

GLOBAL PATTERNS OF GENOTYPE-ENVIRONMENT INTERACTIONS FOR SEED YIELD IN CHICKPEA

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ABSTRACT

Seed yield data from 16 genotypes (G) of chickpea (*Cicer arietinum* L.), tested in 49 trans-continental locations (L) were analyzed using residual maximum likelihood (REML) procedure and pattern analysis methods of classification and ordination to gain an understanding of the structure of Genotype x Environment (GE) interactions. The genotypes included the two major types of chickpea-desi and kabuli drawn from two main areas for chickpea adaptation, the Indian sub-continent and the Mediterranean region. Using hierarchical classification, the 16x49 GL mean data matrix was reduced to 8x9 (G-group x L-group) matrix capturing 50% of GL interaction sums of squares (SS). The genotypes fell into three discernible groups according to their geographic proximity. The location grouping suggested the presence of two mega-environments. Sub grouping of locations showed that generally the tropical (< 23°) locations grouped together and separate from sub-tropical locations. The performance plots of G-groups indicated that two low yielding genotypes, Giza and Harigantars, contributed to large variation from one L-group to another. In general the medium-duration G-group (K 850, L 550, ICC 8 and ICC 4) from India was consistently better in most L-groups. In contrast, the G-group comprising Rabat (Morocco) and ILC 482 (Turkey), generally performed well in higher latitudes. The principal component biplot results were essentially similar to those obtained from the performance plots. It appears that development of early to medium-duration varieties may increase and stabilize seed yields. Based on genotype grouping, separate breeding programs for subtropical, tropical and the Mediterranean regions appear appropriate. This study showed that breeding for kabuli type and relatively bold seed might not necessarily affect varietal productivity adversely. Implications of these findings for chickpea improvement are discussed.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is globally the third most important pulse crop grown over 11 m ha annually in about 50 countries. It is one of the principal high protein food crops cultivated in the semi-arid regions of the world, especially in South Asia, Mediterranean region, eastern Africa and Central America. Two main types are recognized - desi with generally small light brown or other color seeds, and kabuli with larger cream-color seeds. The stover is used as a nutritious fodder for the cattle in the lean season. Around 90% chickpea is cultivated rainfed in the post-rainy season under receding soil moisture conditions. Therefore, selection of suitable high yielding varieties for varying environments is the major objective of most chickpea breeding programs.

Low and erratic yields are forcing chickpea to marginal lands especially in South

Asia, where it has lost large area to more productive and stable crops such as wheat and rice (Kelley and Rao 1994). Several biotic and abiotic stresses cause low and unstable production of this crop. Moreover uncertain and low prices at harvest do not encourage farmers to invest their productive plots and inputs to chickpea.

One of the major objectives of International Agricultural Research Centers (IARCs) is to breed for high yield and wide adaptation. The chickpea improvement program at ICRISAT has been developing and disseminating breeding material and high yielding and disease resistant advanced lines to scientists of National Agricultural Research Systems (NARS) in major chickpea growing regions of the world. This is achieved through the conduct of international chickpea cooperative trials and nurseries. This involves selection of suitable and

representative sites for conduct of multi-environment trials (METs). These not only make improved breeding populations and advanced lines available to NARS but also provide an insight into the adaptation patterns of such materials across widely different environmental conditions (Kumar *et al.*, 1990). Genotype x environment (GE) interactions encountered in these METs mostly manifest themselves qualitatively leading to inconsistent relative ranking of genotypes across environments. Since these METs are conducted on a wide range of environments, GE interactions can influence interpretations (Kumar *et al.*, 1996b).

In recent times the funds for agricultural research have been shrinking and there is a need for economic and objective targeting of METs. At the IARCs a major head for expenditure is organization, conduct and monitoring of these METs (Malhotra and Harris, 1990). With appropriate environmental classification/characterization, effective targeting of the breeding material can reduce such costs. A primary objective in considering relationships among environments for testing genotypes is the identification of the degree of commonality among the environments in relation to the pattern of discrimination among the genotypes (Cooper *et al.*, 1993a). This paper presents the GE interaction analysis of the international chickpea adaptation trial (ICAT) data set to investigate (1) the grouping of genotypes based on their performance across widely diverse transcontinental locations, (2) the grouping of locations according to the similarity of their pattern of genotype differentiation, and (3) the pattern of adaptation of genotypes in different locations.

MATERIAL AND METHODS

Genetic material, test environments, and experimental design: Sixteen genotypes ($n_G=16$), seven desi and one kabuli types from the Indian subcontinent and eight

kabuli types from the Mediterranean region (Table 1), were tested in 70 environments covering $n_L=49$ transcontinental locations over a period of the three ($n_Y=3$) years (Y) 1981/82 to 1983/84. The locations (Table 2) varied in latitude from 37° S to 52° N and in altitude from 0 to 1340 m above mean sea level. A randomized complete block design was used in each environment. The number of replications (R) varied from three to four ($n_R=3,4$). Plot size was 4 rows x 4 m with an inter-row spacing of 30 cm and inter-plant distance of 10 cm in most environments. Seed yield, analyzed in this paper, was recorded from all four rows of each plot.

Statistical methodology: Data on seed yield (kg ha^{-1}) were available from 4368 plots. This represented an unbalanced data set. The imbalance arose from unequal number of replications, 48 missing values, and the lack of presence of each location across all the three years. Rather than forcing this to be a balanced data set, thereby losing considerable information, we decided to use all available data to derive as much information as possible in a statistically efficient way by applying the restricted maximum likelihood (REML) procedure of Patterson and Thompson (1971).

The statistical analysis proceeded in two steps. In the first step, a random YLGR model was fitted to the 4368 plot values using REML to obtain the best linear unbiased predictions (BLUPs) for the performance of different genotypes in different environments. In the second step, these BLUPs were used as basic data to perform pattern analysis to understand the underlying patterns of GE interaction.

REML Analysis: The plot seed yield data y_{ijkl} , corresponding to genotype i grown in block l at location k in year j were analyzed using REML based on the following linear additive random effects model

$$Y_{ijkl} = \mu + Y_j + L_k + (LY)_{jk} + R_{(ijk)} + G_i + (GY)_{ij} + (GL)_{ik} + (GLY)_{ijk} + e_{ijkl} \quad (1)$$

$$i=1, \dots, n_G; j=1, \dots, n_L; k=1, \dots, n_Y; l=1, \dots, n_R$$

where μ , L_k , Y_j , $(LY)_{jk}$, $R_{(ijk)}$, G_i , $(GL)_{ik}$, $(GY)_{ij}$, $(GLY)_{ijk}$, and e_{ijkl} are respectively the general mean, location effect, year effect, LY interaction effect, block-within-(LY) effect, genotype effect, GL interaction effect, GY interaction effect, GLY interaction effect, and the residual. All effects in the model, except μ , are assumed to be independently and identically distributed

normal random variables each with a mean of zero, and variances σ^2_μ , σ^2_L , σ^2_Y , σ^2_{LY} , σ^2_R , σ^2_G , σ^2_{GL} , σ^2_{GY} , σ^2_{GLY} , and σ^2_e respectively. We adopted the conservative approach of treating model (1) as a random model to minimize the chance of claiming differences in genotype performance when no differences actually exist (Gilmour *et al.*, 1996).

Table 1. Name, origin, agronomic characters and grouping of 16 genotypes evaluated in 49 locations

Genotype (Abbreviation)	Origin	Days to flowering ^a	100-seed mass ^a (g)	Mean seed yield (kg ha ⁻¹)	Maximum seed yield (kg ha ⁻¹)	Max./Min. seed yield ratio	CV (%) for yield	Genotype grouping
Desi								
Harigantars (HA)	India	34	14	864	2382	19.7	60	Gp 1
Annigeri (AN)	"	46	18	1441	2903	6.4	44	IndG 2
ICCC 4 (I4)	ICRISAT	55	13	1498	2708	5.4	41	Ggp 7
ICCC 8 (I8)	"	52	24	1410	2640	6.9	45	Ggp 7
K 850 (K8)	India	55	27	1531	2770	5.1	43	Ggp 7
G 130 (G1)	"	64	13	1390	2772	6.8	47	Ggp 2
Pant G-114 (PG)	"	63	11	1442	2926	5.7	45	Ggp 2
Kabuli								
L 550 (L5)	India	60	19	1453	2791	5.5	44	Ggp 7
Cyprus Local (CY)	Cyprus	62	31	1031	2858	14.2	55	Ggp 8
Giza (GZ)	Egypt	47	16	1071	2515	9.7	50	IndG 10
ILC 482 (IL)	Turkey	63	27	1265	2900	10.2	50	Gyp 5
Iranian Local (IR)	Iran	73	23	1114	2401	11.8	53	IndG 12
Jordanian Local (JO)	Jordan	62	24	1142	2506	11.8	51	Ggp 8
Rabat (RA)	Morocco	67	25	1264	2536	7.8	47	Ggp 5
Syrian Local (SY)	Syria	58	30	1052	2649	14.1	53	Ggp 8
Turkish Local (TR)	Turkey	58	31	1134	2831	11.0	49	Ggp 8

^a Data from Patancheru only.

From a GE interaction perspective, the relevant variances are σ^2_G , σ^2_{GL} , σ^2_{GY} , σ^2_{GLY} whose REML estimates were respectively found to be $s^2_G = 41019 \pm 16088$, $s^2_{GL} = 51416 \pm 9931$, $s^2_{GY} = 0 \pm 1749$, and $s^2_{GLY} = 89553 \pm 9754$. In addition to a highly significant s^2_{GL} ($P < 0.01$), the value of s^2_{GL} was 1.25 times that of s^2_G which indicates the presence of GL interaction in this data set. Though the GLY interaction is significant, this, in the absence of GY interaction, will have, from a GEI perspec-

tive, not much GE interaction significance in the presence of significant GL interaction. Accordingly, to meet the objectives of this paper, we chose, as basic data for further GE interaction analysis, the $(n_G \times n_L)$ (= 16x49) GL matrix $Y = (y_{ik})$, ($i=1, \dots, n_G$, $k=1, \dots, n_L$) of the BLUPs of n_G genotypes in n_L locations obtained from the REML analysis of model (1). The REML analysis was carried out using Genstat 5 release 4.1.

Table 2. Latitude, precipitation, mean seed yield and grouping of 49 chickpea testing locations

Location group	Location (abbreviation) name, country	Latitude (degrees)	Precipitation (mm)	Seed yield (kg ha ⁻¹)
Group - ME1				
Egp 36	AC-Alcala-Spain	40:31 N	205	526
	AL-Setif-Algeria	37:00 N	68	548
	B-Pasro Fundo-Brazil	28:15 S	1336	467
	IN-Karaj-Iran	35:50 N	*	946
	AN-Ankara-Turkey	39:55 N	*	583
	DA-Dahod-India	23:00 N	*	2248
	PU-Pullman-USA	46:00 N	169	1723
Egp 38	EG-Mallawi-Egypt	27:50 N	*	1184
	LA-Lam-India	16:50 N	56	1285
	HI-Highmore-USA	44:00 N	429	1174
	IQ-Sulaimania-Iraq	36:50 N	*	699
	KK-Karak-Pakistan	32:33 N	294	448
	SD-Rapid City-USA	44:00 N	241	2455
	SV-Sevilla-Spain	37:90 N	73	929
Egp 39	CA-Casaccia-Italy	42:02 N	317	1569
	T-Terbol-Lebanon	33:52 N	550	1460
	SI-Sicilia-Italy	37:50 N	*	1068
Egp 13	SS-T.Hadya(S)-Syria	36:50 N	340	974
	SW-T.Hadya(W)-Syria	36:50 N	340	2359
Group ME2				
Egp 40	AD-Anand-India	22:50 N	*	1381
	DL-Delhi-India	28:40 N	*	1256
	HR-Hisar-India	29:10 N	400	1789
	KA-Kanpur-India	26:30 N	84	1226
	GW-Gwalior-India	26:13 N	850	1750
	LU-Ludhiana-India	30:56 N	266	1495
	SG-Sriganganagar-India	29:55 N	81	2002
	BH-Bahawalpur-Pakistan	29:35 N	24	849
	CK-Chakwal-Pakistan	32:60 N	*	1820
	MY-Mymensingh-Bangladesh	24:70 N	128	507
	NE-Parwanipur-Nepal	27:20 N	105	1643
	TH-Suwan-Thailand	14:30 N	187	369
	PN-Pantnagar-India	29:00 N	219	1221
	DK-Dokri-Pakistan	27:50 E	38	1195
	RN-Ranchi-India	23:17 N	62	405
Egp 31	BK-Brookings-USA	44:19 N	549	928
	CD-Ridgetown-Canada	52:30 N	445	1879
	CR-Santa Lucia-Costa Rica	10:16 S	167	1376
Egp 35	BU-Debrudja-Bulgaria	44:50 N	280	988
	CH-Temco-Chile	37:00 S	*	2007
	DE-Derol-India	22:00 N	*	2094
	JU-Junagadh-India	21:30 N	235	1668
	SE-Sehore-India	23:12 N	144	553
	RP-Raipur-India	21:14 N	31	1289
Egp 30	HU-Hudeiba-Sudan	17:34 N	*	976
	P-Patancheru-India	17:60 N	750	764
	ME-Inia-Mexico	24:58 N	57	2193
	SH-Shendi-Sudan	16:42 N	0	1631
	RA-Rahuri-India	19:24 N	71	1154
Ind E39	SA-Algassium-S.Arabia	26:04 N	193	505

* Not available

Pattern Analysis: Pattern analysis (Williams 1976) consists of the combined use of complementary classification and ordination techniques. The classification component is used to classify the given number of genotypes and environments into an objectively determined smaller number of disjoint homogeneous groups. The per cent of GE sum of squares retained by a particular number of groups provides an objective basis to determine the number of groups. General experience is that the number of groups decided on the basis of retention of at least 50% of GE interaction sum of squares generally allows understanding the underlying pattern of GE interactions fairly well. Ordination gives a low-dimensional representation of a multidimensional space and helps to determine the relationships among genotypes, among environments, and the interrelationships among genotypes and environments. Since the classification and ordination components are complementary, both exploit the same information to understand the patterns of GE interactions.

Following the suggestion of Fox and Rosielle (1982), the GL data matrix $Y=(y_{jk})$ was first transformed to an environment-standardized matrix $Z=(z_{jk})$, $z_{jk}=\{(y_{jk}-m_k)/s_k\}$, where, m_k and s_k being respectively the mean and standard deviation of the n_G values from location k . This transformation made the mean and variance for each location as 0 and 1 respectively. This, from a GE interaction perspective, helps more effectively to group the locations according to their underlying pattern of similarity of discrimination among genotypes rather than according to their means over genotypes. The matrix Z was subjected to an agglomerative hierarchical classification, based on squared Euclidean distance as dissimilarity measure, using Ward's incremental sum of squares clustering technique as recommended by Eisemann (1982) and Milligan (1989). The performance plot of different genotype groups across differ-

ent location groups was used to determine the specific and broad adaptation of genotypes. Ordination was carried out using the principal component analysis based on the complementary similarity matrix derived from the squared Euclidean distance dissimilarity matrix of the standardized data matrix Z . A biplot was produced from the first two principal components to simultaneously display the genotypes and the locations in a single graph to assess the ability of genotypes for adaptation to different locations.

RESULTS AND DISCUSSION

There was wide variation in mean seed yield for both genotypes and locations. The genotype mean seed yield range, over locations, was 864 kg ha⁻¹ for Harigantars to 1531 kg ha⁻¹ for K 850. The location mean seed yield over genotypes varied from 369 kg ha⁻¹ for Suwan in Thailand to 2455 kg ha⁻¹ for Rapid City in USA (Table 2). The GL interaction mean seed yields varied from 121 kg ha⁻¹ in Thailand to 2926 kg ha⁻¹ at Hisar in India.

Statistics computed from the BLUPs showed that the two lowest yielding genotypes, Harigantars and Giza, were generally very poor in most locations. Maximum to minimum seed yield ratio across 49 locations was 20 for Harigantars (the lowest yielding genotype) compared to 5 for K 850, the overall highest yielding genotype in this trial. Coefficient of variation was also the highest for Harigantars and the least for K 850 (Table 1). Therefore, the poor yielding genotypes contributed relatively more to the variability observed in this MET.

Classification: The results of classification are summarized in dendrograms in Fig 1 for genotypes and Fig 2 for locations. Truncation of genotype dendrogram at eight-group hierarchy and that of location dendrogram at nine-group hierarchy accounted for 50% of GL interaction SS. The details of the classification are given in the following paragraphs.

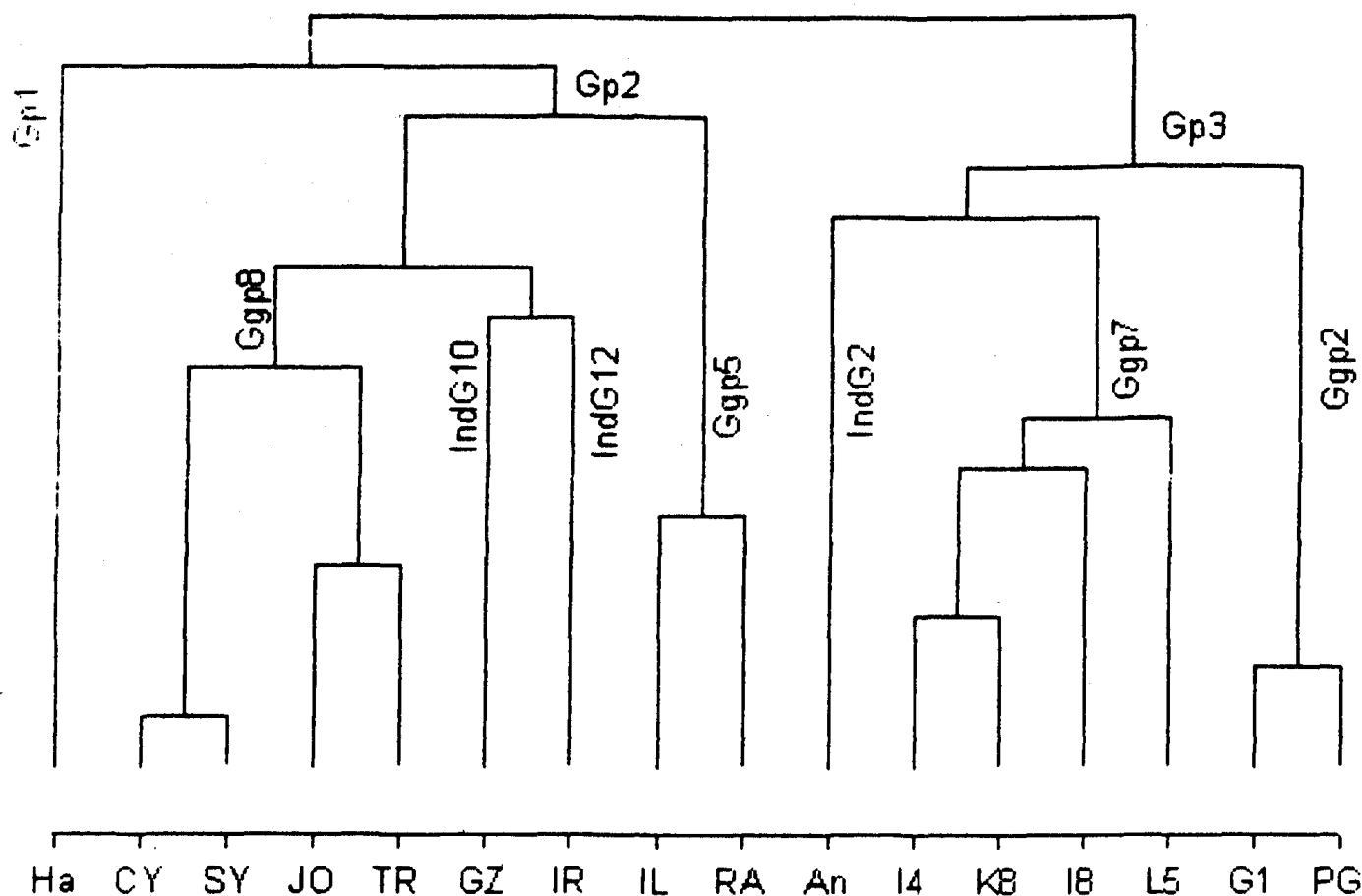


Figure 1. Dendrogram for hierarchical classification of 16 genotypes based on environment-standardized seed yield at 49 locations (Genotype key in Table 1)

Genotype classification: The genotype dendrogram (Fig. 1) although truncated at eight group level, indicated existence of three distinct mega groups of genotypes Gp1=[(Ha)], Gp2=[(CY, SY, JO, TR), (GZ), (IR), (IL, RA)], Gp3=[(An), (I4, K8, I8, L5), (G1, PG)], the parentheses within square brackets indicating the genotypes which are closer to each other within each major genotype group. This classification pattern fitted very well with the selection origin and other known information on these 16 genotypes. Group Gp2 exclusively represents Kabuli genotypes, which originated from the Mediterranean region. These are mainly land races that take too long to mature. The other two groups Gp1 and Gp3 represent desi genotypes (except L 550) which originated from the Indian subcontinent. Gp3 includes breeding lines and varieties with medium

to late maturity. These genotype groupings probably reflect differences in their responses to variation in day-length because of varying latitudes and growing seasons (Group Gp1 consists of a single variety Harigantars, a black-seeded germplasm that has very short growing duration and is susceptible to most pathogens known to attack chickpea. It was the poorest yielder of the lot. This might have influenced its separate grouping. The three groups also showed clearly discernible differences in their mean seed-yields. These were 864 kg ha⁻¹ for Gp1, 1134 kg ha⁻¹ for Gp2 (range 1031-1265 kg ha⁻¹), and 1451 kg ha⁻¹ for Gp3 (range 1390 to 1530 kg ha⁻¹).

Location classification: The location dendrogram (Fig 2) separates the 49 locations into two major classes, which mainly reflect grouping based on differences in their latitudes.

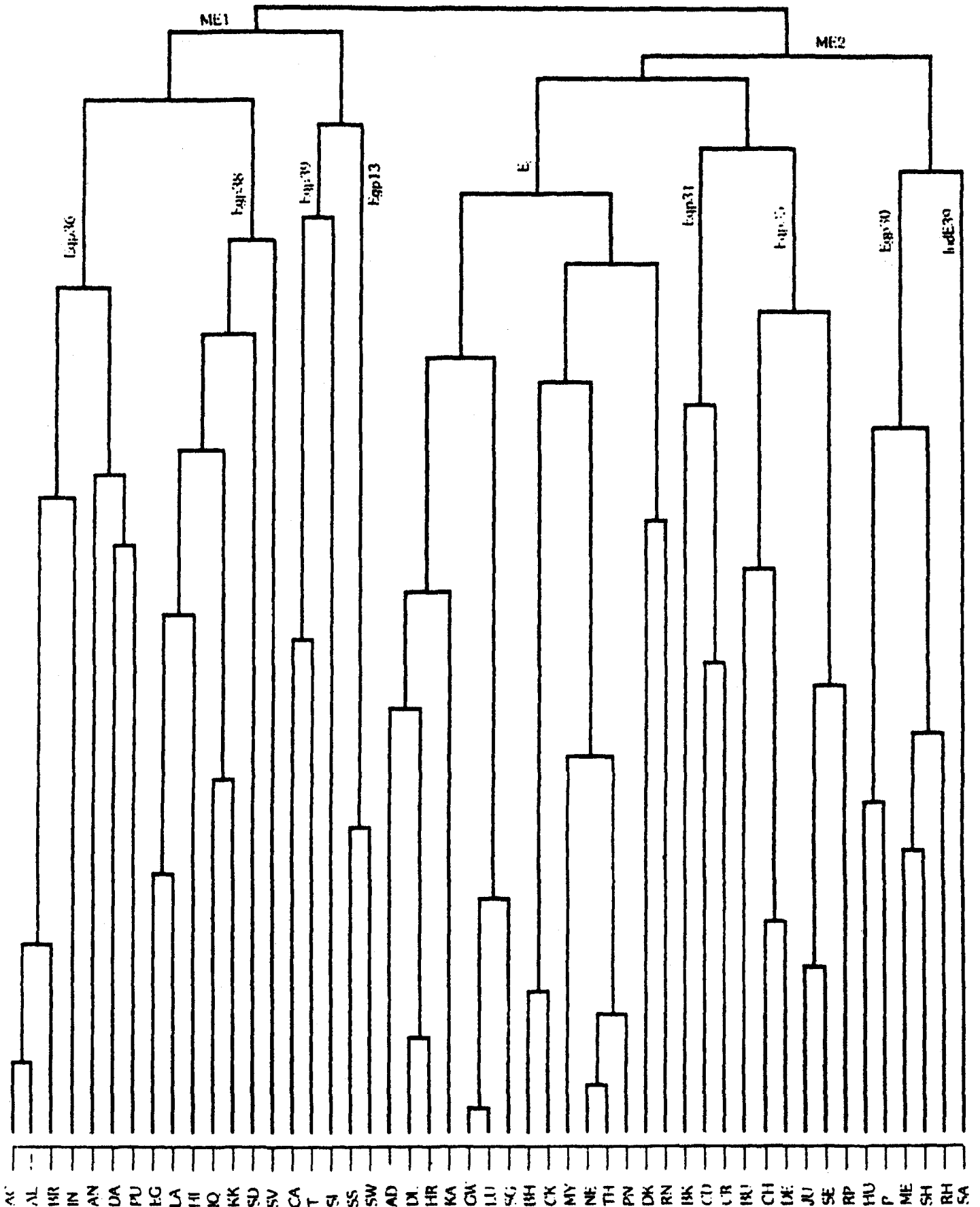


Figure 2. Dendrogram for hierarchical classification of 49 locations based on environment-standardized seed yield of 16 genotypes (Location key in Table 2)

With a few exceptions, mega-environment group ME1 mainly represents locations with latitudes 33-46°N, and group ME2 mainly represents locations having latitudes <32°N. It therefore, appears that variation in latitudes played a major influence in determining the patterns of genotype differentiation. The dendrogram, when truncated at the nine-group hierarchy, allows further meaningful sub-grouping of locations within each of the above two major ME groups, each subgroup representing a cluster of homogeneous locations which more or less distinctly differ from other clusters for latitudes.

The Group ME2, particularly its subgroup Egp40, mainly represents the South Asian sub-tropical locations. All three South American locations appeared in group ME2: BK and CR falling in the same subgroup along with the Canadian location Ridgetown (CD), whereas the Chilean location Temco (CH) grouped with the Bulgarian location Debrudja (BU). The two Sudanese locations (HU, SH) clubbed with the Mexican location Inia (ME) and two Indian locations Patancheru (P) and Rahuri (RH).

The Group ME1 includes locations from US, Spain, Italy, Algeria, Turkey, Egypt, Iran, Iraq, Syria, and Lebanon. Brookings (BR) and Pullman (PU) appeared together in subgroup Egp36, whereas Highmore (HI) and Rapid City (SD) clubbed together in subgroup Egp38. The subgroup Egp39 joined with the two Italian locations Casaccia (CA) and Sicillia (SI). The second Spanish location Sevilla (SV) clubbed with the US location Rapid City (SD) and Highmore (HI) in subgroup Egp38. The winter (SW) and spring (SS) planting at Tel Hadya, Syria formed a separate subgroup Egp13.

Although there were some overlaps of locations among sub-tropical winter cropping, tropical winter cropping and spring planting in the higher latitudes of the Mediterranean re-

gion, Europe and North America, the interactions indicated that broad classification of these locations based on latitudes is relevant and useful in describing genotype adaptation. Chickpea is a quantitatively long day plant (Sethi *et al.*, 1981). Thus varieties bred in longer-day conditions in higher latitudes would flower relatively late and produce low yields in the winters of sub-tropics and tropics. Conversely the varieties bred in the short-day locations will tend to flower earlier in the long-day conditions and may not exhibit their full potential. Thus there should be separate breeding programs to cater to the needs of the two different day-length regimes i.e. spring planting in >33° latitudes and winter planting in <32° latitudes. Similarly testing locations should also be classified accordingly. Further classification of these two mega-environments into nine groups was not solely based on the location mean seed yields. Other important traits such as susceptibility of the genotypes to fusarium wilt, ascochyta blight, pod borer and to abiotic stresses may have played a role in the genotype performance and location grouping.

At Tel Hadya, these trials were planted in winter and spring seasons. The winter planting, because of longer growing season and better moisture regime, produced nearly double the seed yields compared to spring planting. One would expect these to fall in different groups. These however, grouped together (Fig. 2). This suggests that although the yield levels differed, the pattern of responses of genotypes was similar and hence there appears to be little benefit in separate breeding programs for the two situations in that region.

Performance plots: The grouping of 16 genotypes and 49 locations into eight genotype groups and nine location groups appears to have clearly brought out performance differences (Figs. 3a, 3b). This grouping retained 50% of the GL interaction SS. Ggp7 shows

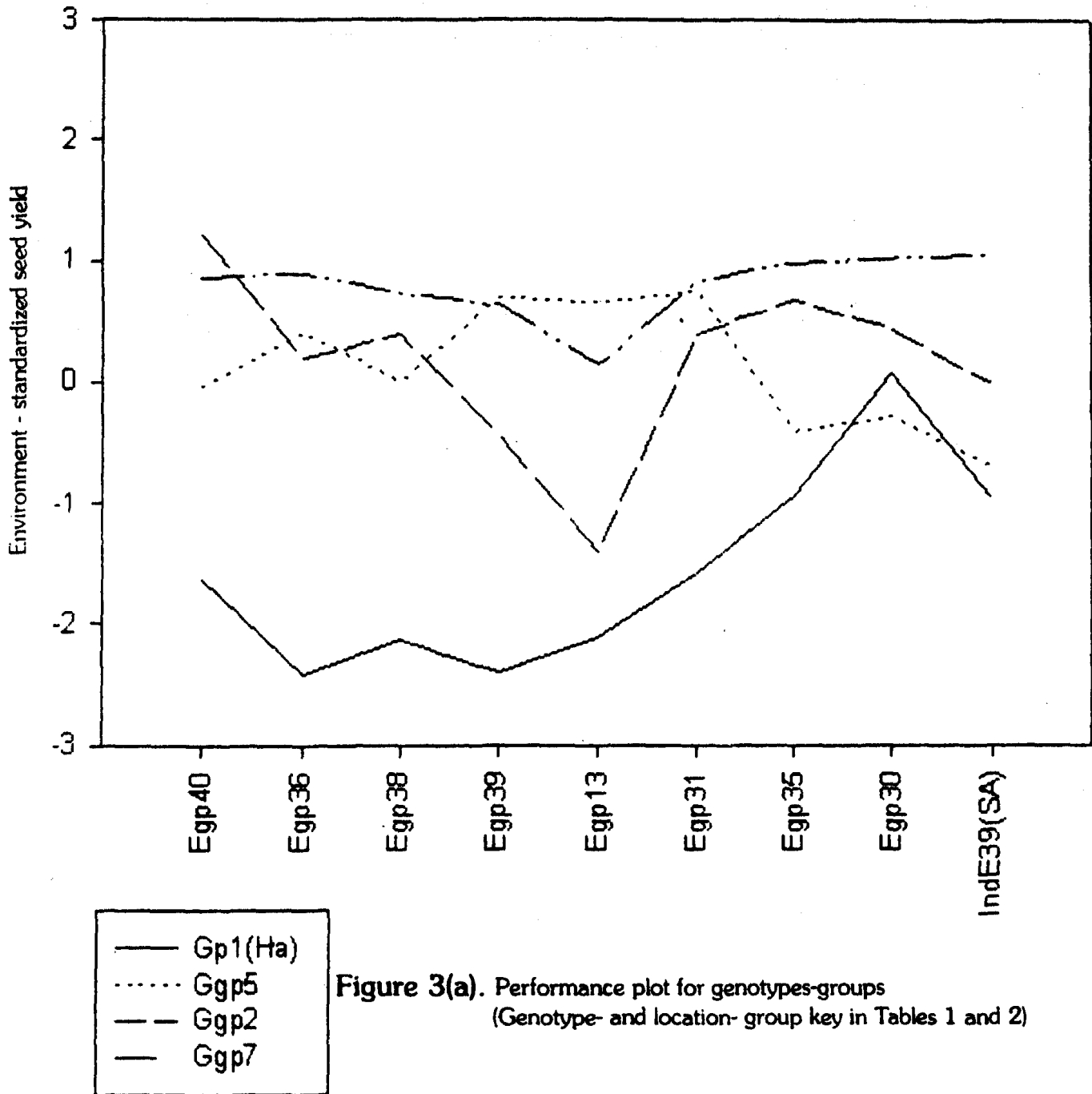


Figure 3(a). Performance plot for genotypes-groups
(Genotype- and location- group key in Tables 1 and 2)

the best performance, which consists of a group of four medium duration genotypes (K 850, ICC 4, ICC 8 and L 550) bred in India. Their performance was very good across all location groups except in Egp13 (Tel Hadya spring and winter plantings). Ggp2 comprising two long-duration genotypes G 130 and Pant G 114 also performed poorly at Egp13 and Egp39. In contrast, Ggp8 comprising of four medium to long duration genotypes from the Mediterranean region (Cyprus Local, Syrian Local, Jordanian Local and Turkish Local)

performed poorly across all the environment groups except Egp13. In Egp13 the performance of Ggp8 was superior compared to Ggp7. Similarly Ggp5 which included ILC 482 (Turkey) and Rabat (Morocco) performed well in high latitude location groups Egp39, Egp13 and Egp31 but poorly in subtropical and tropical South Asia (Egp35, Egp30 and IndE 39). Thus there appear to be clear differences between the adaptation of chickpeas evolved in the Mediterranean region and those bred in South Asia. Therefore, separate breeding pro-

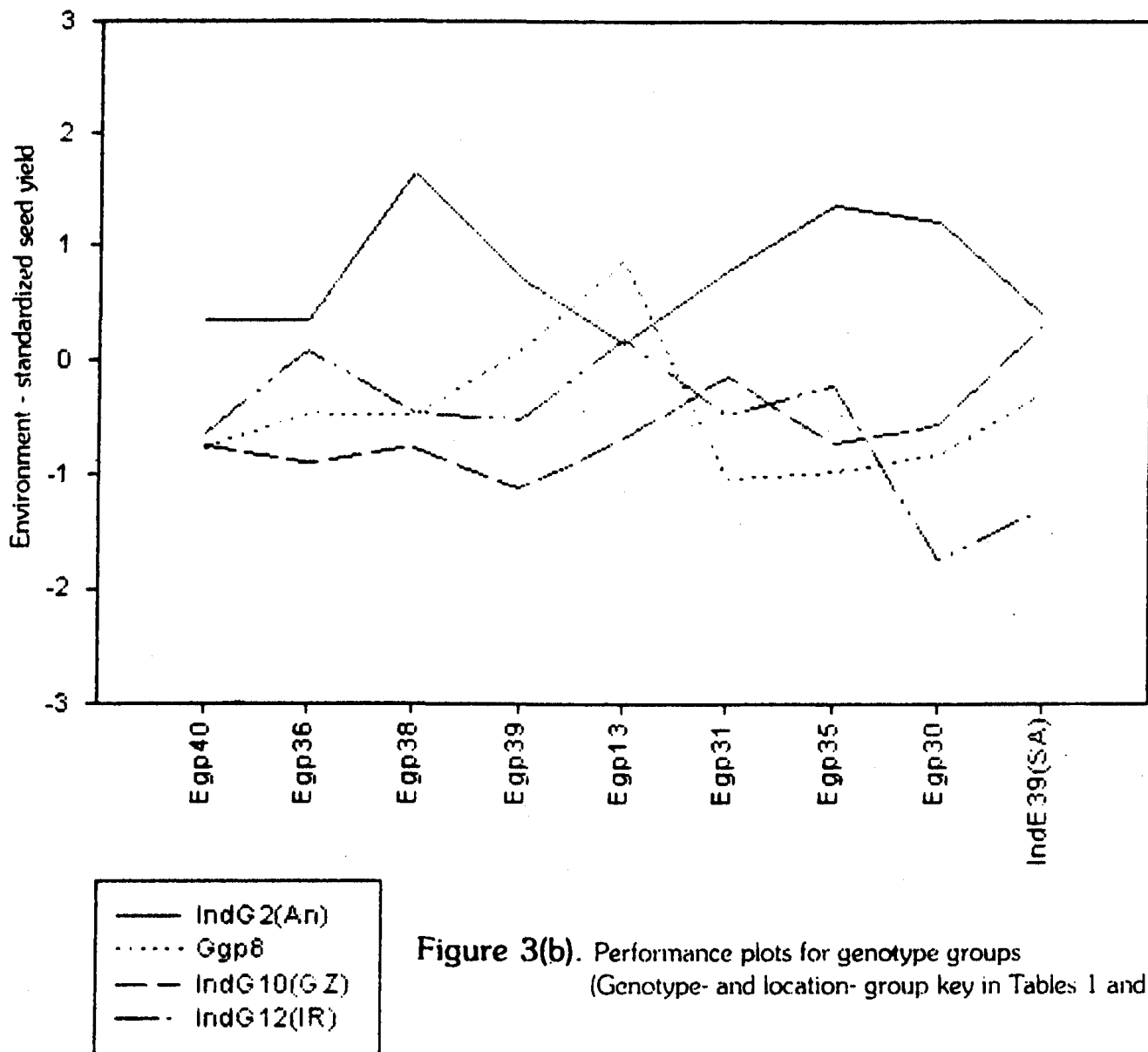


Figure 3(b). Performance plots for genotype groups (Genotype- and location- group key in Tables 1 and 2)

grams and testing locations are required for these two major areas for chickpea adaptation.

The performance of Annigeri (IndG2), a short-duration genotype from tropical India, was on an average good but showed large differences over locations. For example, it performed poor in Egp13, Egp36 and IndE39. We do not know the reasons for its superior performance in Egp38, a high latitude location group but the warm summers may have suited to this variety. Harigantars (Gp1) and Giza (IndG10), both early maturing types and Iranian Local (IndG12) a long-duration kabuli genotype from Iran, all performed poorly across location groups.

Ordination Analysis: The biplot in Fig. 4 summarizes the results of the principal-components (PC)-based ordination analysis. The two PCs together accounted for 76% of GL interaction indicating a good model fit. The location vectors covered a wide range of Euclidean space indicating that the 49 locations represent a population of widely different environments. The range for latitudes (37° S to 52° N) also supports this for these locations.

The genotypes K 850, Annigeri, L 550, and ICC 8, are expected to produce higher seed yield in most locations except at Tel Hadya (winter and spring), where Turkish Local, ILC 482, Syrian Local, Iranian Local,

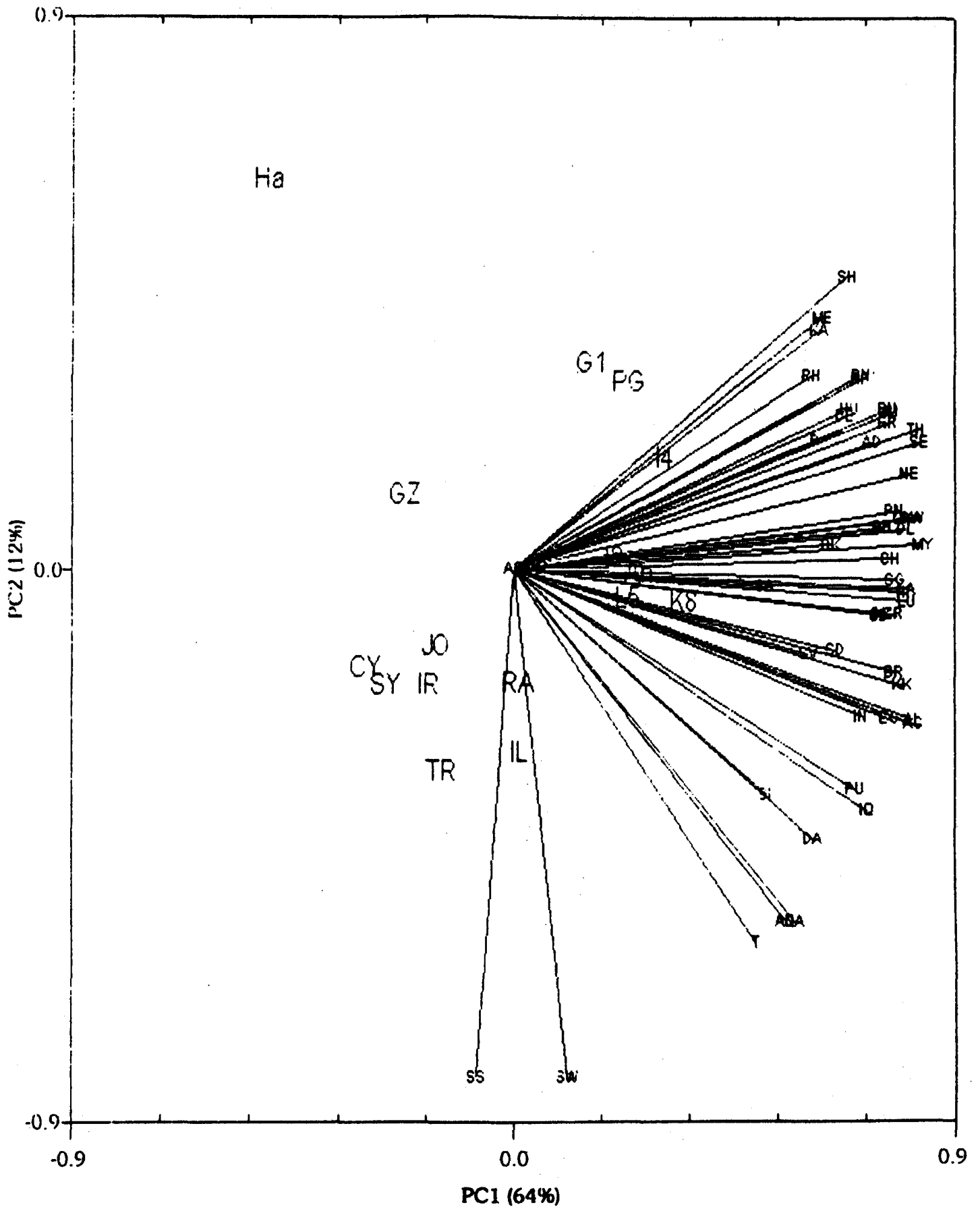


Figure 4. Biplot of 16 genotypes and 49 locations

Cyprus Local, Rabat, and Jordanian Local, produced better seed yields. The genotypes ICCC 4, Pant G-114 and G 130 are expected to give higher yields in most locations falling mainly in location group ME2. The genotypes Harigantars and Giza yield relatively very poorly everywhere.

The angles between vectors in a biplot are useful measures for interpreting similarities and differences among location groups (Basford *et al.*, 1996). The more acute the angle between any two vectors, the more strong is the positive correlation of genotype yields among the concerned locations. Such locations are expected to elicit similar pattern of performance of genotypes. Some of these locations could be dropped as testing sites. The location vectors making an angle of 180° indicate exactly the opposite type of discrimination among genotypes, and location vectors at 90° suggest that there is no correspondence between the pattern of discrimination among genotypes in these locations. Tel Hadya spring and winter planting environments make almost an angle of 90° with locations in group ME2. This indicates that the pattern of genotype differentiation in Egp13 is almost independent of that in locations falling in group ME2.

More than 90 per cent world chickpea is grown rainfed on receding conserved soil moisture. Therefore, the varietal growth and development should match the available moisture during the growing period for achieving a high productivity. Thus the genotypes maturing too soon or too late would produce relatively poor yields. The former would produce too little biomass and consequently low seed yields and the latter would continue vegetative growth and exhaust the available moisture at the expense of seed yield later. In general medium-duration genotypes are expected to perform well in transcontinental METs such as those in the present study. The results of the present study indicate that K 850, a medium

duration variety was the over all top yielder followed by other short- to medium-duration varieties, Annigeri, L 550, ICCC 8 and ICCC 4. This has important implications for the breeding programs. Chickpea growing environments are unlikely to change in the foreseeable future (Kumar *et al.*, 1996a). Therefore, the varieties should be tailored to the available soil moisture regimes. End-of-season drought is a major yield reducer in most chickpea growing environments (Johansen *et al.*, 1994). Breeding for shorter duration varieties may be a useful strategy not only to enhance seed yields but also to increase yield stability for this crop.

Chickpea is a quantitatively long-day plant (Sethi *et al.*, 1981). This makes it difficult to breed for short-day conditions in long-day locations. However, reverse should be possible. This is supported by the results of the present study. The medium- duration varieties K 850 and L 550 bred in India, and ICCC 4 and ICCC 8 bred at ICRISAT have done well in many long-day (high latitude summer planting) locations. Thus our studies are at variance with the findings of Malhotra and Harris (1990) who found no association between days to flower and latitudes.

The general belief that larger seeded varieties are poorer in their seed yield than those with smaller seeds (Tomer *et al.*, 1973) is not supported by the present study. We included genotypes with a range of 12 g 100⁻¹ seeds to 35 g 100⁻¹ seeds. K 850 (28 g 100⁻¹ seeds) was a clear winner whereas Harigantars and Giza (14 -16 g 100⁻¹ seeds) were poor yielders. Thus selection for bolder seed within the size range involved in this study may simultaneously increase seed yield as well since larger seed enhances the sink capacity. Therefore, breeding for larger seed size may be incorporated as an objective in the breeding programs such as those in South Asia, where mostly small seeded varieties are grown.

Some studies (Tomer *et al.*, 1973, Ramanujam *et al.*, 1964 and Ramanujam and Gupta, 1974) implied that in general kabuli types are low yielders and more unstable than desi types. While this may be generally true, Kumar *et al.* (1996b) obtained different results. The kabuli variety L550 was among the highest yielding genotypes and was more stable than some desi types. Thus it should be possible to breed high yielding and stable kabuli varieties which match the performance of desi types. Improvement of L 550 for its seed size and resistances to ascochyta blight and fusarium-wilt may widen its adaptability to the Mediterranean region.

The occurrence of large GL interaction in this crop necessitates more localized breeding (Smithson *et al.*, 1985). However, in recent years varieties with relatively wider adaptation ICCV 10 and ICCV 2 have been released and are being cultivated in varying agroclimatic zones in central and peninsular India, in Bangladesh and Myanmar (Gowda *et al.*, 1995; Kumar *et al.*, 1998). This has been achieved by multilocation testing of advanced breeding lines derived from parents from diverse genetic backgrounds. Thus use of diverse parents may assist in the development of widely adapted chickpea varieties in future.

CONCLUSIONS

The GE interactions studied through pattern analysis showed that the performance of genotypes and environments can be meaningfully described using the statistical methodology proposed in this paper. In the present data set the major day-length responses of various genotypes and planting seasons encountered in different environments grouped appropriately. These showed natural relationships and variations in genotypes. The grouping suggests two mega-environments for breeding crop varieties for chickpea. Separate breeding programs and testing networks for South Asia and Mediterranean region are useful. It also showed

that testing of varieties in spring and winter planting at Tel Hadya may not produce genotype performance differentiation pattern differently. This information can also help in reducing and rationalizing chickpea testing environments in different regions.

The most important implication of this study is that long-duration genotypes may not produce the highest mean seed yields over environments, as in general, the available receding conserved soil moisture under which chickpea is grown, is not enough to support pod development late in the season. In subtropical South Asia major biotic (fusarium-wilt, ascochyta blight, helicoverpa pod borer, botrytis gray mold) and abiotic (drought, chilling) stresses adversely affect chickpea productivity at flowering and podding stages (Kumar *et al.*, 1996a). Thus breeding for relatively earlier maturity may help avoid ill effects of these stresses and might increase the productivity and stability of this crop. A short-term objective for increasing yield and stability to a certain extent can however, be achieved in subtropical zones in South Asia by avoiding damage caused by end-of-season constraints through the use of short- to medium-duration varieties which should mature before such stresses cause significant losses.

Such a strategy should also help chickpea to fit better in crop rotations with cereals such as rice and may lead to newer cropping patterns. Thus a change is required in the chickpea crop breeding objectives where usually higher productivity is linked with longer duration crop. Similarly breeding for relatively large seed size should also help increase yield both in desi and kabuli types.

This study showed that breeding chickpea varieties for high yield and wide adaptation should be possible. This may be achieved by breeding for relatively early and bold seeded varieties, and by incorporating resistance to relevant biotic and abiotic stresses.

ACKNOWLEDGEMENTS

We are thankful to the cooperators

worldwide who conducted the ICAT and sup-

plied the data.

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