Original Research Article

Approaches for Genetic analysis of Chickpea Genotypes under Late Sown Condition

ABSTRACT

Investigation of the genetic potential of chickpeas is crucial in order to achieve durable and high-yielding genotypes through careful parent selection, focused hybridization, and successful trait integration. Therefore, the goal of this study is to identify the genetic potential and personality traits associated. Evaluation of thirty-six *desi* genotypes of chickpea under late sown condition revealed that substantial degree of variation was present, while three traits *viz*., Leaf pattern, flower colour, seed shape and plant pigmentation were found monomorphic, whereas foliage colour, seed surface were dimorphic,polymorphic traits were noted in leaflet size, plant growth habit, plant height, seed colouring, days to 50% flowering and days to maturity. Magnitude of genotypic coefficient of variations, high heritability along with high genetic advance as percentage of mean recorded forharvest index, number of seeds per plant, number of pods per plant and number of effective pods per plantprovides evidence that these parameters were under the control of additive gene effects andeffective selection could be possible for improvement for these traits.Correlation and path analysis revealed biological yield, 100 seed weight, seed per plant, harvest Index and plant height are the mostimportant characters,while imparting selection as these exhibited positive and strong association and maximum positive direct effects on seed yield per plant.Intra cluster D^2 values showed that most diverse genotypes were Phule G13110 and PG 0104, hybridization program between these genotypes may generate desirable sergeants for various yield attributing traits. Genotypes GL 12021, PG 158, PG 0104, JG 24, H 12-62, IPC 2010-134, GNG 2261, GL29098, BG 3067, IPC 2012-98, Phule G13110 and RVSSG 38 were present in more than one PCs hence contributed maximum towards yield and can be used in various breeding programmes for yield improvement under late sown condition.

Keywords: *Chickpea, Association, Path, Heritability,* D^2 *analysis, PCA*

1. INTRODUCTION

Chickpea [*Cicer arietinum*(L.)] is an annual, self-pollinating, diploid pulse crop. Based on seed size and color, cultivated chickpeas are of two types: Macrosperma *(kabuli* type) and

Microsperma (*desi* type). It is one of the cheapest and readily available sources of protein (22%-25%), substitute in making up the deficiency of cereal diets, as well as being an important source of human food and animal feed and helps to improve soil fertility

Chickpea is the most important *rabi* crop, which is predominantly grown in the vast rainfed areas of the country, but it is also grown in irrigated situation under late sown condition. Its area under late-sown conditions is increasing, particularly in northern and central India, due to inclusion of chickpea in new cropping systems and intense sequential cropping practices.

There is dire need toevolve high yielding varieties capable for betterperformance genotypes to bridge the yield gap. Diverse geneticmaterial and its characterization is a pre-requisite forall the breeding programs. Diversity amongparental material provides maximum chances toresearchers to devise desirable breeding strategies. Assessment andexploration of diversity among genotypes isimportance for a successful breeding program. Assessment of diversity is of great importance for the researchersproviding maximum chances for the development ofmost suitable plant genotypes. Therefore, exploration of genetic diversity is of muchimportance for success of a breeding program.Multivariate analysis involves principalcomponent analysis (PCA) and diversity analysis which were found most efficientfor assessment of genetic variation in chickpeagenotypes. Keeping in this view, the present investigation has been planned under the late sowing condition.

2. MATERIAL AND METHODS

Thirty six genotypes of *desi* chickpea were sown in a Randomized Complete Block Design (RCBD) with three replications at JNKVV, Jabalpur under late sown condition. Each genotype was allocated in a 4.8 m^2 plot with plant-to-plant spacing of 10.0 cm. Observations were recorded on four phenological traits *viz*., days to flower initiation (FI), days to 50% flowering(50%F), days to pod initiation (PI), days to maturity (DM), and ten quantitative traits *viz*., plant height (PH), number of primary branches per plant (PB), number of secondary branches per plant (SB), total number of pods per plant (PP), number of effective pods per plant (EP), number of seeds per pod (SP), hundred seed weight (100SW), number of seedsperplant (SP), biological yield per plant (BY), harvest index (HI), and seed yield per plant (SY).The standard biometric techniques were applied for analysis of the data in the present investigation.

3. RESULTS AND DISCUSSIONS

3.1 Morphological characterization

Characterization of morphological traits, variation were found in the foliage colour categorized under 2 type's, 20 accessions had light green foliage colour, while 16 accessions had dark green foliage colour. Based on leaflet size 21 accessions were reported small leaflet size, 8 accessions were medium, while remaining 7 accessions had large leaflet size.

The height of the plant can be grouped into 3 categories, 24 genotypes were medium stature (45-65 cm), 10 genotypes had short (< 45 cm) and remaining 2 genotypes (JG24 and JG24-1) had tall (> 65 cm) stature. In chickpea large variation were recorded on plant growth habit, majority of the genotypes had semi-erect type growth habit only 6 genotypes *viz.,* JG 24, Phule G13110, GNG 2304, JSC 56, PG 0104 and GL 1202had erect type growth habit.

Seed traits areimportant markers for the identification of the genotypes. These traits determinesmarket preference and consumer acceptability. Royal Horticultural Society (RHS) describes 21 color codes for mature seeds of chickpea. Out of 36 genotypes studied, 11 genotypes were brown, 9 genotypes were dark brown, 6 were genotypes yellow (RKG 13-155, IPC 2012-49, GL 12003, H 12-55, GNG 2261, GL 12021) and 5genotypes were grayish brown (GNG 2304, BG 3068, RVSSG 38, IPC 2012-98, IPC 2010-134), 3 genotypes were beige (RKG 13-180, JG 74315-14, NbeG 511) and 2 genotypes were dark brown (JG24, JG24-1).Seed coat texture is an important identification trait, in this investigation thirty one genotypes had smooth seed surface, whereas remaining 5 genotypes *viz.,* CSJ887, PG 158, JG 24, JG 74315-14 and GJG 1319 had rough seed surface.Seed ribbing was present in 27 genotypes and absent in 9 genotypes. Seed size of *desi* genotypes can be classified into 3 categories according to the weight of 100 seeds (seed index), 18 were reported to have small seed size in this study, 4 medium (18-22) and 14 had large seed size (>22g).

Though, these morphological traits showed overlapping of expression in various combination traits, yet proved to be of great utility as identity of all the genotypes could be established individually are in agreement with the previous finding [1, 2].

3.2 Estimates of genetic variability

Estimates of parameters of genetic variability (Table 1). The magnitude of the phenotypic coefficient of variation (PCV %) surpassed the genotypic coefficient of variation (GCV%) for all the observed traits. The highgenotypic and phenotypic coefficient of variation were observed for seed yield per plant followed by number of effective pods per plant, total number of pods perplant, number of seedsper plant, biological yield per plant, 100 seed weight, harvest index, number of secondary branchesperplant, plant height, days to flower initiation. The lowest genotypic coefficient of variation was found for number of primary branchesper plant, days to 50% flowering, days to pod initiationand days to maturity. The results were consistent with the findings reported in previous studies [3, 4, 5]. The heritability ranged from 45.9% to 99.4% across the traits. The high heritability were observed for harvest index, number of seedsperplant, number of effective podsperplant, number of podsperplant, days to flower initiation, plant height, days to pod initiation, days to 50% flowering, biological yieldperplant, days to maturity and seed yieldperplant. These findings indicate that a significant portion of the observed phenotypic variation for these traits can be attributed to genetic factors, with less influence from environmental conditions. Likewise, the range of genetic advance as a percentage of the mean extended from 0.0% to 34.3%.The traits that exhibited notably high values of genetic advance were 100 seed weight, harvest index, seedsperplant and podsperplant. High heritability coupled with high genetic advance as percentage of mean was recorded for harvest index, number of seedsperplant, number of podsperplant and number of effective podsperplant. Such results indicated, predominantly the presence of additive gene action in the expression of these traits and consequently chance of improving these traits through simple selection.A character showing high heritability with low genetic advance mean was recorded for, biological yieldper plant and seed yieldper plant. This reflects the presence of non-additive gene effects. Selection based on such traits may not be rewarding.Consequently, these characteristics emerge as pivotal genetic parameters for the enhancement and selection of high-yielding genotypes.

Table 1: Genetic parameters of variability for yield and its component traits chickpea genotypes.

S.No.	**Character**	**Mean**	**Range**		**Coefficient of variation (%)**		**h^2bs (%)**	**GA as % of mean 5%**
			Min.	**Max.**	**PCV (%)**	**GCV (%)**		
1	FI	50.3	38.0	64.0	15.2	15.0	97.4	30.6
2	50% F	62.2	51.7	74.0	10.5	10.3	96.4	21.0
3	PI	68.8	57.7	82.7	9.2	9.0	96.7	18.3
4	DM	97.1	87.7	107.4	5.5	5.3	92.8	10.6
5	PH	49.1	34.2	66.5	16.5	16.3	96.8	33.0
6	PB	1.9	1.7	2.2	11.1	3.6	45.9	2.4
7	SB	5.1	3.4	6.8	18.4	13.7	54.7	20.8
8	PP	50.8	16.7	54.5	33.2	32.5	97.8	42.1
9	EP	40.5	11.7	66.4	34.2	33.9	98.0	38.3
10	SP	45.6	15.4	64.9	32.3	32.0	98.7	44.9
11	100SW	20.9	12.6	34.4	28.4	27.8	95.9	56.2

12	BY	35.6	7.3	36.4	31.8	30.8	93.3	26.1
13	HI	61.9	26.3	104.7	27.0	26.9	99.4	55.4
14	SY	50.2	24.7	55.7	35.0	33.6	91.9	16.9

Note: *FI=days to flower initiation, 50%F=days to 50% flowering, PI=days to pod initiation, DM=days to maturity, PH=plant height (cm), PB=number of primary branches per plant, SB=number of secondary branches per plant, PP=total number of pods per plant, EP=number of effective pods per plant, SP=number of seeds per pod, 100SW=hundred seed weight (g), SP=number of seeds per plant, BY=biological yield per plant (g), HI=harvest index and SY=seed yield per plant (g).*

3.3 Character association

Seed yieldperplant exhibited positive and significant correlation (Table 2) with biological yieldperplant, 100 seed weight, total number of podsperplant, number of effective podsperplant, number of seedsperplant, harvest index, plant height, and number of primary branchesperplant. Whereas, negative correlation was exhibited days to pod initiation, days to flower initiation, days to 50%flowering, days to maturity, number of secondary branches per plant. The results were in accordance with the earlier findings [6, 7, 8]. From the present investigation on correlation studies, it appeared that biological yieldperplant, 100 seed weight, total number of podsperplant, number of effective pods per plant, number of seedsperplant, harvest index, plant height, number of primary branchesper plant and seed yieldperplant showed significant and positive relationship with most of the characters; hence these traits must be taken into consideration for improvement of seed yield. Highly significant and positive association among the various yield attributing traits indicate immense scope for the seed yield improvement in chickpea.

Table 2: Phenotypic Correlation Coefficient analysis for yield and its contributing traits in chickpea

Characters	**FI**	**50% F**	**PI**	**DM**	**PH**	**PB**	**SB**	**PP**	**EP**	**SP**	**100SW**	**BY**	**HI**	**SY**
FI	1.000	0.914**	0.854**	0.739**	0.543**	0.027	0.462**	-0.374**	-0.294*	-0.303*	-0.248*	-0.178	-0.421**	-0.475
50% F		1.000	0.914**	0.813**	0.604**	0.011	0.496**	-0.316**	-0.228*	-0.231*	-0.148	-0.067	-0.426**	-0.394
PI			1.000	0.805**	0.440**	0.024	0.444**	-0.340**	-0.245*	-0.195*	-0.319**	-0.146	-0.459**	-0.497
DM				1.000	0.401**	0.017	0.513**	-0.168	-0.126	-0.110	-0.177	-0.002	-0.444**	-0.363
PH					1.000	-0.049	0.290*	-0.300*	-0.241*	-0.300*	0.314**	0.233*	-0.219*	0.048
PB						1.000	0.358**	-0.037	-0.017	0.041	0.048	0.117	-0.091	0.072
SB							1.000	-0.085	-0.012	-0.023	0.001	0.210*	-0.440**	-0.104
PP								1.000	0.943**	0.706**	0.160	0.582**	-0.033	0.582
EP									1.000	0.729**	0.143	0.591**	-0.065	0.577
SP										1.000	0.011	0.506**	-0.185	0.395
100SW											1.000	0.548**	0.088	0.617
BY												1.000	-0.361**	0.699
HI													1.000	0.315

*** Significant at 5% and 1% level*

Note: *FI=days to flower initiation, 50%F=days to 50% flowering, PI=days to pod initiation, DM=days to maturity, PH=plant height (cm), PB=number of primary branches per plant, SB=number of secondary branches per plant, PP=total number of pods per plant, EP=number of effective pods per plant, SP=number of seeds per pod, 100SW=hundred seed weight (g), SP=number of seeds per plant, BY=biological yield per plant (g), HI=harvest index and SY=seed yield per plant (g).*

3.4 Path coefficient analysis

The genotypic path revealed (Table 3) that days to 50% flowering, plant height, number of secondary branchesperplant, 100-seed weight, number of seedsperplant, biological yieldperplant and harvest index had positive direct effect on seed yield per plant.Days to maturity, number of primary branchesperplant, number of podsperplant, number of effective podsperplant and number of seedsperpod showed negative direct on seed yieldper plant.Similarly,as direct effect; the indirect effects will also find it contribution via different traits towards the seed yield per plant. Majority of indirect effects of various independent traits via other traits were extremely low of either signs. The indirect effects of number of secondary branches per plant, number of pods perplant, number of effective pods per plant, 100-seed weight, number of seeds per pod, number of seeds perplant, biological yieldper plant and harvest index were positive on seed yield per plant.

Table 3: Genotypic Path coefficient analysis for yield and its component characters in chickpea

Characters	FI	50% F	PI	DM	PH	PB	SB	PP	EP	SP	100SW	BY	HI
FI	0.1351	0.1265	0.1180	0.1040	0.0760	0.0103	0.0872	-0.0515	-0.0408	-0.0411	-0.0348	-0.0251	-0.0575
0.5000	-0.0471	-0.0503	-0.0473	-0.0432	-0.0313	0.0015	-0.0344	0.0162	0.0118	0.0118	0.0081	0.0035	0.0218
PI	-0.0477	-0.0513	-0.0546	-0.0460	-0.0250	-0.0048	-0.0345	0.0189	0.0137	0.0107	0.0177	0.0083	0.0256
DM	-0.0406	-0.0452	-0.0444	-0.0527	-0.0224	-0.0023	-0.0401	0.0094	0.0067	0.0061	0.0096	0.0004	0.0244
PH	0.0036	0.0040	0.0030	0.0027	0.0065	-0.0009	0.0025	-0.0020	-0.0016	-0.0020	0.0021	0.0016	-0.0014
PB	0.0066	-0.0026	0.0077	0.0037	-0.0120	0.0870	0.0421	-0.0111	-0.0045	0.0140	0.0090	0.0253	-0.0299
SB	-0.0289	-0.0307	-0.0283	-0.0341	-0.0176	-0.0217	-0.0449	0.0051	0.0012	0.0011	-0.0007	-0.0111	0.0270
PP	-0.0389	-0.0328	-0.0353	-0.0182	-0.0310	-0.0130	-0.0117	0.1021	0.0978	0.0736	0.0170	0.0623	-0.0037
EP	-0.0127	-0.0098	-0.0106	-0.0054	-0.0103	-0.0022	-0.0011	0.0403	0.0421	0.0313	0.0063	0.0258	-0.0028
SP	0.0105	0.0081	0.0068	0.0040	0.0107	-0.0056	0.0008	-0.0249	-0.0257	-0.0346	-0.0003	-0.0182	0.0064
100SW	-0.0129	-0.0081	-0.0163	-0.0092	0.0161	0.0052	0.0008	0.0084	0.0075	0.0004	0.0503	0.0296	0.0048
BY	-0.1612	-0.0604	-0.1320	-0.0072	0.2168	0.2519	0.2153	0.5289	0.5319	0.4573	0.5111	0.8674	-0.3241
HI	-0.2986	-0.2732	-0.2958	-0.2924	-0.1405	-0.1658	-0.3801	-0.0228	-0.0427	-0.1173	0.0601	-0.2359	0.6312
SY	0.5028	-0.4260	-0.5292	-0.9339	0.0360	0.1396	-0.1981	0.6170	0.5974	0.4113	0.6555	0.7339	0.3287
Partial R	-0.0679	0.0215	0.0289	0.0208	0.0002	0.0122	0.0089	0.0630	0.0251	-0.0142	0.0329	0.6366	0.2075

Note: *FI=days to flower initiation, 50%F=days to 50% flowering, PI=days to pod initiation, DM=days to maturity, PH=plant height (cm), PB=number of primary branches per plant, SB=number of secondary branches per plant, PP=total number of pods per plant, EP=number of effective pods per plant, SP=number of seeds per pod, 100SW=hundred seed weight (g), SP=number of seeds per plant, BY=biological yield per plant (g), HI=harvest index and SY=seed yield per plant (g).*

3.5 Genetic diversity analysis

The percentage contribution towards genetic divergence revealed that, highest for harvest index followed by number of seedsperplant. Other characters *viz* days to flower initiation, plant height, total number of podsper plant, 100 seed weight, biological yield, number of effective podsper plant and days to pod initiation showed low percent of contribution, whereas remaining characters exhibited very low or negligence contribution towards divergence.

On the basis of cluster mean values (Table 4), cluster VI had highest mean value for days to maturity, days to pod initiation, days to 50% flowering, days to flower initiation and number of secondary branchesperplant. Cluster V had highest mean value for number of seedsperpod. Cluster VIII for harvest index; cluster IX for number of podsper plant, number of effective pods perplant, number of seeds per plant, biological yield and seed yield per plant; cluster IV for plant height, 100 seed weight; cluster III for number of primary branches.Intercrossing of genotypes involved in these clusters could be practiced for inducing variability in the respective characters and their rationale improvement for increasing seed yield. These findings align with past observations [7].

Table 4: Cluster mean for yield and yield contributing traits of chickpea genotypes

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
FI	56.97	44.07	47.90	54.33	51.67	57.00	41.00	53.00	42.00
50%F	67.82	56.83	59.38	66.67	59.00	71.67	55.67	65.33	56.00
PI	75.15	63.63	66.48	68.11	66.00	78.00	63.00	72.67	65.33
DM	101.24	94.80	94.19	98.56	92.67	106.33	87.33	100.00	94.00
PH	51.10	43.03	46.50	65.64	47.20	58.13	47.90	59.43	38.90
PB	2.01	1.97	2.04	1.92	1.80	2.00	1.90	1.90	1.90
SB	5.65	4.48	4.84	5.62	4.43	5.80	4.47	4.87	5.03
PP	27.52	31.61	39.17	35.86	16.67	35.13	15.87	18.33	65.90
EP	27.19	27.51	35.77	33.66	15.90	27.03	11.67	16.43	66.47
SP	33.22	34.56	52.49	35.74	28.33	28.90	15.47	26.33	64.90
100SW	18.49	22.81	18.43	32.84	12.87	17.20	23.60	15.40	24.73
BY	14.18	13.47	17.79	22.23	8.43	18.40	8.27	7.30	23.20
HI	51.79	73.48	56.78	59.14	54.53	26.37	98.33	104.67	67.07
SY	7.30	9.63	10.02	12.97	5.03	4.83	7.87	8.17	15.33

***Note:** FI=days to flower initiation, 50%F=days to 50% flowering, PI=days to pod initiation, DM=days to maturity, PH=plant height (cm), PB=number of primary branches per plant, SB=number of secondary branches per plant, PP=total number of pods per plant, EP=number of effective pods per plant, SP=number of seeds per pod, 100SW=hundred seed weight (g), SP=number of seeds per plant, BY=biological yield per plant (g), HI=harvest index and SY=seed yield per plant (g).*

The study comprised of 36 chickpea genotypes, which were assessed for nature and magnitude of genetic divergence based on 15 quantitative characters using Mahalanobis's D^2 statistic. On the basis of D^2 values, the 36 genotypes were grouped into 9 clusters (Table 5), following Tocher's method. Cluster I, II, and cluster III were poly-genotypic consisting of 11, 10, 7 and 3 genotypes respectively and remaining clusters were mono-genotypic.Cluster

II was the most diversified, having highest Intra-cluster cluster. On the basis of inter-cluster distances (Table 6), the highest inter cluster divergence was observed between genotypes of cluster VI and cluster VII, followed by cluster VII and cluster IX, cluster VI and cluster VIII, cluster VIII and cluster IX, cluster VI and cluster IX, cluster V and cluster IX, cluster III and cluster VII, cluster III and VIII, cluster I and VII. Researchers supporting the present findings [4, 7, 8, 9, 10]. Elite genotypes can be selected based on these traits and used as donor parents in future hybridization programs.

Table 5: Distribution of chickpea genotypes in different clusters

Cluster No.	No.of genotypes	Genotypes
I	11	PG158, GL 12021, GNG 2261, BG 3067, H 12-62, GL29098, IPC 2010-134, GNG 2299, JSC 56 , BG 3068
II	10	JG 74315-14, RVSSG 38, NBeG 511, PBC 501, RKG 13-180, NBeG 507, GL29098, RKG 13-155, NDG 14-24, JSC 55
III	7	CSJ887, H 12-55, RVG 203, GJG 1319, IPC 2012-98, CSJ884, RVG 202
IV	3	JG24, JG24-1, JG 24
V	1	GNG 2304
VI	1	PG 0104
VII	1	Phule G13110
VIII	1	GL 12003
IX	1	Phule G0719-10

Note: *FI=days to flower initiation, 50%F=days to 50% flowering, PI=days to pod initiation, DM=days to maturity, PH=plant height (cm), PB=number of primary branches per plant, SB=number of secondary branches per plant, PP=total number of pods per plant, EP=number of effective pods per plant, SP=number of seeds per pod, 100SW=hundred seed weight (g), SP=number of seeds per plant, BY=biological yield per plant (g), HI=harvest index and SY=seed yield per plant (g).*

Table 6: Inter and intra cluster D^2 values for different clusters

Cluster	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**
I	128.07	316.76	266.35	240.51	182.69	266.81	845.37	766.05	703.51
II		155.17	334.59	307.20	250.28	771.77	383.30	468.10	667.63
III			188.54	323.81	350.64	514.38	1006.44	899.93	354.33
IV				72.57	403.40	479.30	733.95	639.73	584.97
V					-0.00	418.33	576.82	691.53	1017.17
VI						0.00	1619.55	1571.25	1022.62
VII							0.00	211.42	1591.68
VIII								0.00	1375.74
IX									0.00

Note: *FI=days to flower initiation, 50%F=days to 50% flowering, PI=days to pod initiation, DM=days to maturity, PH=plant height (cm), PB=number of primary branches per plant, SB=number of secondary branches per plant, PP=total number of pods per plant, EP=number of effective pods per plant, SP=number of seeds per pod, 100SW=hundred seed weight (g), SP=number of seeds per plant, BY=biological yield per plant (g), HI=harvest index and SY=seed yield per plant (g).*

3.6 Principal Component Analysis

In the present study, Rotated component matrix revealed that the PC1 which accounted for the highest variability (28.144%), and was mostly related to yield attributing traits like days to

50% flowering, days to pod initiation, days to flower initiation, days to maturity, seed yield per plant and number of secondary branches per plant (Table 8). PC 2 was dominated by phenological traits *i.e*. number of effective pods per plant, biological yield per plant, number of pods per plant and number of seeds per plant. PC 3 was dominated by physiological traits i.e. 100 seed weight, plant height, PC 4 was dominated by harvest index, while PC5 was dominated by traits *i.e.* number of primary branches per plant. Similar studies on maximum contribution of character towards genetic divergence was performed by [11] for days to 50% flowering, days to maturity and plant height

In PC1, principal component scores (Table 9) ranged from 0.562(GNG 2299) to 4.350 (GL 12021). Maximum value of PC1 component scores was recorded in GL 12021 followed by followed by PG 158, PG 0104, JG 24, H 12-62, IPC 2010-134, GNG 2261, GL29098, BG 3067, IPC 2012-98, Phule G13110, JG24 and RVSSG 38. In PC2, scores ranged from 0.515 (RVG 203) to 4.560 (Phule G0719-10). In PC 3, the value ranged from 0.634 (Phule G13110) to 3.887 (JG24). In PC 4 component scores ranged from 0.552(CSJ884) to 1.638 Phule G13110). While, In PC 5, the value of the component ranged from 0.507 (CSJ887) to 2.173 (BG 3067).

Table 7: Eigen values, % variance and cumulative Eigen values for corresponding 14 traits in chickpea

Traits	Principal component	Eigen value	Variability (%)	Cumulative %
FI	PC1	4.503	28.144	28.144
50%F	PC2	2.823	17.642	45.786
PI	PC3	1.486	9.286	55.072
DM	PC4	1.267	7.916	62.988
PH	PC5	1.074	6.713	69.701
PB	PC6	0.793	4.956	74.657
SB	PC7	0.736	4.599	79.255
PP	PC8	0.631	3.945	83.2
EP	PC9	0.505	3.155	86.356
SP	PC10	0.483	3.021	89.376
100SW	PC11	0.458	2.861	92.237
BY	PC12	0.368	2.301	94.538
HI	PC13	0.327	2.042	96.579
SY	PC14	0.223	1.395	97.974

Note: *FI=days to flower initiation, 50%F=days to 50% flowering, PI=days to pod initiation, DM=days to maturity, PH=plant height (cm), PB=number of primary branches per plant, SB=number of secondary branches per plant, PP=total number of pods per plant, EP=number of effective pods per plant, SP=number of seeds per pod, 100SW=hundred seed weight (g), SP=number of seeds per plant, BY=biological yield per plant (g), HI=harvest index and SY=seed yield per plant (g).*

Table 8: PC values of rotation component matrix for eighteen variables of chickpea

	PCI	PC2	PC3	PC4	PC5
FI	**0.839**	**0.162**	0.005	0.223	-0.039
50%F	**0.852**	**0.209**	0.067	0.273	-0.088
PI	**0.844**	**0.158**	-0.078	0.257	0.006
DM	**0.739**	**0.298**	0.01	0.17	-0.026
PH	0.46	0.096	0.572	0.046	-0.203
PB	0.14	0.259	0.137	-0.289	**0.774**
SB	0.526	0.453	0.196	-0.139	0.308
PP	-0.465	0.684	-0.174	0.277	-0.035
EP	-0.407	0.728	-0.17	0.307	0.030
SP	-0.343	0.566	-0.429	0.039	0.054
100SW	-0.327	0.232	0.618	-0.195	-0.348
BY	-0.234	0.745	0.295	-0.21	-0.07
HI	-0.464	-0.378	0.103	0.479	0.065
SY	-0.586	0.345	0.431	0.184	0.056

Note: *FI=days to flower initiation, 50%F=days to 50% flowering, PI=days to pod initiation, DM=days to maturity, PH=plant height (cm), PB=number of primary branches per plant, SB=number of secondary branches per plant, PP=total number of pods per plant, EP=number of effective pods per plant, SP=number of seeds per pod, 100SW=hundred seed weight (g), SP=number of seeds per plant, BY=biological yield per plant (g), HI=harvest index and SY=seed yield per plant (g).*

Table 9: PCA scores of chickpea genotypes having positive >0.5 values in each PCs

PC1	**PC2**	**PC3**	**PC4**	**PC5**
GL 12021	Phule G0719-10	JG24	Phule G13110	BG 3067
PG 158	JSC 56	JG24-1	GL12003	GL29098
PG 0104	JG24	RVG 202	CSJ887	RKG 13-155
JG 24	JG24-1	NbeG 507	GNG 2299	NbeG 507
H 12-62	PG 0104	BG 3067	RKG 13-180	H 12-55
IPC 2010-134	H 12-55	IPC 2012-49	RVSSG 38	H 12-62
GNG 2261	GJG 1319	GJG 1319	H 12-55	CSJ884
GL29098	CSJ884	PG 158	PBC 510	BG 3068
BG 3067	IPC 2010-134	RKG 13-180	JG24	PG 158
IPC 2012-98	JSC 55	GL 12003	JG24-1	GJG 1319
Phule G13110	IPC 2012-98	Phule G13110	CSJ884	CSJ887
RVSSG 38	BG 3068	-	-	-
	GNG 2261	-	-	-
-	BG 3067	-	-	-
-	RKG 13-155	-	-	-
-	GL 12021	-	-	-
-	PG 158	-	-	-
-	RVG 203	-	-	-

4. CONCLUSION

On the basis of phonological and yield attributing traits, five genotypes *viz*., JG 24, Phule G0719-10, RVG 203, GJG 1319 and RKG 13-180 were found promising under late sown condition. High magnitude of genotypic coefficient of variations, high heritability along with high genetic advance as percentage of mean recorded for harvest index, number of seeds per plant, number of pods per plant and number of effective pods per plant provides evidence that these traits were under the control of additive gene effects. Selection of these traits will be effective and rewarding for improvement of chickpea under late sown condition. Seed yield per plant showed highly significant and positive association with biological yield, 100 seed weight, number of pods per plant, number of effective pods per plant, number of seeds per plant and harvest index. For genetic improvement of seed yield, these traits should be given prime importance. Path analysis revealed that biological yield per plant, harvest index, days to flower initiation, number of pods per plant and number of primary branches per plant exerted maximum positive direct effect on seed yield per plant. High biological yield, harvest index, more number of pods and primary branches should be consider for constructing plant type of chickpea under late sown condition.

Harvest index, number of seeds per plant, days to flower initiation, plant height, number of pods per plant and 100 seed weight showed maximum contribution towards genetic divergence. The hybridization between genotypes with maximum inter cluster distance from cluster VII (Phule G13110) and VI (PG 0104) may leads to the formation of superior segregants/transgressive segregates in breeding program. The genotypes Phule G0719-10, GL 12021, PG 158, PG 0104, JG 24 and H 12-62 have highest PC values for yield related traits. These genotypes can be used for further breeding programs for the development of high yield under late sown condition.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that no generative AI technologies such as large language models (chatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

CONSENT

All authors declare that ‘written informed consent was obtained from the patient (or other approved parties) for publication of this case report and accompanying images. A copy of the written consent is available for review by the Editorial office/Chief Editor/Editorial Board members of this journal.

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