



Genetic Diversity Studies and Fusarium Wilt Screening in Chickpea (*Cicer arietinum* L.) Germplasm

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ABSTRACT

Background: The genetic base of chickpea has narrowed substantially during the domestication and recent crop improvement is unable to meet the demands due to very few common parents in hybridization process. Therefore, increasing the genetic divergence of chickpea has been a major goal for breeders. The assessment of genetic diversity of chickpea germplasm can provide a valuable information to the breeder for parental selection strategies in plant breeding programs.

Methods: Two hundred and eighty chickpea germplasm including two checks (JG-11 and SA-1) were tested with an objective to explore the genetic divergence by using Mahalanobis D^2 statistics. Among the 280 germplasm lines, 269 germplasm lines were selected from ICRISAT core set chickpea germplasm and 11 advanced breeding lines and varieties from AICRP, scheme from ZARS Kalaburagi. The field experiment was carried out in augmented block design (ABD) during *Rabi* 2021-22. The magnitude of genetic divergence was studied using data obtained from five quantitative traits.

Result: The 280 genotypes including checks were divided into seventeen clusters based on their D^2 values. Out of seventeen clusters, cluster II (89 genotypes) was the largest followed by cluster I (83 genotypes), cluster III (31 genotypes), cluster VIII (29 genotypes), cluster VII (24 genotypes), cluster VII (15 genotypes). Same set of germplasm were also screened for fusarium wilt in wilt sick plot, 30 germplasm lines showed resistant (10.71%), 83 moderately resistant (29.64%), 44 moderately susceptible (15.71%), 31 susceptible (11.07%) and 92 highly susceptible reaction to fusarium wilt. Clusters XIV and XVI had extreme genetic distance and the germplasm lines in these cluster also showed moderate resistance to fusarium wilt (ICC 1098, ICC 11284 and ICC 10466).

Key words: Chickpea, Diversity, Fusarium wilt, Germplasm.

INTRODUCTION

Chickpeas are a nutrient dense food, serving as an important source of protein, dietary fibre, minerals and folate for a large portion of the global population. It is self-pollinated diploid ($2n = 2x = 16$) crop having a genome size of 740 Mbp (Varshney *et al.*, 2013) and is cultivated in about 57 countries under diverse environmental locations. India tops in production and consumption of chickpeas in the world, accounting for 66 per cent of total world's production. It is cultivated in an area of 9.69 Mha with a production of 11.91 MT and productivity of 1142 kg/ha (Anonymous, 2021). To attain self-sufficiency by 2050, the total pulse production in India needs to reach 39 MT (Vision 2050; IIPR) and amongst all pulses, chickpea production alone needs to reach about 16-17.5 MT from a limited area of 9.69 Mha with a mean productivity of 1500-1700 kg/ha. We can achieve the production goal by exploring the genetic distance present among genotype using D^2 statistics for effective choice of parents in the hybridization (Saha *et al.*, 2018).

The genetic base of chickpea has narrowed substantially during the domestication process (Thudi *et al.*, 2016). Therefore, increasing the genetic divergence of chickpea has been a major goal for breeders. The assessment of genetic diversity of chickpea germplasm can provide valuable information to the breeder for parental

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selection strategies in plant breeding programs. Chickpea wilt (*Fusarium oxysporum* f. sp. *Ciceri*) is a very important disease and the pathogen in association with other soil-borne pathogens like root rots and foot rot also causes extensive damage to chickpea. It causes around 10% yield loss in India but under certain conditions and specific locations, the losses may go up to 60%. Thus, the present

study was commenced to estimate the extent of genetic diversity present and field screening for fusarium wilt among 280 chickpea germplasm.

MATERIALS AND METHODS

Two hundred and eighty chickpea germplasms including two checks (JG-11 and SA-1) were evaluated during *Rabi* 2020-21 at Zonal Agricultural Research Station (ZARS), Kalaburagi. Sowing was carried out by hand dibbling method and approximately 40 seeds were sown per genotype. Sowing was done on 6th October, 2021 for germplasm characterization and the field experiment was carried out in augmented block design (ABD) with two checks in each block. Each entry was planted in one row of 4-meter length having a spacing of 30 cm between the rows and 10 cm between the plants respectively. The data was noted for five polygenic traits *viz.*, days to 50 per cent flowering, plant height (cm), days to maturity, 100 seed weight (grams) and seed yield/plant (grams) (Plate 1). The

data were analysed with the technique of D^2 statistics (Mahalanobis 1936), as advocated by Rao (1952). The software package INDOSTAT version 8.5 was used to analyse the statistical data. Experimental layout for screening Fusarium wilt was laid out on National Wilt Sick Plot maintained at Agricultural Research Station, Kalaburagi [Latitude (N) 17° 35' and Longitude (E) 76° 01']. The sick plot is maintained since 1985-86 to till date. It is one of the national sick plot for screening AICRP and local genotypes. The wilt sick plot was maintained by adding chopped plants of *Fusarium oxysporum* f. sp. *ciceris* infested chickpea plants every year.

All the genotypes were sown in single row along with wilt susceptible (JG-62) and resistant check varieties (WR-315) during the *rabi* 2019 season. A row length of 4 meters each was maintained with a spacing of 30 cm and 10 cm between the rows and plants respectively (Plate 2). The observations on per cent disease incidence was recorded at 30, 60, 90 days after sowing by counting the number of diseased and dead plants (due to Fusarium wilt) among

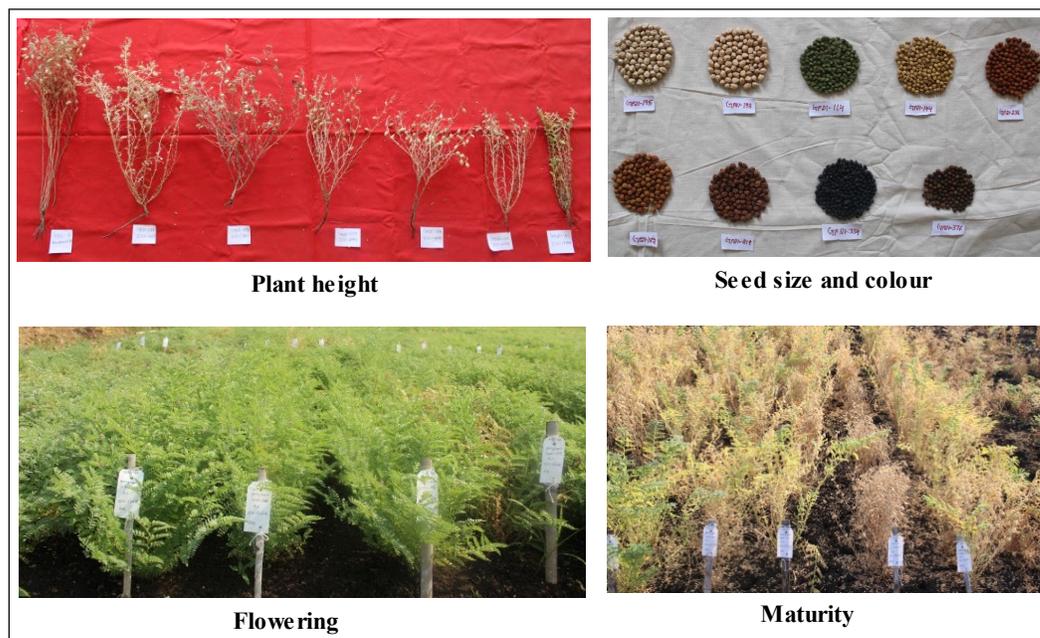


Plate 1: Diverse chickpea germplasm for major traits.



Plate 2: Field screening of 280 chickpea germplasm for *Fusarium* wilt.

the total number of plants present per genotype and per cent disease incidence was estimated. Disease rating was categorized as per the standard wilt scoring format of All India Coordinated Research Project (AICRP) on chickpea, IIPR, Kanpur.

$$\text{Per cent disease incidence (PDI)} = \frac{\text{Number of plants wilted}}{\text{Total number of plants}} \times 100$$

Percent mortality	Reaction
0-10% plants infected	Resistant (R)
10.1-20% plants infected	Moderately resistant (MR)
20.1-30% plants infected	Moderately susceptible (MS)
30.1-50% plants infected	Susceptible (S)
50.1-100% plants infected	Highly susceptible (HS)

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) is an important tool to determine the variability present among the genotypes. The analysis (ANOVA) revealed the presence of considerable variability among 280 genotypes including checks (JG-11 and SA-1) for all the five polygenic traits (Table 1). The results show ample scope incorporating the promising genotypes in the breeding programmes aimed improvement in seed yield and its component characters.

Group constellations by tocher method

On the basis of D^2 values, two-hundred and eighty genotypes including two checks (JG-11 and SA-1) were clustered into 17 clusters based on Tocher's method (Rao, 1952). Out of 17 clusters, Cluster II has the highest number of genotypes (89) followed by cluster I with 83 genotypes, cluster III with 31 genotypes, cluster VIII with 29 genotypes, cluster VI with 24 genotypes, cluster VII with 15 genotypes (Table 2 and Fig 1). Whereas, the remaining clusters IV, V, IX, X, XI, XII, XIII, XIV, XV, XVI, XVII are mono-genotypic containing one genotype each, which shows that the genotypes included in these clusters are more divergent than the genotypes belonging to other clusters. The results are in accordance with the results obtained by Gediya *et al.*,

(2018), Bohare *et al* (2020). The solitary clusters are obtained due to the fact that they exhibit some distinctive characters which make them diverse from the other clusters.

Relative contribution of each character towards genetic divergence

The analysis revealed that, days to maturity had contributed maximum towards divergence (29.92%) followed by 100 seed-weight (28.02%), plant height (22.45%), days to 50 per cent flowering (18.67%). Whereas, least contribution was made by seed yield/plant (0.57%) towards the genetic divergence (Fig 2).

Intra-cluster and inter-cluster distances among the chickpea germplasm

Intra-cluster and inter-cluster distances were calculated using D^2 values. Out of 17 clusters, intra cluster distances were lower than inter-cluster distances indicating that genotypes included in different clusters are more diverse compared to the genotypes included in the same clusters. The mean intra-cluster D^2 values were ranged from 0 to 425.66. Cluster VII logged highest intra-cluster distance (425.66), followed by cluster VIII (401.40), indicating that wide genetic divergence was existing among the genotypes within these clusters. So, more emphasis will be given to the genotypes included in these clusters while selecting parents for future crop improvement. The clusters *viz.*, cluster VI (260.71), cluster III (221.62), cluster II (176.78), cluster I (148.70) had moderate intra cluster distance. Whereas, no intra cluster distance was observed in nine clusters IV, V, IX, X, XI, XII, XIII, XIV, XV, XVI, XVII as they are mono-genotypic with one genotype per cluster (Table 3).

Cluster mean values of seventeen clusters

Cluster mean value ranged from 31 days (cluster XIV) to 83 days (cluster XVI) for the trait days to 50 per cent flowering. Cluster XIV genotypes exhibited early flowering habit with average number of days taken to flowering were 31, indicating that the Cluster XIV composed of early flowering genotypes. Cluster mean for the trait days to maturity ranged from 90 (cluster XI) to 130 days (cluster XVI). The genotypes of Cluster XI demonstrated a unique early maturing

Table 1: Summary of analysis of variance (ANOVA).

Source of variation	df	Days to 50% flowering	Days to maturity	Plant height	100 seed-weight	Seed yield/plant
Block (Ignoring treatments)	12	213.721***	634.293***	65.063*	34.769***	596.924***
Treatment (eliminating blocks)	281	44.416***	49.200**	57.907*	3.603*	42.164***
Checks	1	252.346***	133.885**	286.913**	1.858	63.711**
Checks + var vs var	280	43.673***	48.898**	57.089*	3.610*	42.087***
Block (Eliminating check + var.)	12	10.124	38.852*	14.012	2.485	2.514
Entries (Ignoring blocks)	281	53.110***	74.628***	60.087*	4.982**	67.548***
Varieties	279	50.038***	74.350***	53.940*	4.971**	67.758***
Check vs varieties	1	711.072***	93.032**	1548.416***	11.071**	12.808
Error	12	6.427	12.879	18.261	1.459	5.488

*= Significance at P = 0.05, **= Significance at P = 0.01, ***= Significance at P = 0.001 probability levels.

behaviour, taking only 90 days to reach maturity. In terms of plant height, genotypes from cluster IX displayed the greatest cluster mean value (66 cm), indicating that they were taller than genotypes from other clusters. Cluster VI had the lowest cluster mean value (34.03 cm) indicating that the genotypes included in this cluster are dwarf. Cluster mean value for

Table 2: Clustering pattern of chickpea genotypes based on D² analysis.

Cluster no.	Number of genotypes	Name of genotypes lines
I	83	JG-11XWR-315(F5)-55, JG-14X WR-315(F4)-66, ICCV-171101, ICCV-171113, ICC-506 ICC-1052, ICC-1230, ICC-1923, ICC-3776, ICC-9137, ICC-1008, ICC-10341, ICC-10466, ICC-11303, ICC-11498, ICC-13764, ICC-13892, ICC-16207, ICCV-14314, ICC-67, ICC-283, ICC-456, ICC-708, ICC-867, ICC-1161, ICC-2072, ICC-2482, ICC-2593, ICC-2629, ICC-2679, ICC-2737, ICC-2884, ICC-2919, ICC-2990, ICC-3230, ICC 3239, ICC 3325, ICC 3362, ICC 4495, ICC 4533, ICC 4567, ICC 4593, ICC 4639, ICC 4657, ICC4958, ICC 4991, ICC 5135, ICC 5504, ICC 5613, ICC 5878, ICC-7184, ICC-7554, ICC-7571, ICC-7819, ICC-7867, ICC-8384, ICC-8515, ICC-8521, ICC-8752, ICC-9418, ICC-9434, ICC-9586, ICC-9636, ICC-9643, ICC-9702, ICC-9712, ICC-9848, ICC-9872, ICC-9942, ICC-10399, ICC-10685, ICC-16915, IG-5909, ICCV-2, JG-11, ICCV-10, KAK-2, ICC-8318, ICC-9402, ICC-1180, ICC-2969, ICCV-08108, ICC-10673
II	89	GKB-10, ICC-1882, ICC-9002, ICC-11664, ICC-11879, ICC-11903, ICC-11944, ICC-12028, ICC-12037, ICC-12155, ICC-12299, ICC-12324, ICC-12328, ICC-12379, ICC-12537, ICC-12824, ICC-13816, ICC-14051, ICC-14077, ICC-14831, ICC-15333, ICC-15406, ICC-16269, ICC-16654, ICC-16796, ICCV-12109, ICCV-12113, ICCV-12115, ICCV-12304, ICCV-13110, ICCV-13115, ICCV-13304, ICCV-14308, ICCV-14313, ICCV-14315, ICCV-15109, ICCV-15110, ICCV-16105, ICCV-16110, ICCV-16117, ICC4872, ICC-12307, ICC-12726, ICC-12851, ICC-12947, ICC-13077, ICC-13441, ICC-13523, ICC-13719, ICC-14815, ICC-15762, ICC-15618, ICC-15785, ICC-15868, ICC-15888, ICC-16374, ICC-16487, IG-6044, IG-6055, IG-72109, IG-73458, ICCV-12101, ICCV-12118, ICCV-13106, ICCV-13107, ICCV-13108, ICCV-13117, ICCV-13301, ICCV-13303, ICCV-13305, ICCV-13307, ICCV-13308, ICCV-13310, ICCV-15315, ICCV-16106, ICCV-16107, ICCV-16113, ICCV-16114, ICCV-16115, ICCV-16116, ICCV-16118, ICCV-16312, ICCV-12108, ICCV-13113, ICC-12654, ICC-1083, ICC-1098, SA-1, ICCV-13311
III	31	ICC-14799, ICCV-12116, ICCV-13306, ICC-1392, ICC-1397, ICC-1356, ICC-1398, ICC-1422, ICC-1456, ICC-1510, ICC-1715, ICC 3391, ICC 3410, ICC 3421, ICC-3512, ICC 3582, ICC 3631, ICC 3892, ICC-4918, ICC 5879, ICC 6306, ICC-8855, ICC-8950, ICC-9862, ICC-11279, ICC-11378, ICC-11584, ICCV-13109, ICCV-16301, ICCV-16310, GBM-2
IV	1	ICC-1431
V	1	ICCV-16307
VI	24	ICCV-171111, ICC-11764, ICC-16261, ICCV-14310, ICCV-14312, ICC-1194, ICC-2277, ICC-1205, ICC-2580, ICC 4418, ICC 4814, ICC 4853, ICC-10018, ICCV-13114, ICC-15802, ICC-16903, ICCV-12301, ICCV-12313, ICCV-13309, ICCV-15317, JG-14, ICCV-96029, JG-16, A-1
VII	15	ICC-13283, ICC-13524, ICC-13599, ICC-13124, ICC-13219, ICCV-13302, ICCV-16302, ICCV-16303, ICCV-16309, ICCV-16313, ICCV-16305, ICC-13628, ICCV-16306, ICCV-16314, ICC-14098
VIII	29	BG-256XWR-315(F4)-6, GBM-2WR-315(F4)104, RCBM-3, ICC-637, ICC-10393, ICC-11284, ICC-13863, ICC-95, ICC-440, ICC-791, ICC-2720, ICC-3218, ICC5221, ICC5337, ICC-1627, ICC5383, ICC6537, ICC-6875, ICC-8522, ICC-8621, ICC-9590, ICC-14669, ICC-14778, ICC-10945, ICCV-16316, ICCV-16317, ICCV-16318, ICCV-196856, ICC-9895
IX	1	IG-10701
X	1	ICCV-16311
XI	1	ICCV-14114
XII	1	ICC-14199
XIII	1	ICCV-16103
XIV	1	ICC-5845
XV	1	ICCV-15117
XVI	1	ICCV-16308
XVII	1	MNK-1

100 seed-weight was ranged from 8 g (cluster XI) to 56.8 g (cluster XVII), the genotypes of the cluster XVII showed the highest 100 seed-weight followed by cluster III (31.7 g) which shows that the genotypes of this cluster have bold

seed characters which are preferred by the consumers. The genotype MNK-1 (56.80 g) showed the highest 100 seed-weight and the genotype ICC-14077 (4.8 g) has the lowest 100 seed-weight. Cluster mean for seed yield/plant values

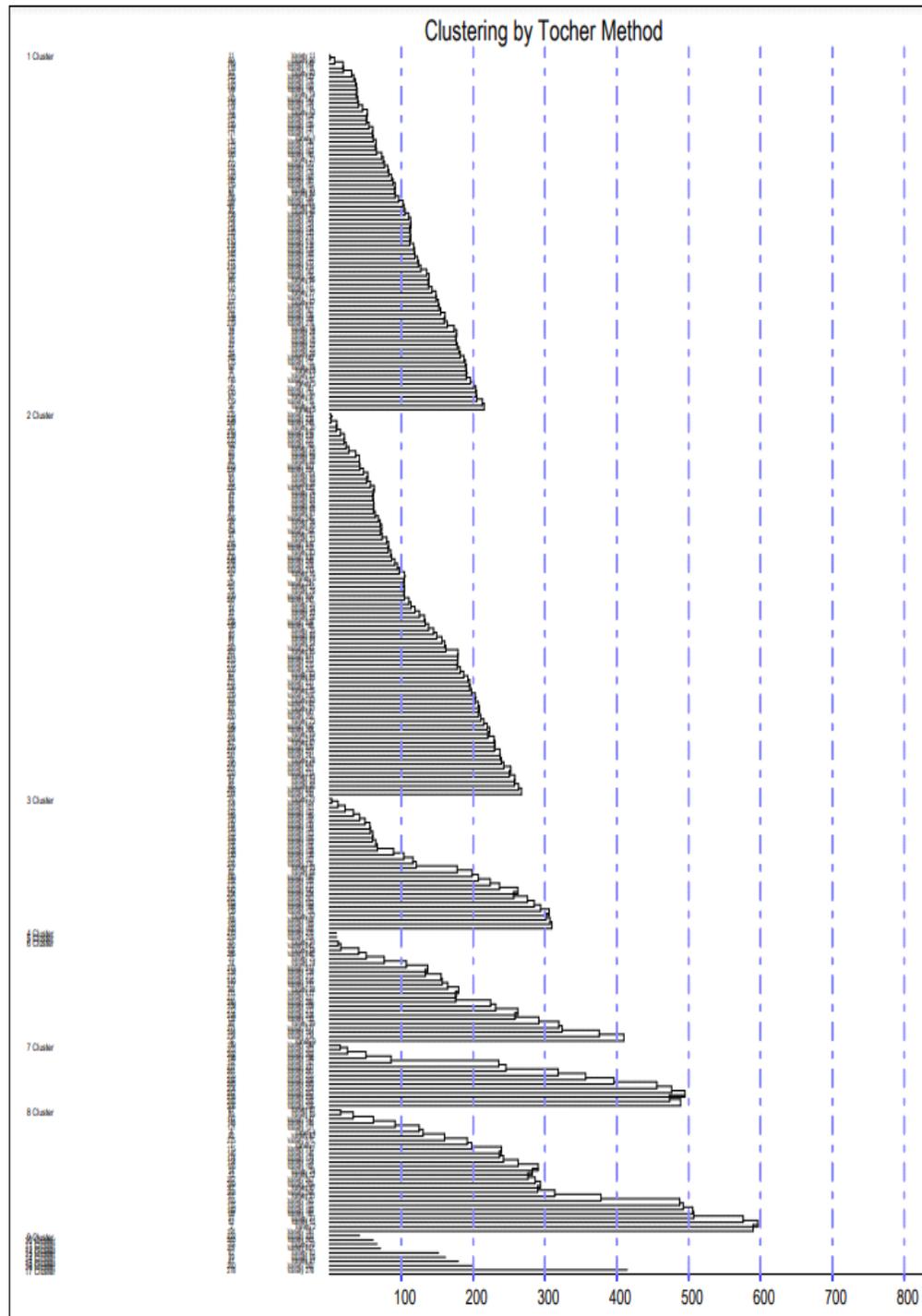


Fig 1: Dendrogram showing clustering pattern of 280 genotypes and 2 checks of chickpea.

Table 3: Intra (diagonal) and inter cluster distances (D^2 value) of 280 genotypes along with checks of chickpea.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII
I	148.70	420.85	423.29	881.74	762.35	329.88	887.78	387.13	1021.45	1734.51	507.29	1449.52	1093.58	811.29	1225.70	2597.49	1531.66
II		176.78	579.57	303.30	475.75	536.82	441.15	655.84	675.24	885.86	356.94	615.58	520.04	1456.31	830.88	1443.93	2190.71
III			221.62	821.23	401.79	853.80	718.36	602.79	1060.61	1196.20	1065.90	1163.56	908.89	1072.94	728.29	1872.58	816.74
IV				0.00	361.50	933.77	354.05	1287.44	1143.43	276.18	617.03	292.15	166.86	2515.76	419.58	769.12	2634.50
V					0.00	1042.66	308.62	1052.02	1098.74	536.34	1256.65	710.63	654.17	1614.56	538.81	1066.52	1450.79
VI						260.71	1091.26	746.18	1483.84	2025.85	479.30	1766.90	1315.54	1221.82	1623.57	3050.80	2458.78
VII							425.66	1115.46	891.35	619.61	1000.35	564.56	623.67	1870.03	771.43	1027.54	2182.55
VIII								401.40	732.93	2061.60	785.90	1556.69	1426.11	682.57	1590.57	2698.39	1528.85
IX									0.00	1554.67	986.26	794.27	1267.25	1239.13	1705.81	1578.25	2428.32
X										0.00	1511.45	209.54	233.74	3578.44	268.45	199.00	2675.55
XI											0.00	983.00	693.03	1909.41	1271.22	2193.01	3032.23
XII												0.00	206.03	3019.81	511.98	250.01	2836.66
XIII													0.00	3028.20	179.58	618.00	2438.23
XIV														0.00	3063.34	4352.70	1628.12
XV															0.00	735.94	1641.32
XVI																0.00	3383.30
XVII																	0.00

ranged from 2.38 g (cluster XII) to 8.13 g (cluster XVII), with genotypes from cluster XVII had the highest seed yield/plant (8.13 g) suggesting that the genotypes of this cluster are preferred for the seed yield improvement of chickpea (Table 4).

Fusarium wilt screening in chickpea (*Cicer arietinum* L.) germplasm

Among the two hundred and eighty-two chickpea genotypes along with two checks screened against wilt, there was a significant variation between genotypes for their disease reaction. Out of 280 germplasm screened, 30 showed resistant (10.71%), 83 moderately resistant (29.64%), 44 moderately susceptible (15.71%), 31 susceptible (11.07%) and 92 highly susceptible reaction to fusarium wilt. The

per cent disease incidence (PDI) ranged from 0.44 (ICCV 16116) to 49.49 (ICCV-171101) among germplasm with resistance check WR-315 and susceptible check JG-62 recording the wilt incidence of 4.25 and 86.42 per cent respectively. The lowest PDI was observed for the line ICCV 16116 (0.44) followed by ICC 9942 (1.77), ICC 4657 (3.48) and ICC 9872 (5.50) and can be re-validate and used in fusarium wilt resistance breeding program (Table 5). Similar study was conducted by Ayyub *et al.* (2003) who reported high level of resistance to *Fusarium* wilt in chickpea germplasm originating from different sources. Bakhsh *et al.* (2007) reported 3 genotypes with disease incidence 0, 6.7 and 8.3 per cent as resistant and 4 with disease incidence of 18.2 to 20 per cent as tolerant Kumar *et al.* (2013) reported that out of 100 genotypes, 44 showed resistant reaction, 11 MR,

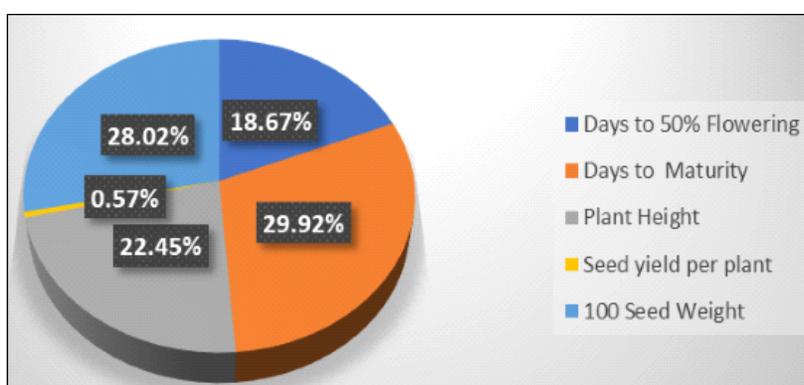


Fig 2: Diagrammatic representation of per cent contribution of each character towards divergence in genotypes.

Table 4: Cluster means of 17 clusters for yield and its related traits in chickpea genotypes.

Cluster No.	No. of germplasm lines	DDF	DM	PH	SY/PP	100-SW	Overall score	Rank
I	83	49.53 (3)	95.40 (4)	42.06 (10)	5.93 (4)	23.63 (5)	26	15
II	89	57.15 (8)	104.54 (7)	42.11 (9)	3.58 (11)	13.00 (12)	47	9
III	31	55.29 (6)	106.77 (8)	45.62 (7)	7.38 (2)	31.70 (2)	25	2
IV	1	65.00 (12)	114.00 (11)	34.33 (16)	4.00 (10)	11.00 (13)	62	12
V	1	55.00 (5)	121.00 (15)	41.66 (11)	4.10 (9)	23.60 (6)	46	10
VI	24	45.50 (2)	94.13 (2)	34.03 (17)	4.53 (8)	16.76 (8)	37	13
VII	15	58.13 (9)	116.73 (14)	43.62 (8)	3.53 (12)	14.78 (11)	54	7
VIII	29	50.72 (4)	94.28 (3)	52.84 (4)	4.95 (5)	23.54 (7)	23	17
IX	1	59.00 (10)	104.00 (6)	66.00 (1)	2.52 (14)	9.50 (15)	46	11
X	1	76.00 (13)	125.00 (16)	38.00 (12)	4.68 (7)	15.50 (10)	58	5
XI	1	61.00 (11)	90.00 (1)	38.00 (13)	2.40 (16)	8.00 (17)	58	6
XII	1	76.00 (14)	116.00 (13)	47.00 (6)	2.38 (17)	9.00 (16)	66	8
XIII	1	76.00 (15)	110.00 (10)	36.0 (14)	2.56 (13)	16.00 (9)	61	3
XIV	1	34.00 (1)	96.00 (5)	61.33 (2)	6.00 (3)	28.40 (3)	26	15
XV	1	76.00 (16)	115.00 (12)	35.33 (15)	4.86 (6)	28.20 (4)	63	1
XVI	1	79.00 (17)	130.00 (17)	48.00 (5)	2.50 (15)	11.00 (14)	59	4
XVII	1	56.00 (7)	108.00 (9)	54.40 (3)	8.13 (1)	56.80 (1)	37	14

Where, Numbers in parenthesis are overall score for characters in chickpea genotypes.

DDF: Days to 50% flowering; 100-SW: 100 seed weight (g); SY/PP: Seed yield per plant (g); DM: Days to maturity; PH: Plant height (cm).

Table 5: Chickpea lines identified as resistant against fusarium wilt under field condition.

Entry name	Per cent disease incidence (%)	Reaction
ICCV 16116	0.44	R
ICC 9942	1.77	R
ICC 4657	3.48	R
ICC 9872	5.50	R
ICC 11279	6.17	R
ICC 440	6.30	R
ICC 95	6.41	R
ICC 2679	6.48	R
ICC-1882	7.11	R
ICC 2990	7.24	R
ICC-16269	7.88	R
ICC-11944	8.33	R
ICC 1392	8.33	R
ICC 3230	8.33	R
ICCV-14314	8.60	R
MNK-1	8.66	R
ICC 791	8.69	R
ICC 1398	8.88	R
ICC 3218	8.88	R
ICC 3325	8.88	R
ICC 867	9.09	R
ICC 4495	9.33	R
ICC-10466	9.40	R
ICC-11664	9.50	R
ICC 9643	9.52	R
ICC 2629	9.60	R
GBM-2	9.62	R
ICC-637	9.80	R
ICC 2072	9.80	R
ICC 67	9.84	R

22 tolerant, 15 moderately susceptible and 8 susceptible to *Fusarium* wilt. Similar results were also reported by Shah *et al.* (2015) and Kumar *et al.* (2015); Ayana *et al.* (2019). Laxuman *et al.* (2025) used various wilt resistant chickpea genotypes and breeding lines for evaluating yield response in different environments. They observed higher average yields of KCD-11 and ICCV 191106 with wilt resistance.

CONCLUSION

In this current divergence study, the relative contribution of each character towards genetic divergence will provide effective data to assist the plant breeders in selecting superior genotypes from available germplasm collection to use them as parents in the future crop improvement programme. The maximum intra cluster distance (425.66) was observed in the cluster VII, followed by cluster VIII (401.40), indicating the existence of wide genetic diversity among the genotypes within these cluster. The maximum inter cluster distance was observed between cluster XIV

and cluster XVI (4352.70), followed by cluster X and cluster XIV (3578.44), cluster XVI and cluster XVII (3383.30), cluster XIV and cluster XV (3063.34), cluster VI and cluster XVI (3050.80), revealing that genotypes included in these clusters are genetically diverse and is vital for future hybridization programme. The field screening for *Fusarium* wilt of two hundred and eighty chickpea genotypes in the wilt sick plot yielded thirty resistant genotypes, of which ICCV 16116 (0.44) followed by ICC 9942 (1.77), ICC 4657 (3.48), ICC 9872 (5.50) showed significantly higher level of resistance for wilt as they produced narrow range of per cent disease incidence (PDI) value. The characters which contributed more to genetic divergence may be given more weightage in future plant breeding programmes to improve the yield through selection. The *Fusarium* wilt resistant genotypes which were screened using sick plot can be directly released as variety or choice of parents for hybridization programme.

Conflict of interest

All authors declared that there is no conflict of interest.

REFERENCES

- Anonymous (2021). Agriculture at glance, Directorate of Economic and Statistics, Department of Agriculture and Co-operation. pp: 105-108.
- Ayana, A., Hailu, N. and Taye, W. (2019). Screening desi and kabuli chick pea varieties against *Fusarium* wilt resistance in West Gojam, Northwestern Ethiopia. *Journal of Plant Pathology and Microbiology*. **10**: 2.
- Ayyub, M.A., Khan, S.M., Ahmad R. and Iftikhar K. (2003). Screening of chickpea germplasm for the sources of resistance against chickpea wilt. *Pakistan Journal of Phytopathology*. **15(1-2)**: 25-27.
- Bakhsh, A., Iqbal, S.M. and Ikram-UI-Haque. (2007). Evaluation of chickpea germplasm for wilt resistance. *Pakistan Journal of Biotechnology*. **39(2)**: 583-593.
- Bohare, T.V., Kulwal, P.L., Chahande, R.V., Bedis, M.R. and Shinde, L.B.M.S.D. (2020). Genetic diversity analysis in chickpea (*Cicer arietinum* L.) genotypes. *Journal of Pharmacognosy and Phytochemistry*. **9(2)**: 899-903.
- Gediya, L., Patel, D.A., Parmar, D.J., Patel, R. and Rahevar, R. (2018). Assessment of genetic diversity of chickpea genotypes using D² statistics. *International Journal of Childhood and Society*. **6(4)**: 3177-3181.
- Kumar, S.S.V., Prakash, J.C. and Kumar, A.B. (2013). Identification of chickpea genotypes for resistance to pod borer and fusarium wilt. *Bioinfolet*. **10(2)**: 745-749.
- Kumar, A., Nath, A.S. and Kumar, Y. (2015). Screening for resistant sources in chickpea. *Indian J. Agri. Sci*. **4(8)**: 2319-7064.
- Ayana, A., Hailu, N. and Taye, W. (2019). Screening Desi and Kabuli Chick Pea Varieties against *Fusarium* Wilt Resistance in West Gojam, Northwestern Ethiopia. *Journal of Plant Pathology and Microbiology*. **10**: 2.
- Laxuman, Sidramappa, P.H., Kumar, K.S. and Kumar, G.A. (2025). Seed yield stability assessment of chickpea genotypes through AMMI and Bi Plot analysis. *Legume Research*. **48(2)**: 218-223. doi: 10.18805/LR-4911.

- Mahalanobis, P.C. (1936). Study on the Generalized Distance in Statistic. Proceedings of National Institute of Sciences India. **2**: 49-55.
- Rao, C.R. (1952). Advanced Statistical Methods in Biometrical Research. John Wiley and Sons, New York.
- Shah, T.M., Imran, M., Atta, B.M., Aslam, M. and Hussain, K. (2015). Screening of chickpea advanced lines for sources of resistance against blight and wilt two major diseases of chickpea. *Pak. J. Bot.* **47(6)**: 2443-2448.
- Saha, S., Babbar, A. and Singh, S. (2018), Genetic diversity in elite lines of chickpea (*Cicer arietinum* L.) for phenological and quantitative traits. *Journal of Pharmacognocny and Phytochemistry.* **7(2)**: 2705-2709.
- Thudi, M., Chitikineni, A., Liu, X., He, W., Roorkiwal, M., Yang, W. and Samineni, S. (2016). Recent breeding programs enhanced genetic diversity in both Desi and Kabuli varieties of chickpea (*Cicer arietinum* L.). *Scientific Reports.* **6**: 38636.
- Varshney, R.K., Song, C., Saxena, R.K., Azam, S., Yu, S. and Sharpe, A.G. (2013). Draft genome sequence of chickpea (*Cicer arietinum*) provides a resource for trait improvement. *Natational Biotechnology.* **31(3)**: 240-246.