

Genotype x Environment Interaction and Stability Analysis of Chickpea (*Cicer arietinum* L.) in Northern part of Ethiopia

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ABSTRACT

The study was conducted to assess genotypes and delineate environments to refine recommendation domain. Genotype-environment interaction (GE), helps to know the presence of GE i.e. differential genotype responses in different environments, complicates cultivar evaluation in turn the stability analysis indicate the stable genotypes across environments. The sum square of G x environment interaction was partitioned by AMMI model into two significant interaction principal component axes (IPCA). Genotypes based on seed yield Akaki, ICC-V91022, ICC-V 91014, and ICC-V 92006 best perform at Inewari-2, Adet-2, Inewari -1 and sirinka-2 and Sirinka -1 respectively. GGE biplot depicted the presence of three mega environments among the test environments used for evaluation of genotypes. Where Inewari -2 and Adet -2 were exceptional environments for seed yield and the rest environments cluster together. Besides, hundred seed weight explained PC1 and PCA2 about 59.3 and 40.7%. There was positive correlation among environments except Inewari-3 and Sirinka-3 where ICC-V 89303 and ILL-2872 perform well. Pattern analysis has assisted in analyzing the Chickpea testing environments leading to the identification of the existence of three and two mega-environment clusters for seed yield and hundred seed weight respectively. Thus applying Biplot and breeding view present in the breeding Management system tool (BMS) assist in cultivar recommendation and identifying target environments.

Keywords: Chickpea, Genotype x environment interaction, stability, analysis, Biplot and breeding view.

INTRODUCTION

Chickpea with 17-24% protein and 41-50.8% carbohydrates is one of the most important food crops (Witcombe and Erskine, 1984). Chickpea (*Cicer arietinum* L.) is an important pulse crop in Ethiopia that contribute more than 1.91 % (about 231298.5 Hectares) and 1.83 % (about 400207.72 tone) of both in area and production among pulses that account 13.38 (1616809.4 hectare) and 10.6% (about 2,316,012 tone) of grain crops area and production in the country and its' productivity is 1.73 tone/hectare (CSA ,2011). Ethiopia is the largest producer of chickpea in Africa accounting for about 46% of the continent's production during 1994-2006. The country is also the seventh largest producer worldwide and contributes about 2% to the total world chickpea production (Menale, et.al. 2009).

MET data analysis, prior to cultivar evaluation, should be to investigate the relationships among the test environments and the possibility of mega-environment differentiation within the target environment. Identification of mega-environments would allow exploitation of the GE that is repeatable across years. For a given mega-environment, genotypes should be evaluated for mean yield (or, in more general terms, mean performance) and stability across test environments. The ideal cultivar should be one that is both high-yielding and stable (W. Yan and L.A. Hunt, 2002).

Yield is a complex quantitative trait, and such traits are often controlled by many genes, influenced by prevailing environmental conditions, with each gene having a small effect. In order to identify the most stable and high yielding genotypes, it is important to conduct multi-environment trials (Luquez et al., 2002).

Multi-location trials, or more generally, multi-environment trials (MET) are conducted routinely to generate essential information for breeding line selection, new cultivars release, and cultivar re commendation. MET are essential because of the existence of genotype -by-environment interactions (GE), which complicates genotypes evaluation /selection, and for this reason, analysis of genotype-by-environment data from MET trials has been an important component of plant breeding and cultivar recommendation.

In a MET, a number of genotypes are evaluated at a number of geographical locations for a number of years in the hope that the pattern of stresses that the genotypes experience is representative of future growing environments (Malosetti, et. al., 2013). While A large number of genotypes are tested over a number of sites and years, and it is often difficult to determine the pattern of genotypic responses across environments without the help of graphical display of data (Yan et al., 2001).

A mega-environment is a group of environments or sub-regions in which a single genotype or a group of similar genotypes are specifically adapted and champion in performance (Gauch and Zobel, 1997). Differences in genotype stability and adaptability to environment can be qualitatively assessed using the biplot graphical representation that scatters the genotypes according to their principal component values (Vita et al., 2010). The cosine of angle between a pair of environment vectors approximates correlation between them (Yan and Kang, 2003). The position and perpendicular projection of genotypic points onto an environmental vector can be used to identify a genotype or genotypes having specific adaptation in that environment(s) (Yan et al., 2000). The lines that connect the biplot origin and the marker of the environments are called environment vectors. The angle between the vectors of the two environments is related to the correlation coefficient between them. When the biplot adequately approximate the environment-centered data, and when the environment - focused scaling is used, the cosine of the angle between the vectors of two environments approximates the correlation coefficient between them (Karooneburg, 1995). It has to be emphasized that mega-

environment delination must be based on data from multiple years because repeatability of a GE pattern is the key for making decisions that have long-term impacts (Yan et al., 2011).

The objectives of this study was to assesses stability , genotype-by-environment (GEI)pattern of “multi-environment trials” (METs) of chickpea genotypes growing in vertisol areas of Northern part of Ethiopia and model the data using AMMI and GGE using Biplot and breeding view present in breeding Management System tool (BMS).

MATERIALS AND METHODS

Plant materials

In collaboration with the International Center for Agricultural Research in the Dry Areas (ICARDA), Syria, the National chickpea research program of the Ethiopian Institute of Agricultural Research (EIAR) had introduced desi chickpea germplasms. Where initially the germplasms were grown on a sick plot to screen for wilt /root rot disease tolerance, then, the screening nurseries and advanced yield trials were conducted at Enewari. Lastly fifteen desi chickpea genotypes together with two commercial varieties and one farmer's variety were used in this study. The names, origin and genotypic codes of these genotypes are given in Table 1.

Design and environments

The genotypes were examined in Randomized Complete Block Design (RCBD) with three replications in three different environments (Enewari 2600, Adet 2240, and Sirinka 1860 m.a.s.l, respectively) and three consecutive growing seasons (Total of 9 environments). Where each year at each location was considered as a separate environment resulted a total of nine test environments. All the genotypes were planted on a broad bed (considered as a plot), which had 1.2 width and 4 meter length. The furrow between any two plots was 40 cm

wide. Each plot consisted of 4 rows each row being 4m long and 0.3m spaced apart. Data on seed yield and hundred seed weight were recorded from two central rows of each plot, where the total harvestable area was 2.4m².

The Additive Main Effects and Multiplicative Interaction (AMMI) and GGE model was used to investigate GEI. Stastical analysis was performed by statistical packages Genstat Discovery Edition 4 and breeding view present in the breeding Management system tool (BMS).

Table 1. The codes and names of 15 chickpea genotypes

Genotype names		Genotype names	
1	ICC-V-91014	9	ICC-V-91022
2	ICC-V-89240	10	ICC-V-90035
3	ILL-2872	11	ICC-V-89223
4	ICC-V-92010	12	ICC-V-92942
5	ICC-V-92006	13	ICC-V-91030
6	ICC-V-92032	14	Worku*
7	ICC-V-89303	15	Akaki*
8	ICC-V-93102	16	Local checks

**and *: standard checks and released genotype

RESULTS AND DISCUSSION

RESULTS

Combined analysis of variance

The analysis of variance (ANOVA) for 15 chickpea genotypes tested in 9 environments showed that chickpea flowering and physiological maturity, were significantly ($P < 0.01$) affected by Location (L), genotypes (G) and genotype \times Location \times Year where as There was no significant difference ($P < 0.05$)

for Plant height, pod /plant and seed/pod for genotype \times Location (Table 2). Similarly, The AMMI model Analysis of 15 chickpea genotypes tested in 9 environments showed that chickpea grain yield was Significantly ($P < 0.01$) affected by environments (E), genotypes (G) and genotype \times environment interaction (GEI) (Table 3) indicating the presence of genetic

variation and possible selection of stable entries.

The Seed yield in the AMMI model, GEI is explained by two axes (principal component 1, PCA1, and principal component 2, PCA2) that are highly significant at $P < 0.001$. Genotypes ICC- V 9206, followed by ICC- V 92032 and ICC-V 89223, being closer to the biplot origin, were average in their performances for seed yield across the environments and they are stable (Fig1). The genotypes that are farther along the positive direction of the vector tend to give higher yields, and are better adapted to those environments.

Genotypes based on seed yield Akaki, ICC-V91022, ICC-V 91014, and ICC-V 92006 best perform at Inewari-2, Adet-2, Inewari -1 and sirinka-2 and Sirinka -1 respectively.

GGE biplot depicted the presence of three mega environments among the test environments used for evaluation of genotypes (Figure 2). Where Inewari -2 and Adet -2 were exceptional environments for seed yield and the rest environments cluster together. Where Akaki best perform at Inewari -2 and ICC-V91022 at Adet -2 in the contrary ICC-V91014 best perform in all environments except Inewari -2 and Adet -2.

Hundred seed weight explained PCA1 and PCA2 about 59.3 and 40.7%. There was positive correlation among environments except Inewari-3 and Sirinka-3 where ICC-V 89303 and ILL-2872 perform well

respectively Table 3. Further GGE biplot analysis showing the two mega environments and their respective high hundred seed weighting genotypes presented in (Fig. 4).

The correlation coefficients among the nine environments are presented in Table 4 and 5 for seed yield and hundred seed weight respectively. If correlation coefficient value is positive and close to 1 it is possible to consider the environments as one recommendation domain and vice versa. Admirably, the vector view of a GGE biplot Fig. 2 and 4 provide the succinct summary of the interrelationships among environments.

DISCUSSION

Identifying favorable environments for chickpea genotypes Environment that appears almost in a perpendicular line have similar means and those that fall almost in a horizontal line have similar interaction pattern. AMMI1 biplot (Figure 1) thus exhibited that environment differed in main and interactions. The environment Adet-3 and Adet-1 and Inewari -3 had similar main effect but differed in interaction with genotypes. The ranking in such environments is likely to be quite variable, thus making it complex to produce variety recommendations. Further the environment Inewari-2 and Adet-2 were the highest yielding and highly interacting, hence are most suitable only for the specifically adapted genotypes.

The genotypes and environments that are farthest from the origin being more responsive fit the worst. Genotypes and environments that fall into the same sector interact positively; negatively if they fall into opposite sectors (Osiru et al., 2009). A genotype showing high positive interaction in an environment obviously has the ability to exploit the agro-ecological or agro-management conditions of the specific

environment and is therefore best suited to that environment like genotypes Akaki, ICCV-91022 and ICCV-91014 of this study. In general MET data are valuable not only in selecting superior genotypes but also in identifying test environments that are more effective for genotype evaluation in the country like Ethiopia has got diverse agro-ecologies.

Table 2. Mean square values of agronomic characters for combined analysis of variance over three years and locations.

Source	DF	Mean square Error				
		Days to flower	Days to maturity	Plant Height(cm)	P/P	S/P
Year	2	337.3**	3852.6**	1385.5**	4978.5**	0.8*
Loc	2	2443.6**	20168.5**	3052**	11425.8**	1.5*
Genotype	14	208.1**	86.5**	181.2*	542**	0.6**
Genotype x year	28	6.5**	19*	21.9**	164.8NS	0.3*
Genotype x loc	28	11.2**	32.1**	13.6NS	133.3NS	0.2NS
Genotype x year x loc	56	9.3**	15.7**	16.2*	164.2*	0.2NS
Pooled error	250	2.7	12.4	11.4	120	0.2

The local checks were omitted from the combined analysis and only two standard checks and 13 genotypes were considered.

*, ** Indicate Significance at 0.05 and 0.01 probability levels, respectively. Ns: Non- significant

G x L=Genotypes x location Interaction, G x Y = Genotypes x years Interaction,

G x Lx Y= Genotypes x years x location Interaction

DTF, days to flower; DTM, days to mature; PH, plant height (cm); P/P, pod/plant; S/P, seed.pod

Table 3. AMMI analysis of 15 chickpea genotypes seed yield performance evaluated across 9 environments

Source	Df	Seed yield		Hundred seed weight	
		Sum of square	Mean square	Sum of square	Mean square
Genotypes	14	3.904	0.2789*	986.9	70.49**
Environments	8	35.102	4.3877**	52.9	6.61**
Interactions	112	8.065	0.0720	53.8	0.48
IPCA 1	21	4.552	0.2167*	31.9	1.52**
IPCA 2	19	3.513	0.1849*	21.9	1.15**
Residuals	72	0.000	0.0000	0.0	0.00

* and **: significant at 5% and 1% probability level, respectively

Table 4. Correlation coefficient among test environments for seed yield

Adet- 1	1.0000							
Adet- 2	-0.2119	1.0000						
Adet- 3	0.9414	0.5006	1.0000					
Inewari -1	0.7306	0.0766	0.7564	1.0000				
Inewari -2	0.2674	0.0059	0.1034	-0.4530	1.0000			
Inewari -3	0.9937	0.3015	0.9727	0.7612	0.2003	1.0000		
Sirinka -1	0.8862	0.1694	0.8921	0.9629	-0.2075	0.9080	1.0000	
Sirinka -2	0.6254	0.3247	0.5305	0.9178	-0.4095	0.6172	0.8521	1.0000
Sirinka -3	0.5103	0.5160	0.2044	0.0334	0.7238	0.4114	0.1977	0.2582
Adet- 1		Adet- 2	Adet- 3	Inewari -1	Inewari -2	Inewari -3	Sirinka -1	Sirinka -2

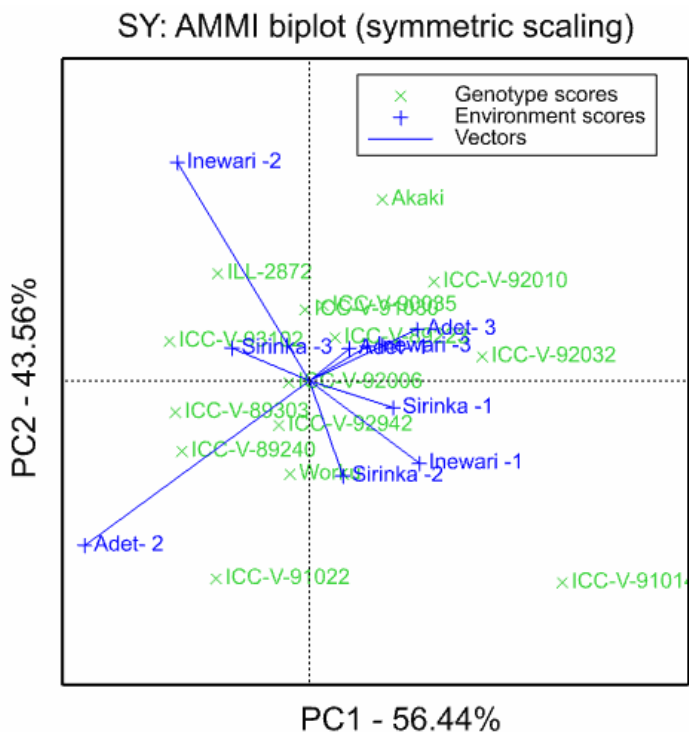


Fig.1. AMMI biplot analysis showing the mega environments and their respective yielding genotypes

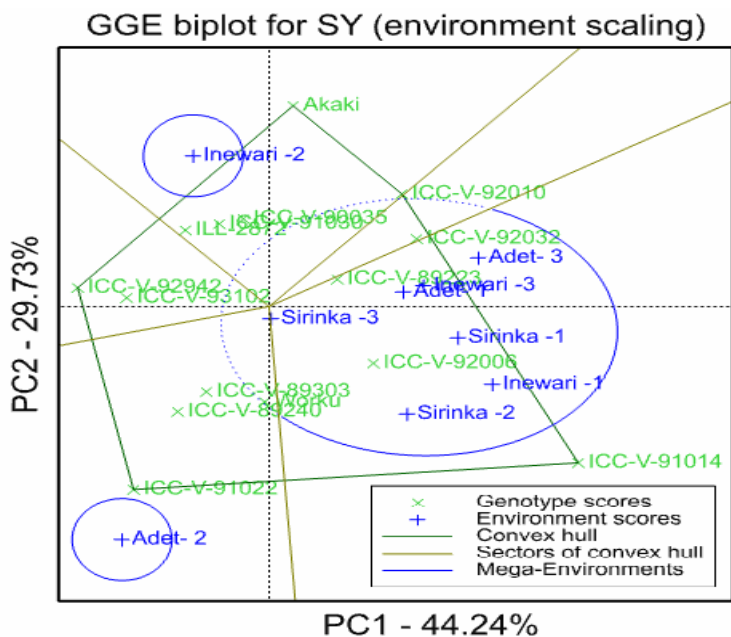


Fig.2. GGE biplot analysis showing the three mega environments and their respective yielding genotypes presented

Table 5. Correlation matrix for hundred seed weight

Adet- 1	1.0000							
Adet- 2	0.9999	1.0000						
Adet- 3	0.9647	0.9671	1.0000					
Inewari -1	0.9233	0.9271	0.9912	1.0000				
Inewari -2	0.9592	0.9620	0.9992	0.9942	1.0000			
Inewari -3	0.8578	0.8611	0.9550	0.9693	0.9522	1.0000		
Sirinka -1	0.9829	0.9846	0.9967	0.9780	0.9946	0.9311	1.0000	
Sirinka -2	0.9741	0.9755	0.9954	0.9766	0.9908	0.9517	0.9959	1.0000
Sirinka -3	0.8779	0.8769	0.8982	0.8660	0.8808	0.9229	0.8960	0.9313
Adet- 1	Adet- 2	Adet- 3	Inewari -1	Inewari -2	Inewari -3	Sirinka -1	Sirinka -2	

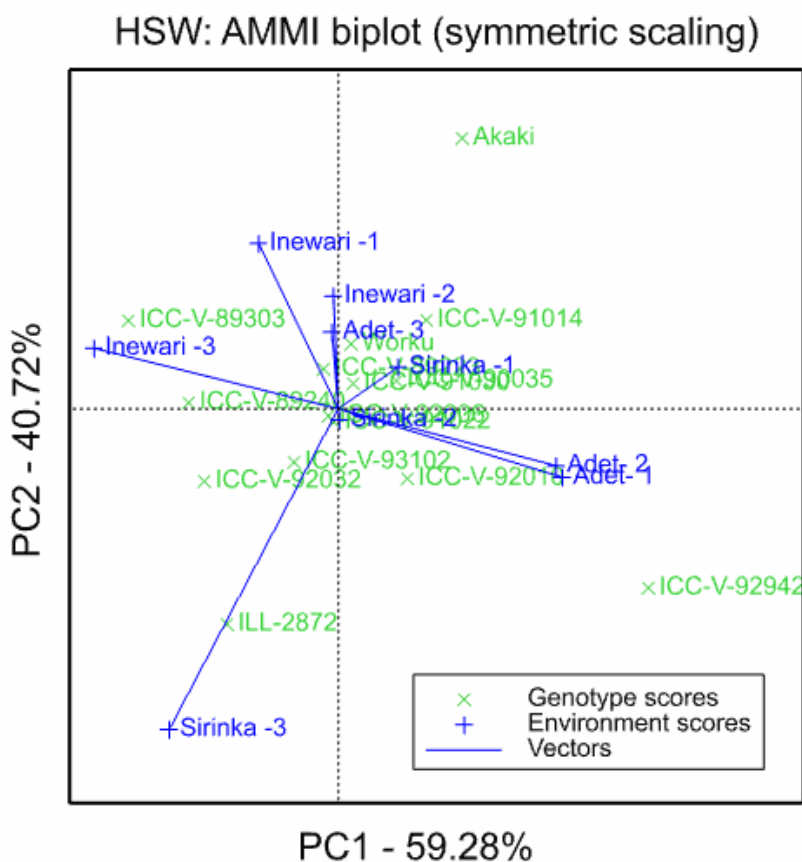


Fig.3. Biplot for PC1 vs. PC2 scores obtained from hundred seed weight data of 15 chickpea genotypes across nine environments.

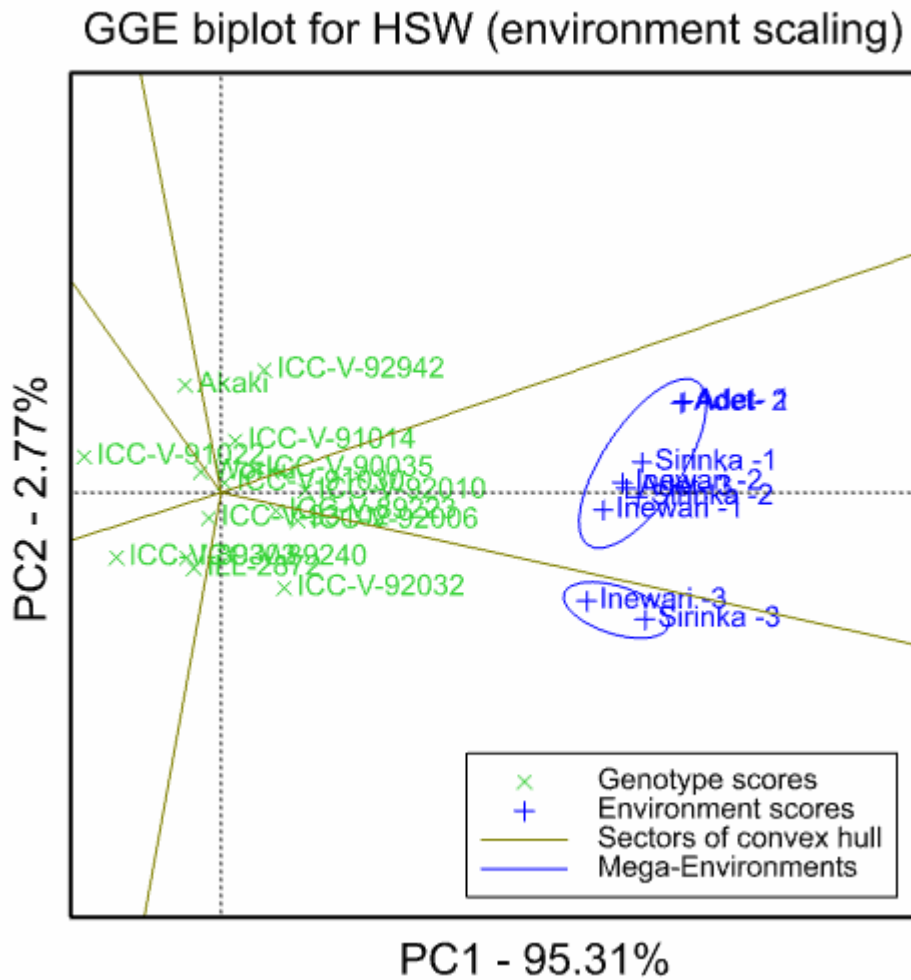


Fig4. GGE biplot analysis showing the two mega environments and their respective high hundred seed weighting genotypes presented

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