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Full Length Research Paper

Performance of chickpea genotypes under two different environmental conditions

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Seed yield of 20 genotypes of chickpea was investigated under two different environmental conditions of Pakistan during 2007 to 2008. The experiment was carried out in randomized complete block design with three replications in each environment. Within environment, genotype main effect was significant. Similarly, genotype by environmental interaction was also significant. Genotypes at Karak produced significantly greater seed yield than at Peshawar. Cluster analysis of chickpea genotypes based on seed yield resulted in two main clusters. These two clusters were again subdivided into three and two sub-clusters indicating considerable diversity for grain yield among the chickpea genotypes. GGE biplot analysis ranked genotypes on above average seed yield across environments as Lo-3, Lo-2, Pk-2, Lo-4 and Pk-3 as top five genotypes, while the bottom five genotypes were identified as Sy-7, Pk-1, Sy-4, Sy-5 and Pk-5. For stability of performance across environments, Pk-4, In and Pk-3 were identified as most stable genotypes followed by Lo-2, Pk-2, Pk-3 and Lo-3. On the basis of both stable performance and mean seed yield across environment, the GGE biplot ranked genotypes Lo-3 as the best among all, followed by Lo-2, Pk-2, Pk-3 and Lo-4, while the rest of the genotypes were identified as inferior. Karak was identified as representative environment as compared to Peshawar.

Key words: Genotype × Environment interaction (GEI), bioplot analysis, *Cicer arietinum L.,* Seed yield.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is an important leguminous crop grown under a wide range of environments. Chickpea, which is drought tolerant and performs well in low input agriculture, was cultivated on an area of 1052.3 thousand hectares with a production of 837.8 thousand tones in Pakistan. While in the North-West Frontier Province (NWFP) of Pakistan, it was cultivated on an area of 50.1 thousand hectares with a production of 23.1 thousands tones (Anonymous, 2009). In NWFP, about 75% chickpea is grown on rainfed lands and its cultivation is concentrated in the southern part of the province.

Chickpea seeds are eaten fresh as green vegetables, parched, fried, roasted and boiled; as snack food, sweet and condiments; seeds are ground and the flour can be used as soup, dhal, and to make bread; prepared with pepper, salt and lemon it is served as a side dish (Duke, 1981).

Genotype × Environment interaction (GEI) is an important aspect of plant breeding programs. It may arise when certain genotypes are grown in diverse set of environments. A significant G × E interaction for a quantitative trait such as seed yield can seriously limit the efforts on selecting superior genotypes for both new crop production and improved cultivar development (Kang and Gorman, 1989).

The lack of consistency in performance across environments complicates cultivar selection; it can provide useful information to the researcher (Busey, 1983; Kang, 1998). For example, it can help justify the need for additional

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Abbreviations: GEI, Genotype × environment interaction; **MET,** multi-environment trials.

Table 1. Chickpea genotypes name, code name of genotypes for GGE biplot and their origin.

S/N	Genotype	Code	Origin	S/N	Genotype	Code	Origin
1	NDC-727	Pk-1	NIFA, Pakistan	11	NKC-5-S16	Sy-4	ICARDA, Syria
2	NDC-15-4	Pk-2	NIFA, Pakistan	12	NKC-5-S17	Sy-5	ICARDA, Syria
3	NDC-4-15-3	Pk-3	NIFA, Pakistan	13	NKC-5-S23	Sy-6	ICARDA, Syria
4	NDC-4-20-1	Pk-4	NIFA, Pakistan	14	NKC-5-S24	Sy-7	ICARDA, Syria
5	NDC-4-20-3	Pk-5	NIFA, Pakistan	15	SL-05-42	Lo-1	Karak, Pakistan
6	NDC-4-20-7	Pk-6	NIFA, Pakistan	16	SL-05-53	Lo-2	Karak, Pakistan
7	NDC-5-S11	In	ICRISAT, India	17	SL-03-14	Lo-3	Karak, Pakistan
8	NKC-5-S12	Sy-1	ICARDA, Syria	18	SL-03-15	Lo-4	Karak, Pakistan
9	NKC-5-S14	Sy-2	ICARDA, Syria	19	SL-03-29	Lo-5	Karak, Pakistan
10	NKC-5-S15	Sy-3	ICARDA, Syria	20	SL-03-64	Lo-6	Karak, Pakistan

broad-based testing in different environments and predict the variability expected among testing locations (Busey, 1983). The GEI can be properly exploited to advantage through various approaches (Gauch and Zobel, 1996; Kang, 1998; Annicchiarico, 2002; Yan and Kang, 2003). Most agronomically and economically important traits, such as grain yield, are quantitative in nature and routinely exhibit GEI. This necessitates genotype evaluations across multiple environments (called multi-environment trials [MET]) in the advanced stages of selection (Annicchiarico, 2002; Kang et al., 2004). By growing cultivars in different environments, the highest yielding and most stable cultivars can be identified (Lu’quez et al., 2002). When selecting genotypes for wide adaptation, plant breeders look for a noncrossover GEI or preferably the absence of GEI (Matus-Ca´diz et al., 2003). Thus, the estimation of stability of performance becomes important to identify consistent-performing and high-yielding genotypes (Kang, 1998).

Many stability statistics have been used to determine whether or not cultivars evaluated in MET are stable (Lin et al., 1986; Hu¨hn, 1996; Flores et al., 1998; Hussein et al., 2000; Robert, 2002; Sabaghnia et al., 2006). Because the most stable genotype(s) may not be the highest yielding, the use of methods that integrate yield performance and stability to select superior genotypes becomes important (Kang, 1988; Pham and Kang, 1988; Kang and Pham, 1991; Kang, 1993; Kang and Magari, 1996).

Recently, Yan (1999) and Yan et al. (2000) proposed a GGE biplot that allows visual examination of the GE interaction pattern of MET data. The GGE biplot emphasizes two concepts. First, although the measured yield is the combined effect of genotypes (G), environment (E), and genotype by environment interaction (GE), only G and GE are relevant to and must be considered simultaneously, in cultivar evaluation. Second, the biplot technique developed by Gabriel (1971) was employed to approximate and display the GGE of a MET and is commonly known as GGE biplot. This GGE biplot is constructed by the first two principal components (PC1 and PC2, also referred to as primary and secondary effects, respectively) derived from subjecting environment-centered yield data, that is, the yield variation due to GGE, to singular value decomposition (Yan, 1999; Yan et al., 2000). In addition, the GGE biplot also has a usage in selecting superior cultivars and test environments for a given mega-environment. Provided the genotypic PC1 scores have a near-perfect correlation with the genotype main effects, ideal cultivars should have a large PC1 score (high yielding ability) and a small (absolute) PC2 score (high stability). Similarly, ideal test environments should have a large PC1 score (more discriminating of the genotypes in terms of the genotypic main effect) and small (absolute) PC2 score (more representative of the overall environment) (Yan, 1999; Yan et al., 2000). Thus, the objectives of this study are to investigate the efficacy of the test sites using the GGE biplot technique and to determine the stability performance of different chickpea genotypes at two contrasting sites in North-West Frontier Province of Pakistan.

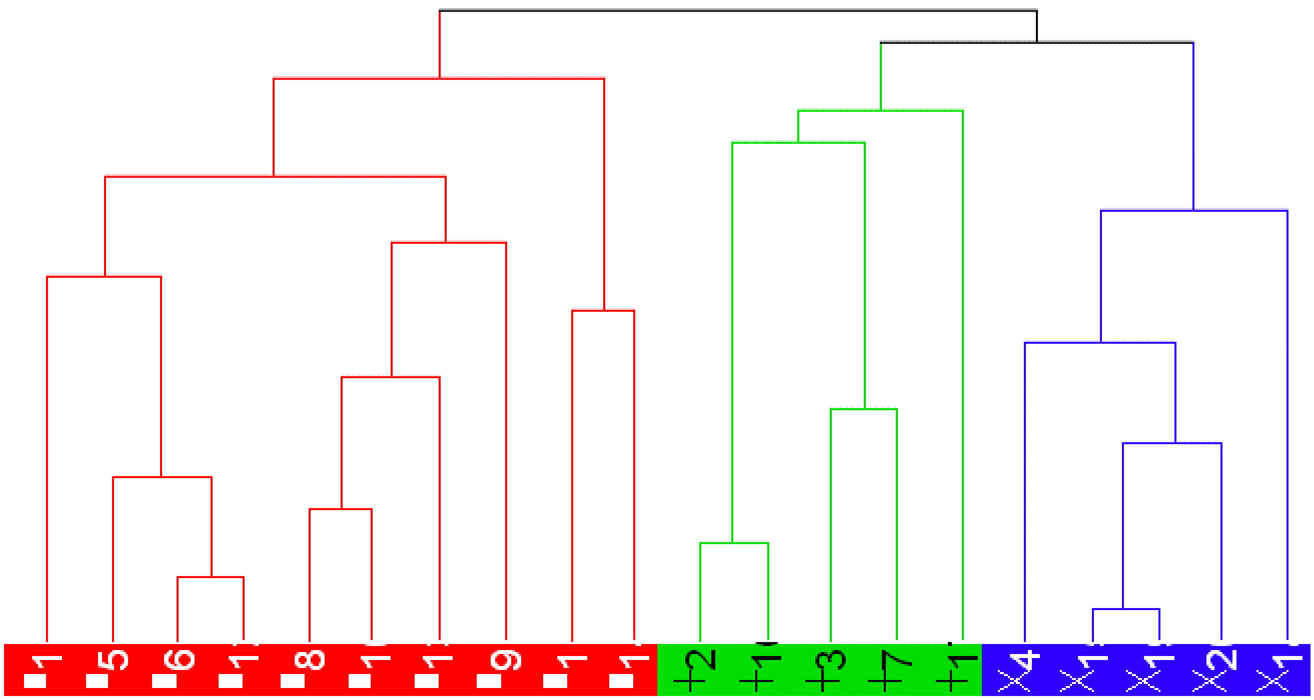
MATERIALS AND METHODS

The present research was conducted at the Agricultural Research Farm, NWFP Agricultural University, Peshawar (latitude and longitude, 34°02'N, 71°37'E) and Agricultural Research Station, Ahmad Wala, Karak (latitude and longitude, 32°93'N, 71°23'E), during winter 2007 to 08. The experimental material consisted of 20 genotypes. Original genotype name, origin and code name of genotypes are shown in Table 1.

The crop was sown in the field in October 2007 using randomized complete block design with three replications at each location. Plant to plant distance and row to row distance was 10 and 40 cm, respectively.

Statistical analysis

The grain yield data were subjected to combined analysis of variance across locations. Cluster analysis of chickpea genotypes (Figure 1) based on dissimilarity matrix was determined by JMP (window version 5.0, SAS Institute). Since, genotype × location interaction was significant, the data was subjected for biplot analysis (Figure 2). The GGE biplot software (Yan, 2001) was used



Varieties: Pk-1 (1), Pk-2 (2), Pk-3 (3), Pk-4 (4), Pk-5 (5), Pk-6 (6), In (7), Sy-1 (8), Sy-2 (9), Sy-3 (10), Sy-4 (11), Sy-5 (12), Sy-6 (13), Sy-7 (14), Lo-1 (15), Lo-2 (16), Lo-3 (17), Lo-4 (18), Lo-5 (19), and Lo-6 (20).

Figure 1. Dendrogram of cluster analysis of 20 chickpea genotypes based on dissimilarity matrix for seed yield (kg ha^{-1}).

to generate graphs showing "which-won-where" pattern (Figure 3), ranking of cultivars on the basis of yield and stability (Figure 4), comparison of genotypes with ideal genotype (Figure 5), ranking location on the basis of representativeness and discriminating ability (Figure 6) and relationship among genotypes (Figure 7; Yan and Kang, 2003).

RESULTS AND DISCUSSION

Analysis of variance for seed yield (kg ha^{-1}) revealed highly significant differences among environments, genotypes and genotype by environment interaction (Table 2). Hakim et al. (2006), Shaukat et al. (2003) and Vijay (2001) also reported significant genotype by location interaction. Seed yield at Karak was higher (830 kg ha^{-1}) than Peshawar (316 kg ha^{-1}). Across environments, maximum seed yield produced by SL-03-14 was 1126 kg ha^{-1} while NKC-5-S24 produced the lowest seed yield of 100 kg ha^{-1}. Genotype SL-03-14 produced maximum seed yield of 712 and 1541 kg ha^{-1} at Peshawar and Karak, respectively, while genotype NKC-5-S24 produced minimum seed yield of 54 and 146 kg ha^{-1} at Peshawar and Karak, respectively (Table 2).

Cluster analysis

Combine cluster analysis of 20 diverse chickpea genotypes based on seed yield (kg ha^{-1}) resulted in two main clusters (Figure 1). The first cluster was again subdivided into three sub-clusters. First sub-cluster consisted of four genotypes which included NDC-727, NDC-4-20-3, NDC-4-20-7 and NKC-5-S17, while second sub-cluster contained genotypes that is, NKC-5-S12, NKC-5-S15, NKC-5-S23 and NKC-5-S14. The third sub-cluster consisted of two genotypes that is, NKC-5-S16 and NKC-5-S24. The second main cluster was divided into two sub-cluster in which the first sub-cluster contains five genotypes that is, NDC-15-4, SL-05-53, NDC-4-15-3, NDC-5-S11 and SL-03-14. Similarly, the second sub-cluster consisted of five genotypes which included NDC-4-20-1, SL-05-42, SL-03-29, SL-03-64 and SL-03-15. First sub-cluster of first group and the second main group contained only desi genotypes except NKC-5-S17 (which is kabuli). While the remaining sub-clusters of first group consisted of only kabuli genotypes. Hasan and Abdullah (2007) also examined eleven varieties of chickpea and separated them into two main groups and three sub-clusters by cluster analysis.

Genotypes grouping via GGE biplot

On the basis of average seed yield, chickpea genotypes were divided in two main sectors as shown in Figure 2. The first sector (in the direction of performance line)

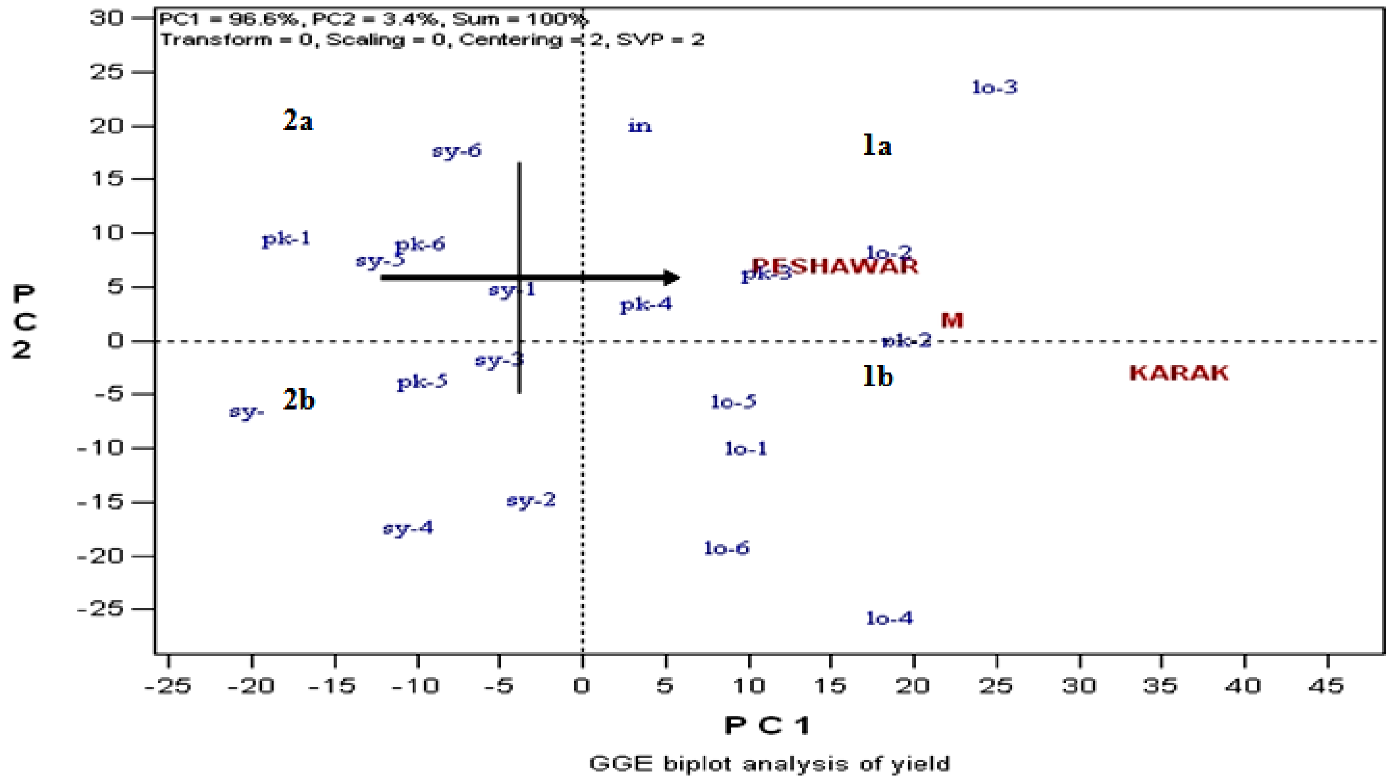


Figure 2. GGE biplot based on seed yield data of 20 chickpea genotypes. Environments along with mean are in upper case while genotypes are coded and in lower case.

exhibited genotypes with above average seed yield in kg ha^{-1}, while the rest (in sector 2) were inferior in performance with below average seed yield. Each main sector is further divided into two sub-sectors. Sector 1a consisted of chickpea genotypes Lo-3, Pk-2, Lo-2, Pk-3, In and Pk-4, while Lo-4, Lo-1, Lo-5 and Lo-6 lie in sector 1b. On the other hand, sector 2a consisted of genotypes Sy-1, Sy-6, Pk-6, Sy-5 and Pk-1, while genotypes Sy-2, Sy-3, Pk-5, Sy-4 and Sy-7 occupied positions in sector 2b. This distribution exhibits a diversified genetic makeup of the studied chickpea genotypes.

Best genotype in each environment

A polygon view of the biplot drawn on genotypes shows that all other genotypes are inside the polygon while some genotypes are on the vertices (Figure 3). These vertex genotypes are the most responsive genotypes since they have the longest distance from the biplot origin. Responsive genotypes are those that are either the best or the poorest in one or all environments (Yan and Rajcan, 2002). Both the environments lie in the sector where Lo-3 is the vertex genotypes exhibiting that Lo-3 was the best in both environments, followed by genotypes Lo-2, Pk-2, Pk-3, Pk-4 and In. Therefore these genotypes

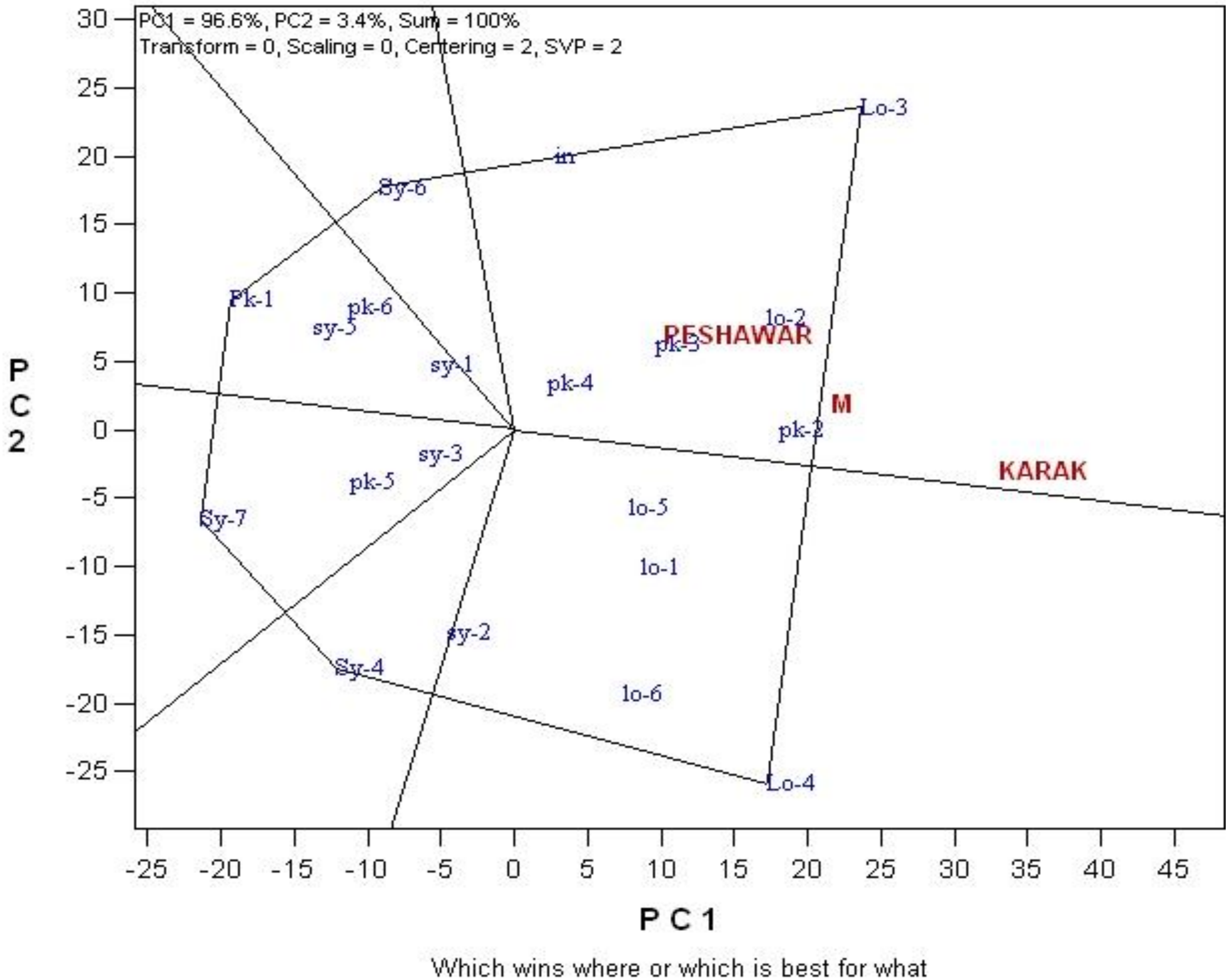


Figure 3. GGE biplot of seed yield data of 20 chickpea genotypes in two environments along with the mean of environments.

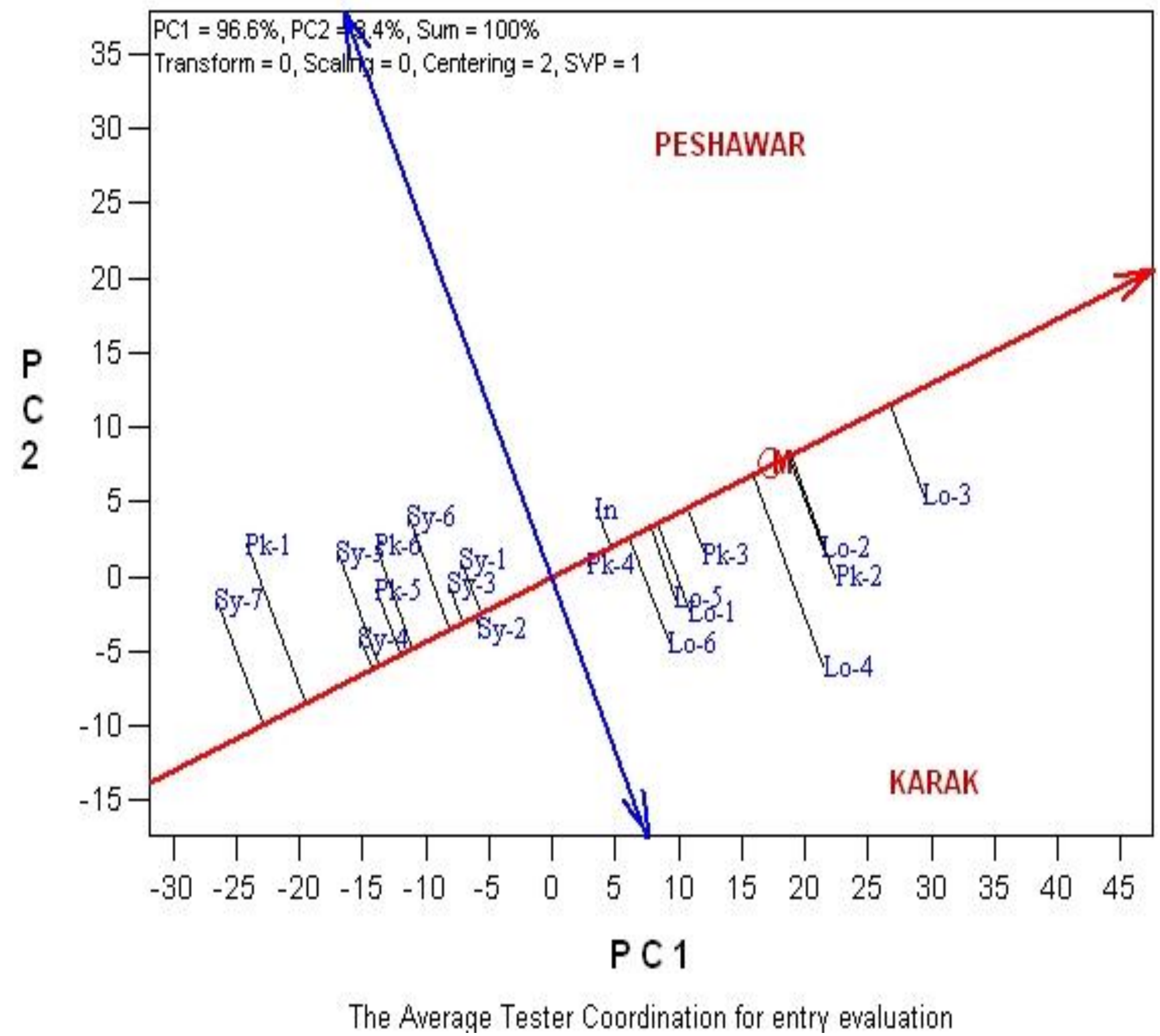


Figure 4. Average tester coordination (ATC) view of the GGE biplot, hybrids in lower case and locations are in upper case. PC1 and PC2 are first and second principal components,

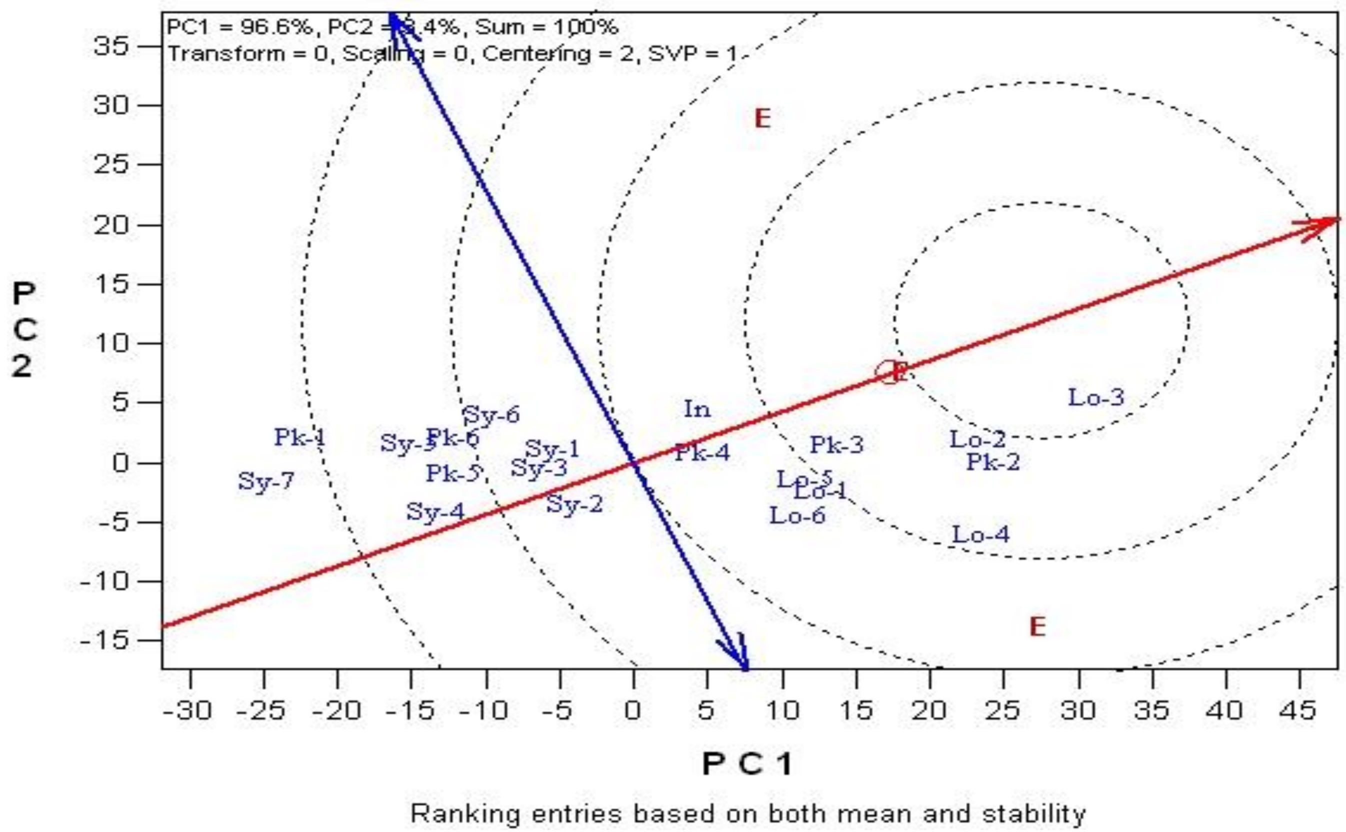


Figure 5. Comparison of genotypes with the ideal genotype. Environments are denoted by 'E' while genotypes are in lower case.

especially Lo-3 can be grown for achieving higher yields in both Karak and Pehsawar.

Average yield and stability of genotypes

The average testers coordinate (ATC X-axis) passes through the biplot origin and the arrow indicates the positive end of the axis (Figure 4). The ATC Y-axis passes the plot origin and is perpendicular to the ATC X-axis. The average yield of the genotypes is approximated by the projections of their markers to the ATC X-axis and the stability of the genotypes is approximated by the projections of their markers to the ATC Y-axis (Yan, 2001). Thus genotypes Lo-3, Lo-2, Pk-2, Lo-4 and Pk-3 were identified as top five genotypes (on the basis of seed yield) and Sy-7, Pk-1, Sy-4, Sy-5 and Pk-5 as the bottom five genotypes. For only stability of performance across test environments, Pk-4, In and Pk-3 were best among all other genotypes. However, genotype with high seed yield and relatively stable performance is important for growers. Therefore genotype widely adapted across test environments should be selected. When an "ideal" genotype view was drawn, chickpea genotype Lo-

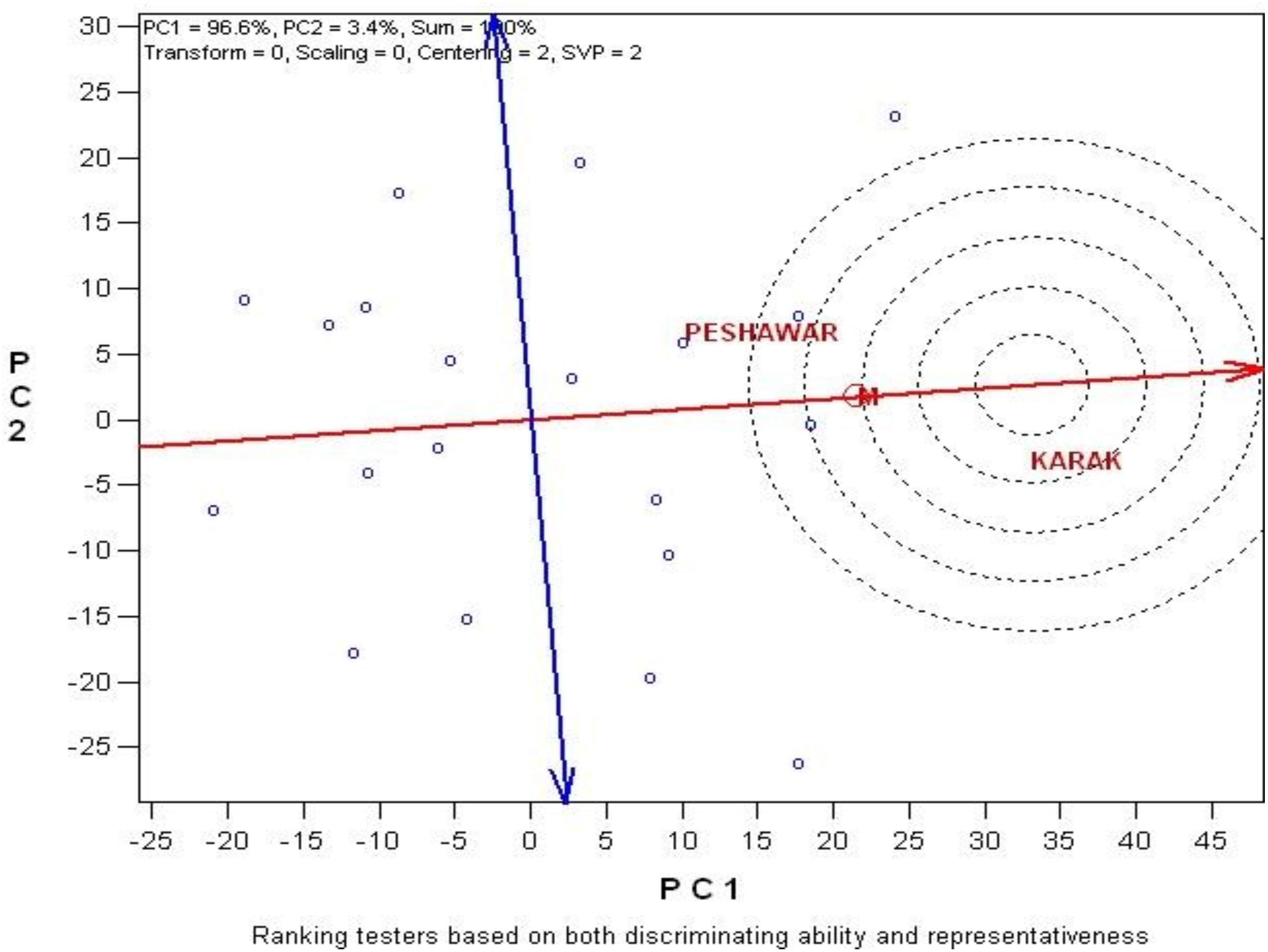


Figure 6. Comparison of locations with an ideal location.

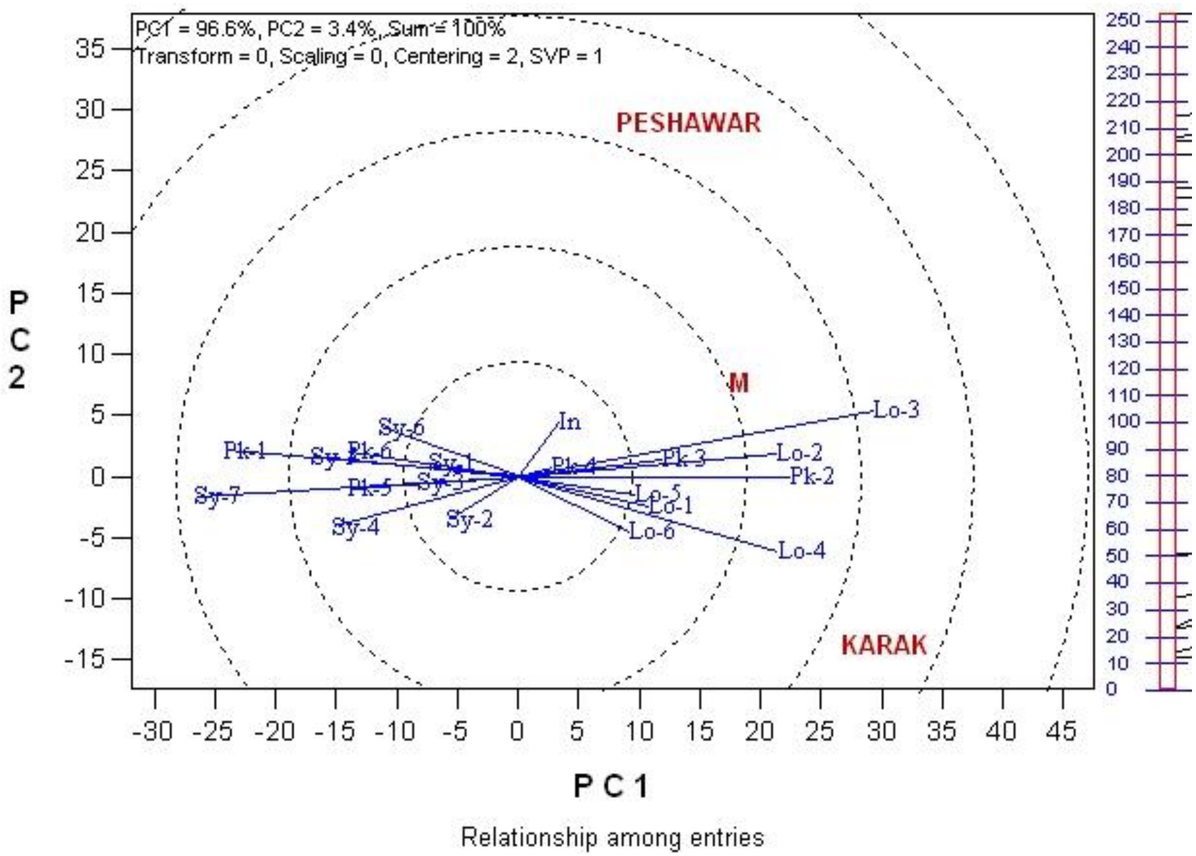


Figure 7. A Genotype + Genotype × Environment interaction bi-plot showing relationships among 20 genotypes.

3 (GGE distance 5.6) was the closet to the ideal genotype, followed by Lo-2 (10.7) and Pk-2 (11.8; Figure 5 and Table 2). An ideal genotype is defined as one that is the highest yielding (longest projection on ATC X-axis) across test environments and is absolutely stable (Shortest projection on ATC Y-axis) in performance (that is, one that ranks the highest in all test environments (Yan and Kang, 2003; Fan, et al., 2007).

The representativeness and discriminating ability of the environments

Genotype by environment interaction with respect to discriminating ability and representativeness of test environments is a measure of desirability (Blanche and Myers, 2006; Yan, 1999; Yan, et al. 2000). Discriminating ability and representativeness of the test environments can be measured as the absolute distance of an environment from the biplot origin and the length of the projection from the marker of an environment onto the ATC Y-axis (Yan, 2001) as shown in Figure 6. Thus, environment of Karak was the best as it had small projection onto ATC Y-axis (representative of test environments) and large projection onto ATC X-axis (highly discriminating ability for genotypes). On the other hands,

Table 2. Mean values for seed yield (kg ha^{-1}), distance from "ideal genotype" and ranking of 20 chickpea genotypes evaluated at Peshawar and Karak during 2007 to 2008.

S/N	Genotypes	Code	Seed yield kg ha^{-1}			GGE parameters	
			Peshawar	Karak	Mean	Ranking	Distance
1	NDC-727	Pk-1	181	159	170 GH	19	52.4
2	NDC-15-4	Pk-2	498	1430	964 AB	3	11.8
3	NDC-4-15-3	Pk-3	454	1132	793 BCD	5	18.1
4	NDC-4-20-1	Pk-4	361	896	628 DE	10	26.5
5	NDC-4-20-3	Pk-5	176	472	324 FG	16	43.0
6	NDC-4-20-7	Pk-6	260	430	345 FG	15	42.3
7	NDC-5-S11	In	476	861	669 D	9	24.8
8	NKC-5-S12	Sy-1	288	625	457 EF	11	36.0
9	NKC-5-S14	Sy-2	168	726	447 EF	12	36.2
10	NKC-5-S15	Sy-3	236	619	427 F	13	37.4
11	NKC-5-S16	Sy-4	75	483	279 FGH	17	45.2
12	NKC-5-S17	Sy-5	226	354	290 FGH	18	45.4
13	NKC-5-S23	Sy-6	340	472	406 F	14	39.4
14	NKC-5-S24	Sy-7	54	146	100 H	20	55.5
15	SL-05-42	Lo-1	336	1152	744 CD	6	21.2
16	SL-05-53	Lo-2	544	1375	959 AB	2	10.7
17	SL-03-14	Lo-3	712	1541	1126 A	1	5.60
18	SL-03-15	Lo-4	317	1486	902 BC	4	17.8
19	SL-03-29	Lo-5	356	1111	734 CD	7	21.5
20	SL-03-64	Lo-6	261	1138	699 D	8	23.7
Mean			316	830			

$LSD_{(0.05)}$ for locations = 156.2; $LSD_{(0.05)}$ for Genotypes = 198.4; $LSD_{(0.05)}$ for G × L = 281.7.

environment of Peshawar is representative but not having discriminating ability (small projection onto ATC X-axis). A highly discriminating location is one that maximizes the observed genotypic variation among genotypes for a given trait (Blanche and Myers, 2006). The center of the concentric circles is the place where an "ideal" environment is located (Yan, 2001). An ideal environment is one that is most discriminating for genotypes and is representative of all other environments (Yan and Kang, 2003; Fan, et al. 2007; Blanche and Myers, 2006). When both the environments were compared with an ideal environment, Karak was considered the best as compared with Peshawar.

Relationship among genotypes

The vectors of all 20 chickpea genotypes represent their inter-relationship and the linear map to the right of the graph (in degrees) helps indicate relationship between genotypes (Figure 7). The cosine of the angle between two vectors of genotypes represents correlation between them (Yan and Kang, 2003; Fan, et al. 2007). The biplot drawn for the relationship among genotypes exhibited two different groups of genotypes. The first group on the right side of the biplot origin is comprised of local collection of Karak (Lo-1 to Lo-6) and some of the varieties developed at Nuclear Institute of Food and Agriculture (NIFA), Pakistan (Pk-2, Pk-3 and Pk-4). The second group on the left side of the biplot origin mainly comprised of introduced genotypes from Syria, ICARDA (that is, Sy-1 to Sy-7, Pk-5, 6 and 1). The only genotype 'In' which was introduced from India has slightly similar angle to those of national genotypes.

Conclusions

The GGE biplot was identified Lo-3 as the most desirable genotype across environments, followed by Lo-2, Pk-2, Lo-4 and Pk-2, while Sy-7, Pk-1, Sy-4, Sy-5 and Pk-5 were the most undesirable genotypes across environments. Karak was identified best for genetic differentiation of genotypes, while location Peshawar was the least representative. Thus, the GGE biplot methodology was a useful tool for identifying locations that optimized genotypes performance and for making better use of limited resources available for the testing program.

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