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Stability analysis of elite chickpea genotypes tested under diverse environments

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Abstract

Twelve elite chickpea genotypes along with two check varieties were grown at four diverse locations in Punjab province to check their stability. The analysis of variance for seed yield at individual locations showed significant to highly significant differences between genotypes. Pooled analysis of variance over locations displayed highly significant differences between genotypes, locations and genotype x location interaction. Among 14 genotypes, the maximum mean seed yield over the locations was produced by the CC119/00 (1.229 t ha^{-1}) and the highest mean seed yield producing location was NIAB (1.412 t ha^{-1}). The cluster analysis effectively grouped the locations and genotypes into three clusters each viz. low, medium and high yielding ones. G x E interaction was of crossover in nature. Partitioning of total variance revealed significant differences among environments and genotypes for grain yield demonstrating the presence of considerable variations among genotypes as well as diversity of environments at various locations. The analysis of stability based on mean grain yield, regression coefficient and deviation from regression revealed that the genotypes; CC119/00, CC117/00 (Colchicine mutants), CM256/99, CH38/00 and K-70022 were most stable and adapted to the diverse environmental conditions of Punjab. Previously colchicine was only known to cause chromosome doubling but now it is also known to induce mutations. This is the first report of the systematic work on the mutants induced through colchicine treatments and demonstrated their yield superiority and stability over the locations. These genotypes are recommended for commercial cultivation and can also be effectively utilized in the recombination breeding programs to enhance genetic variability in kabuli chickpea.

Key words: *Cicer arietinum* L.; Cluster analysis; Colchicine; G x E interaction; Mutant; Seed yield; Stability

Introduction

Chickpea (*Cicer arietinum* L.) is an annual legume and the only cultivated specie within genus *Cicer*. Pakistan ranks second in terms of acreage and third in terms of chickpea production in the world. Chickpea provides a cheap, high quality and rich source of protein. It is two types, desi and kabuli and there are strong consumer preferences for one or the other. Chickpea is the major rabi legume crop of Pakistan. During 2006-07 the crop was grown on an area of 1052.3 thousand hectares with annual production of 837.8 thousand tones (Anonymous, 2006-07). Average yield of world is 700 kg ha^{-1} and that of Pakistan is 550-700 kg ha^{-1}, which is quite low from its potential of four tons ha^{-1}. This gap between the average yield and the yield potential is due to its susceptibility to various biotic and abiotic stresses (Shah et al., 2005). The major biotic factor limiting chickpea yields in Pakistan are the fungal diseases; *Ascochyta* blight and *Fusarium* wilt. The blight epidemics of 1980s reduced chickpea production by almost 50% (Malik and Bashir, 1984; Malik et al., 1991). During the past several years 10-50% losses caused by *Fusarium* wilt have been reported in chickpea in the dry areas of Pakistan (Khan et al., 2002). Resistance break down is possibly the greatest challenge in breeding for diseases in chickpea.

Table 1. General features of the chickpea experimental material used in the study

S. No.	Genotypes	Breeding Institute	Type	Pedigree	100 seed weight
1.	CC121/00	NIAB[1]	Mutant	C_8, Pb.1, 0.05% Colchicine	23.9
2.	CC119/00	NIAB	Mutant	C_8, Pb.1, 0.05% Colchicine	24.5
3.	CC118/00	NIAB	Mutant	C_8, Pb.1, 0.05% Colchicine	25.1
4.	CC117/00	NIAB	Mutant	C_8, Pb.1, 0.05% Colchicine	23.3
5.	CM256/99	NIAB	Mutant	M_9, Pb.1, Gamma rays, 200Gy	24.1
6.	CM305/99	NIAB	Mutant	M_9, Pb.1, 0.2% EMS	23.6
7.	CM1589/01	NIAB	Mutant	M_7, P40/91, Gamma rays, 300Gy	22.6
8.	CH38/00	NIAB	Recombinant	F8, P8-3, P40/91 x Noor91	23.1
9.	CH41/00	NIAB	Recombinant	F8, P13-2, P40/91 x Noor91	26.0
10.	CH44/00	NIAB	Recombinant	F8, P13-6, P40/91 x Noor91	26.9
11.	K-90395	AARI[2]	Recombinant	AARI advance line	25.5
12.	K-70022	AARI	Recombinant	AARI advance line	24.6
13.	Pb-1	AARI	Check	Selection from local collection	17.4
14.	CM2000	NIAB	Check	ILC195, Gamma rays, 150Gy	22.1

[1] NIAB: Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad
[2] AARI: Ayub Agricultural Research Institute (AARI), Faisalabad

Use of resistant or tolerant cultivars is often practiced in many breeding programmes in order to control *Ascochyta* blight of chickpea (Ali et al., 2008a).

In Pakistan, desi type chickpea is grown on about 90% area and kabuli type on around 10% area. The contribution of kabuli is further declining due to its greater vulnerability to various stresses than desi type. As a result the price of kabuli remains high and we have to spend huge foreign exchange annually on its import. The variability in environment has been long recognized as an important factor influencing the performance of genotypes (Singh and Bejiga, 1990). Multi-environment trials (METs) are typically used in plant breeding programmes to evaluate material across a range of sites representing target environments for the crop (Berger et al., 2007). Genotype x environment interaction is the change in relative performance of genotypes across sites (DeLacy et al., 1996). G x E interaction should be investigated so that the breeder can decide to restructure the programme to minimize the interaction effect, or exploit it to produce varieties with specific adaptation to particular environments (Eisemann et al., 1990). A key concept in G x E analysis is genotype stability and by definition, genotypes exhibiting a high degree of G x E interaction are unstable across sites (Berger et al., 2007). The first systematic approach to the analysis of phenotypic stability of cultivars or genotypes was made by Finlay and Wilkinson in 1963. They used two parameters, (i) mean performance over environments and (ii) regression of performance in different environments over the respective environmental mean (Phundan and Narayanan, 2004). According to this model, a genotype with regression coefficient (b) value less than 1.0 has above average stability and is specially adapted to low-performing environments, a genotype with b value greater than 1.0 has below average stability and is specially adapted to high performing environments and a genotype with b value equal to 1.0 has average stability and is well or poorly adapted to all environments depending on having a high or low mean performance (Finlay and Wilkinson, 1963). Whereas, Eberhart and Russell (1966) model consists of three parameters, (a) mean yield over locations or seasons, (b) regression coefficient and (c) deviation from regression. According to this model a stable variety is one with a regression coefficient of unity (b=1) and a minimum deviation from the regression line ($S^2d=0$). Using their definition a breeder would usually desire to develop a variety with high mean yield and satisfying the above requirements for stability (Phundan and Narayanan, 2004).

Stability analysis was successfully used to determine stable chickpea genotypes by other workers (Singh and Bejiga, 1990; Kumar et al., 1996; Ozdemyr and Engyn, 1996; Yadava et al., 2000; Sood et al., 2001; Arshad et al., 2003; Bakhsh et al., 2006, Prakash, 2006). Acikgoz et al. (2009) carried out genotype x environment interaction and stability studies in field pea and identified the genotypes for low and high yielding environments. Fikere et al. (2009) tested 16 field pea genotypes across 12 environments in South Eastern Ethiopia and by using stability analysis identified two most stable genotypes for the region. A tremendous genetic variability has been produced in desi and kabuli chickpea through induced mutations and hybridization at NIAB, Faisalabad. The advanced mutants/recombinants are

Table 2. Analysis of variance of chickpea genotypes at different locations during 2006-07

Sr. No.	Source of variation	Degrees of Freedom	Mean Squares			
			NIAB	BARI	AZRI	AARI
1.	Replications	2	0.028^{NS}	0.005^{NS}	0.097**	0.059^{NS}
2.	Genotypes	13	0.794**	0.072**	0.105**	0.046*
3.	Error	26	0.013	0.003	0.016	0.022
4.	Total	41				

NS = Non significant, * and ** = Significant at 5% and 1% level of probability, respectively

Table 3. Pooled analysis of variance over locations for seed yield in chickpea

Sr. No.	Source of variation	Degrees of Freedom	Sum of Squares	Mean Squares
1.	Replications within locations	2	0.083	0.041^{NS}
2.	Genotypes	13	4.550	0.350**
3.	Locations	3	12.353	4.118**
4.	Genotypes x Locations	39	8.673	0.222**
5.	Error	110	1.719	0.016
6.	Total	167	27.377	

NS = Non significant, ** = Significant at 1% level of probability

needed to be tested at multi-locations to check their stability and adaptability. In the present study efforts were made to examine the genotype x environment interactions for seed yield in the elite kabuli chickpea genotypes to identify the stable genotypes that are best suited to the diverse environments of Punjab province.

Materials and Methods

The general features of the experimental material used in the study have been presented in the Table 1. Among the twelve test genotypes; four were developed by using colchicines as a chemical mutagen, one from ethyl methane sulphonate (EMS), two from gamma rays and five were developed through hybridization. Ten elite kabuli chickpea genotypes of NIAB and two kabuli elite lines of AARI along with two check varieties (Pb.1 and CM2000) were evaluated for stability of grain yield at four diverse locations viz., Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad; Barani Agricultural Research Institute (BARI), Chakwal; Arid Zone Research Institue (AZRI), Bhakkar; and Ayub Agricultural Research Institute (AARI), Faisalabad**,** in the Punjab province during 2006-07. The trials were laid out in randomized complete block design with three replications having a plot size of 6.0 m^2 keeping row and plant distance as 30 and 15 cm, respectively. Normal agronomic and cultural practices prevailing with the local requirements were applied at each location.

Data was collected for seed yield per plot (g) from different locations and converted to tones per hectare (t ha^{-1}). The data was analyzed as a split plot with locations as main plots and genotypes as sub-plots according to Steel and Torrie (1985). Stability parameters were estimated following the Eberhart and Russell model (1966). Cluster analysis was performed and tree diagrams were developed by STATISTICA 4.1 program based on linkage distances using Ward's method. A genotype with high mean seed yield, regression coefficient (b) close to unity and deviation from regression (S^2d) near to zero was defined as a stable cultivar (Eberhart and Russell, 1966).

Results and Discussion

The genotypes in the present study (Table 1) were developed taking into consideration the consumers demand for bold seed size. Therefore, all the test genotypes were having more seed weight (22.6 to 26.9 g) as compared to the recent check variety CM2000 (22.1 g). The development of high yielding and large seed size genotypes is the most basic demand of the chickpea growers to get ultimate return from their product (Khattak et al., 2007). The present study is among the rare reports in which the kabuli chickpea mutants developed through the application

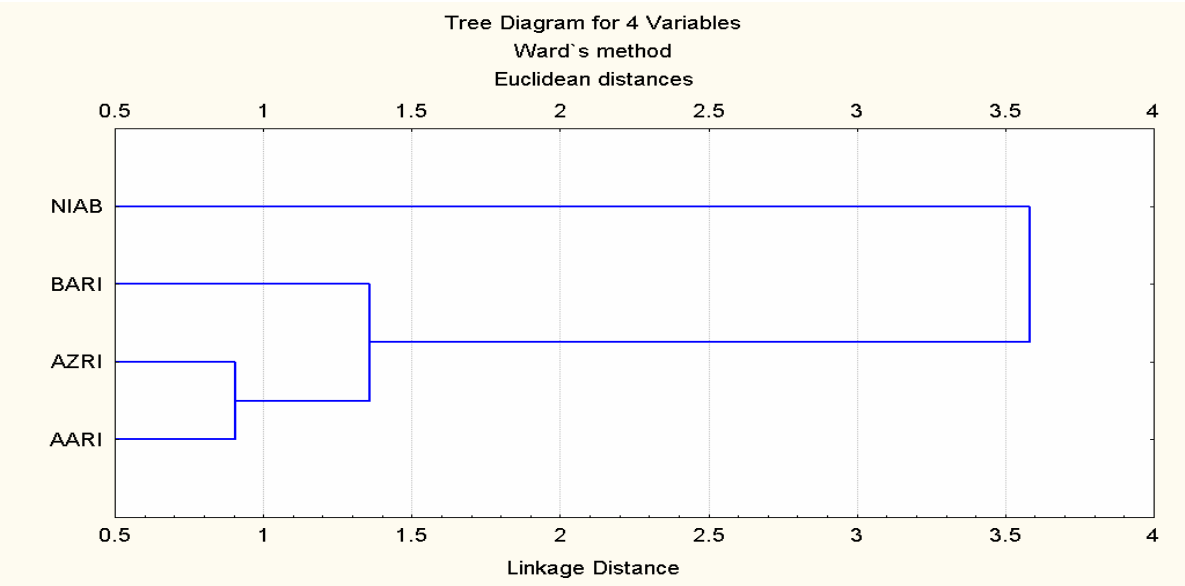

Fig 1. Tree diagram of four locations for seed yield in kabuli chickpea

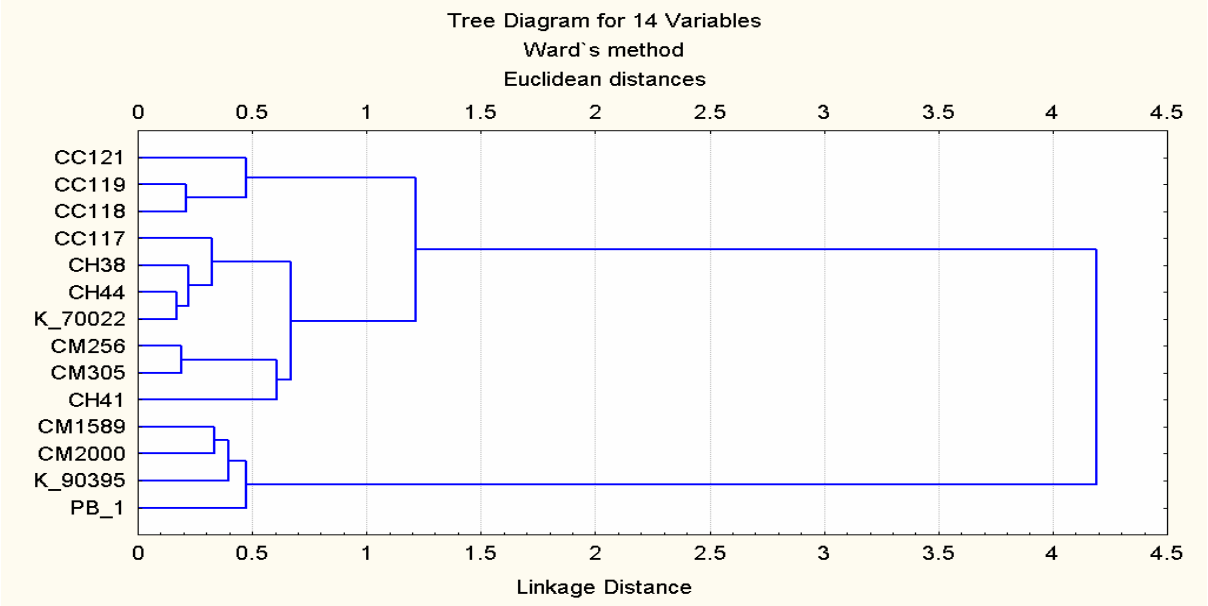

Fig 2. Tree diagram of fourteen genotypes for seed yield in kabuli chickpea

of colchicine were used as an experimental material. The colchicine was mostly used for chromosome doubling but it also induces mutations. In 1994 the IAEA data bank on induced mutant cultivars contained a total of 141 chemically induced mutant cultivars amongst which six were colchicine mutants (Harten, 1998).

The analysis of variance of chickpea genotypes at individual locations (Table 2) was highly significant for mean seed yield at NIAB, BARI and AZRI, whereas significant at AARI. The pooled analysis of variance over locations (Table 3) showed non-significant differences between replications within locations and highly significant ($P<0.01$) differences between genotypes, locations and genotype x locations interaction, thus indicating substantial variability among these for seed yield. Significant genotype x environment (G x E) interaction was also reported by Arshad et al. (2003) and Bakhsh et al. (2006) in chickpea, by Abbas et al. 2008 in mungbean, by Ali and Sarwar (2008) in cowpea and by Karasu et al. (2009) in soybean. The mean seed yield of genotypes at each location has been presented in Table 4. Maximum yield was produced

Table 4. Grain yield (tons/ha) of 14 chickpea genotypes at 4 different locations during 2006-07

Sr. No.	Genotype	NIAB[1] Faisalabad	BARI[2] Chakwal	AZRI[3] Bhakkar	AARI[4] Faisalabad	Mean
1.	CC121/00	1.819 abc	0.927 a	1.245 ab	0.844 abcd	1.209 ab
2.	CC119/00	1.962 ab	0.644 e	1.328 a	0.980 ab	1.229 a
3.	CC118/00	2.019 a	0.527f	1.354 a	0.815 abcd	1.179 abc
4.	CC117/00	1.756 bc	0.661 de	0.979 c	1.042 a	1.109 bcd
5.	CM256/99	1.784 bc	0.394 g	0.985 c	0.869 abcd	1.008 de
6.	CM305/99	1.724 cd	0.517 f	0.873 c	0.795 abcd	0.977 ef
7.	CM1589/01	0.721 g	0.688 de	0.990 c	0.729 bcd	0.782 hi
8.	CH38/00	1.456 ef	0.800 c	1.030 bc	0.833 abcd	1.030 de
9.	CH41/00	1.314 f	0.533 f	0.911 c	0.613 d	0.843 gh
10.	CH44/00	1.638 cde	0.755 cd	0.998 c	0.950 ab	1.085 cde
11.	K-90395	0.710 g	0.827 bc	0.658 d	0.644 cd	0.710 i
12.	K-70022	1.532 de	0.661 de	1.094 bc	0.930 abc	1.054 de
13.	Pb-1	0.452 h	0.694 de	0.923 c	0.934 ab	0.751 hi
14.	CM2000	0.881 g	0.916 ab	0.898 c	0.892 abcd	0.897 fg
Location mean		1.412 a	0.682 d	1.019 b	0.848 c	0.990

Mean values carrying similar letter(s) do not differ significantly at 5% level of probability

[1] NIAB: Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad

[2] BARI: Barani Agricultural Research Institute (BARI), Chakwal

[3] AZRI: Arid Zone Research Institue (AZRI), Bhakkar

[4] AARI: Ayub Agricultural Research Institute (AARI), Faisalabad

by CC118/00 (2.019 t ha^{-1}) at NIAB. The highest mean seed yield (1.229 t ha^{-1}) over the locations was achieved by the genotype CC119/00 followed by CC121/00 (1.209 t ha^{-1}) and CC118/00 (1.179 t ha^{-1}). Among the locations maximum mean seed yield wasproduced at NIAB (1.412 t ha^{-1}) followed by AZRI (1.019 t ha^{-1}), AARI (0.848 t ha^{-1}) and BARI (0.682 t ha^{-1}).

Cluster analysis was used as a tool to classify chickpea growing environments (Malhotra and Singh, 1991). The cluster analysis and AMMI (Additive Main effects and Multiplicative Interaction) analysis techniques differentiate the high yielding and low yielding environments into groups and sub-groups based on genotypic mean yield performance over environments (Arain et al., 2001). The tree diagram of the locations based on grain yield of 14 genotypes resulted in three main clusters (Fig.1). The first cluster consists of single location (NIAB) producing highest yield of 1.412 t ha^{-1}. The second cluster included one lowest yielding (0.682 t ha^{-1}) location BARI and the third cluster comprised of AZRI and AARI producing 1.019 and 0.848 t ha^{-1} mean seed yield, respectively. This difference among various locations may be due to the heterogeneous soils and imprecision in field operations (Crossa et al., 1991).

The cluster diagram of 14 genotypes based on the average yield produced at all the locations showed three main clusters (Fig. 2). First cluster comprised of top yielding genotypes viz. CC121/00, CC119/00 and CC118/00 with mean grain yield ranging from 1.179 to 1.229t ha^{-1}. Second cluster consisted of CC117-/00, CH38/00, CH44/00, K-70022, CM256/99, CM305/99 and CH41/00 with mean seed yield of 0.843 to 1.109 t ha^{-1}. This group included the medium yielding genotypes. Similarly, cluster three included the medium (CM2000) and low (CM1589/01, K-90395 and Pb-1) yielding genotypes. Both the check varieties were included in this group and the mean yield of the genotypes ranged from 0.751 to 0.897 t ha^{-1}. So, it is apparent that through cluster analysis it is possible to differentiate high, medium and low yielding locations and/ or genotypes. Ali et al. (2008b) also identified the high yielding wheat varieties through cluster analysis. Acikgoz et al. (2009) reported that cluster analysis could be a powerful tool to examine G x E interaction and suggested that the use of both stability and cluster analysis might give better results and if the number of environments was sufficient, a separate stability analysis could be run in each cluster.

In case the variance due to varieties x locations is found significant (as in Table 3) the analysis may be further proceeded for estimating the stability parameters (Singh and Chaudhary, 1979; Phundan and Narayanan, 2004). Eberhart and Russell in 1966 made improvement in stability analysis by partitioning the genotype-environment interaction of each variety into two parts, (i) slope of the regression line and (ii) deviations from the regression line. In this model, the total variance is first divided into two components i.e. genotype and environment plus interaction (E+ G x E). The second component (E+ G x E) is further subdivided into three components viz.

Table 5. Pooled analysis of variance for grain yield in kabuli chickpea genotypes.

Source	Degree of freedom	Mean square
Total	55	0.155**
Environments	3	0.310*
Varieties	13	0.273**
Env. + Var. x Env.	42	0.132*
Env. (Linear)	1	0.931**
Var. x Env. (Linear)	13	0.160*
Pooled Dev.	28	0.070**
Pooled Error	112	0.016

Table 6. Stability parameters for 14 chickpea genotypes estimated by Eberhart and Russell (1966) model.

Sr. No.	Genotype	Seed yield (tons/ha)	% difference from mean	% difference from better check CM2000	Regression coefficient (b)	Deviation from regression (S^2d)
1.	CC121/00	1.209	22.12	34.78	3.077	0.079**
2.	CC119/00	1.229	24.14	37.01	0.505	0.035
3.	CC118/00	1.179	19.09	31.43	-0.874	0.138**
4.	CC117/00	1.109	12.02	23.63	0.724	0.049
5.	CM256/99	1.008	1.81	12.37	2.790	0.028
6.	CM305/99	0.977	-1.31	8.91	-0.667	0.038
7.	CM1589/01	0.782	-21.01	-12.82	1.543	0.369**
8.	CH38/00	1.030	4.04	14.82	1.118	0.018
9.	CH41/00	0.843	-14.84	-6.02	3.218	0.126**
10.	CH44/00	1.085	9.59	20.95	-1.110**	0.002
11.	K-90395	0.710	-28.28	-20.84	1.605	0.023
12.	K-70022	1.054	6.46	17.50	-0.157	0.020
13.	Pb-1	0.751	-24.14	-16.27	2.807	0.056*
14.	CM2000	0.897	-9.39	-	-0.580*	0.005
	Grand mean	0.990				

* = Significant at 5% level of probability, ** = Significant at 1% level of probability

(a) environment linear, (b) genotype x environment (linear) and (c) pooled deviations (Phundan and Narayanan, 2004).

Partitioning of analysis of variance (Table 5) displayed highly significant results for genotype, environment linear and pooled deviations, whereas, significant for Env. + Var x Env. and var. x Env. Linear. A significant G x E interaction may be either crossover in which a significant change in rank occurs from one environment to another (Matus et al., 1997) or a non-crossover type in which ranking of genotype remains constant across environments and the interaction is significant due to change in the magnitude of response (Baker, 1988; Blum 1983, Matus et al., 1997). In the present study G x E interaction was of crossover in nature.

The stability parameters for 14 genotypes have been given in the Table 6. The CC119/00 was the top yielding and a stable genotype with 24.14 and 37% higher yield from the grand mean and better check CM2000, respectively and non-significant regression coefficient and deviations from regression. Similarly, CC117/00 gave 12.02 and 23.63% more yield than the mean and check with regression close to unity and non-significant deviation from regression. The less than one b values of CC119/00 and CC117/00 indicated above average stability and their response to the poor environments. Both these mutants were developed by the use of colchicine and showed promise for yield and its stability. This was a good example that demonstrated the use of colchicine for viable mutations.

CM256/99 and CH38/00 gave higher yields from mean and the check combined with high value of regression coefficient indicated their response to the favourable conditions. The negative regression value may be an indicator of better response to poor environment (Abbas et al., 2008) in case of K-70022 coupled with higher yield from mean and check and non-significant deviation from regression. Similarly CM305/99 showed lower value of regression coefficient and close to zero (0.029) standard deviation to regression which indicated its stability under poor environments though displayed lower

yield from mean and higher yield (9%) from the check. Stability in the seed yield was earlier reported by many workers (Arshad et al., 2003; Bakhsh et al., 2006; Swamy and Reddy, 2004; Khan et al., 2007; Abbas et al., 2008, Ali and Sarwar, 2008). Prakash et al. (2006) by using stability analysis identified some stable chickpea genotypes for different environments.

CC121/00, CC118/00 and CH44/00 although showed higher yields (10 to 35%) from mean and check yet can't be considered as stable genotypes due to either significant regression coefficient or deviation from regression values. Similarly, the genotypes, CM1589/01, CH41/00, K-90395, Pb-1 and CM2000 were the lower yielders with significant b or S^2d, hence does not fulfill the requirements of stable genotypes.

Conclusion

The results of the present study indicated that seed yield was influenced by the environmental changes because there were significant variations in seed yield of the genotypes tested at diverse environments. Chickpea crop yields in the Punjab province were generally low and not stable. The stability based on the mean seed yield, regression coefficient and deviation from regression indicated that the genotypes, CC119/00, CC117/00, CM256/99, CH38/00 and K-70022 were the most stable and adapted to the diverse environments of the Punjab province. The cluster analysis also grouped all these genotypes in high and medium yielding clusters. These genotypes are recommended for commercial cultivation and can also be effectively utilized in the recombination breeding programs to enhance genetic variability in kabuli chickpea.

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