Genetic Variability and Diversity Analysis for Yield and its Associated Traits in Chickpea (*Cicer arietinum* L.)

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Original Research Article

ABSTRACT

Chickpea (*Cicer arietinum* L.) is a leguminous self-pollinating crop belongs to family- Leguminosae (Fabaceae). The aim of a plant breeder is to identify or develop high yielding cultivars. In the present investigation, 83 genotypes grown during *Rabi* 2021-22 to investigate genetic variability, heritability and genetic advance, correlation, direct and indirect effects and genetic divergence (D^2 analysis) among yield and its attributing traits. High GCV and PCV recorded for the numbers of pods per plant

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and biological yield indicating the presence of substantial amount of genetic variability in the experimenting material. High heritability coupled with high genetic advance was shown for seed yield per plant, hundred seed weight. Selection based on these traits may be proved worthwhile. Significant and positive correlation was documented for seed yield per plant with numbers of pods per plant and biological yield and path analysis signified that biological yield had the highest positive direct effect on seed yield per plant. The data obtained from the present investigation may be proved helpful in the selection of high yielding superior genotype (s) of chickpea.

1. INTRODUCTION

Chickpea, also known as gram, Bengal gram, Egyptian pea, Garbanzo or Garbanzo bean, is a self-pollinated, annual diploid ($2n = 2x = 16$) species [1] with a genome size of 738 Mb [2] which aids in increasing soil fertility by biological nitrogen fixation. The taxonomic hierarchy of chickpea is family Fabaceae (Leguminoseae), sub-family Faboideae (Papilionaceae) and tribe *Cicereae*. "According to the seed morphology, chickpeas can be separated into: *desi* type, which has small seeds with a brown coat colour, and *kabuli* type, which has big seeds with a cream- or beige-colored coat" [3-5]. "It is highly nutritious encompassing of vitamins, minerals, and vital amino acids, including lysine, methionine, threonine, valine, and leucine, as well as ß-carotene, calcium, phosphorus magnesium, and potassium" [6-10]. "Chickpea productivity is reduced by abiotic factors *viz.*, drought; heat, excessive salt and cold" [11] and "biotic factors including Ascochyta blight, Fusarium wilt and Helicoverpa" [12].

"The basic information on the existence of genetic variability in a population and the relationship between different traits is essential for any successful plant breeding programme" [13-22]. "The genotypic coefficient of variation estimates the heritable variability, while the phenotypic co-efficient measures the role of the environment on the genotype. Hence, Selection depends on heritability, selection intensity, and the genetic advance of traits" [3,23-31]. "The efficiency of selection with higher yield is depends upon the existing variability and other genetic factors" [32]. "The assessment of major characteristics and their interrelatedness is important in developing selection criteria for improving existing genotypes" [33]. "Path coefficient analysis helps to determine the direct effect of traits and their indirect effects on other traits. A directional model based on seed yield and its components that provides the chance for selection is used in correlation analysis to evaluate the mutual relationship between two parameters" [34]. Mahalanobis's D^2 statistics is a powerful tool in quantifying the degree of variability at the genotype level.

The current investigation was aimed to investigate genetic variability, heritability and genetic advance, correlation, direct and indirect effects and genetic divergence (D^2 analysis) among yield and its attributing traits.

2. MATERIALS AND METHODS

The investigation was carried out to know the genetic variability, correlation and path analysis of 83 chickpea (63 desi and 20 kabuli type) genotypes (Table 1). The experiment was carried out at Agriculture Research Farm, Department of Plant Breeding & Genetics College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya (RVSKVV), Gwalior, Madhya Pradesh. India. All the 83 genotypes were sown in randomized block design (RBD) with two replications. The genotypes were planted during November, 2021 and harvested during the March 2022. "Each entry was planted in 4 rows of 3m length, keeping row to row and plant to plant distance of 30 x 15, respectively. All the recommended package of practices was followed. Data were recorded on 10 different characters including days to 50 % flowering, days to maturity, plant height, numbers of branches per plant, numbers of pods per plant, total numbers of seeds per pod, 100- seed weight, harvest index, biological yield per plant and seed yield per plant. Five plants from each replication were randomly selected from each genotype for recording observations for all the traits" [28].

Table 1. List of chickpea genotypes used in the present study

S. No.	Name of genotype	S. No.	Name of genotype	S. No.	Name of genotype	S. No.	Name of genotype	S. No.	Name of genotype
1	SAGL 162380	18	BGD 112	35	SAGL 152216	52	NBeG 47	69	RVSSG 77
2	SAGL 162379	19	RVG 205	36	SAGL 152218	53	JG 322	70	BG 362
3	SAGL 152320	20	RVSSG 71	37	SAGL 152405	54	GJG 3	71	ICCV 2
4	SAGL 152348	21	ICC 4958	38	SAGL 171015	55	JG 218	72	RVKG 111
5	JGG 1	22	ICCV 10	39	SAGL 161015	56	JSC 35	73	RVKG 151
6	RVSSG 44	23	RVSSG 72	40	SAGL 190028	57	RVSSG 54	74	RVSSG 78
7	RVSSG 42	24	RVSSG 74	41	JG 14	58	HC 5	75	RVSSG 89
8	JAKI 9218	25	JG 33	42	JG 315	59	GG 2	76	RVSSG 36
9	RVG 202	26	ICC 4812	43	RVG 201	60	GCP 101	77	SAGL 190004
10	SAGL 190001	27	JG 130	44	JG 74	61	GG 1	78	SAGL 190006
11	SAGL 190002	28	SAGL 190007	45	JG 12	62	GBM 2	79	SAGL 162304
12	JG 11	29	SAGL 190008	46	SAGL 190029	63	VIJAY	80	SAGL 152228
13	JG 16	30	RVSSG 70	47	JSC 37	64	RVSSG 30	81	SAGL 171017
14	SAGL 190003	31	SAGL 190009	48	JG 63	65	RVSSG 31	82	SAGL 171005
15	RVSSG 88	32	RVSSG 86	49	RVG 203	66	JGK 3	83	MNK 1
16	SAGL 190005	33	SAGL 190011	50	JG 36	67	JGK 5		
17	RVSSG 68	34	SAGL 190012	51	ANNAGIRI	68	JGK 2		

Genotypic (GCV) and phenotypic coefficient of variation (PCV) was calculated as per formulae suggested by Burton Burton [35], heritability in the broad sense (h^2) as proposed by Burton and De [36] and genetic advance as per the method described by Johnson et al. [37]. The correlation coefficients were determined the degree of a character's relationship with yield as well as among the variables that contribute to yield. The Weber and Moorthy [38] and Miller et al. [39] formulae was employed to calculate the correlations between genotype and phenotype. The method initially given by Wright [40] and later developed by Dewey and Lu [41] was used to perform path coefficient analysis in order to figure out the direct and indirect impacts of the various characters on yield. The genetic divergence was estimated by using D^2 analysis given by Mahalanobis [42] and the genotypes were grouped into different clusters according to Tocher's method as described by Rao [43]. "Contribution of individual characters towards divergence was estimated according to the method described" by Singh and Choudhary [44].

3. RESULTS AND DISCUSSION

3.1 Variability Studies

The ANOVA implies that the mean sums of squares due to genotypes were significant for all the traits under study *viz.*, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, numbers of pods per plant, 100-seed weight, biological yield per plant, harvest index and seed yield per plant except total numbers of seeds per pod (Table 2). This substantial variability provides a good prospect for improving traits of interest in chickpea breeding programmes as suggested by Dehal et al. [45], Katkani et al. [46], Sharma et al. [47] and Sharma et al. [48].

Results revealed that PCV% was higher than GCV% for all the traits under investigation (Table 3). High genotypic and phenotypic coefficient of variance were recorded for numbers of pods per plant, biological yield, seed yield per plant, harvest index, 100- seed weight and plant height. Similar findings were also reported by Hailu et al. [49] and Ningwal et al. [28]. This suggests that substantial phenotypic variation is present among the genotypes in respect to investigated traits indicating the scope of exploiting variability

for further improvement of these traits. "High heritability coupled with higher genetic advance as percentage of mean was documented for seed yield per plant, hundred seed weight, plant height, numbers of branches per plant, biological yield per plant, harvest index, numbers of pods per plant. It means these characters are governed by additive gene action" Thakur et al. [50] and Ningwal et al. [28].

3.2 Correlation Coefficient Analysis

Correlation provides the magnitude of linear association between pairs of characters and form the basis of selection index, thereby aiding the breeder in crop improvement programme through simultaneous manipulation of the paired traits. Genotypic and phenotypic correlations, for various yield-attributing traits were estimated considering seed yield per plant as a dependent variable (Table 4, Table 5). It was revealed from the results that the genotypic correlation coefficients for most of the characters were higher than the phenotypic correlation coefficients. This indicated that there was a strong inherent association between various characters investigated and was less influenced by environmental effects. Highly significant and positive genotypic correlation for seed yield per plant was recorded with numbers of pods per plant followed by biological yield per plant, total numbers of seeds per plant, plant height, harvest index and days to 50% flowering. These results are in accordance with the findings of Bhanu et al. [51], Jain et al. [22], Ningwal et al. [28] and Rajput et al. [30].

3.3 Path-Coefficient Analysis

The direct and indirect effects of different independent characteristics on the dependent character are measured via path coefficient analysis. It demonstrates the relationship between these independent characters and seed yield results from their direct influence on yield or from their indirect impact through other accrediting characters. In the present investigations, path coefficient analysis has been performed at genotypic and phenotypic levels taking yield as a dependent variable (Table 6, Table 7, Fig. 1, Fig. 2). In general, genotypic direct and indirect effects were somewhat higher in magnitude when equated to the phenotypic effects.

Table 2. Analysis of variance for 10 characters of 83 chickpea genotypes

Source of variation	df	Mean sum of squares									
		DT50%F	DTM	PH	NBPP	NPPP	TNSPP	100S-W	BY	HI%	SYPP
Replication	1	0.4879**	32.9879**	1081.4049**	36.1355**	571.4328**	1.6780**	4.0566**	2.4396**	1.1522**	2.9987**
Treatments	82	44.1564**	169.8630**	196.9068**	2.5969**	936.8304**	0.1834	58.6552**	214.7388**	261.3937**	31.5860**
Error	82	25.7318	33.0855	28.7998	4.9471	23.8805	0.1079	10.1639	6.5720	3.9516	8.3553

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

DT50%F=Days to 50% flowering, DTM=Days to maturity, PH=Plant height, NBPP=Numbers of branches per plant, NPPP=Numbers of pods per plant, TNSPP=Total numbers of seeds per pod, 100-SW=Hundred seed weight, BY=Biological yield per plant, HI%=Harvest Index, SYPP=Seed yield per plant

Table 3. Genetic parameters of variability for yield and its contributing traits for chickpea genotypes

S. No.	Traits	Range		Grand Mean	Coefficient of variance		h²	Genetic advance as % mean
		Min	Max		GCV%	PCV%	(b)%	
1.	DT50%F	44	70	56.3	5.39	8.34	41.7	7.173
2.	DTM	83	128	107.4	7.69	8.57	80.5	14.229
3.	PH	26	77	43.8	20.92	22.64	85.4	39.826
4.	NBPP	2.8	7.6	5.53	19.59	20.59	90.5	38.390
5.	NPPP	7.67	91	39.9	53.41	54.1	97.5	18.620
6.	TNSPP	1.0	2.0	1.34	14.5	22.6	41.2	19.161
7.	100-SW	8.9	37	20	24.58	27.04	82.7	46.055
8.	BY	6.5	52	20.6	49.40	50.18	96.9	37.210
9.	HI%	11	67	45	25.18	25.37	98.5	35.488
10.	SYPP	1.25	23	8.3	41.03	47.84	73.5	56.490

Table 4. Phenotypic correlation coefficient for yield and its attributing traits in chickpea genotypes

Character	DT50%F	DTM	PH	NBPP	NPPP	TNSPP	100-SW	BY	HI%	SYPP
DT50%F	1.000	0.1070	0.0697	0.2164	0.3060**	0.1704	-0.2370*	0.0034	0.2111	0.2598*
DTM		1.000	-0.1600	-0.1770	-0.2577**	0.0442	-0.2220*	0.0805	-0.1620	-0.1370
PH			1.000	0.1922	0.1597	0.1157	-0.0020	0.0051	0.0555	0.3077**
NBPP				1.000	0.3804**	0.2254*	0.0071	-0.3020**	0.2894**	0.1417
NPPP					1.000	0.2060	-0.212	0.0382	0.3878**	0.5068**
TNSPP						1.000	-0.035	-0.01	0.2059	0.1873
100-SW							1.000	-0.014	0.1576	-0.0830
BY								1.000	-0.4289**	0.4244**
HI%									1.000	0.2857**
SYPP										1.000

* Significant at 5% and ** Highly Significant at 1%

Table 5. Genotypic correlation coefficient for yield and its attributing traits in chickpea genotypes

Character	DT50%F	DTM	PH	NBPP	NPPP	TNSPP	100-SW	BY	HI%	SYPP
DT50%F	1.0000	-0.2444*	-0.0451*	-0.2306*	0.3673**	0.8173**	-0.6235**	0.1475	0.2807*	0.2500*
DTM		1.0000	-0.2508*	0.1932	-0.3292**	0.1636	-0.3168**	0.1358	-0.1968	-0.2586*
PH			1.0000	-0.2103*	0.1467	0.2404*	-0.0553	0.0319	0.0401	0.3174**
NBPP				1.0000	-0.3739**	-0.8634**	0.1536	0.3052**	-0.2843**	-0.1062
NPPP					1.0000	0.3681**	-0.2578*	0.0559	0.3853**	0.5464**
TNSPP						1.0000	0.0184	-0.0607	0.3383**	0.3701**
100-SW							1.0000	0.0066	0.1659	-0.1566
BY								1.0000	-0.4295**	0.5184**
HI%									1.0000	0.3127**
SYPP										1.0000

* Significant at 5% and ** Highly Significant at 1%

Table 6. Phenotypic path coefficient analysis for yield and its component traits in chickpea genotypes

Character	DT50%F	DTM	PH	NBPP	NPPP	TNSPP	100-SW	BY	HI%	SYPP
DT50%F	**0.0539**	0.0058	0.0038	0.0117	0.0165	0.0092	-0.0128	0.0002	0.0114	0.2598
DTM	-0.0048	**-0.0451**	0.0072	0.008	0.0116	-0.002	0.0100	-0.0036	0.0073	-0.1368
PH	0.0156	-0.0358	**0.2235**	0.043	0.0357	0.0259	-0.0005	0.0011	0.0124	0.3077
NBPP	0.0134	-0.011	0.0119	**0.062**	0.0236	0.014	0.0004	-0.0187	0.0179	0.1417
NPPP	0.0619	-0.0521	0.0323	0.0769	**0.2022**	0.0417	-0.0429	0.0077	0.0784	0.5068
TNSPP	0.0018	0.0005	0.0012	0.0024	0.0022	**0.0107**	-0.0004	-0.0001	0.0022	0.1873
100-SW	0.0231	0.0216	0.0002	-0.0007	0.0207	0.0034	**-0.0975**	0.0014	-0.0154	-0.0832
BY	0.0021	0.0503	0.0032	-0.1887	0.0238	-0.0059	-0.0088	**0.625**	-0.2681	0.4244
HI%	0.0928	-0.0711	0.0244	0.1272	0.1704	0.0905	0.0693	-0.1885	**0.4396**	0.2857

Table 7. Genotypic path coefficient analysis for yield and its component characters in chickpea genotypes

Character	DT50%F	DTM	PH	NBPP	NPPP	TNSPP	100-SW	BY	HI%	SYPP
DT50%F	**0.1866**	-0.0456	-0.0084	-0.043	0.0686	0.1525	-0.1163	0.0275	0.0524	0.2500
DTM	-0.0184	**0.0753**	-0.0189	0.0145	-0.0248	0.0123	-0.0239	0.0102	-0.0148	-0.2586
PH	-0.0129	-0.0715	**0.2852**	-0.06	0.0419	0.0685	-0.0158	0.0091	0.0114	0.3174
NBPP	0.0824	-0.069	0.0752	**-0.3574**	0.1337	0.3086	-0.0549	-0.1091	0.1016	-0.1062
NPPP	0.0841	-0.0754	0.0336	-0.0856	**0.2289**	0.0843	-0.059	0.0128	0.0882	0.5464
TNSPP	-0.319	-0.0638	-0.0938	0.3369	-0.1437	**-0.3902**	-0.0072	0.0237	-0.132	0.3701
100-SW	-0.0167	-0.0085	-0.0015	0.0041	-0.0069	0.0005	**0.0268**	0.0002	0.0044	-0.1566
BY	0.1141	0.105	0.0246	0.2359	0.0432	-0.0469	0.0051	**0.7732**	-0.3321	0.5184
HI%	0.1498	-0.105	0.0214	-0.1517	0.2056	0.1805	0.0885	-0.2292	**0.5336**	0.3127

Table 8. Distribution of chickpea genotypes into different clusters

Cluster No.	No. Of genotypes	Name of the genotypes
Cluster I	35	ICCV 2, RVSSG 89, JG16, SAGL 152228, JG 130, RVG 202, SAGL 190028, RVG 201, JGG 1, JG 33, SAGL 17005, SAGL 161015, SAGL 190004, RVSSG 78, SAGL 152348, SAGL 152320, ICC 4958, RVSSG 42, SAGL 190001, SAGL 162379, RVSSG 44, SAGL 162380, SAGL 190003, RVSSG 71, RVG 205, RVSSG 88, SAGL 190011, JG 74, JG 12, SAGL 171015, SAGL 152216, RVSSG 30, JGK 2, RVSSG 72
Cluster II	28	SAGL 190008, RVSSG 54, SAGL 190012, JG 14, ICCV 10, GBM 2, RVSSG 70, HC 5, GG 1, SAGL 190009, SAGL 171017, RVSSG 68, ICC 4812, SAGL 152405, JG 218, RVSSG 74, GCP 101, GJG 3, SAGL 190007, JG 315, NBeG 47, JG 11, JG 36, ANNAGIRI, SAGL 190029, RVG 203, JSC 35, GG 2
Cluster III	8	SAGL 190006, MNK 1, BG 362, SAGL 162304, VIJAY, JGK 3, RVSSG 77, RVSSG 36
Cluster IV	1	JG 322
Cluster V	4	JGK 5, RVKG 151, RVSSG 31, SAGL 190005
Cluster VI	1	JG 63
Cluster VII	1	SAGL 152218
ClusterVIII	1	JSC 37
Cluster IX	1	RVKG 111
Cluster X	1	SAGL 190001
Cluster XI	1	JAKI 9218
Cluster XII	1	BGD 112

Table 9. Inter and intra cluster D^{2}values for different clusters

Cluster No.	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII
Cluster I	**10.21**	15.92	20.48	17.19	17.23	21.36	22.99	21.53	21.71	18.53	17.73	28.78
Cluster II		**10.8**	19.29	15.07	21.28	14.42	14.93	14.03	16.87	18.74	22.3	19.1
Cluster III			**11.09**	27.48	17.98	16.93	17.07	21.33	16.84	17.59	25.69	24.18
Cluster IV				**0**	28.75	23.14	20.85	16.07	19.74	20.19	16.39	22.41
Cluster V					**12**	21.89	26.41	28.32	27.32	24.41	28.66	33.82
Cluster VI						**0**	10.13	13.27	17.77	19.39	27.3	17.99
Cluster VII							**0**	9.86	10.37	16.29	24.05	11.41
Cluster VIII								**0**	13.11	15.84	21.33	12.82
Cluster IX									**0**	12.66	19.55	13.39
Cluster X										**0**	15.35	23.26
Cluster XI											**0**	29.07
Cluster XII												**0**

Table 10. Cluster mean for yield and its component traits of chickpea genotypes employing Tocher's Method

Cluster	DT50%F	DTM	PH	NBPP	NPPP	TNSPP	100-SW	BY	HI%	SYPP
Cluster I	55.53	109.34	43.37	5.53	26.51	1.32	21.67	**15.19**	47.83	7.12
Cluster II	57.91	104.30	43.60	5.90	61.12	1.41	18.88	18.72	48.26	9.05
Cluster III	52.88	112.69	41.29	4.12	22.29	1.25	19.02	40.10	**24.68**	7.22
Cluster IV	57.50	100.00	32.83	6.84	58.00	1.30	17.00	15.25	**67.77**	**3.41**
Cluster V	52.63	108.50	46.38	4.79	**12.83**	**1.13**	15.32	16.76	24.81	3.72
Cluster VI	57.50	98.50	**77.83**	5.67	72.50	1.30	**12.32**	27.35	42.10	**23.50**
Cluster VII	**70.00**	114.50	62.00	6.66	73.00	1.25	17.95	34.46	46.40	15.90
Cluster VIII	**51.50**	**83.00**	58.83	6.50	70.50	1.25	**26.91**	34.44	55.24	17.25
Cluster IX	61.00	**120.50**	**29.00**	3.33	48.00	**2.00**	20.85	**44.44**	45.19	14.00
Cluster X	63.50	92.50	33.67	**7.34**	22.50	1.34	23.78	41.81	45.42	17.50
Cluster XI	60.50	113.50	52.17	5.66	15.00	1.34	26.00	31.00	63.85	4.47
Cluster XII	53.50	111.50	36.00	6.34	**91.50**	1.25	16.75	41.39	50.77	18.00

Table 11. Contribution of various traits towards clustering in chickpea genotypes

S. No.	Source	Contribution %
1	Days To 50% Flowering	0.06
2	Days To Maturity	3.56
3	Plant height	1.88
4	Numbers of primary branches per plant	0.03
5	Numbers of pods per plant	28.83
6	Total numbers of seeds per pod	0.18
7	100 -seed weight	3.67
8	Biological yield per plant	30.97
9	Harvesting index	30.56
10	Seed yield per plant	0.26
	Total	100.00
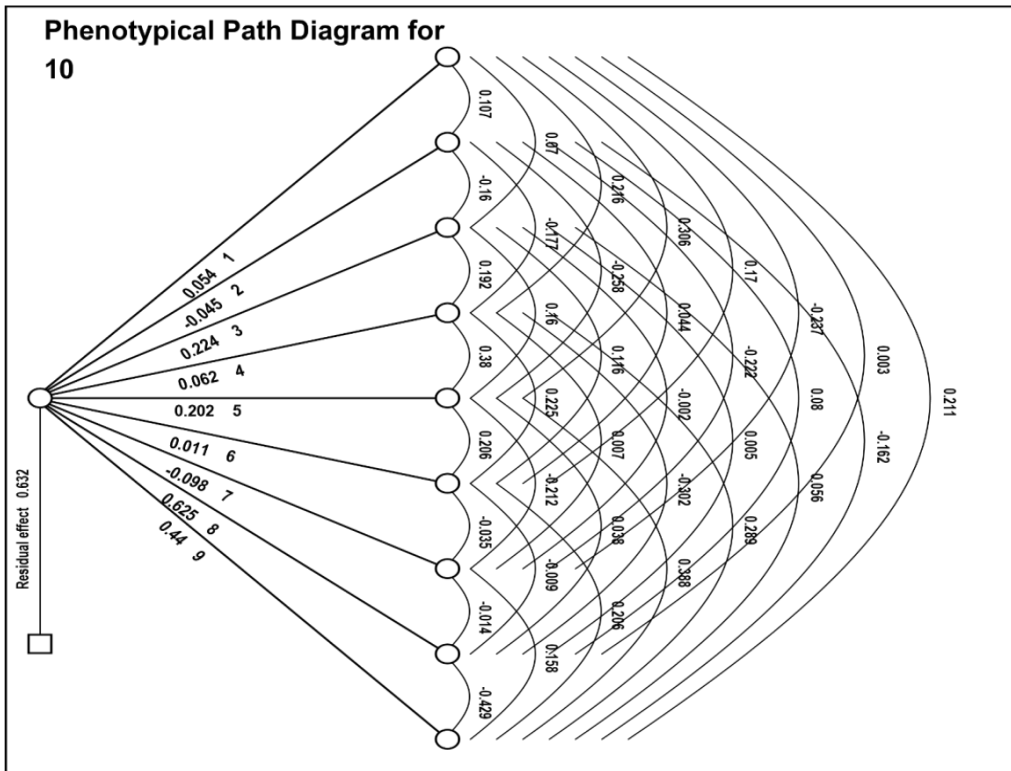
Fig. 1. Phenotypic path diagram for 10 characters in chickpea genotypes
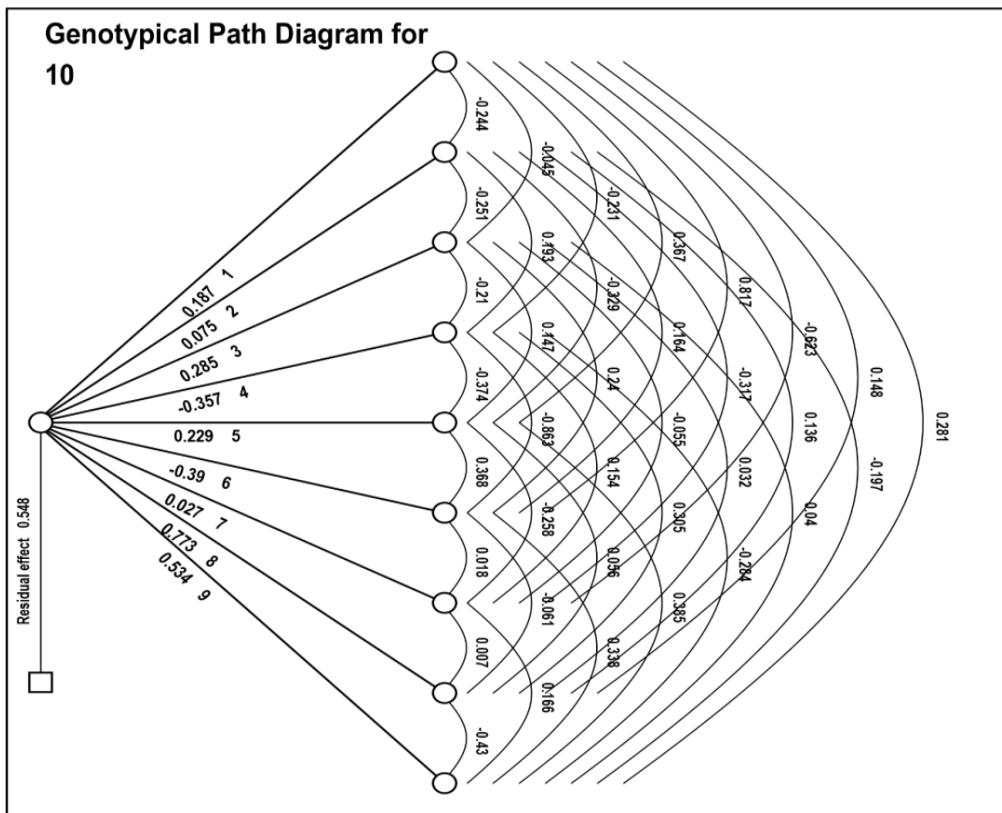
Fig. 2. Genotypic path diagram for 10 characters in chickpea genotypes
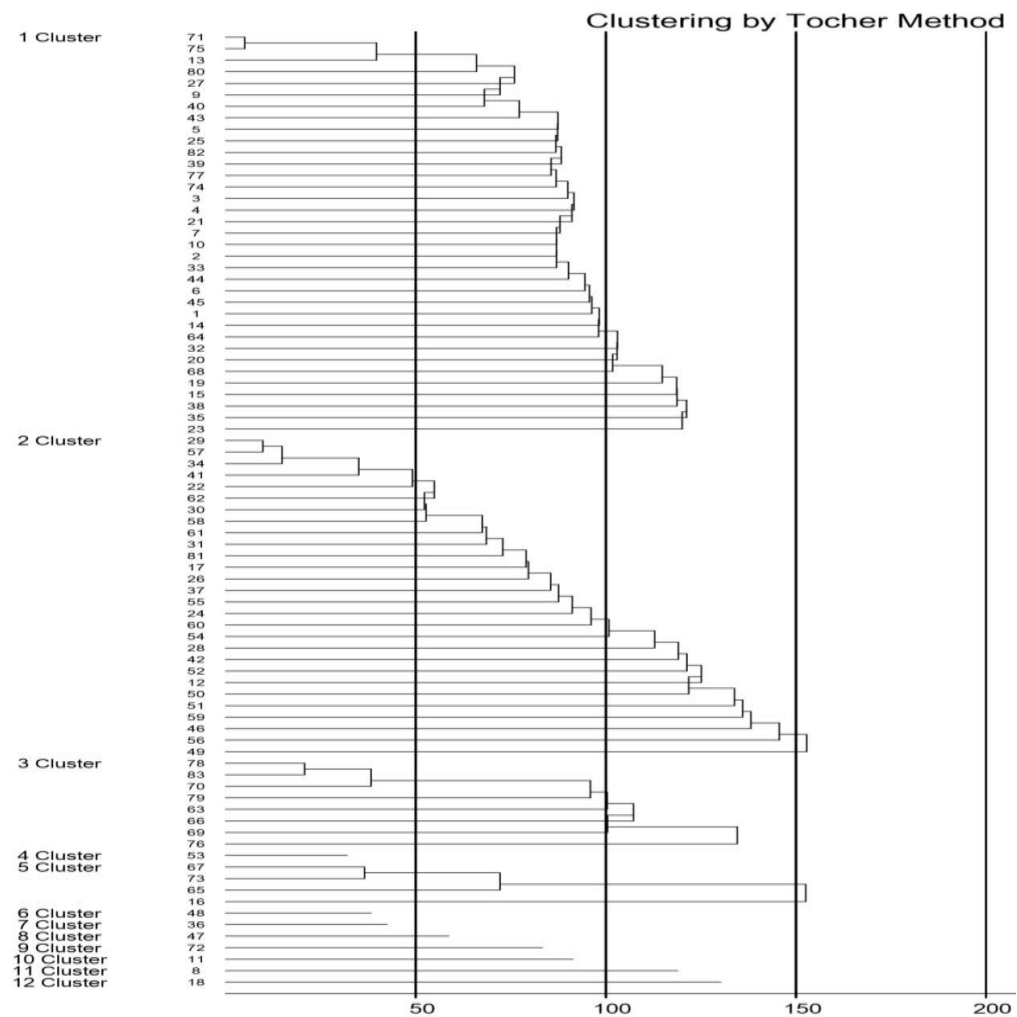
Fig. 3. Cluster diagram of diverse chickpea genotypes based on D^2 analysis
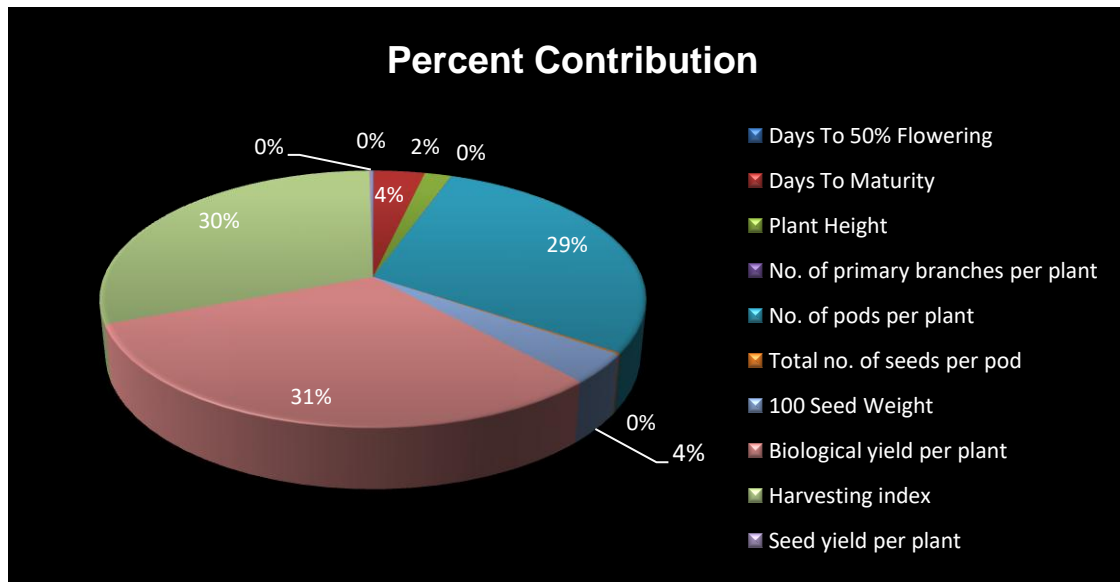
Fig. 4. Percent contribution of traits in cluster

Genotypic path coefficient analysis revealed that biological yield per plant had the highest positive direct effect on seed yield per plant tracked by harvest index, plant height, numbers of pods per plant, days to 50% flowering and days to maturity. Whilst phenotypic path coefficient analysis exposed that biological yield had the highest positive direct effect on seed yield per plant trailed by harvest index, plant height, numbers of pods per plant, numbers of branches per plant and days to 50% flowering. These findings are closely similar with earlier results of Shrivastava et al. [52] and Jain et al. [22] for days to 50% flowering, plant height, numbers of pods per plant and days to maturity. Moreover, Kumawat et al. [53] reported comparable findings for biological yield per plant and harvest index.

3.4 Genetic Divergence (D^2 Analysis)

Mahalanobis (D^2) statistics is a compelling tool widely used by plant breeders to measure the degree of divergence at genotypic level.

3.5 Composition of Clusters

Grouping of the genotypes (Table 8) was carried-out by Tocher's method as per suggested by Rao [43]. Eighty-three chickpea genotypes which were evaluated for nature and magnitude of genetic divergence were grouped into 12 clusters. Cluster IV, VI, VII, VIII, IX, X, XI and XII were mono genotypic, whereas cluster I, II, III and V were poly genotypic. This confirmed the diversity present in the experimented material.

Cluster I was the largest comprising of 35 genotypes followed by cluster II which had 28 genotypes, cluster III had 8 genotypes while cluster V had 4 genotypes. Cluster IV, VI, VII, VIII, IX, X, XI and XII had only one genotype in each. Therefore, it can be concluded that the selection of parents for hybridization should not be based on geographical diversity only, but it should have a base of both geographical origin as well as genetic divergence.

3.6 Intra and Inter Cluster Distances

The intra and inter cluster distances D^2 between all possible pairs of 12 clusters were computed and presented in Table 9 and depicted in Fig. 3. Cluster V showed maximum intra cluster D^2 value (D^2 = 12.00), while cluster III had 11.09 intra cluster value, cluster II showed 10.80. The highest inter cluster distance (D=33.82) was observed between genotypes of cluster V and cluster XII, tracked by cluster XI and cluster XII (D=29.07). These clusters are quite divergent from each other and the genotypes belonging to them can be used for hybridization programme as crosses between genotypes belonging to the clusters with maximum inter cluster distance, may give higher heterotic response resulting in better recombinants.

3.7 Cluster Means for Various Characters

The results clearly indicated appreciable difference among cluster means for most of the characters (Table 10). Highest cluster mean for

days to maturity, plant height and seed yield per plant was evident in cluster IX, whereas cluster IX had high values of mean for biological yield per plant which indicated that genotypes having high seed yield and tall plants were concentrated in these clusters. Therefore, it is suggested that parent selected for hybridization among the genotypes of above said clusters would produce higher heterosis and segregants for more than one economic character. The potential lines are identified from different clusters and used as parents in a hybridization programme. These findings are in accordance of earlier studies of Janghel et al. [54] and Katkani et al. [46].

3.8 Contribution of Various Characters towards Genetic Divergence

The utility of D^2 analysis is enhanced by its application to estimates the relative contribution of various characters to genetic divergence. The contribution of each character towards total genetic diversity is presented in Table 11 and Fig. 4. The percentage contribution of 10 quantitative characters towards genetic divergence exposed that biological yield per plant had maximum share towards genetic divergence followed by harvest index, numbers of pods per plant, 100 -seed weight, days to maturity, plant height and seed yield per plant. These characters were liable for expressing maximum diversity among the clusters. These findings are similar to the results of Tiwari and Babbar [55], Nimbalkar et al. [56], Tiwari et al. [15] and Biswal and Babbar [57].

4. CONCLUSION

based on the Analysis of variance it is concluded that significant difference was exist for the entire seed yield and its contributing traits indicating presence of considerable amount of variability among the genotypes. High phenotypic and genotypic coefficient of variation recorded for numbers of pods per plant followed by biological yield per plant indicating the pre-dominance of additive gene action and selection based on these traits may be rewarding. Seed yield per plant shared highly significant and positive association with biological yield per plant and total numbers of seeds per plant. The path analysis revealed that biological yield per plant showed a highest direct effect on seed yield per plant tracked by harvest index and plant height. Cluster I was the largest comprising of thirty-five genotypes trailed by cluster II having twenty-eight genotypes. Genotypes belongs to these

clusters may be used as parents to produce transgressive segregants.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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