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Genetic diversity in new chickpea accessions for *fusarium* wilt resistance, canopy temperature and yield components under drought milieus

Muhammad Naveed*, Muhammad Shafiq, Chaudhry Muhammad Rafiq, Muhammad Afzal Zahid

Pulses Research Institute, Ayub Agricultural Research Institute, Faisalabad, Pakistan

***Corresponding author: naveed1735@yahoo.com**

Abstract

Chickpea *fusarium* wilt is one of the major causes of low productivity under water deficit environments in Pakistan. Searching newly developed chickpea genotypes for the desirable recombinants possessing wilt resistance along with other yield components was the objective of this experiment. Sixty accessions were laid out in an alpha lattice design with two replications. Analysis of variance for various traits revealed significant diversity among the genotypes which can be exploited for the development of superior chickpea segregants in productivity improvement programs. High to moderate estimates of heritability and genetic advance were recorded for *fusarium* wilt incidence, days to 50% flowering, total branches per plant, pods per plant, 100-seed weight, grain yield and harvest index. Significant relationship of grain yield with these characters was further established by means of principal component analysis. First four PCs out of total ten achieved eigenvalues > 1 and explained 75.5% of overall variability. Days to 50% flowering, 100-seed weight and grain yield contributed highest weight on PC_1 that explained 31.80% of total variation. PC_2 described 21.60% of digression and was mainly related to pods per plant, plant height and canopy temperature. Cluster analysis classified the genotypes into 3 clusters with maximum 33 genotypes in cluster II. Cluster I comprised of drought tolerant accessions based on canopy temperature while cluster III consisted of bold seeded genotypes regarding 100-seed weight. Cluster II incorporated wilt resistant, early flowering yet late maturing genotypes having highest pods per plant, grain yield and harvest index. D^2 statistics further confirmed the versatility of cluster II genotypes over cluster I and III for most of the studied characters.

Keywords: Diversity; chickpea; *fusarium* wilt; canopy temperature; yield components.
Abbreviations: FWI_*Fusarium* wilt incidence, CT_Canopy temperature, DF_Days to 50% flowering, DM_Days to maturity, PH_Plant height, TBPP_Total branches per plant, PPP_Pods per plant, HSW_100-seed weight, GY_Grain yield, HI_Harvest index, PCs_Principal components.

Introduction

Chickpea (*Cicer arietinum* L.) is the second leading food legume after drybeans being cultivated in cool seasons of arid and semi-arid environments worldwide (Varshney et al., 2013; Jha et al., 2014). Its seeds are substitute to meat due to rich source of carbohydrate, crude protein, minerals, vitamins and various other essential nutrients (El-Adawy, 2002). Two major chickpea types i.e. *desi* have angular microsperma with rough coat while *kabuli* have round macrosperma with smooth coat (Naghavi and Jahansouz, 2005). Globally, it is cultivated in 54 countries with major production share from India (66.3%), followed by Australia (6.2%), Pakistan (5.7%), Turkey (3.9%) and Burma (3.7%). Despite ranking second in chickpea acreage, average productivity of 276 kg/ha of Pakistan is far below than worlds average of 941 kg/ha (Gaur et al., 2012; FAOSTAT, 2013)where 90% of the crop is being grown on rainfed and marginal lands with major portion (>80 %) on sand dunes of Thal zone of Punjab province. Years receiving rainfall during cropping season yield satisfactory production and *vice versa* (Khan et al., 1991; Shafiq et al., 2011). Beside drought, chickpea wilt caused by *fusarium oxysporum* is another major production limiting factor responsible for approximately 1.2 million dollars annual yield losses in Pakistan (Shah et al., 2009).

Genetic crop improvement depends upon exploitation of traits diversity available in the genepool by providing useful information in parents' selection and their further utilization through plant breeding approaches. Diversified germplasm is a source that may have genes of biotic and abiotic stress resistance for future breeding programs. Recent plant breeding practices have narrowed genetic base of cultivated chickpea. However, characterization of newly developed genotypes for economic traits will assist in the development / evolution of superior cultivars (Robertson et al., 1997; Van Esbroeck and Bowman, 1998; Naghavi and Jahansouz, 2005). Genetic diversity can be accessed by characterizing morphological plant traits or by the application of molecular markers. Magnitude of variation present among genepool entries can be evaluated through multivariate methods such as cluster analysis, D^2 statistics and principal component analysis (Malik et al., 2014). According to Sharma (1998), the main advantage of principal component analysis (PCA) over other biometrical techniques is that one test entry can be alloted to only one cluster in addition to revealing the magnitude of largest contributor to total variability at each axis of separation. Genetic variability in agronomic and morphological chickpea indices have been examined earlier efficiently using cluster and principal component analysis (Arshad et al. 2003; Naghavi and Jahansouz, 2005; Malik et al., 2014). In view of the above mentioned facts, the current study was planned and executed for assessing genetic variability among new chickpea genotypes developed through conventional and mutational breeding strategies. This will help to identify potential parents that can be utilized in

hybridization for improving chickpea plant against biotic and abiotic stresses coupled with other economic features.

Results

Variance and variability analysis

Mean square values obtained from analysis of variance for different traits revealed significant differences among the tested genotypes (Table 2). Descriptive statistics worked out for ten variables are presented in Table 3. Highest CVs were found for *fusarium* wilt incidence (47.5%), pods per plant (29.1%), grain yield (28.2%), harvest index (19.4%) and 100 seed weight (18.8%). Whereas, CVs recorded for days to maturity, canopy temperature, days to 50% flowering, plant height and total branches per plant were small. High GCV was measured for *fusarium* wilt incidence (63.3%), grain yield (28%) and pods per plant (27.4%). Broad sense heritability estimates were higher for grain yield (98.4%), 100-seed weight (97.8%), days to 50% flowering (97.8%), harvest index (97.0%), *fusarium* wilt incidence (89.2%), pods per plant (89.2%), plant height (80.8%) whereas moderate for days to maturity (54.1%), total branches per plant (50.9%) and lowest for canopy temperature (31.9%). Genetic advance mean percentage was highest for *fusarium* wilt incidence (92.3) followed by grain yield (57.1), pods per plant (53.3), harvest index (38.8) and 100-seed weight (37.8) while least for days to maturity (1.0) and canopy temperature (1.8).

Association studies

Pearson correlation coefficients among various traits are presented in Table 4. *Fusarium* wilt incidence revealed positive and significant association with days to 50% flowering, plant height while negative and significant with grain yield. Canopy temperature exhibited negative but significant correlation with plant height, pods per plant and grain yield. Association of days to 50% flowering with days to maturity, plant height and 100-seed weight was significantly positive while with pods per plant, grain yield and harvest index was significantly negative. Correlation of days to maturity with plant height and 100-seed weight was observed positive and statistically significant. Positive and negative relationship measured for plant height with 100-seed weight and harvest index was significant respectively. Significant linkage observed for total branches per plant with pods per plant, grain yield was positive while negative with 100-seed weight. Pods per plant and 100-seed weight associated negatively with each other, however pods per plant, grain yield and harvest index correlated positively among each other. 100-seed weight exhibited negative relationship with grain yield while grain yield revealed positive and significant association with harvest index.

Contribution of traits in total diversity

Principal component analysis of various traits yielded 10 PCs. First four PCs attained eigenvalues > 1 and explained 75.5% of diversity existed in the genotypes, thereby condensed the 10 traits to 4 PCs (Table 4). Remaining six PCs had eigenvalues < 1, therefore not presented here. PC_1, PC_2, PC_3 and PC_4 explained 31.80%, 21.6%, 11.70% and 10.30% of the overall diversity present in the genotypes respectively. Days to 50% flowering (-0.425), 100-seed weight (-0.414) and grain yield (0.382) contributed highest weight on the most important component i.e. PC_1 while PC_2 was greatly influenced by pods per plant (0.498), plant height (0.441) and canopy temperature (-0.420). Plant traits which exhibited maximum weight on PC_3 were harvest index (-0.662), total branches per plant (0.469) and canopy temperature (-0.370). PC_4 was mainly controlled by *fusarium* wilt incidence (0.718), canopy temperature (0.497) and total branches per plant (0.366).

Genotypes categorization

Cluster analysis classified the genotypes into 3 clusters (Table 5). Cluster I comprised of 20 genotypes, cluster II of maximum 33 accessions and cluster III of 7 entries. Mean values for each cluster indicated that cluster I comprised of entries with least values for canopy temperature, 100-seed weight, and medium for no. of days required for flowering, maturity, pods per plant, grain yield and harvest index while highest for plant height, total branches per plant (Table 5). Cluster II which comprised of early flowering but relatively late maturing genotypes exhibited least *fusarium* wilt incidence coupled with highest pods per plant, grain yield and harvest index. However, cluster III incorporated accessions with highest values for canopy temperature and 100-seed weight. Results of Mahalanobis and Rao D^2 statistics for 3 clusters are presented in Table 7 which revealed that for most of characters investigated, genotypes of cluster II displayed highest assortment against the genotypes of cluster I and then by cluster III. PC_1 and PC_2 which in combination elucidated 53.40% of total variance were plotted against each other in a biplot depicting share of each trait in genetic diversity among the experimental genotypes (Fig. 1). Dendrogram using centroid linkage displayed that all the three clusters were linked with each other (Fig. 2).

Discussion

Significant differences from analysis of variance revealed that sufficient genetic diversity existed among the accessions. Simultaneous consideration of ranges, CVs and variances disclosed greater values for *fusarium* wilt incidence, plant height, pods per plant, 100-seed weight, grains yield and harvest index which suggested utilization of current experimental genotypes in future breeding schemes and in plant selections aimed for these traits in yield improvement programs. Smaller values for canopy temperature, days to 50% flowering, days to maturity and total branches per plant proposed exploration of further germplasm for creation of more variability regarding these characters (Sewak et al., 2012; Malik et al., 2014). If the value of PCV is greater than GCV, it means that the apparent distinction is due to both genotypes and environment (Singh and Chaudhury, 1996). In the present study, considering GCV and PCV for each trait at once indicated that days to 50% flowering and plant height were least influenced by environment. Both these traits were under the control of non-additive type of gene action due to high heritability (97.8 & 80.8) coupled with low genetic advance (12.6 & 17.0) respectively. High heritability along with high to moderate genetic advance was observed for grain yield, 100-seed weight, harvest index, *fusarium* wilt incidence and pods per plant which recommended that sufficient prospect existed in experimental plant material for the improvement of these characters. Moderate to low heritability and genetic advance estimates were recorded

Table 1. Chickpea *fusarium* wilt disease rating scale given by Iqbal et al. (1993).

Disease Incidence	Response	Rating Scale
0-10 %	Highly Resistant	1
11-20 %	Resistant	3
21-40 %	Moderately Resistant	5
41-80 %	Susceptible	7
81-100 %	Highly Susceptible	9

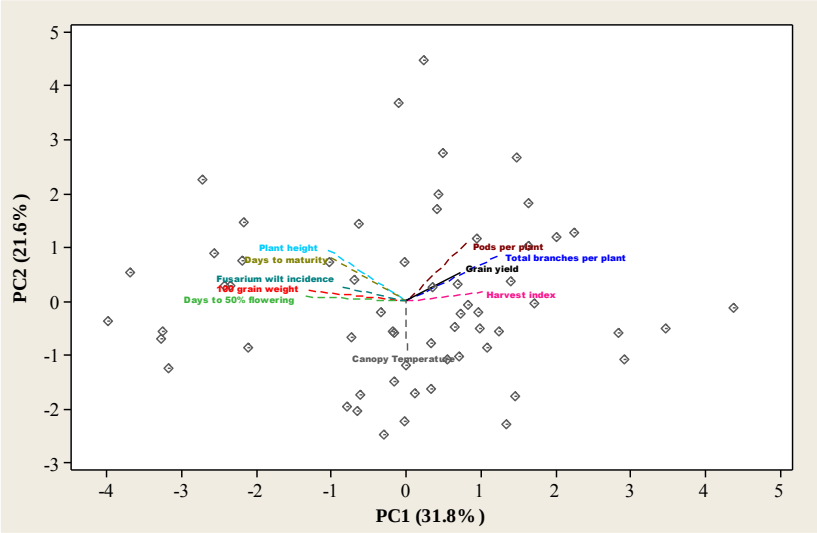

Fig 1. Biplot of first two principal components depicting contribution of various traits in diversity of new chickpea germplasm

Table 2. Mean square values acquired from ANOVA of 10 chickpea traits

S.O.V	D.F.	FWI (%)	CT (°C)	DF (50 %)	DM	PH (cm)	TBPP	PPP	HSW (g)	GY (kg/ha)	HI (%)
Replications	1	64.54	10.70	30.00	30.00	0.125	4.330	210.7	0.672	29856.0	3.078
Genotypes	59	129.2 **	0.684 *	79.83 **	3.808 *	64.73 **	4.092 *	575.4 **	38.58 **	299375.7 **	43.04 **
Error	59	13.94	0.466	1.736	1.748	12.40	2.008	62.38	0.861	4824.7	1.310

*, ** = Significant at 5% and 1% level of probability, FWI_*Fusarium* wilt incidence, CT_Canopy temperature, DF_Days to 50% flowering, DM_Days to maturity, PH_Plant height, TBPP_Total branches per plant, PPP_Pods per plant, HSW_100-seed weight, GY_Grain yield, HI_Harvest index, PCs_Principal components

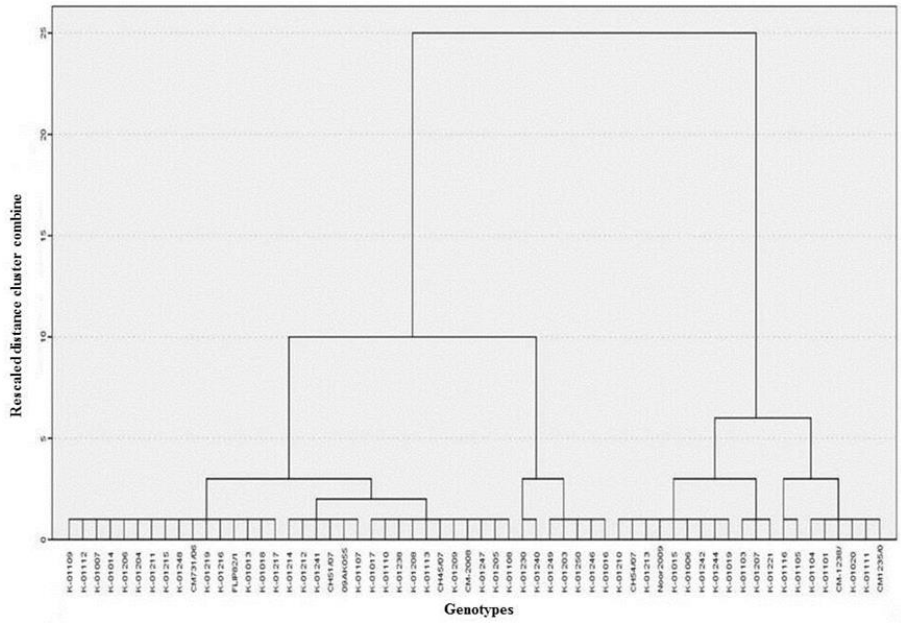

Fig 2. Dendrogram illustrating centroid linkage of 60 chickpea genotypes based on 10 traits.

Table 3. Descriptive statistics for various traits of 60 chickpea genotypes.

Variables	Traits Range			Mean	±	SE	C.V. (%)	Variance	PCV (%)	GCV (%)	$h^2_{B.S.}$ (%)	GA (mean %)
FWI (%)	0.0	-	52.9	16.0	±	1.0	66.8	64.6	50.2	47.5	89.2	92.3
CT (°C)	19.6	-	21.9	20.9	±	0.1	2.4	0.3	2.8	1.6	31.9	1.8
DF (50%)	88.5	-	110.5	101.0	±	0.8	6.3	39.9	6.3	6.2	97.8	12.6
DM	151.5	-	158.5	155.7	±	0.2	0.9	1.9	0.9	0.7	54.1	1.0
PH (cm)	39.8	-	67.7	55.7	±	0.7	10.2	32.4	10.2	9.2	80.8	17.0
TBPP	6.8	-	13.3	9.9	±	0.2	14.5	2.0	14.4	10.3	50.9	15.2
PPP	26.0	-	99.4	58.4	±	2.2	29.1	287.7	29.0	27.4	89.2	53.3
HSW (g)	18.0	-	34.0	23.4	±	0.6	18.8	19.3	18.8	18.6	97.8	37.8
GY (kg/ha)	625.0	-	2208.5	1372.5	±	49.9	28.2	149688.0	28.2	28.0	98.4	57.1
HI (%)	14.9	-	46.6	23.9	±	0.6	19.4	21.6	19.4	19.1	97.0	38.8

FWI_*Fusarium* wilt incidence, CT_Canopy temperature, DF_Days to 50% flowering, DM_Days to maturity, PH_Plant height, TBPP_Total branches per plant, PPP_Pods per plant, HSW_100-seed weight, GY_Grain yield, HI_Harvest index, PCs_Principal components.

Table 4. Pearson correlation coefficients of various traits in chickpea.

Variables	FWI (%)	CT (°C)	DF (50 %)	DM	PH (cm)	TBPP	PPP	HSW (g)	GY (kg/ha)
CT (°C)	0.063								
DF (50%)	0.416**	-0.054							
DM	0.194	-0.213	0.401**						
PH (cm)	0.319*	-0.337**	0.389**	0.588**					
TBPP	-0.003	-0.115	-0.219	-0.124	-0.057				
PPP	0.049	-0.277*	-0.317*	0.135	0.206	0.384**			
HSW (g)	0.248	0.063	0.415**	0.535**	0.503**	-0.260*	-0.254*		
GY (kg/ha)	-0.240*	-0.310*	-0.398**	-0.060	-0.044	0.382*	0.595*	-0.347**	
HI (%)	-0.189	0.181	-0.318*	-0.115	-0.283*	-0.022	0.360**	-0.207	0.572**

*, ** = Significant at 5% and 1% level of probability. FWI_*Fusarium* wilt incidence, CT_Canopy temperature, DF_Days to 50% flowering, DM_Days to maturity, PH_Plant height, TBPP_Total branches per plant, PPP_Pods per plant, HSW_100-seed weight, GY_Grain yield, HI_Harvest index, PCs_Principal components.

Table 5. Principle component analysis of various traits in chickpea.

	PC_1	PC_2	PC_3	PC_4
Eigen value	3.177	2.163	1.175	1.031
% of total variance	31.80	21.60	11.70	10.30
Cumulative variance %	31.80	53.40	65.10	75.50
Contributions by various traits				
Variables	PC_1	PC_2	PC_3	PC_4
FWI (%)	-0.269	0.122	0.079	0.718
CT (°C)	0.001	-0.420	-0.370	0.497
DF (50%)	-0.425	0.039	0.024	0.121
DM	-0.318	0.380	-0.269	-0.128
PH (cm)	-0.329	0.441	-0.005	-0.055
TBPP	0.227	0.241	0.469	0.366
PPP	0.252	0.498	-0.064	0.22
HSW (g)	-0.414	0.091	-0.311	-0.046
GY (kg/ha)	0.382	0.384	-0.157	-0.04
HI (%)	0.324	0.082	-0.662	0.134

FWI_*Fusarium* wilt incidence, CT_Canopy temperature, DF_Days to 50% flowering, DM_Days to maturity, PH_Plant height, TBPP_Total branches per plant, PPP_Pods per plant, HSW_100-seed weight, GY_Grain yield, HI_Harvest index, PCs_Principal components.

for days to maturity, total branches per plant and canopy temperature. Presence of high genetic advance for *fusarium* wilt incidence, grain yield and pods per plant specified that selection may be more useful as these traits are governed by additive gene action (Kumar et al., 1998; Sewak et al., 2012). Presence of variation in genotypes for different traits necessitates association studies. Correlation coefficient analysis measures the mutual association between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. Correlation analyses in this experiment indicated significant associations for f*usarium* wilt incidence with days to 50% flowering, plant height and grain yield, for canopy temperature with plant height, pods per plant and grain yield, for days to 50% flowering with days to maturity, plant height, 100-seed weight, pods per plant, grain yield and harvest index. Similarly significant relationship was found for days to maturity with plant height and 100-seed weight, for plant height with 100-seed weight and harvest index, for total branches per plant with pods per plant, 100-seed weight and grain yield. Likewise significant correlation coefficients were recorded for pods per plant with100-seed weight, grain yield and harvest index, for 100-seed weight with grain yield, and for grain yield with harvest index. These research findings are in accordance with that of earlier ones of Saleem et al., 2002; Kumar et al., 2003; Arshad and Bakhsh, 2004; Malik et al., 2010; Biabani et al., 2011; and Malik et al., 2014. Based on significant associations with grain yield, the present investigation suggests that traits like *fusarium* wilt incidence, canopy temperature, days to 50% flowering, total branches per plant, pods per plant, 100-seed weight and harvest index can be utilized as decisive features in the evolution of high

Table 6. Cluster membership of various chickpea genotypes.

Cluster No.	Entries No.	Detail of Genotypes
Cluster I	20	K-01006, K-01104, K-01242, CM1235/08, K-01116, K-01015, K-01213, CM-1238/08, K-01244, K-01210, K-01105, CH54/07, K-01103, K-01020, K-01221, K-01101, K-01207, K-01111, K-01019, & Noor2009.
Cluster II	33	K-01238, K-01013, K-01018, K-01248, K-01109, CM-2008, K-01014, K-01214, K-01113, K-01216, K-01241, K-01112, K-01007, K-01017, K-01108, K-01208, K-01107, K-01219, K-01247, CH51/07, K-01206, FLIP82/150C, CM731/06, K-01209, K-01217, K-01205, K-01215, K-01110, 09AK055, CH45/07, K-01211, K-01212, & K-01204.
Cluster III	7	K-01250, K-01249, K-01230, K-01246, K-01016, K-01203, & K-01240.

Table 7. Mean values of clusters for various traits in chickpea.

Variables	Cluster I	Cluster II	Cluster III
FWI (%)	12.34	2.17	12.71
CT (°C)	20.87	20.95	21.03
DF (50%)	101.14	95.50	101.50
DM	155.63	156.50	156.0
PH (cm)	55.75	53.10	55.55
TBPP	9.92	9.70	8.65
PPP	58.57	74.50	36.30
HSW (g)	23.21	25.25	25.50
GY (kg/ha)	1368.57	2198	656.25
HI (%)	23.61	37.13	18.71

FWI_*Fusarium* wilt incidence, CT_Canopy temperature, DF_Days to 50% flowering, DM_Days to maturity, PH_Plant height, TBPP_Total branches per plant, PPP_Pods per plant, HSW_100-seed weight, GY_Grain yield, HI_Harvest index, PCs_Principal components.

Table 8. D^2 statistics among 3 clusters.

	Cluster I	Cluster II	Cluster III
Cluster I	0.00	829.78	712.69
Cluster II	829.78	0.00	1542.38
Cluster III	712.69	1542.38	0.00

yielding chickpea kabuli genotypes under water deficit conditions. Principal component methodology is a useful technique for creating variability among breeding populations by selecting diverse parents (Akter et al., 2009). In our study on chickpea, first four PCs out of ten contributed largely to the total variability and explained 75.5% of diversity present in the accessions similar to the earlier reported findings (Shiv et al, 2012 and Malik et al., 2014). PC_1 was largely due to differences in days to 50% flowering, 100-seed weight and grain yield and these findings were confirmed from relationship studies which revealed significant association among these traits. PC_2 was mainly due to contributions from pods per plant, plant height and canopy temperature. Similarly PC_3 was explained by diversity present in harvest index, total branches per plant, canopy temperature, and *fusarium* wilt incidence while PC_4 by canopy temperature and total branches per plant. Further, scattering of experimental treatments in all the four segments of biplot suggested the existence of considerable genetic assortment among the genotypes (Fig. 1). Accessions in close proximity to each other and origin had small or no valuable variability while those distant from the origin had useful diversity for the characters being investigated and can be introgressed in already cultivated chickpea cultivars or newly developed genotypes with a view of expanding its genetic base. Moreover, cluster analysis sorted out experimental genotypes into 3 clusters regarding particular traits. Accessions in cluster I with least canopy temperature can be exploited for developing drought tolerant genotypes with more plant height and total branches per plant while genotypes in cluster III can be utilized for bold seed feature. Cluster II involving 33 entries are of realistic significance for breeding against *fusarium* wilt resistance with early flowering but relatively late maturing genotypes possessing highest pods per plant, grain yield and harvest index. D^2 statistics recommended that accessions in cluster II had valueable variability for most of the traits and can be incorporated in hybrid breeding and selection of desirable segregants in crop improvement programs. Centroid linkage dendrogram revealed that even a single cluster did not illustrated any separation and confirmed that all the three clusters were correlated with each other because a number of chickpea accessions exhibited differences and similarities in various traits among them. These results are in agreement with the reported ones of Grenier et al., 2001 and Malik et al., 2014.

Materials and Methods

Plant materials

It is the genetic source material often referred as germplasm used by plant breeders to develop new cultivars. The genes required for crop improvement are present in different lines, varieties, strains or populations of the crop species and their relatives. Germplasm evaluation consists of assessment of the accessions for their various features or traits of some known or potential use in breeding programmes. In the present study, newly evolved sixty chickpea kabuli genotypes were evaluated for various plant traits during cropping season 2013-14. These genotypes were selected from uniform F_6 and M_6 filial generations developed by means of conventional plant breeding and mutational breeding techniques respectively.

Experimental site

The present study was conducted at Pulses Experimental Area, Ayub Agricultural Research Institute, Faisalabad, Pakistan located on latitude of 31° 21′ 52″ N and longitude of 72° 59′ 40″ E with altitude of 184 meters.

Layout design, plot size and production practices

Experiment was conducted on wilt sick land using alpha lattice design with two replications. Seeds of all the treatments were sown upto 6" depth using dibbler manually. Plot size measured was 4.0 × 0.6 m^2, comprising 2 rows of each treatment. Plant to plant and row to row distances maintained were 15 cm and 30 cm respectively. One bag of diammonium phosphate (DAP) was applied pre-sowing while pesticide was sprayed to protect the crop from pod borer attack during cropping period. Other production practices i.e. weeding and hoeing were carried out when the crop needed. However, no irrigation was applied to experimental crop.

Fusarium wilt incidence (%)

Reaction of each genotype to *fusarium oxysporum* was determined by using modified 1-9 scale (Table 1) proposed by Iqbal *et al*., (1993). The observations were recorded on plant basis from seedling stage to maturity and wilt incidence calculated for each test entry by using the formula;
Fusarium wilt incidence (%) =
No. of plants wilted / Total ≠ of plants

Canopy temperature (°C)

Ten readings of canopy temperature for each test entry were taken on consecutive days using infrared thermometer (RAYPRM 30 CFRJ, RAYTEK, USA). These observations were recorded before the onset of reproductive stage between 1.00-2.00 pm when the plants were fully exposed to sun light.

Yield components

Observations were recorded on days to 50%flowering, days to maturity, plant height, total branches per plant, pods per plant, 100-seed weight, grain yield and harvest index. Days to flowering and maturity were calculated from date of sowing to 50% of flowering and 90% of maturity, respectively while plant height (cm), total branches per plant, pods per plant were taken on randomly selected ten plants. 100-seed weight (g) for each entry was recorded from 3 samples per replication whereas grain yield was recorded per plot (g) and then converted into kg/ha. Harvest index was obtained as percentage of grain yield to total biological yield.

Statistical computations

The replicated data for each character was subjected separately to analysis of variance technique using GenStat v.14.1 software (Payne et al., 2011). Means of each trait over genotypes were computed and used for obtaining descriptive statistics i.e. range, standard error, coefficient of variation and variance. Then phenotypic, genotypic and environmental variances were computed (Wricke and Weber, 1986). Further, heritability ($h^2_{B.S.}$) and genetic advance over mean (%) were worked out following Allard (1999) and Shukla et al. (2006). Pearson correlation coefficients, cluster and principal component analysis were performed in statistical software packages; Statistica v. 6.0 and Minitab v.16.1 (Sneath and Sokal, 1973). Based on elucidation distances, k-means clustering was used for cluster analysis while Ward's method was used for developing tree diagram. D^2 statistics were calculated using Mahalanobis (1936) and Rao (1952). Diversity pattern among the genotypes for various studied traits was graphically assessed by plotting first two principal components against each other using Minitab version 16.1.

Conclusion

Various statistical procedures such as principal component and cluster analysis employed for assessing genetic diversity of various chickpea traits provided assistance in realizing and further grouping of genotypes possessing drought and *fusarium* wilt resistance coupled with high yield potential. The information gained from these analyses along with association studies will facilitate in the selection of potential parents to be utilized in the hybridization schemes aimed at the improvement of chickpea plant against major biotic and abiotic stresses responsible for low productivity.

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