

Research Article

Additive Main Effect and Multiplicative Interaction Analysis for Grain Yield of Chickpea (*Cicer arietinum* L.) in Iran

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Selection of chickpea (*Cicer arietinum* L.) cultivars with wide adaptability across diverse farming environments is important before recommending them to achieve a high rate of cultivar adoption. Multienvironment trials including 3 years and 5 locations for 17 genotypes of autumn chickpea were carried out in Iran. Additive main effect and multiplicative interaction (AMMI) were used to understand the GE interaction pattern. Analysis of variance of grain yield showed that 68.36% of the total sum of squares was attributable to environmental effects, only 15.9% to genotypic effects and 13.55% to GE interaction effects. Biplot of the first principal component and mean grain yields for genotypes and environments revealed that high yielding genotypes were not stable cultivars regarding final yield. The AMMI2 mega-environment analysis identified four chickpea megaenvironments in Iran. The first megaenvironment contained locations, Ghachsaran and Lorestan, where genotype Arman was the winner; the second megaenvironment contained locations Gorgan, where genotype FLIP 98-126C was superior. The tertiary megaenvironment contained locations in Ilam, where genotype FLIP 98-82C was superior and the location of Kermanshah made up the other megaenvironment, with FLIP 98-201C as superior.

1. Introduction

Legumes have been considered a rich source of protein throughout the world and contain approximately three times more proteins than cereals. Legumes and specially chickpea (*Cicer arietinum* L.) are important sustainable production of food in the arid and semiarid countries of west Asia such as Iran. Major producing countries include India, Pakistan, and Iran [1], where the crop is generally planted after the main rainy season and grown on stored soil moisture making terminal drought stress a primary constraint to productivity. West, northwest and northeast of Iran are favorable for the production of Kabuli chickpea. Food legume and specially chickpea in Iran accounts nearly 1.32% of the world pulses area and 0.9% of the world production [2].

Although chickpea-breeding programs have some priorities in common, the major objective of increasing the genetic

potential of yield for most, if not for all, can be achieved via breeding for higher yield potential or eliminating hazards that reduce yield. The improved chickpea genotypes are evaluated in multienvironment trials to test their performance across different environments and to select the best genotypes in specific environments. Crop yield stability is an important issue for farmers, breeders, geneticists, and production agronomists. Successful new genotypes must show high performance for yield and other essential agronomic traits. Chickpea cultivars must show high performance for yield and other essential agronomic traits.

Multienvironment trials (METs) play an important role in selecting the best cultivars to be used in future years at different locations and in assessing a cultivar's stability across environments before its commercial release. When the performance of cultivars is compared across sites, several

cultivar attributes are considered, of which grain yield is one of the most important. Cultivars grown in MET trials react differently to environmental changes. This differential response of cultivars from one environment to another is called genotype \times environment (GE) interaction. GE interactions are an important issue facing plant breeders and agronomists. A significant GE interaction for a quantitative trait such as grain yield can seriously limit progress in selection. The study of the GE interaction may assist understanding of stability concept. Information on the structure and nature of GE interaction is particularly useful to breeders because it can help determine if they need to develop cultivars for all environments of interest or if they should develop specific cultivars for specific target environments. Several methods have been proposed for analysis of GE interaction with the aim of explaining the information contained in the GE interaction data matrix [3–7]. They each reflected different aspects of stability and no single method can adequately explain cultivar performance across environments. An alternative and complementary method of evaluating cultivars is through multivariate analysis of GE interactions [4, 8]. A comprehensive description of GE interaction requires more sophisticated statistical methods than standard analysis of variance (ANOVA). A popular extension of ANOVA for studying GE interaction is the additive main effects and multiplicative interaction (AMMI) model [9]. The AMMI model is a hybrid analysis that incorporates both the additive and multiplicative components of the two-way data structure. The AMMI analysis uses analysis of variance (ANOVA) followed by principal component analysis (PCA) applied to the sums of squares allocated by the ANOVA to the $G \times E$ interaction. One of the most important purposes in analysis of MET data is megaenvironment identification. A megaenvironment is defined as a group of locations that consistently share the same best cultivars [10]. The other important purpose is identification of suitable genotypes with both high mean performance and high stability within a megaenvironment. The megaenvironment analysis is an effective tool for study of these purposes.

The objectives of this study are to (i) interpret G main effect and GE interaction obtained by AMMI analysis, (ii) use the AMMI megaenvironment analysis to examine the possible existence of different megaenvironments in chickpea-growing regions in Iran.

2. Materials and Methods

2.1. Field Experiments and Plant Material. Field experiments were conducted during three growing seasons (2008–2010) at five different research stations in Iran, which include Ghachsaran, Gorgan, Ilam, Kermanshah, and Lorestan (Table 1). In each environment (year \times location combination), 17 genotypes were tested. The names, codes, and origin of the genotypes are provided in Table 2. The experiments were carried out in a randomized complete block design with four replications over all environments. The trial fields were plowed and disc harrowed few days prior to seeding. The experimental plots consisted of four rows of 4 m length each. Row-to-row and plant-to-plant distances were kept at 30 cm

and 10 cm, respectively at all the environments. Weeds were controlled by hand-weeding two or three times as required. Neither herbicides nor insecticides were used in any trials as there was no need for them. Data on seed yield were taken from the middle two rows of each plot, leaving aside the guard rows on either side of a plot. Upon harvested seed yield was determined for each genotype at each test environment, the average was computed in accordance with the experimental design.

2.2. Statistical Analysis. The measured yield of each cultivar in each test environment is a measure of environment main effect (E), genotype main effect, and GE interaction. Typically, E explains up to 80% or higher of the total yield variation however; it is G and GE that are relevant to cultivar evaluation [11]. The interaction makes it difficult to select the best performing and most stable genotypes in plant breeding. Genotype stability across environments is important in breeding programs because it enhances the progress from selection in any one environment. A genotype is considered to be stable if its response in all environments is constant. Several methods have been proposed for analysis of GE interaction. The additive main effects and multiplicative interactions (AMMI) model, which combines standard analysis of variance with principal component analysis [12], was used to investigate of GE interaction. This method extracts genotype and environment main effects and uses principal component analysis (PCA) to explain patterns in the GE interaction or residual matrix, which provides a multiplicative model and is applied to analyze the interaction effect from the additive ANOVA model [13].

The AMMI model is:

$$Y_{ij} = \mu + \alpha_i + \beta_j + \sum_N \lambda_n \xi_{in} \eta_{jn} + \rho_{ij} + \varepsilon_{ij}, \quad (1)$$

where Y_{ij} is the observed mean yield of genotype i in environment j , μ the grand mean, α_i the genotype main effect, β_j the environment main effect, λ_n the eigenvalues of the interaction IPCA, ξ_{in} and η_{jn} are the genotype and environment scores for the IPCA axis, ρ_{ij} interaction residual, N the number of IPCA retained in the model and ε_{ij} the random error term. MATMODEL software [14] and the associated program, AMMIWINS, include megaenvironment analysis for the AMMI model. AMMIWINS identifies each megaenvironment by its winning genotype, counts its number of wins, and calculates the average expected yield over those environments included in that megaenvironment. In this study, PROC GLM of SAS [15] was run to calculate genotype and environment and genotype by environment interactions.

3. Results

Results of the combined analysis of grain yield of chickpea genotypes are given in Table 3. The differences among genotypes for grain yield were significant ($P < 0.01$). The E and L effects were significant at $P < 0.01$ and $P < 0.05$, respectively; however, the Y effect was not significant. Significant L effect showed that the response of genotype to changes

TABLE 1: Agroclimatic characteristics of testing environments.

Location	Environments		Code	Mean (kg·ha ⁻¹)	Latitude Longitude	Altitude (m)	Temp (°C) ^a		Max	Rainfall (mm)		Soil condition	
	Year	Year					Min	Max		PS ^b	GS ^c	Texture	Type ^d
Ghachsaran	2008	E1	2117.8	30° 10' N 50° 50' E	669.5	5.3	39.2	180	575	Silt-loam	Regosols		
	2009	E2	1752.8			0	47.8	195.3	515.2				
	2010	E3	1253.1			-2.6	44.6	190.1	560.7				
Gorgan	2008	E4	2328.3	36° 51' N 54° 16' E	13.3	3.8	34.2	135	425	Sandy-loam	Cambisols		
	2009	E5	2603.2			-3	41	1758	700.6				
	2010	E6	1636.2			-3.2	34.5	114.2	410.3				
Ilam	2008	E7	848.6	33° 38' N 46° 25' E	1363.4	4.9	37.6	150.3	458	Silt-loam	Cambisols		
	2009	E8	913.9			4.2	36.1	113	505.2				
	2010	E9	1357.9			3	35	170.4	576				
Kermanshah	2008	E10	1569.3	34° 19' N 47° 07' E	1322	5.3	37	128.4	398.5	Silt-loam	Cambisols		
	2009	E11	850.8			-10	41.6	149.2	431.5				
	2010	E12	1473.1			-8	38.6	169	515				
Lorestan	2008	E13	2123.5	23° 26' N 48° 17' E	1147.7	4	32	140.1	430.8	Silt-loam	Regosols		
	2009	E14	1744.0			-5	39	110	482.8				
	2010	E15	1707.3			-6	41	125.2	442.3				

^a Mean seasonal temperature.^b Preseasonal rainfall.^c Growing season.^d According to FAO system of soil classification.

TABLE 2: Genotype code, cultivar name, and cultivar origin of 17 chickpea genotypes.

Genotype code	Name	Origin
G1	FLIP 97-50C	ICARDA
G2	X94TH45K11	ICARDA
G3	X94TH151K10	ICARDA
G4	X95TH1K14	ICARDA
G5	X95TH9K1	ICARDA
G6	FLIP 98-82C	ICARDA
G7	FLIP 98-36C	ICARDA
G8	FLIP 98-55C	ICARDA
G9	Gokce	ICARDA
G10	FLIP 98-74C	ICARDA
G11	FLIP 98-126C	ICARDA
G12	FLIP 98-197C	ICARDA
G13	FLIP 98-201C	ICARDA
G14	FLIP 98-22C	ICARDA
G15	FLIP 98-40C	ICARDA
G16	Arman	Iran
G17	Bivanij	Iran

ICARDA: International Center for Agricultural Research in Dray Areas.

in the locations was under genetic control. Mean squares associated with the GE interaction were significant at $P < 0.01$. The significant GE interaction for yield confirms the differential rankings of cultivars to environments. Analysis of variance also indicated significant genotype \times year \times location interaction ($P < 0.01$). It shows the influence of changes in environment on the yield performance of the genotypes evaluated. Mean squares associated with the GY and GL interaction are not significant.

The grain yield of the genotypes across environments ranged from 233 to 3963 kg·ha⁻¹ and grand mean grain yield was 1618 kg·ha⁻¹. Among the genotypes, the mean grain yields of nine genotypes were above the grand mean grain yield while the rest gave below the grand mean grain yield. The analysis of variance of grain yield of the 17 genotypes tested in fifteen environments showed that 68.36% of the total sum of squares was attributable to environmental effects, only 9.23% to genotypic effects, and 22.41% to GE interaction effects (Table 3). Thus, only about 32% of the variation was relevant for identifying highest yielding genotypes in different environments as only G and GE interaction affect the ranking. The use of the AMMI model revealed, successively, smaller patterns within the GE interaction. Partitioning of GE interaction indicated the AMMI5 model described the GE interaction patterns for yield using the first five IPCA scores based on cross-validation. Results from AMMI analysis also showed that the first PC axis (IPCA 1) of the interaction captured 33.71% of the interaction sum of squares in 29.68% of the interaction degrees of freedom. Similarly, the second PC axis (IPCA2) explained a further 26.65% of the G \times E interaction sum of squares. Two principal components (PC1 and PC2) explained only 60.37% of the G \times E interaction sum of squares. The largest IPCA1

TABLE 3: Analysis of variance on grain yield of 17 chickpea genotypes in 15 environments of Iran.

Source	Df	MS	RMSPD [†]	Explained (%)
Environment (E)	14	19050789**		68.36
Year (Y)	2	8798258 ^{NS}		
Location (L)	4	42253254*		
L \times Y	8	10014496**		
repeat (E)	45	150401		
G	16	2251338**		9.23
G \times E	224	390364**		22.41
IPCA 1	29	1016470**	382.23	33.71
IPCA 2	27	863187**	359.61	26.65
IPCA 3	25	431236**	355.55	12.33
IPCA 4	23	367192**	349.83	9.66
IPCA 5	21	299114**	344.85	7.18
G \times Y	32	302721 ^{NS}		
G \times L	64	502035 ^{NS}		
††IPCA 1	19	436117**	201.40	77.37
IPCA 2	17	97155**	193.63	15.42
G \times L \times Y	128	356421**		
Error	720	87608		
Total	1019			

^{NS}, *, and **: nonsignificant, significant at the 0.05, and 0.01 probability level, respectively.

[†], RMSPD, the root mean square prediction differences in units of yield kg/ha.

^{††}, AMMI analysis for the set of cultivar \times location means averaged across years.

scores were for Arman and it were close to zero for FLIP 98-55C and FLIP 98-22C. The largest IPCA1 scores for environments were for E4 and E7 (Figure 1). Higher IPCA1 and IPCA2 scores both positive and negative contribute to higher GE interaction. The largest IPCA2 scores were for X95TH1K14 and it were close to zero for Bivanij and FLIP 98-22C (Figure 2).

The biplot of IPCA1 against IPCA2 compares relative magnitude and sign of the GE interaction controlled by each genotype and each environment. Genotypes with large IPCA1 or IPCA2, or both, have high interactions, whereas genotypes with IPCA1 or IPCA2 scores near zero have small interactions for the corresponding axis. This is exemplified by FLIP 98-22C which was close to the center of both axes.

Whether the genotypes and environments have similar or opposite GE interaction patterns is indicated by their same or opposite horizontal and/or vertical direction from the center. For example, FLIP 98-55C, X94TH45K11, and FLIP 98-74C produced similar interaction effects than those by X94TH151K10, X95TH9K1, and Arman. Simultaneous assessment of IPCA scores for genotypes and environments facilitates the interpretation and identification of specific interactions among them. For example, genotypes with appositive IPCA would be particularly adapted to environments with a positive IPCA and poorly adapted to environments with a negative IPCA [9]. The Arman, FLIP 98-40C, FLIP 98-82C, and FLIP 98-36C have the best performer (due

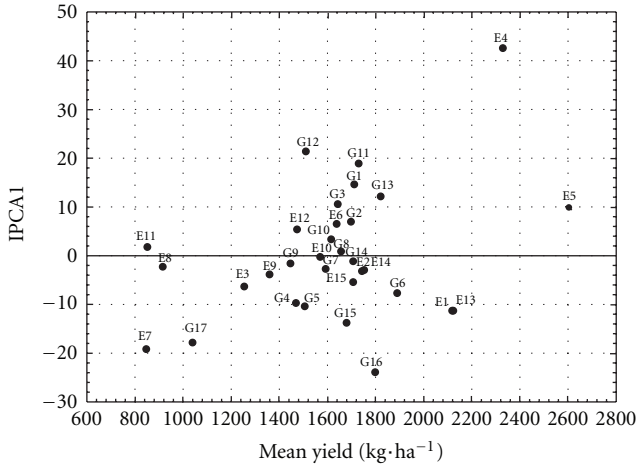


FIGURE 1: Biplot of interaction principal component axis (IPCA1) against mean yield ($\text{kg}\cdot\text{ha}^{-1}$) of 17 chickpea genotypes in 15 environments.

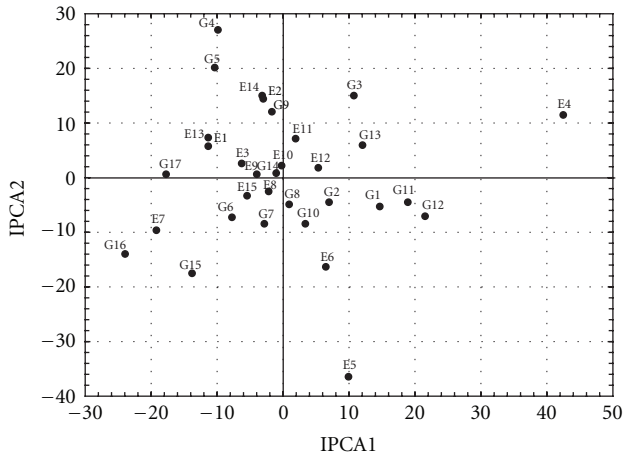


FIGURE 2: Biplot of interaction principal component axis (IPCA1) against IPCA2 for yield ($\text{kg}\cdot\text{ha}^{-1}$) of 17 chickpea genotypes in 15 environments.

to large positive GE interaction) in E7, E15, but these are the worst performer (due to large negative GE interaction) in others environments in the opposite sector of the biplot.

4. Discussion

FLIP 98-22C and FLIP 98-55C showed small interactions, therefore they were selected for yield stability across locations and years. Thus, these genotypes may have broad adaptation and make good sources for breeding chickpea cultivars. Unfortunately, the recommend genotypes by IPCA had low yield. It indicates that simultaneous selection for yield and broad adaptation to diverse environments is not possible. Limitations in the availability of farming inputs in developing countries such as Iran increase the need for stable genotypes that cope with environmental variation. In these situations, where the availability of farming inputs

TABLE 4: AMMI2 megaenvironment and their winning genotypes for the 17 chickpea genotypes grown in 5 locations of Iran.

AMMI2 megaenvironment	Winner genotypes	Expected values for Yield
Megaenvironment 1		
Ghachsaran	Arman	1990.8
Lorestan	Arman	2134.6
Megaenvironment 2		
Gonbad	FLIP 98-126C	2781.1
Megaenvironment 3		
Ilam	FLIP 98-82C	1379.3
Megaenvironment 4		
Kermanshah	FLIP 98-201C	1591.3

is not ensured, genotypes with good performance and stability should be recommended. Therefore, we used AMMI megaenvironment analysis. In a cultivar \times location \times year experiment, one of the problems associated with cultivar evaluation is that the effect of location can vary considerably from year to year [16]. This is usually evidenced by a significant location by year interaction in the analysis of variance. The presence of such an interaction presents a serious problem to anyone wishing to recommend a cultivar to a region. Because the environment factor in this analysis is a combination of locations and years, it is not helpful when recommendations of cultivars to specific locations are required. Lin and Butler [17] used the set of cultivar \times location means averaged across years. They assumed that the mean across years at each location was representative of the fixed component (refer to [16]). Therefore, we used the set of cultivar \times location means averaged across years for megaenvironment analysis and Site regression analysis. The GL megaenvironment analyses for years also were similarly constructed and are not presented. Partitioning of GL interaction indicated the AMMI2 model described the GL interaction patterns for yield using the first two IPCA scores based on cross-validation. Two principal components explained only 92.79% of the $G \times L$ interaction sum of squares (Table 3). The first megaenvironment contained locations in Ghachsaran and Lorestan, where genotype Arman was the winner (in terms of yield and stability); the second megaenvironment contained locations in Gorgan, where genotype FLIP 98-126C was the winner. The tertiary megaenvironment contained locations in Ilam, where genotype FLIP 98-82C was the winner and the location of Kermanshah made up the other megaenvironment, with FLIP 98-201C as the winner (Table 4). According to the present assessment, FLIP 98-126C is adapted to high-yielding environments and recommend for Gorgan location. This genotype was released by Dry land Agricultural Research Institute. This genotype can also be grown successfully in other locations in Iran.

5. Conclusion

It is clear that the AMMI model is an excellent tool for study of MET data. The objective of AMMI strategy is to explore

multidirectional aspects of the GE interaction and to extract more information from this component. Analysis of stability and identification of megaenvironments on chickpea using this method have not been already reported. In addition, this study indicated the possibility of improving progress from selections under diverse location conditions by applying AMMI strategy.

Abbreviations

AMMI:	Additive main effect and multiplicative interaction
ANOVA:	Analysis of variance
E:	Environment main effect
G:	Genotype main effect
GE:	Genotype \times environment interaction
GL:	Genotype \times location interaction
ICARDA:	International Center for Agricultural Research in Dry Areas
L:	Location main effect
METs:	Multienvironment trials
PCA:	Principal component analysis
Y:	Year main effect.

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