops that are vital sources of plant-based proteins and essential amino acids. In addition to their nutritional value, legumes play a crucial role in sustainable agriculture by enhancing soil health through symbiotic nitrogen fixation and contributing high-quality organic matter to the soil.

India is largest producer of chickpea in the world with 115.76 lakh tonnes from an acreage of 104.74 lakh hectares, with productivity of 12.6 quintals per hectare. according to ANGRAU, 2023–2024. Maharashtra's chickpea area was reported at 26.30 lakh hectares, while production reached 27 lakh tonnes and productivity was 702 kg per hectare. Chickpea is widely consumed across the world in various forms, with its culinary use often shaped by ethnic and regional traditions. On the Indian subcontinent, chickpeas are commonly split into cotyledons and consumed as 'dal' or ground into flour (besan), which is then used in a variety of snacks and dishes. Globally, especially in Asia and Africa, chickpeas are incorporated into soups, salads, and stews, and are also eaten in roasted, boiled, salted, or fermented forms. These diverse methods of consumption not only cater to cultural preferences but also provide substantial nutritional value and significant health benefits to consumers (Jukanti *et al.*, 2012) [16].

Genetic variability is a vital tool for plant breeders, serving as a fundamental source of variation and a key driver of yield improvement. The success of crop enhancement efforts relies heavily on identifying traits that contribute to yield, which in turn depends on the presence of heritable variation and the heritability of specific traits. To ensure reliable estimation of genetic parameters, a precise and environmentally stable approach to measuring genetic variability is required.

The progress achieved in crop improvement through selection is directly influenced by the level of genetic variability available in the breeding material. However, environmental factors can also impact the expression of this variability. Therefore, it is imperative to collect, analyze, and document all available genetic diversity within chickpea genotypes to meet the increasing demand for varietal development and higher productivity.

For any crop improvement program, a breeder must possess a thorough understanding of genetic variability and heritability. These factors are critical at various stages of the breeding process. Specifically, the degree of variability and heritability for economically important traits in early-generation populations will determine the overall success of the breeding program. Estimating heritability and expected genetic gain is crucial to accurately assess the potential of selecting superior individuals under specific conditions (Johnson *et al*., 1955) [12].

2.Materials and Methods

The field experiments related to the present investigation entitled "Assessment of genetic variability in Chickpea (*Cicer arietinum* L.) was carried out during Rabi season, 2023-2024 at Pulse Improvement Project, MPKV, Rahuri. The materials used in the present investigation consisted of forty- four genotypes of chickpea. The material was obtained from the Pulse Improvement Project, MPKV, Rahuri. The experiment used a randomized block design with three replications with spacing 30cm x 10cm. All other intercultural operation like thinning, weeding, In order to facilitate better germination, a light irrigation after sowing, at time of pod formation.

3. Result and discussion

The mean data for ten characters were subjected to analysis of variance which showed that the mean sum of square for nine characters due to genotypes were found significant under study, which indicates that considerable amount of variability is present among genotypes. This significant heterogeneity offers a strong opportunity to enhance desirable features in chickpea breeding efforts. The similar findings for all the characters have been reported by Akhtar *et al*. (2011) [2], Jivani *et al*. (2013) [14], Jain *et al*. (2020) [13], Manasa *et al*. (2020) [20], Nikita and Lal (2022) [23] and Munazza moin (2023) [22].

3.1 Genetic variability parameters

Parameters of genetic variability were recorded on ten quantitative traits viz., days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight, harvest index, and seed yield per plant.

3.2 Genotypic and Phenotypic Coefficients of Variation

Estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were classified as suggested by Sivasubramanian and Madhavamenon (1973) and are presented in Table 4. Genotypic coefficient variation (GCV) was highest for seed yield per plant (g) (37.51%) followed by 100 seed-weight (20.84%) and number of primary branches (18.74%). The character days to maturity (3.30%) recorded lowest GCV. The maximum phenotypic coefficient of variation (PCV) was recorded for seed yield per plant (38.03%), followed by Number of Primary branches (25.54%). In general, the magnitude of phenotypic coefficient of variation was higher than the genotypic coefficient of variation. High magnitude of GCV and PCV was observed for seed yield per plant and 100 seed weight. This was in conformity with the results of Kuldeep *et al.* (2014) [17], Singh *et al.* (2018) [28], Jain *et al.* (2020) [13] and Devi *et al*. (2021) [7], Nikita and Lal (2022) [23] Bharathi *et al*. (2022) [6] and Munazza moin (2023) [22]. While, low magnitude of GCV and PCV was observed for days to maturity, which was in conformity with Akhtar *et al*. (2011) [2], Kuldeep *et al*. (2014) [17] and Manasa *et al*. (2020) [20].

3.3 Heritability

Heritability in broad sense was estimated for various characters as suggested by Hanson *et al.* (1956) [11]. Estimates of heritability in broad sense are presented in Table 5. High estimates of heritability (>60%) was observed for nine studied characters. The highest estimates of heritability exhibited in days to Harvest index (97.80%) followed by 100 seed weight (97.60%), Seed yield (97.30%), Number of pods per plants (97.30%), days to 50% flowering (96.20%),Plant height (95.20%), days to maturity (94.80%) number of seeds per pod (89.40%) and number of secondary branches (88.50%) and number of primary branches (53.90%) showed moderate heritability range (30-60%).In the current study, traits such as Harvest index, 100 seed weight, Seed yield per plant, number of pods per plant, Plant height, number of secondary branches per plant all exhibited a high estimates of heritability (broad sense), along with high genetic advance as a percentage of mean, indicating that these traits are largely governed by additive gene action and that selection of these traits could be more effective for the desired genetic improvement. These findings supported by similar noting of Jivani *et al*. (2013) [14], Sharanappa *et al*. (2014) [27], Banik *et al*. (2018) [4], Kumar *et al.* (2019) [18], Manasa *et al*. (2020) [20] and Devi *et al*. (2021) [7], Munazza moin *et al*. (2023) [22].

3.4 Genetic advance

Genetic advance (at 5% selection intensity) was calculated by the formula cited by Allard (1960) [1]. The range of genetic advance observed from 0.06 to 19.83. The highest estimate of GA for number of pods per plant (19.83) followed by seed yield per plant (13.58), 100 seed weight (12.91), harvest index (12.90), plant height (11.20) and days 50% flowering (7.13). The range of genetic advance as per cent of mean is classified as suggested by Johansson, *et al.* (1955) [12]. High estimates of genetic advance as per cent of mean observed for seed yield per plant (76.24%), followed by 100 seed-weight (42.43%), harvest index (37.38%) While, days to maturity (6.63%%) showed the lowest performance in genetic advance as per cent of mean.

Table 1: Analysis of variance for ten different quantitative characters in chickpea.

Characters	Mean sum of square		
	Replication (df. 2)	Treatment (df. 43)	Error (df. 86)
Days to 50% Flowering	8.96	37.83**	0.48
Days to maturity	11.87	38.26**	0.69
Plant height	15.88	94.73**	1.55
pods/plant	8.62	288.5**	2.66
seeds/pod	0.003	0.003	0.0001
Primary branches	1.00	0.62**	0.13
Seecondary branches	8.39	17.33**	0.72
100 seed weight (g)	0.19	121.82**	0.98
Harvest index	0.92	121.27**	0.92
Yield/plant	1.15	135.37**	1.23

The data collected on individual characters were subjected to the method of analysis of variance commonly applicable to the Randomized Block Design.

Table 2: Estimates of variability parameters for seed yield and yield contributing characters in forty four chickpea genotypes

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	ECV (%)	Heritability (bs) (%)	Genetic Advance	Genetic Advance% of Mean
1	Days to 50% flowering	48.84	43.66-56.33	7.22	7.36	1.43	96.20	7.13	14.59
2	Days to maturity	106.9	100.66-115.33	3.30	3.40	0.77	94.80	7.09	6.63
3	Plant height (cm)	46.55	36.83-56.26	11.97	12.26	2.67	95.20	11.20	24.06
4	Number of pods per plant	56.55	41.76-78.93	17.26	17.50	2.88	97.30	19.83	35.07
5	Number of seeds per pod	1.00	1.00-1.20	3.50	3.70	1.20	89.40	0.069	6.82
6	Number of Primary branches per plant	2.15	1.33-2.66	18.74	25.59	17.35	53.90	0.61	28.33
7	Number of secondary branches per plant	12.91	8.73-18.3	18.22	19.37	6.57	88.50	4.56	35.31
8	100 seed-weight (g)	30.44	20.63-45.43	20.84	21.10	3.25	97.60	12.91	42.43
9	Harvest index (%)	41.09	32.26-53.57	15.41	15.58	2.33	97.80	12.90	37.39
10	Seed yield per plant (g)	17.82	9.33-35.00	37.52	38.03	6.23	97.30	13.58	76.24

Table 3: Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients in chickpea

Sr. No.	Name of character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of pods per plant	Number of seeds per pod	Number Primary branches per plant	Number of secondary branches per Plant	100 seed weight (g)	Harvest index (%)	Seed yield per plant (g)
1.	Days to 50% flowering	1.000	0.6430**	0.0199	-0.0777	-0.1369	-0.0500	-0.1125	0.0113	-0.0034	-0.0137
2.	Days to maturity	0.6434**	1.000	0.0299	-0.0374	-0.1406	0.2054*	0.0601	-0.0667	-0.0175	-0.0384
3.	Plant height (cm)	0.0190	0.0318	1.000	-0.0744	0.0437	-0.0406	-0.0022	-0.0616	-0.0816	-0.0730
4.	Number of pods per plant	-0.0704	-0.0285	-0.0635	1.000	0.4956**	0.7177**	0.6282**	0.9577**	0.9593**	0.9682**
5.	Number of seeds per pod	-0.1208	-0.1134	0.0523	0.4812**	1.000	0.4438**	0.4397**	0.5363**	0.4517**	0.5651**
6.	Number of Primary branches per plant	-0.0022	0.1884*	-0.0430	0.5180**	0.3277**	1.000	1.0231**	0.6405**	0.6590**	0.6708**
7.	Number of secondary branches per plant	-0.1092	0.0493	-0.0050	0.5892**	0.3918**	0.7635**	1.000	0.5809**	0.5980**	0.6098**
8.	100 seed-weight (g)	0.0147	-0.0576	-0.0571	0.9525**	0.5158**	0.4664**	0.5509**	1.000	0.9669**	0.9791**
9.	Harvest Index (%)	0.0009	-0.0096	-0.0763	0.9520**	0.4315**	0.4888**	0.5590**	0.9564**	1.000	0.9794**

Table 4: Estimates of genotypic direct (diagonal) and indirect effects (above and below diagonal) of component characters on seed yield in Forty four chickpea genotypes

Sr. No.	Name of character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of pods per plant	Number of seeds per pod	Number of Primary branches per plant	Number of secondary branches per plant	100 seed weight (g)	Harvest index (%)	Genotypic correlation with seed yield per plant (g)
1.	Days to 50% flowering	0.0188	-0.0057	-0.0001	-0.0147	-0.0160	-0.0021	0.0053	0.0025	-0.0018	-0.0137
2.	Days to maturity	0.0121	-0.0088	-0.0002	-0.0071	-0.0164	0.0087	-0.0028	-0.0146	-0.0094	-0.0384
3.	Plant height (cm)	0.0004	-0.0003	-0.0055	-0.0140	0.0051	-0.0017	0.0001	-0.0135	-0.0436	-0.0730
4.	Number of pods per plant	-0.0015	0.0003	0.0004	0.1887	0.0578	0.0303	-0.0295	0.2091	0.5126	0.9682**
5.	Number of seeds per pod	-0.0026	0.0012	-0.0002	0.0935	0.1166	0.0188	-0.0207	0.1171	0.2414	0.5651**
6.	Number of Primary branches per plant	-0.0009	-0.0018	0.0002	0.1354	0.0518	0.0423	-0.0481	0.1398	0.3522	0.6708**
7.	Number of secondary branches per plant	-0.0021	-0.0005	0.0000	0.1185	0.0513	0.0432	-0.0470	0.1268	0.3196	0.6098**
8.	100 seed-weight (g)	0.0002	0.0006	0.0003	0.1807	0.0625	0.0271	-0.0273	0.2183	0.5167	0.9791**
9.	Harvest index (%)	-0.0001	0.0002	0.0005	0.1810	0.0527	0.0279	-0.0281	0.2111	0.5344	0.9794**

3.1 Correlation coefficient analysis
To establish a cause and effect relationship, the first step used was to partition genotypic and phenotypic correlation coefficient into direct and indirect effects by path analysis as suggested by Dewey and Lu (1959) [8] and developed by Wright (1921).

The degree of association between yield and its components was shown by the examination of the correlation coefficient given the interdependence of the yield components. Both phenotypic and genotypic levels of the correlation between various features and seed yield were evaluated, and the study revealed that genotypic correlation coefficient values were higher than phenotypic values. This showed how much the environment affects the phenotypic correlation coefficient. The seed yield per plant and its correlation with the number of pods per plant, number of seeds per pod, number of primary branches, number of secondary branches, 100 seed weight and harvest index were all positive and statistically significant. The seed yield per plant and its correlation with the number of pods per plant, number of seeds per pod, number of primary branches, number of secondary branches, 100 seed weight and harvest index were all positive and statistically significant. Similar results also reported by Kuldeep *et al.* (2014) [17], Banik *et al.* (2017) [5], Nitesh *et al.* (2018) [24], Kumar *et al.* (2019) [18], Makarand *et al.* (2019) [19] and Nikita and Lal (2022) [23], Gulwane *et al*. (2022) [10] and Reddy *et al*. (2023) [25].

4.1 Path coefficient analysis
The correlation coefficient demonstrated the association between the two characters, but a dependent trait is an interaction of many component traits that are mutually associated, and a change in any one of them will disrupt the entire network of cause and effect system. Wright (1921) developed the path analysis, a statistical tool that takes into account the cause-and-effect relationships between variables. The results of path coefficient based on genotypic coefficient taking seed yield per plant as dependent variable indicated that the characters days to 50% flowering, number of pods per plant, number of seeds per pod, number of primary branches, 100 seed weight and harvest index exhibited positive direct effect on grain yield per plant while traits like days to maturity and plant height showed negative direct effect on seed yield per plant. The number of secondary branches per plant had effect on seed yield through the number of pods per plant, number of seeds per pod, number of primary branches, 100 seed weight and harvest index and indicating the indirect selection of such characters would be successful in increasing yield. Highest direct effect on seed yield per plant showed by harvest index followed by 100 seed weight with positive correlation coefficient so that the direct selection of this trait for seed yield per plant is useful. Highest positive indirect effect was showed by number of secondary branches per plant via number of pods per plant. The component of residual effects of path analysis was 0.1190. Low residual effect indicated that characters for path analysis were adequate and appropriate. Highest direct effect on seed yield per plant showed by harvest index followed by 100 seed weight with positive correlation coefficient so that the direct selection of this trait for seed yield per plant is useful. These findings are in consonance to the results obtained by Kuldeep *et al.* (2014) [17], Shafique *et al.* (2016) [26], Banik *et al.* (2017) [5], Gulawane *et al*. (2022) [10] and Nikita and Lal (2022) [23].

Genetic divergence
Rao (1952) recommended adopting D^2 statistics in plant breeding to examine genetic diversity. Improvement of seed yield or any other traits is normally attained through involvement of genetically diverse parents in breeding programme. For identifying such parents for crossing, multivariate analysis by means of Mahalanobis' D^2 statistics has been used in several crops. It is powerful tool used to quantify the degree of genetic diversity between the genotypes and to relate clustering pattern with the geographic region.

Table 5: Grouping of 44 genotypes of chickpea into different clusters based on D^2 values

Cluster No.	Number of genotypes	Name of genotypes
I	11	RSGD 1253, Kalinga chana 1, DC 2305, RKG 23-2, Phule G 0405, NBeG 1639, BAUG 121, RKG 23-1 GJG 2101, NBeG 1632, GL 18046
II	15	RG 2022-30, Phule Vikram, GJG 2109, JG 2023-79, GNG 2624, AKG 1303, BG 4048, IPC 2019-246, DC 2306, CGS 20-1, GNG 2619, AKG 1809, RSGD 1182, H 20-08, JG 2023-78
III	4	PG 362, IPC 2020-208, RVSSG-125, BDNG 2020-78
IV	11	BDNG 2020-61, GL 19065, NDG 22-10, H 20-02, GDG 2008, TSRCH 1455, Phule G 1521-12-2, BGM 20211, BG 4047, RVSSG-126, Phule G 1504-5-7
V	1	RLBG-13
VI	1	PG 357
VII	1	NDG 22-6

5.1 Clustering pattern of the genotypes
The clustering pattern obtained on the basis of magnitude of D^2 values was made and presented in Table 5 and clustering as per Tocher method. The 44 genotypes were grouped into seven clusters. Cluster II was biggest and consisted of 15 genotypes. Cluster IV and Cluster I was the second largest with 11 genotypes, Cluster III consist 4 genotypes. Cluster V, VI, VII were solitary, with whereas the only one genotype in each of these cluster. The crosses involving the parents with extreme divergence have also been reported to exhibit decrease in heterosis (Moll *et al.*, 1964) [21]. Therefore, while selecting the parents by considering the genetic diversity and *per se* performance and cluster mean for the characters also need due consideration in the crop improvement programme. In the present investigation Forty four genotypes were grouped into seven clusters.

Table 6 showed the highest inter cluster distance (D = 19.80) was found between the clusters V and VI, followed by the cluster III and VI (D = 19.13) and cluster I and VI (D =15.48). This indicated that hybridization among the genotypes between these clusters would produce successful hybrids and desirable segregants in further generations. The intra cluster value was highest in cluster IV had maximum intra cluster distance (D= 9.35) followed by cluster II (D = 6.98), indicating that this cluster is more heterogeneous. Singh *et al.* (2020) [28] studied 20 genotypes into five clusters, cluster I had the highest intra-cluster distance. Reena Kumari *et al.* studied 35 genotypes divided into six clusters, Cluster I and II comprised majority of genotypes. Kumari Pragati *et al.* Studied 60 elite lines of chickpea genotypes were grouped into 10 clusters, Cluster I was largest. Vijay Kumar *et al.* studied 40 genotypes of chickpea divided into eight clusters, Cluster III was largest including 10 genotypes.

Table 6: Average intra (bold) and inter-cluster D and D^2 values (in parenthesis) for seven clusters in forty four chickpea genotypes

Cluster	I	II	III	IV	V	VI	VII
I	6.56 (43.03)	9.26 (85.74)	8.86 (78.49)	11.66 (135.95)	12.29 (151.04)	15.48 (239.63)	9.41 (88.54)
II		6.98 (48.72)	10.75 (115.56)	11.26 (126.78)	9.05 (81.90)	14.90 (222.01)	11.36 (129.04)
III			4.52 (20.43)	14.15 (200.22)	9.68 (9.68)	19.13 (365.95)	9.40 (88.36)
IV				9.35 (87.42)	15.22 (231.64)	11.97 (143.28)	11.40 (129.96)
V					0.00 (0)	19.80 (392.04)	13.81 (190.71)
VI						0.00 (0)	15.53 (241.18)
VII							0.00 (0)

Table 7: Mean values of the seven clusters for ten characters in forty four chickpea genotype

Cluster No.	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of pods per plant	Number of seed per pod	Number of Primary branches per plant	Number of secondary branches per plant	100 seed weight (g)	Harvest index (%)	Seed yield per plant (g)
I	50.94	105.79	47.61	49.87	1.00	1.82	11.34	27.41	37.83	14.55
II	45.84	105.36	43.82	53.59	1.00	2.13	12.91	27.74	38.47	14.82
III	53.58	113.75	52.44	47.91	1.00	2.00	11.19	25.32	34.84	11.80
IV	48.91	107.27	46.81	69.37	1.02	2.42	14.34	38.85	49.51	26.33
V	44.67	109.00	52.63	49.87	1.00	2.00	11.97	21.43	34.13	11.00
VI	48.00	105.33	43.33	78.93	1.20	3.00	17.07	45.43	53.58	35.00
VII	56.33	112.33	46.97	61.97	1.00	3.00	18.30	31.83	43.47	19.00
Population mean	49.75	108.40	47.65	58.78	1.03	2.33	13.87	31.14	41.69	18.92

Table 8: Percent contribution of different characters

Sr. No.	Character	Contribution%
1	Days to 50% flowering	20.82%
2	Days to maturity	13.42%
3	Plant height (cm)	16.38%
4	Number of pods per plant	31.92%
5	Number of seeds per pod	2.43%
6	Number of Primary branches per plant	0.02%
7	Number of secondary branches per plant	0.95%
8	100 seed-weight (g)	7.61%
9	Harvest index (%)	5.92%
10	Seed yield per plant (g)	0.53%

6. Conclusions

1. Analysis of variance revealed highly significant differences among genotypes for all the traits indicating that that is ample amount of variability.
2. The phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters. High GCV and high PCV were observed for Seed yield per plant, 100 seed weight. This indicates that these characters provide good source of variation and hence are useful in crop improvement programme in chickpea.
3. High heritability coupled with high genetic advance as per cent mean observed for number of Plant height, number of pods per plant, number of secondary branches, 100 seed weight, harvest index and seed yield per plant which indicates that these traits were predominantly governed by additive gene action and selection of these traits would be more effective for desired genetic improvement.
4. Seed yield per plant had significant and positive relationship with number of pods per plants, number of seeds per pod, number of primary branches, number of secondary branches, 100 seed weight, harvest index.
5. The highest direct positive effect on seed yield per plant was showed by Harvest index, 100 seed weight, number of pods per plant, number of seeds per pod. Hence selection based on these characters can help in improvement of seed yield in chickpea.
6. The 44 genotypes studied were grouped in seven diverse clusters. The maximum intra cluster distance was registered between cluster IV whereas maximum inter cluster showed by cluster V and cluster VI.
7. Among the 10 characters studied, the Number of pods per plant showed maximum contribution towards divergence followed by days to 50% flowering, plant height, days to maturity, 100 seed weight, harvest index, number of seeds per pod.
8. Considering the performance of genotypes Phule G 1521-12-2, PG 357, BG 4047, Phule Vikram, RG 2230, NDG 22-10, NDG 22-6 should be used in incorporated into future breeding efforts or may be tested in multi-location trial.

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