

Morpho-Physiological Grouping of Indian Chickpea (*Cicer arietinum* L.) Genotypes Based on Terminal Drought Stress Response

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ABSTRACT: Drought is a serious constraint in limiting seed yield of chickpea. Identification of major seed yield limiting trait under drought conditions is critical to breed varieties for more drought resilience. This study was conducted for characterization of the chickpea genotypes on the basis of morpho-physiological responses under drought stress to select promising drought tolerant line. The set consisted of forty chickpea genotypes including released varieties, identified donors and the advanced breeding lines. A field experiment was conducted in randomized complete block design (RCBD) under normal and drought stressed conditions in Rabi season of 2020-21 and 2021-22. Morpho-physiological observations were recorded on relative water content (RWC), saturation water deficit (SWD), canopy temperature depression (CTD), chlorophyll content index (CCI), plant height (PH), number of primary branches (NPB), number of secondary branches (NSB), biological yield per plant and seed yield per plant of these chickpea genotypes. Data of both seasons were pooled for calculation of summary statistics including genetic parameters; inter correlation and path coefficient analysis. Genotypes performing better in drought stressed conditions can be used as drought tolerant lines for developing promising drought tolerant cultivars.

Keywords: Morpho-physiological, drought stress, genetic parameters, correlation, path analysis.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a self-pollinating, diploid ($2n=2x=16$) pulse crop with a 738Mbp genome (Varshney *et al.*, 2013). Chickpea seeds are a good source of carbohydrates and proteins for the vegetarian diets of resource-poor consumers. Globally chickpea covers 14.8 million ha (mha) area with an annual production of 15.1 million tons (FAO, 2021). In India, 'Pulse Revolution' is majorly contributed by chickpea to move the country towards self-sufficiency in pulses. An all-time high of 12.61 mt chickpea production recorded during 2020-21 (Dixit, 2021).

Drought is being most detrimental abiotic stress by limiting production and productivity of crops more than other abiotic stresses (Shao *et al.*, 2009). Drought

mainly affects yield, membrane integrity, osmotic adjustment, pigment content and photosynthetic activity. In India, there has been substantial shift of region of chickpea cultivation from cooler Northern climatic conditions zones to hot southern Indian conditions limited to drought prone marginal and sub marginal tracts. That's greatly affected chickpea yields of country over the past few years. Further, late onset of raining delayed chickpea sowing in rice fallows conditions and exposing chickpea to heat and drought stresses during reproductive stage as terminal heat and drought stresses (Sachdeva *et al.*, 2017).

The crop responses to various abiotic stresses are complex involving morpho-physiological, biochemical and gene regulatory mechanisms for drought resilience. Thus, this study was conducted for characterization of

the chickpea genotypes on the basis of morpho-physiological responses under drought stress to select promising drought tolerant line.

MATERIAL AND METHOD

The experimental material consists of 40 chickpea genotypes including released varieties, identified donar and advance breeding lines (Table 1). The research trial was laid out in RCBD with three replications during rabi seasons 2020-21 and 2021-22 at field of Biotechnology center, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur. Three row of 1 m length was planted for each genotype with 10 cm of plant to plant and 45 cm of row to row distance. Standard agronomical practices have been implemented to maintain ten numbers of plants in each row.

Five evocative plants are carefully chosen from each line for recording the observations on chlorophyll content index (CCI), plant height (PH), number of primary branches (NPB), number of secondary branches (NSB), biological yield per plant and seed yield per plant. Relative water content was calculated according Sachdeva *et al.* (2017). Saturation Water Deficit was calculated by subtracting RWC from 100. Canopy temperature depression was calculated by subtracting canopy temperature of plant from air temperature. Statistical analysis of pooled data of both seasons was done by using Window Stat 9.1 software. Genetic diversity was calculated using Mahalanobis's D2 (Mahalanobis's, 1936) while and clustering of genotypes was conducted according to Tocher's method (Rao, 1952).

Table 1: Details of chickpea genotypes used in the study.

Sr. No.	Genotype	Source	Pedigree
1.	ICC4958	ICRISAT, Patancheruvu	JGC 4958
2.	JAKI9218	JNKVV, Jabalpur	(ICCC 37 × GW5/7) × ICCV 107
3.	JG6	JNKVV, Jabalpur	(Phule G-5 × Narsinghpur bold) × ICCC 37
4.	JG11	JNKVV, Jabalpur	ICCC 44 × ICCV 10
5.	JG14	JNKVV, Jabalpur	Single Plant selection from JG 62
6.	JG16	JNKVV, Jabalpur	A composite from genetic stock
7.	JG17	JNKVV, Jabalpur	(ICCV10XK850) × (H208XRS11)
8.	JG24	JNKVV, Jabalpur	(GW5/7XP326)XICCL83149
9.	JG28	JNKVV, Jabalpur	BDNG 9-3 × Narshingpur Bold
10.	JG32	JNKVV, Jabalpur	(JG 74 × ICC 4958)-21
11.	JG33	JNKVV, Jabalpur	[(JM - 1 X IPC 9239)X JG 7] - 14-11
12.	JG36	JNKVV, Jabalpur	[(JM - 1 × IPC 4958) × JG 315] - 2
13.	JG42	JNKVV, Jabalpur	[(JM - 1 × IPC 9239) × JG 322] - 30-3
14.	JG63	JNKVV, Jabalpur	JG 12 × JG 16
15.	JG74	JNKVV, Jabalpur	[(JM 1 × IPC 9239)JG7] 14-11-2011-42
16.	JG226	JNKVV, Jabalpur	JG 74 × JG315
17.	PG205	JNKVV, Jabalpur	JG 315×ICC 96029
18.	ICCV15102	ICRISAT, Patancheruvu	ICCV03112 × ICCV10
19.	ICCV15115	ICRISAT, Patancheruvu	ICCV10 × ICCV 96970
20.	ICCV15118	ICRISAT, Patancheruvu	ICCV 05530 × ICCV 88510
21.	ICCV19616	ICRISAT, Patancheruvu	JAKI 9218/ICCV 05103
22.	ICCV181664	ICRISAT, Patancheruvu	ICC 4958 TM/JG 130
23.	JG2003-14-16	JNKVV, Jabalpur	[(JM1 x ICC4929) × ICC4958]-2-14-16
24.	JG2016-44	JNKVV, Jabalpur	(ICC 96029 × ICC11551) 44
25.	JG2016-45	JNKVV, Jabalpur	(JG 74 × ICC11551) 45
26.	JG2016-1411	JNKVV, Jabalpur	JG 14 × JG 11
27.	JG2016-1614	JNKVV, Jabalpur	JG 16 × JG 14
28.	JG2016-9605	JNKVV, Jabalpur	JG 74 × ICC 96029
29.	JG2016-9651	JNKVV, Jabalpur	JG 130 × ICC 96029
30.	JG2016-74315	JNKVV, Jabalpur	[{(JG 74 × WR 315) × JG 74} -2010 -1- 3- 5- 11-15-10-2]
31.	JG2016-634958	JNKVV, Jabalpur	JG 63 × ICC 4958
32.	JG2016-921814	JNKVV, Jabalpur	JAKI 9218 × JG 14
33.	JG2017-48	JNKVV, Jabalpur	(JG 315 × ICC 96029)48
34.	JG2018-51	JNKVV, Jabalpur	JG63 × ICC1205
35.	JG2022-74	JNKVV, Jabalpur	JG12 × JG74
36.	JG2016-36	JNKVV, Jabalpur	JG12 × JG16-1
37.	JG2022-75	JNKVV, Jabalpur	JG12 × ICC4958
38.	JG2021-6301	JNKVV, Jabalpur	JG12 × ICCV06301
39.	JG2021-1424	JNKVV, Jabalpur	JG14 × JG24
40.	JG2021-1617	JNKVV, Jabalpur	JG16 × JG17

RESULTS AND DISCUSSION

In India, chickpea is third most important legume crop occupying 45% of total pulse production. Drought and heat both limit chickpea production critically. The mean of the studied characters indicate presence of moderate amount of variation in the tested genotypes. on the basis

of pooled data analysis of both seasons, RWC, SWD, CTD, CCI, PH, NPB, NSB, biological yield per plant and seed yield per plant of the forty genotypes were recorded.

Under normal condition, the average RWC value was recorded 73.5 + -4.6 with range from 65.2 to 79.5, mean SWD was found 31.7 + -6.3 with range from 20.6

to 43.0, mean CTD was obtained 3.3± 0.4 with range from 2.6 to 4.0, mean CCI was observed 58.8 ± 2.0 with range from 55.5 to 62.5, PH was recorded 50.9 ± 4.7 with range from 38.7 to 58.2 cm, mean NPB was recorded 3.0 ± 0.2 with range from 2.6 to 3.6, mean NSB was found 8.5 ± 0.8 with range from 7.5 to 10.3, mean biological per plant was observed 34.4 ± 4.7 g with range from 25.5 g to 48.0 g and mean seed yield per plant was recorded 13.7 ± 1.8 g with range from 11.7 to 21.7 g (Table 2).

Under drought stress situations, the mean RWC value was recorded 68.3 ± 6.3 with range from 57.0 to 79.4,

mean SWD was found 31.7 ± 6.3 with range from 20.6 to 43.0, mean CTD was obtained 1.7 ± 0.3 with range from 1.1 to 2.2, mean CCI was observed 54.8 ± 2.1 with range from 51.2 to 58.9, PH was obtained 45.3 ± 4.5 with range from 33.5 to 51.5 cm, mean NPB was recorded 2.5 ± 0.2 with range from 2.0 to 3.1, mean NSB was found 7.4±0.7 with range from 6.6 to 9.3, mean biological per plant was observed 23.5 ± 3.8 g with range from 17.4 g to 33.9 g and mean seed yield per plant was recorded 8.9 ± 0.7 g with range from 6.1 to 9.9 g (Table 3).

Table 2: Pooled morpho-physiological mean performance of different chickpea genotypes under normal conditions.

Sr. No.	Genotype	RWC	SWD	CTD	CCI	PH	NPB	NSB	BY	SY
1.	ICC4958	77.4	22.6	3.8	59.3	48.2	3.2	10.3	33.6	11.8
2.	JAKI9218	77.6	22.4	3.6	60.9	55.1	3.1	9.0	34.6	15.6
3.	JG6	76.0	24.0	3.6	58.8	52.2	3.3	9.7	42.7	21.7
4.	JG11	79.3	20.7	4.0	60.9	47.0	3.6	10.3	36.3	14.9
5.	JG14	73.0	27.0	3.5	59.2	54.8	2.6	8.5	32.4	13.1
6.	JG16	77.2	22.8	3.9	60.6	54.5	3.2	9.7	48.0	15.7
7.	JG17	70.8	29.2	3.4	57.4	54.4	3.0	9.5	30.7	13.6
8.	JG24	79.5	20.5	3.3	61.0	58.2	3.5	9.8	34.1	12.3
9.	JG28	75.7	24.3	3.3	59.7	55.9	2.7	7.8	25.5	11.7
10.	JG32	74.4	25.6	3.2	58.5	54.8	2.6	7.8	29.1	12.6
11.	JG33	71.4	28.6	3.9	57.3	57.0	2.7	8.8	28.3	14.4
12.	JG36	75.0	25.0	3.1	60.0	50.7	2.8	8.1	42.6	11.8
13.	JG42	74.9	25.1	2.9	58.6	50.1	2.7	9.7	28.4	13.1
14.	JG63	78.8	21.2	3.7	60.8	52.0	3.2	9.3	32.4	15.0
15.	JG74	77.6	22.4	2.6	60.1	56.1	2.9	8.5	33.4	14.1
16.	JG226	77.1	22.9	3.0	60.3	50.4	2.9	7.8	34.9	15.1
17.	PG205	78.8	21.2	2.7	62.3	50.1	3.4	8.9	45.5	14.8
18.	ICCV15102	73.5	26.5	3.5	57.5	49.0	3.0	7.8	33.1	15.3
19.	ICCV15115	79.2	20.8	3.3	60.6	51.2	3.4	7.5	35.0	14.4
20.	ICCV15118	77.0	23.0	3.0	60.2	57.0	3.1	7.7	33.3	14.4
21.	ICCV19616	67.0	33.0	3.6	56.5	53.2	2.9	8.8	29.7	12.2
22.	ICCV181664	78.8	21.2	2.8	61.3	54.7	3.2	8.2	31.9	12.0
23.	JG2003-14-16	78.5	21.5	3.2	60.3	53.9	2.8	8.2	40.5	14.9
24.	JG2016-44	78.1	21.9	3.3	62.5	57.6	3.0	8.1	37.3	13.8
25.	JG2016-45	68.6	31.4	2.7	55.9	53.4	2.6	7.6	33.0	14.0
26.	JG2016-1411	75.9	24.1	2.9	59.9	54.7	2.8	7.8	33.6	13.4
27.	JG2016-1614	66.2	33.8	3.2	56.2	44.7	2.7	7.8	36.6	12.5
28.	JG2016-9605	67.2	32.8	2.6	56.4	50.1	2.9	8.6	28.8	13.5
29.	JG2016-9651	69.9	30.1	3.3	57.5	47.0	3.1	8.8	35.8	14.5
30.	JG2016-74315	72.0	28.0	3.1	57.1	44.8	3.3	8.5	34.6	12.3
31.	JG2016-634958	76.0	24.0	2.9	62.5	45.8	3.1	8.0	32.3	13.3
32.	JG2016-921814	72.4	27.6	2.9	58.4	47.7	2.9	8.0	30.8	11.9
33.	JG2017-48	66.4	33.6	3.7	56.1	48.6	3.1	7.8	33.2	13.7
34.	JG2018-51	72.1	27.9	3.7	58.2	50.0	3.0	8.3	39.9	14.3
35.	JG2022-74	68.7	31.3	3.4	56.3	46.8	3.1	7.7	31.1	12.5
36.	JG2016-36	65.2	34.8	2.8	56.3	40.2	3.1	7.7	32.2	14.1
37.	JG2022-75	66.1	33.9	3.1	55.5	45.0	3.1	8.8	35.3	12.2
38.	JG2021-6301	69.2	30.8	3.1	57.6	38.7	3.0	9.4	37.0	12.8
39.	JG2021-1424	69.8	30.2	3.4	58.0	53.9	3.0	8.1	35.8	12.9
40.	JG2021-1617	66.9	33.1	3.0	56.6	47.2	2.8	7.5	31.3	11.8
	Min	65.2	20.5	2.6	55.5	38.7	2.6	7.5	25.5	11.7
	Max	79.5	34.8	4.0	62.5	58.2	3.6	10.3	48.0	21.7
	Mean	73.5	26.5	3.3	58.8	50.9	3.0	8.5	34.4	13.7
	SD	4.6	4.6	0.4	2.0	4.7	0.2	0.8	4.7	1.8

The dendrogram based on Tocher clustering grouped the forty tested genotypes into ten major clusters (Table 4, Fig. 1). The largest cluster, cluster I comprised of 13 genotypes (ICCV15118, JG2016-1411, JG32, JG24, JG33, JG28, JG2016-921814, ICCV181664, JG2016-45, ICCV15102, JG2003-14-16, JG2016-9651 and JG2021-1617) followed by cluster II, III and IV

consisted with 9 (JAKI9218, JG63, ICC4958, JG11, JG16, JG2018-51, JG17, ICCV19616), 6 (JG42, JG28, JG2022-74, JG2016-36, JG2016-1614, JG2016-44) and 6 (JG14, JG74, JG226, JG2016-45) genotypes, respectively. Rest six clusters comprised with single-single genotypes (JG2021-6301, JG2021-1424, JG36, JG2016-74315, PG205, JG2016-634958 respectively).

Table 3: Pooled morpho-physiological mean performance of different chickpea genotypes under drought stressed conditions.

Sr. No.	Genotype	RWC	SWD	CTD	CCI	PH	NPB	NSB	BY	SY
1.	ICC4958	75.2	25.8	2.1	55.6	45.4	2.5	9.3	24.7	9.2
2.	JAKI9218	74.7	25.3	2.0	56.3	50.5	2.8	8.1	23.5	9.8
3.	JG6	69.7	30.3	1.1	55.0	46.7	2.7	8.1	27.6	9.4
4.	JG11	75.9	24.1	2.0	56.6	42.8	2.5	8.5	24.9	9.9
5.	JG14	64.4	35.6	1.1	54.7	48.5	2.2	7.6	21.6	8.8
6.	JG16	73.8	26.2	2.0	56.4	51.3	2.8	8.5	30.6	9.8
7.	JG17	63.7	36.3	2.0	53.0	48.0	2.3	8.1	27.5	9.0
8.	JG24	77.0	23.0	1.7	57.2	51.3	2.7	7.8	21.9	8.1
9.	JG28	68.5	31.5	1.7	55.2	51.5	2.5	6.6	25.1	7.9
10.	JG32	71.4	28.6	1.7	55.4	47.8	2.5	6.8	23.0	8.7
11.	JG33	67.6	32.4	1.7	53.8	50.5	2.4	7.3	20.1	8.7
12.	JG36	77.2	22.8	1.6	58.6	44.3	2.3	7.3	33.9	9.1
13.	JG42	71.3	28.7	1.4	55.0	44.0	2.7	7.9	21.5	8.9
14.	JG63	77.7	22.3	2.1	57.4	49.2	2.7	8.6	25.6	9.1
15.	JG74	69.1	30.9	1.1	56.1	49.2	2.0	6.9	17.4	6.1
16.	JG226	70.9	29.1	1.1	56.6	45.0	2.3	6.9	26.2	9.1
17.	PG205	77.6	22.4	1.7	58.9	45.8	3.1	7.9	32.3	9.5
18.	ICCV15102	69.7	30.3	1.7	53.7	43.3	2.3	7.0	23.3	9.9
19.	ICCV15115	74.3	25.7	1.4	56.1	44.5	2.7	6.6	25.3	9.7
20.	ICCV15118	72.3	27.7	1.6	56.3	50.5	2.3	6.7	20.0	9.5
21.	ICCV19616	62.2	37.8	2.2	52.8	47.5	2.5	7.6	20.1	8.4
22.	ICCV181664	72.9	27.1	1.8	56.5	47.8	2.4	7.4	18.4	8.6
23.	JG2003-14-16	72.4	27.6	1.6	55.4	47.2	2.5	7.4	28.0	9.6
24.	JG2016-44	79.4	20.6	1.5	58.9	51.0	2.3	7.4	20.2	9.0
25.	JG2016-45	62.9	37.1	1.8	52.0	47.3	2.7	6.7	20.5	9.1
26.	JG2016-1411	73.1	26.9	1.6	56.6	49.2	2.5	6.9	21.7	9.0
27.	JG2016-1614	58.6	41.4	1.6	52.0	39.0	2.7	6.8	20.8	7.8
28.	JG2016-9605	57.6	42.4	1.1	51.8	43.2	2.3	6.9	21.1	9.3
29.	JG2016-9651	63.0	37.0	1.8	53.3	41.8	2.3	7.8	28.0	9.6
30.	JG2016-74315	64.8	35.2	1.9	52.6	39.5	2.7	7.5	20.8	8.4
31.	JG2016-634958	66.8	33.2	1.7	57.5	41.0	2.8	7.1	23.4	8.8
32.	JG2016-921814	65.6	34.4	1.7	54.4	42.7	2.5	7.2	21.4	8.6
33.	JG2017-48	62.4	37.6	2.1	52.6	43.2	2.3	6.8	22.7	9.1
34.	JG2018-51	67.4	32.6	2.1	54.2	43.3	2.3	7.5	29.3	9.5
35.	JG2022-74	62.0	38.0	1.4	52.2	40.2	2.2	6.9	20.1	8.7
36.	JG2016-36	57.0	43.0	1.5	52.0	35.0	2.3	6.9	19.9	9.2
37.	JG2022-75	58.7	41.3	1.2	51.2	39.7	2.4	7.9	25.9	7.9
38.	JG2021-6301	61.4	38.6	1.7	53.5	33.5	2.2	8.4	20.9	8.7
39.	JG2021-1424	62.2	37.8	1.9	53.6	47.7	2.5	7.0	21.3	8.1
40.	JG2021-1617	59.8	40.2	1.8	52.4	40.3	2.4	6.7	20.9	7.8
	Min	57.0	20.6	1.1	51.2	33.5	2.0	6.6	17.4	6.1
	Max	79.4	43.0	2.2	58.9	51.5	3.1	9.3	33.9	9.9
	Mean	68.3	31.7	1.7	54.8	45.3	2.5	7.4	23.5	8.9
	SD	6.3	6.3	0.3	2.1	4.5	0.2	0.7	3.8	0.7

Table 4: Distribution of chickpea genotypes in various clusters.

Sr. No.	Cluster No.	No. of genotypes	Name of genotypes
1.	Cluster I	13	ICCV15118, JG2016-1411, JG32, JG24, JG33, JG28, JG2016-921814, ICCV181664, JG2016-45, ICCV15102, JG2003-14-16, JG2016-9651 and JG2021-1617
2.	Cluster II	9	JAKI9218, JG63, ICC4958, JG11, JG16, JG2018-51, JG17, ICCV19616
3.	Cluster III	6	JG42, JG28, JG2022-74, JG2016-36, JG2016-1614, JG2016-44
4.	Cluster IV	6	JG14, JG74, JG226, JG2016-45,
5.	Cluster V	1	JG2021-6301
6.	Cluster VI	1	JG2021-1424
7.	Cluster VII	1	JG36
8.	Cluster VIII	1	JG2016-74315
9.	Cluster IX	1	PG205
10.	Cluster X	1	JG2016-634958

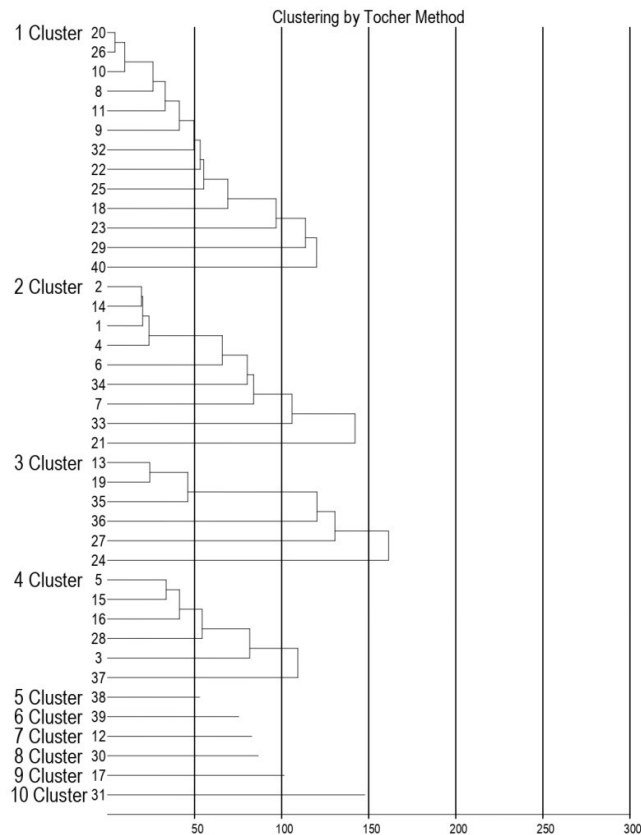


Fig. 1. Clustering of Chickpea Genotypes.

Bharadwaj *et al.* (2001) suggested that phenotypic and/or genotypic diversity per se is an inferential criterion so should not be used as a direct measure of genetic diversity. It may not be more useful for selecting the genotypes as parents for breeding program, generally done by most breeders. Numerous clustering techniques have been utilized by different researchers to quantify the genetic diversity in a given set of germplasm/ genotypes on the basis of collected data (Bharadwaj *et al.*, 2011; Sachdeva *et al.*, 2017; Katkani *et al.*, 2022).

Tocher clustering could clearly delineate the drought tolerant chickpea genotypes from the susceptible genotypes. In this study, Tocher clustering clearly grouped most drought tolerant genotypes into cluster II (JAKI9218, JG63, ICC4958, JG11, JG16, JG2018-51, JG17, ICCV19616) and discriminated from drought sensitive genotypes which were grouped into cluster VI (JG14, JG74, JG226, JG2016-45). Rest clusters contained with moderately drought tolerant chickpea genotypes. Sachdeva *et al.* (2017) also grouped chickpea genotypes on the basis of morpho-physiological traits dendrogram and found that Cluster IIa contained with most drought tolerant genotypes *viz.*, ICC4958, ICCV10313, ICCV10 and ICCV97309 while cluster I and cluster III had the most susceptible chickpea genotypes. The clustering pattern of genotypes clearly depicted that considerable amount of diversity was present in the utilized material of study. This could be due to differential selection executed by breeders for selection of seed yield attributing and other

traits which have been considered as genetic drift because of selection (Murty and Arunachalam 1966).

Further, the intra and inter cluster Mahalanobis D₂ values depicted wide range of intra cluster distance from 0.00 to 12.29 (Table 5). Cluster III demonstrated highest intra cluster D₂ mean value (D₂ = 12.29) followed by Cluster II (D₂ = 10.14), Cluster IV (D₂ = 9.80) and Cluster I (9.13), whereas remaining six clusters (Cluster V, VI, VII, VIII, IX and X) revealed zero value for Intra cluster distance due to having single genotype in each cluster. These monogenotypic clusters represented minimum diversity for the present study. The maximum inter cluster divergence distance was depicted between genotypes of Cluster II and Cluster IV (56.04) representing their highest suitability for utilizing in crossing programme. Outcomes of the study clearly specified the remarkable possibilities of incorporation of allelic resources existing in these genotypes by using a systematic breeding program.

The mean of clusters for all studied traits in pooled data analysis are presented in (Table 6). Cluster IX (77.6) revealed highest mean for RWC while Cluster V was found with minimum cluster mean (61.44). Maximum SWD was recorded for Cluster V (38.56) while minimum SWD was observed in Cluster IX (22.40). Highest CTD was depicted by Cluster II (2.08) whereas lowest SWD was found in Cluster IV (1.12). Utmost superior CCI was demonstrated by Cluster Cluster IX while utmost inferior value recorded from Cluster VIII. Tallest plants were showed by Cluster VI (47.67) with shortest plants in Cluster V (33.50). Maximum NPB

was recorded in Cluster XI (3.13) with minimum NPB in Cluster V (2.17). Highest NSB found in Cluster V (8.40) with lowest NSB in Cluster VI (7.02). Utmost high biological yield per plant (33.87 g) were noted down in Cluster VII while utmost low biological yield per plant (20.83 g) were noted in Cluster VIII. Maximum seed yield per plant was demonstrated by

Cluster IX (9.50 g), while minimum was observed in Cluster VI with 8.13 g mean value. These findings approved in earlier research of Tiwari and Babbar (2017); Gediya *et al.* (2018); Ponnuru *et al.* (2019); Dar *et al.* (2020); Janghel (2020); Boparai *et al.* (2021); Katkani *et al.* (2022); Biswal *et al.* (2022).

Table 5: Inter and intra cluster divergence values for different clusters generated by Tocher method.

	Group. 1	Group. 2	Group. 3	Group. 4	Group. 5	Group. 6	Group. 7	Group. 8	Group. 9	Group. 10
Group. 1	9.13	23.35	17.79	35.22	13.40	15.16	15.58	14.12	13.84	16.11
Group. 2		10.14	37.34	56.05	22.72	14.47	30.22	14.52	21.49	25.53
Group. 3			12.29	22.43	21.00	28.41	17.91	26.69	23.36	23.06
Group. 4				9.80	38.69	46.64	30.78	45.79	39.36	38.51
Group. 5					0.00	13.77	19.57	12.38	16.61	12.16
Group. 6						0.00	23.96	10.74	16.75	14.51
Group. 7							0.00	23.91	10.07	17.87
Group. 8								0.00	17.93	20.02
Group. 9									0.00	14.53
Group. 10										0.00

Table 6: Cluster Means of different traits generated by Tocher method.

	RWC	SWD	CTD	CCI	PH	NPB	NSB	BY	SY
Group. 1	68.93	31.07	1.71	54.80	47.03	2.46	7.07	22.48	8.85
Group. 2	70.21	29.79	2.08	54.98	46.81	2.53	8.11	25.43	9.31
Group. 3	67.13	32.87	1.46	54.37	42.28	2.48	7.07	21.33	8.87
Group. 4	65.09	34.91	1.12	54.25	45.36	2.31	7.39	23.30	8.45
Group. 5	61.44	38.56	1.75	53.52	33.50	2.17	8.40	20.95	8.75
Group. 6	62.22	37.78	1.90	53.64	47.67	2.54	7.02	21.26	8.13
Group. 7	77.16	22.84	1.58	58.55	44.33	2.33	7.27	33.87	9.13
Group. 8	64.84	35.16	1.91	52.62	39.50	2.71	7.52	20.83	8.37
Group. 9	77.60	22.40	1.73	58.87	45.83	3.13	7.93	32.26	9.50
Group. 10	66.85	33.15	1.67	57.47	41.00	2.83	7.10	23.45	8.84

CONCLUSION

The genotypes JAKI9218, JG63, ICC4958, JG11, JG16, JG2018-51, JG17 and ICCV19616 had lower variability in studied traits under drought stress conditions and higher yield also, thus, are very promising chickpea genotypes to be utilized as drought tolerant donors. When breeding program needs to create variation for these studied traits, crossing of the genotypes of cluster II with cluster VI would be ideal. Crosses of such diverse parents will produce a broad range of variation for selection of the desirable traits.

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REFERENCES

Bharadwaj, C., Satyavath, C. T. and Subramanyam, D. (2001). Evaluation of different classificatory analysis methods in some rice (*Oryza sativa* L.) collections. *Ind. J. Agric. Sci.*, 71(2): 123-125.

Bharadwaj C., Srivastava R., Chauhan S. K., Satyavathi C. T., Kumar J., Faruqui A., Yadav S., Rizvi A. H. and Kumar T. (2011). Molecular diversity and phylogeny in geographical collection of chickpea (*Cicer* sp.) accessions. *J. Genet.*, 90, e94-e100.

Biswal, M. and Babbar, A. (2022). Cataloguing for diverse advance breeding lines of desi chickpea (*Cicer arietinum* L.) for phenological and yield attributing

traits. *Biological Forum- An International Journal*, 14(1): 303-307.

Boparai, Arshivir, K., Sood, V. K., Singh, M. and Katna, G. (2021). Genetic diversity for various agromorphological traits in advanced interspecific derivatives of chickpea (*Cicer arietinum* L.). Abstract: Pulse WebCom, S2: 67:87.

Dar, M. A., Khuroo, N. U. S., Mir, R. U. R., Dar, Z. A., Sofi, P. A., Dar, S. A., Lone, B. A., Sheikh, F. A. and Bhat, U. R. (2020). Diversity Analysis in chickpea (*Cicer arietinum* L.) genotypes under temperate conditions. *Current Journal of Applied Sciences and Technology*, 39(29): 9-14.

Katkani, D., Babbar A., Upadhyay, S. and Goyal, V. (2022). Computation of Genetic Variability and Divergence Analysis in Advance Breeding Lines of Chickpea. *Biological Forum – An International Journal*, 14(2): 611-617.

Dixit, G. P. (2021). Sustaining Chickpea growth in India: Breeder's Perspective. *Journal of Food Legumes*, 34(2), 73-75.

Food and Agriculture Organization (FAO). (2021). FAOSTAT Statistical Database of the United Nation Food and Agriculture Organization (FAO) statistical division. Rome.

Gediya, L. N., Patel, D. A., Kumar, D., Vekariya, K. J. and Nayak, J. J. (2018). Characterization of chickpea genotypes based on morphological traits. *Journal of Pharmacognosy and Phytochemistry*, 7(4): 3008-3015.

Janghel, D. K., Kumar, K., Sunil, R and Chhabra, A. K. (2020). Genetic Diversity Analysis, Characterization and Evaluation of Elite Chickpea (*Cicer arietinum* L.)

- Genotypes. *International Journal of Current Microbiology and Applied Sciences*, 9(1): 199-209.
- Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proceedings of National Academy of Science (India)*, 2: 49-55.
- Murthy, B.R. and Arunachalam, V. (1966). The nature of genetic divergence in relation to breeding system in crop plants. *Indian J. Genet. & Plant Breed.*, 26A: 188-189.
- Ponnuru, A., Lal, G. M. and Munagala, S. K. (2019). Genetic diversity studies in chickpea (*Cicer arietinum* L.) Germplasm. *Jr. of Pharmacognosy and Phytochemistry*, 8(4): 2549-2552.
- Rao, C. R. (1952). *Advance statistical methods in biometrics research*. Hafer Pub. Co. Darion., 371-378.
- Sachdeva, S., Bharadwaj, C., Sharma, V., Kumar, N., Bhat, K. V., Patil, B. S., & Varshney, R. (2017). Morpho-physiological grouping of chickpea (*Cicer arietinum* L.) genotypes on the basis of their response to drought stress. *Intl. J. Trop. Agri.*, 35, 15-23.
- Shao, H. B., Chu, L. Y., Jaleel, C. A., Manivannan, P., Panneerselvam, R., & Shao, M. A. (2009). Understanding water deficit stress-induced changes in the basic metabolism of higher plants—biotechnologically and sustainably improving agriculture and the ecoenvironment in arid regions of the globe. *Critical reviews in biotechnology*, 29(2), 131-151.
- Tiwari, A. and Babbar, A. (2017). Genetic divergence in chickpea (*Cicer arietinum* L.) genotypes under normal and late planting. *Environment and Ecology*, 35(2C): 1357-1363.
- Varshney, R. K., Song, C., Saxena, R. K., Azam, S., Yu, S., Sharpe, A. G., & Cook, D. R. (2013). Draft genome sequence of chickpea (*Cicer arietinum*) provides a resource for trait improvement. *Nature biotechnology*, 31(3), 240-246.

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