Australian Journal of
Crop Science

AJCS

AJCS 11(02):212-219 (2017) ISSN:1835-2707
doi: 10.21475/ajcs.17.11.02.p297

Genotype by environment interaction on yield stability of desi type chickpea (*Cicer arietinum* L.) at major chickpea producing areas of Ethiopia

Assefa Funga[1,2], Megersa Tadesse[2], Million Eshete[1], Asnake Fikre[4], Lijalem Korbu[1], Nigussie Girma[1], Dagnachew Bekele[1], Ridwan Mohamed[1], Zewdie Bishaw[3], Ganga Rao NVPR[4], Moses Siambi[4], Emmanuel Monyo[4], Pooran Gaur[5], Chris Ojiewo*[6]

[1]Ethiopian Institute of Agricultural Research, Debre-Zeit Agricultural Research Center, Ethiopia
[2]Research Methods Program, Department of Horticulture, Jomo Kenyatta University of Agriculture and Technology, Kenya
[3]ICARDA-Sub Saharan Africa Program, Ethiopia
[4]ICRISAT - Eastern and Southern African Program, Nairobi, Kenya
[5]ICRISAT - South Asian Program, Patancheru, Hyderabad, Telangana, India
[6]ICRISAT - Global Program on Genetic Gains, Addis Ababa, Ethiopia

***Corresponding author: C.Ojiewo@cgiar.org**

Abstract

This study was conducted to determine the interaction between chickpea genotypes with the environment (GxE) on the yield stability and adaptability of desi type chickpea genotypes (*Cicer arietinum* L.). Seventeen chickpea genotypes were evaluated for two cropping years (2012/2013 – 2013/2014) at four locations i.e., eight environments (locations x years combination). Chickpea grain yield was significantly ($p<0.01$) affected by genotypes, the environments and GxE interaction, indicating that the varieties and the test environments were diverse. GxE was further partitioned by principal component axes. The first two principal components cumulatively explained 53.1% of the total variation, of which 32.7% and 20.4% were contributed by IPCA1 and IPCA2, respectively. This implies that the interaction of 17 chickpea genotypes with eight environments was predicted by the first two principal components. AMMI1 biplot analysis showed five adaptive categories of genotypes based on similarities in their performance across environments. The AMMI2 biplot generated using genotypes and environmental scores for the first two IPCAs revealed positioning of the five genotype groups (GC) into four sectors of the biplot. Among them, two genotypes in GC 5 (G5 and G11) exhibited high yields across environments, low IPCA1 scores, low AMMI stability value (ASV) and yield stability index (YSI). G5 was released as a new variety, 'Dimtu' and registered in the Official Varieties Catalogue of Ethiopia, 2016.

Keywords: AMMI model, GxE, Desi type, chickpea, genotype, stability.
Abbreviations: ASV_ AMMI Stability Value, AMMI_ Additive Main Effect and Multiplicative Interaction, E_Environment, EC_Environment Category, G_Genotype, GC_Genotype Category, GxE_Genotype by Environment Interaction, IPCA_Independent Principal Component Analysis PC_Principal Component, YSI_Yield Stability Index.

Introduction

Chickpea (*Cicer arietinum* L.) is the world's second most important food legume next to dry bean. In 2014, 14.25 million of tons of chickpea grain was produced on about 14.8 million hectares across the world with an average productivity of 0.96 ton ha^{-1} (FAOSTAT, 2016). In Ethiopia, chickpea is mainly grown in the central, northern and eastern highland areas at an altitude of 1400-2800 m.a.s.l., with annual rainfall range of 700-2000 mm (Anbessa and Bejiga 2002). During the 2014/2015 cropping year, 1.08 million smallholder Ethiopian farmers produced 458,682 tons of chickpea on 239,755 ha of land with an average productivity of 1.913 tons ha^{-1} (CSA, 2015). Israel achieved an average of 6 tons ha^{-1} in 2013 (FAOSTAT, 2014) showing that Ethiopia can potentially attain such yields with proper management and appropriate varieties. This yield gap between achieved and potential yield of chickpea in Ethiopia could be partially be due to varietal and environmental variability.

Evaluating genotypes of annual crops for grain yield on a multi-locational or multi-year basis frequently shows GxE interaction that complicates the selection or recommendation of materials. According to Annicchiarico (1997), it is possible to cope with genotype x year or genotype x location x year interaction effects only through selection for yield stability across environments defined as location x year combinations. In doing so, there are two possible strategies for developing genotypes with low G x E interactions:1. Sub-division or stratification of heterogeneous area into smaller, more homogeneous sub-regions, with breeding programs aimed at developing genotypes for specific sub-regions. However, even with this refinement, the level of interaction can remain high, because breeding area does not reduce the interaction of genotypes with location on years (Eberhart and Rusell, 1966; Tai, 1979). 2. The second and most plausible strategy for reducing GxE interaction involves selecting genotypes with better stability across a wide range of environments in order to better predict their behavior (Farshadfar et al., 2011).

GxE analysis is important to identify superior varieties and their adaptation to and stability in diverse agroecologies (Kanouni, et al., 2015). Differential performance of chickpea under diverse environmental conditions decreases yield stability (Padi, 2007). Inefficiency in the GxE analysis of variance may result in wrong selection of genotypes for yield. There are many models for conducting GxE whose applicability depends on the experimental data, the number of environments, and the accuracy of collected data and environmental information. In this study, we used AMMI model in yield stability analysis as its reliability recently reviewed by several authors (Adugna, 2007; Gauch et al., 2008; Gauch, 2013; Hongyu & Garc, 2014; Bose et al., 2014). On the AMMI biplot, the displacements along the x-axis indicate differences in main (additive) effects, whereas displacements along the y-axis indicate differences in interaction effects (Kempton, 1984; Yan, 2003). Genotypes that group together have similar adaptation while environments which group together influence the genotypes in the same way. If a genotype or an environment has an IPCA1 score of close to zero, this implies that its interaction effects are minimal and therefore, it is stable (Carbonell et al., 2004). A genotype and environment with the same sign on the IPCA1 axes, have a positive interaction; the converse is also true (Yan, 2003). The AMMI model lacks provision for a quantitative stability measure, such a measure is essential in order to quantify and rank genotypes according to their yield stability. Purchase et al. (2000) (proposed the AMMI stability value (ASV) measure to cope with such inadequacy of the AMMI model in providing a quantitative stability measure. Actually, ASV is the distance from the origin (0, 0) of the biplot graph of IPCA1 scores against IPCA2 scores. Since the IPCA1 score contributes more to GxE sum of square, it has to be weighted by the proportional difference between IPCA1 and IPCA2 to the scores to compensate for the relative contribution of IPCA1 and IPCA2 total GxE sum of squares. The distance from the origin is then determined using Pythagoras theorem (Purchase et al. 2000). AMMI2 biplot is used to explain the magnitude of GxE. The genotypes and environments that are far away from the origin are more interactive. Genotypes and environments that fall into the same sector interact positively. On the contrary, genotypes and environments that fall in opposite sectors interact negatively (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 (Osiru et al, 2009; Rashidi et al, 2013). Stability is evaluated in the y-axis (IPCA1) by AMMI1 i.e., the closer the y-value to zero line from both (positive and negative) sides, of the more stable a genotype is. On the other hand AMMI2 analysis evaluates stability of environments and genotypes when they are located near the origin, with low scores for IPCA1 and IPCA2 axes of the interaction (Purchase, 1997). Thangavel et al. (2011) also pointed out that the distances from the origin (0, 0) are indicative of the amount of interaction that was exhibited by either genotypes over environments or environments over genotypes.

Results and Discussion

AMMI analysis of variance for G, E and GxE Interactions

AMMI model is fundamentally effective where the assumption of linearity of responses of genotype to a change in environment is not fully explained, which is important in stability analysis (Gauch, 1996). The combined analysis of variance (ANOVA) for grain yield (kgha^{-1}) of 17 chickpea genotypes tested in eight environments showed highly significant differences ($p<0.01$) for environments (E), genotypes (G) and environments by genotypes interaction (GxE) (see Table 1). The total variation explained was 60.3% for environment, 4.7% for genotype and 16.5% for GxE. The high percentage of the variation explained by E implies that the environments were diverse, resulting in large differences among environmental means causing most of the variation in the grain yield. This is an indication that environmental influence is a major factor on yield performance of chickpea in Ethiopia. The presence of GxE interaction was clearly demonstrated by the AMMI model (Figure1) in which five of the principal component axes were significant ($p<0.01$). As a result, 92.6% of the interaction sum of squares were cumulatively explained, of which 32.7%, 20.4%, 17.8%, 11.5% and 10.2% were explained by IPCA1, IPCA2, IPCA3, IPCA4 and IPCA5, respectively (Table 2). However, to simplify the complexity of the analysis and to graph the results of AMMI using a biplot, two interaction principal component axes for AMMI model were sufficient for a predictive model. Other interaction principal component axes captured mostly non-predictive random variation and did not fit to predict validation observations (Gauch and Zobel, 1996; Yan and Manjit, 2002). Thus, the results indicated that the AMMI model fits the data well, and justifies the use of AMMI2. Therefore, the interaction of the 17 chickpea genotypes with eight environments was predicted by the first two interaction principal component axes (Tables 3 and 4). The yield response of the 17 chickpea genotypes evaluated in the present study are shown in table 3. The mean grain yield value of genotypes averaged over environments indicated that genotypes G5 and G17 had the highest (3090 kg ha^{-1}) and the lowest (2439 kg ha^{-1}) yield, respectively. The performance of different genotypes was found to be inconsistent across all environments (Table 3). Similarly the environment mean grain yields ranged from 3582 kg ha^{-1} for CD2 to 1354 kg ha^{-1} for AK1 and grand mean of grain yield over environments and genotypes was 2786 kg ha^{-1}.

Graphical representation of the AMMI1 biplot for additive and interaction effects

Genotypes (G6, G13, G2, G8, G14, G10, G7, and G16) and environments (AN1, DZ1, DZ2) that were located on quadrants I and II of AMMI1 biplot AMMI1 (Figure 1) have positive interaction because they have the same positive sign of IPCA1 score. Similarly the genotypes and environments distributed on quadrants III and IV of AMMI1 biplot graph (Fig 1) have positive interaction because they all have the same negative value of IPCA1 score. Genotypes and environments on the same parallel line (ordinate) such as G2 and G17 (Fig 1) have similar yields performance. Genotypes or environments on the right side of the midpoint of the axis have higher yields than those on the left hand side. Therefore, genotypes G10, G14, G3, G1, G12, G15, G8 and G16 had higher average yield than grand mean, while genotypes G11, G13, G6, G7, G4, G9, G2 and G17 were identified as moderately low to low yielding genotypes (Fig1).

A high genotypic absolute IPCA1 score shows high interaction and reflects more specific adaptation to the environments with IPCA1 values of the same sign. Genotypes (G1, G3, G7, G12, G15, and G16) and environments (CD1, CD2, DZ1, DZ2, and AN1) on Fig 1 with large magnitude of IPCA1 score and had high

Table 1. ANNOVA for AMMI analysis of genotype by environment interaction on yield of desi chickpea.

Source of variation	DF	SS	MSS	F	Pr>F	Explained %
Total	407	324738000.6				
Environment (E)	7	195883470.3	27983352.9	40.6617	5.064e-09 ***	60.3
Rep(Env)	16	11011184.0	688199.0	3.5841	7.192e-06 ***	3.4
Genotype(G)	16	15265112.0	954069.5	4.9687	6.469e-09 ***	4.7
(GxE)	112	53422394.3	476985.7	2.4841	1.345e-09 ***	16.5
Residuals	256	49155825	192015.000			

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Grand mean = 2786.3 R-squared = 0.8486 C.V. = 15.73%

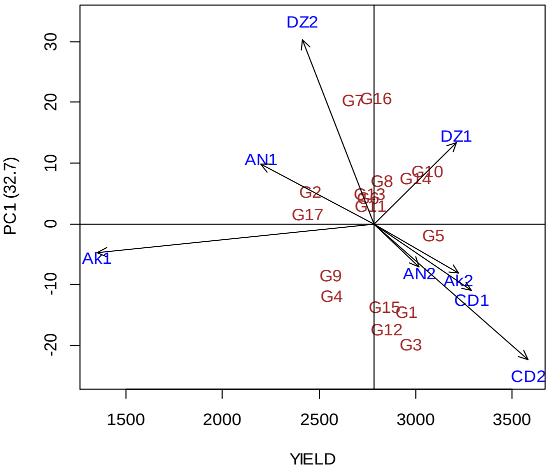

Fig 1. Plot of Genotype and Environment IPCA 1 scores versus grand means. G1 – G17 with red color represent genotypes while environments are represented by two letters and numbers in blue color. The details of the genotypes and environments are presented in tables 3 and 4.

Table 2. Principal component analyses of genotype by environment interaction on yield of desi chickpea.

Mult_Interaction Effect	Df	SS	Ms	F	Pr.F	GxE expl. (%)	Cumulative %
IPCA1	22	17481049.4	794592.8	4.14	0.0000	32.7	32.7
IPCA2	20	10883413.8	544168.9	2.83	0.0001	20.4	53.1
IPCA3	18	9489058.7	527167.3	2.75	0.0002	17.8	70.9
IPCA4	16	6162014.8	385126.1	2.01	0.0130	11.5	82.4
IPCA5	14	5442458.5	388748.1	2.02	0.0168	10.2	92.6
IPCA6	12	2495760.2	207978.8	1.08	0.3773	4.7	97.3
IPCA7	10	1468638.8	146864.7	0.76	0.6673	2.7	100

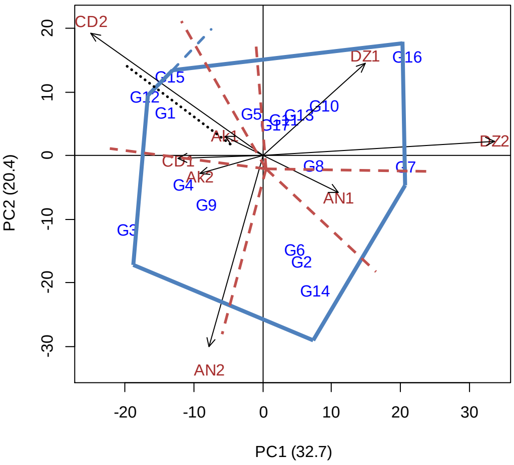

Fig 2. Plot of IPCA1 versus IPCA2 scores. G1 – G17 with blue color represent genotypes while environments are represented by two letters and numbers in red color. The details of the genotypes and environments are presented in tables 3 and 4.

Table 3. Performance and stability of 17 chickpea genotypes based on mean grain yield (kg/ha), PC1, PC2 scores and AMMI stability value (ASV).

Genotype	G-Mean	G-PC1	G-PC2	ASV	YSI	Rank ASV	Rank YSI
G1	2953	-14.23	7.06	19.37	16	11	5
G2	2453	5.53	-16.39	17.83	26	10	16
G3	2974	-19.67	-11.47	27.44	20	16	4
G4	2562	-11.50	-4.37	15.22	22	8	14
G5	3090	-1.73	6.94	7.28	4	3	1
G6	2753	4.55	-14.52	15.63	21	9	12
G7	2673	20.69	-1.46	26.27	28	15	13
G8	2825	7.35	-1.32	9.41	12	4	8
G9	2558	-8.25	-7.40	12.81	21	6	15
G10	3062	8.90	8.06	13.87	9	7	2
G11	2770	3.16	5.90	7.13	12	2	10
G12	2852	-17.06	9.51	23.62	20	14	6
G13	2762	5.23	6.76	9.47	16	5	11
G14	3002	7.66	-21.04	23.17	16	13	3
G15	2842	-13.40	12.75	21.24	19	12	7
G16	2798	20.94	15.82	30.89	26	17	9
G17	2439	1.83	5.17	5.66	18	1	17

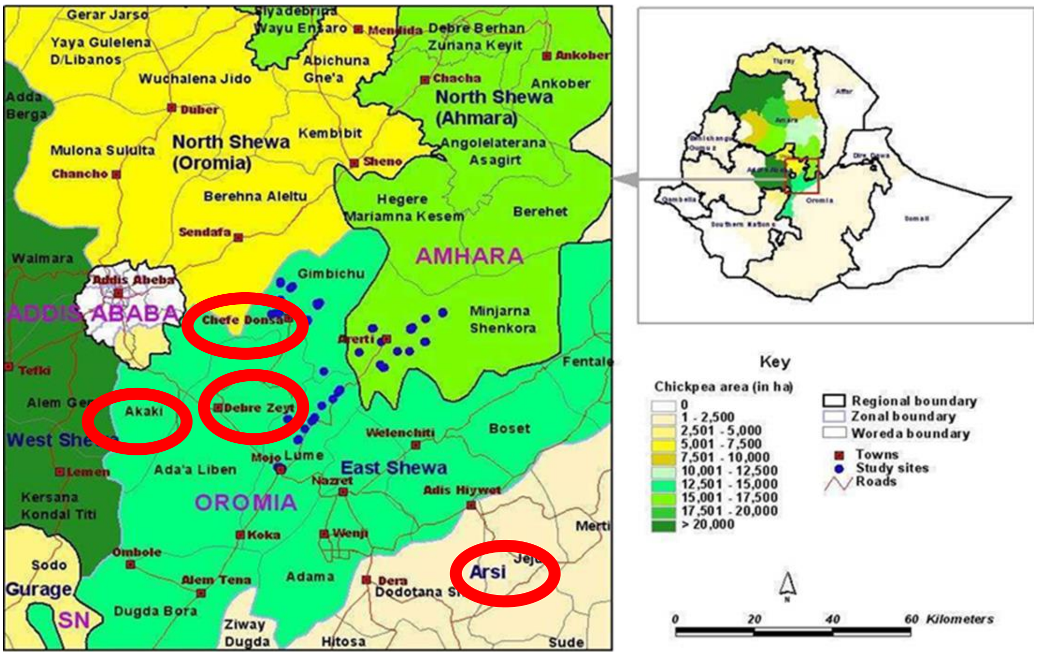

Fig 3. Study sites and distribution of area (ha) under chickpea production in Ethiopia.

interaction. Adaptation behavior of these genotypes was also specific; G3 which had a large negative IPCA1 value was more adaptive to CD1 environment with large negative IPCA1 value; G12 and G15 were both adaptive to CD2 environment with large negative IPCA1 score. G16 was adaptive to DZ1, G7 to DZ2 and G14 to AN1 with corresponding large positive IPCA1 scores.

The environments showed variability in both main effects and interactions (Fig 1). Based on yield performance, environments were categorized as either high or low yielder. Environments CD2, CD1, AK2, and DZ1and AN2 were higher yielders than grand mean while DZ2, AN1 and AK1 were low yielders. Based on their distribution on biplot graph (Fig 1) four environment categories (EC) were identified:

EC-1 consisted of one environment (DZ1), had large positive IPCA1 and IPCA2 and therefore had high interactions. The fourth highest yield (3212 kg ha^{-1}) response was obtained from this environment implying a fairly high yield attribute.

EC-2 consisted of environments located on quadrant II (DZ2 and AN1). This category had medium to large positive IPCA1 and small negative to positive IPCA2 scores, thereby contributing high interaction to GxE.

EC-3 consisted of one environment (AK1) that was located on quadrant III and had small negative IPCA1 and small positive IPCA2 score implying that the environment was less interactive (more stable) with lower yield (1354 kg ha^{-1}) response.

EC-4 had environments such as CD2, CD1, AK2 and AN2 which were located on the fourth quadrant of the AMMI1 biplot. This group had medium to large negative IPCA1 and wide range of large negative to large positive IPCA2 scores ranging between -33.46 to 21.42, thereby contributing high interaction to GxE. The highest yield (3582 kg ha^{-1}) response was observed in this category. Thus, the biplot indicated CD2 as the highest yielding environment and AK1 as the lowest.

Table 4. Performance and stability of 8 test environments based on mean grain yield (kg/ha), PC1, PC2 scores and AMMI stability value (ASV).

Environment	Mean	IPCA1	IPCA2	ASV	YSI	Rank ASV	Rank YSI
AK1	1354	-5.41	3.35	7.63	9	1	8
AK2	3222	-9.06	-3.10	11.90	5	2	3
AN1	2201	10.95	-6.39	15.28	10	3	7
AN2	3017	-7.84	-33.46	34.90	11	6	5
CD1	3288	-12.26	-0.46	15.55	6	4	2
CD2	3582	-24.87	21.42	38.11	8	7	1
DZ1	3212	14.85	16.06	24.74	9	5	4
DZ2	2416	33.64	2.57	42.71	14	8	6

Table 5. Mean response of five genotype categories (GC) to eight environments (E), range of IPCA1 and IPCA2 scores.

GC	Genotypes	Mean(kgha^{-1})	ASV range	IPCA1 range	IPCA2 range
GC 1	G10, G14, G8,G16	2922	9.14 to 30.89	8.9 to 20.94	-21.04 to 8.06
GC 2	G2, G13, G6, G7	2723	9.47 to 26.27	5.23 to 20.69	-16.39 to 6.76
GC 3	G4.G9	2560	12.81 to 15.22	-8.25 to -11.5	-7.4 to -4.37
GC 4	G3, G1, G12, G15	2905	19.37 to 27.44	-13.4 to -19.67	-11.47 to 12.75
GC 5	G5, G11, G17	2766	5.66 to 7.28	-1.73 to 3.16	5.17 to 6.94

Table 5. Description of chickpea genotypes used in the study.

Trial Code	Original Name	Genotype code	Remark
DZ-2012-Ck-0027	ICCV-09108	G1	Advanced breeding line
DZ-2012-Ck-0028	ICCV-07104	G2	Advanced breeding line
DZ-2012-Ck-0029	ICCX-060039F3P65-BP	G3	Advanced breeding line
DZ-2012-Ck-0030	ICCX-060039F3P38-BP	G4	Advanced breeding line
DZ-2012-Ck-0031	ICCV-10107	G5	Advanced breeding line
DZ-2012-Ck-0032	ICCV-10102	G6	Advanced breeding line
DZ-2012-Ck-0033	ICCRIL-03-0208	G7	Advanced breeding line
DZ-2012-Ck-0034	ICCX-060045F3P203-BP	G8	Advanced breeding line
DZ-2012-Ck-0035	ICCX-060039F3P44-BP	G9	Advanced breeding line
DZ-2012-Ck-0036	D058	G10	Advanced breeding line
DZ-2012-Ck-0037	D051	G11	Advanced breeding line
DZ-2012-Ck-0038	ICCV-10108	G12	Advanced breeding line
DZ-2012-Ck-0039	ICCV-10103	G13	Advanced breeding line
DZ-2012-Ck-0040	ICCV-08111	G14	Advanced breeding line
Natoli	ICCX-910112-6	G15	Released variety
Minjar	ICCV-03107	G16	Released variety
Local	DZ-10-11	G17	Released variety

Table 6. Description of the test environments.

Location	Altitude	Longitude	Latitude	Year	Environment code	Rainfall (mm) (Aug.-Dec.)
Akaki	2339	38.75°E	8.96°N	2012/2013	AK1	350
				2013/2014	AK2	276
Chefe Donsa	2410	39.12°E	8.97°N	2012/2013	CD1	490
				2013/2014	CD2	489
Debre Zeit	1900	38.98°E	8.75°N	2012/2013	DZ1	360
				2013/2014	DZ2	221
Arsi Negele	1913	38.66°E	7.35°N	2012/2013	AN1	152
				2013/2014	AN2	131

The chickpea genotypes also showed wide variability in yield performance. Genotypes and environments with IPCA1 scores of the same sign produce positive interactions effects, while the combinations of IPCA1 scores of opposite signs have negative specific interactions. Five genotype categories (GC) were identified from the biplot generated from this study (Fig 1):

GC1 included four genotypes (G10, G14, G8 and G16) with mean yield of 2922 kg ha^{-1} which was higher than the grand mean (2786 kg ha^{-1}). This group of genotypes had small positive to high positive IPCA1 scores ranging from 8.90 to 20.94 and a wide range of ASV values. They had medium to high interactions and relatively stable yields.

GC2 consisted of four genotypes (G2, G13, G6 and G7) in quadrant II with a mean yield of 2723 kg ha^{-1}(Table 5) which was less than the grand mean. They had small to large positive IPCA1 scores ranging from 5.23 to 20.69, large negative and small positive IPCA2 scores ranging from -16.39 to 6.76 and a wide range of ASV values. These genotypes had small to high interactions with relatively stable low yielding attributes.

GC3 included two genotypes (G4 and G9) in quadrant III with a mean yield response of 2560 kg ha^{-1}, which is much less than the grand mean. This group of genotypes had -8.25 to -11.5 IPCA1 scores range and relatively small negative IPCA2 scores ranging from -7.4 to -4.37. They showed medium range of ASV values. They had moderate interactions and hence were highly unstable across the environments but well adapted to low yielding environments

GC4 consisted of four genotypes (G3, G1, G12 and G15) in quadrant IV with the highest mean yield of 2905 kg ha^{-1}. This group had large negative IPCA1 scores of -13.4 to –19.67, large negative and large positive IPCA-2 score ranging from -11.47 to 12.75, large ASV value, and were well adapted to the high yielding environments such as CD2. This genotype group had high interactions and hence had specific adaptation performance.

GC5 consisted of the three genotypes (G5, G11 and G17) with considerable mean yield of 2766 kg ha^{-1}, which is very close to the grand mean (2786 kg ha^{-1}). This group had the smallest negative and positive IPCA-1 scores, ranging from -1.73 to 3.16 and small positive IPCA2 scores ranging from 5.17 to 6.94, smallest ASV value, and were well adapted to the environment. This genotype group was less interactive, and hence was highly stable across tested environments.

AMMI stability value (ASV) for measuring quantitative stability

A genotype with the least ASV score is considered the most stable; therefore, genotype G17 was the most stable followed by G11 and G5. Despite being the most stable, G17 showed the least grain yield performance of the 17 genotypes. It follows that, stability alone cannot be the basis for screening and selection of genotypes for release since some genotypes are stable for poor yields across environments (Yan and Kang, 2003) and selecting them would lead to development of a variety which is consistently low-yielding.

AMMI2 biplot for demonstrating the magnitude of GxE

Genotypes G12, G15, G16, G7, G14, G3 and environments CD2, DZ1, DZ2 and AN2 were the least responsive/interactive based on their far distance from the origin on the AMMI2 biplot. Genotypes G17, G11 and G5 which were close to the origin were considered non-sensitive to environmental interaction.

The relationships among and between environments and genotypes on the graph of AMMI2 biplot help to predict relative performance of a given genotype in a given environment by drawing connecting segments (blue line) between all the genotypes located at the outer side and then creating lines from the origin (0, 0) that cut these segments perpendicularly (i.e. the red dotted line is perpendicular to the green line) as shown in Fig 2. If any environment point lies on the red dotted line, genotypes found at the two ends of the segment will produce equal yields in that environment. On the other hand, if an environment point lies on one side of the red line, the closer genotype will produce a higher yield in that environment (Yan and Kang, 2003; Yan and Manjit, 2002; Yan et al., 2000). Thus, genotypes in the current study were assigned to their adaptive environments.

On the segment formed by G15,G16 genotype G10, G13, G11, G13, G17 and G16 were the most adapted to environment DZ1. DZ1 was located in quadrant I on the AMMI1 biplot graph (Fig 1) which is the ideal location for the highest yielder and most stable genotypes and environments. AMMI2 biplot graph therefore confirms these genotypes as most adapted to this environment (DZ1). Genotypes G7 from segment G16-G7 and G8 from segment G7-G14 were most adapted to environments DZ2 and AN2 since they were located closer to the two environments on AMMI2 biplot. Genotype G14, G2 and G6 were adapted to environment AN2, while G3, G9 and G4 were adapted to environments AK2 and CD1. G12 and G1 were most adapted to environment AK1 whereas genotypes G15 and G5 were most adapted to environment CD2.

Selective nature of the environment can be determined by its scores from AMMI model. Environments with large IPCA scores are more discriminative of genotypes, while environments with IPCA scores near zero exhibit little interaction across genotypes and less discrimination among genotypes. In this regard, CD2, DZ2 and AN2 are most discriminative as indicated by long distance from the origin of the biplot graph (Fig 2). Genotypes with positive IPCA1 scores respond positively (adaptable) to the environments that have positive IPCA1 scores (i.e. their interaction is positive). Those that respond negatively to the environments (less adapted) have negative IPCA1 scores (Samonte et al., 2005). The biplot revealed that the genotypes G2, G13, G6, G7, G10, G14, G8, G16, G17 and G11 with positive IPCA1 scores responded positively to the environments AN1, DZ1 and DZ2 and hence are adaptable to these environments. Similarly, genotypes G3, G1, G12, G15, G4, G9 and G5 with negative IPCA-1 scores are adapted to the environments CD2, CD1, AK2, AN2 and AK1.

Materials and Methods

Plant materials

The experiments were conducted at four locations representing major chickpea producing areas of Ethiopia for two cropping years (2012/2013 and 2013/2014) resulting in 8 environments. Seventeen genotypes consisting of 14 advanced lines (G1-G14) and three released varieties (G15 – G17) were used as experimental materials (Table 6). The experiments were carried out in a randomized complete block design (RCBD), with four replications. The description of test locations is provided in Table 7 and Fig 3. Each plot consisted of four rows of 4 meter length and the spacing was 30 cm between and 10 cm within rows. Data on seed yield was taken from the middle two rows of each plot. At harvest seed yield was determined for each genotype at each test environments.

Biometrical genetic analysis

AMMI model

The AMMI model equation for ith genotype in jth environment in r blocks (replication) formulated by Gauch, (1992) was used to analyze GxE interactions.

$$Y_{ijr} = \mu + G_{\mathrm{i}} + E_j + B_r\,(E_j) + \sum_{\mathrm{k=1}}^{\mathrm{n}} \lambda_k \gamma_{jk}\, \alpha_{en} + P_{ij} + \varepsilon_{ij}$$

Where Y_{ijr} is the yield of genotype (i) in environment (j) for replicate (r), μ is the total yield mean, G_i is the main effect of genotype or the genotype (i) mean deviation (genotype mean minus total yield mean), E_j is the main effect of environment or the environment (j) mean deviation, $B_r\,(E_j)$ is the effect of the block r within the environment j, r is the number of blocks, λ_k is the singular value for IPCA axis k (k is the number of remain IPCA axis in AMMI model) γ_{jk} and α_{jk} are the genotype (i) environment (j) eigen vector value (i.e. the left and right singular vectors) for IPCA axis k, P_{ij} is the residual containing all multiplicative terms not included in the model, n is the number of axes or principal components (IPCA) retained by the model, and ε_{ij} is the experimental error, assumed independent with identical distribution.

Calculations were performed using R software version 3.1.3 using the full data (including all replicates data) for AMMI model. In addition to this, the AMMI stability value (ASV) as described by Purchase, 2000 was calculated as follows:

$$\sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}}(IPCA1_i)\right]^2 + (IPCA2_i)^2}$$

Where $\frac{SS_{IPCA1}}{SS_{IPCA2}}$ is the weight given to the IPCA1-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares, $IPCA1_i =$ IPCA1 score of the i^{th} genotype and $IPCA2_i$ = IPCA2 score of the i^{th} genotype. The larger the IPCA score, either negative or positive, the more specifically adapted a genotype is to certain environments. Smaller ASV scores indicate a more stable genotype across environments.

Another component of stability in AMMI model is yield stability index (YSI) and was calculated as: YSI = rASV+ rY where, rASV is the rank of AMMI stability value and rY is the rank of mean grain yield of genotypes (rY) across environments. YSI incorporates both mean yield and stability in a single criterion. Low values of this parameter show desirable genotypes with high mean yield and stability.

Conclusion

Stability and adaptation of chickpea genotypes were analyzed over eight environments using AMMI models to select stable genotypes in major chickpea producing areas of Ethiopia. Genotypes G5 with mean yield of 3090 kg ha^{-1}(highest) and G11 with mean yield of 2770 kg ha^{-1} (comparable to grand mean 2786 kg ha^{-1}) were found to be stable and adaptable to all environments. Genotypes which were distributed in the first quadrant of AMMI I biplot showed high level of yield performance in under ideal environments. Based on the results of this study and other traits, genotypes G5 was released and registered as a new variety, 'Dimtu' in 2016 for promotion and production in chickpea growing areas of Ethiopia.

Acknowledgment

The authors acknowledge the technical staff of Debre-Zeit Agricultural Research Center for their support during data collection. This study was conducted jointly by Debre-Zeit Agricultural Research Center, the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) and The International Center for Agricultural Research in Dry Areas (ICARDA). Financial support coming through the Ethiopian Federal Ministry of Agriculture, CGIAR Research Program on Grain Legumes (CRP-GL) and Tropical Legumes Projects (TL2 and TL3) are hereby acknowledged.

References

Adugna A (2007) Assessment of yield stability in sorghum. Afr Crop Sci J. 15(2):83 – 92.

Anbessa Y, Bejiga G (2002) Evaluation of Ethiopian chickpea landraces for tolerance to drought. Gen Res and Crop Evol. 49(6):557-64.

Annicchiarico P (1997) Additive main effects and multiplicative interaction (AMMI) analysis of genotype-location interaction in variety trials repeated over years. Theor Appl Gen. 94(8): 1072-1077.

Bejiga G, Tullu A, Tsegaye S (1994) Effect of sowing date and seeding rate on the yield and other characters of chickpea (*Cicer arietinum* L.). Eth J Agric Sci. 14: 7-14.

Bose LK, Jambhulkar NN, Singh ON (2014) Additive main effects and multiplicative interaction (AMMI) analysis of grain yield stability in early duration rice. J Anim Plant Sci 24(6):1885-1897.

Carbonell SA, Filho JA, Dias LA, Garcia AA, Morais LK (2004) Common bean genotypes and lines interactions with environments. Sci Agric. 61:169-177.

Central Statistical Authority (CSA) (2015). Agricultural Sample Survey, 2014/15. Results on Area, Production and Yield of Major Crops by Sector and Season. Statistical bulletin 171. Addis Ababa, Ethiopia.

Eberhart SAT, Russell WA (1966) Stability parameters for comparing varieties. Crop Sci. 6(1): 36-40.

FAOSTAT (2016) Agriculture Organization of the United Nations. Statistics Division. http://faostat3.fao.org/ download/Q/QC/E (accessed 24.10.16).

FAOSTAT (2014) Agriculture Organization of the United Nations. Statistics Division. http://faostat3.fao.org/ download/Q/QC/E (accessed 14.02.16).

FAOSTAT (2013) Food and agriculture organization of the United Nations. Statistical database. http://faostat3.fao.org/ download/Q/QC/E (accessed 14.02.16).

Gauch HG (2006) Statistical analysis of yield trials by AMMI and GGE. Crop Sci. 46(4): 1488-1500.

Gauch HG (2013) A simple protocol for AMMI analysis of yield trials. Crop Sci. 53(5): 1860-1869.

Gauch HG, Zobel RW (1996) AMMI analysis of yield trials. In: Kang MS, Gauch HG (Eds) Genotype by Environment Interaction. pp. 85–122.

Gauch HG (1992) Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Elsevier Science Publishers. Amsterdam, The Netherlands. 278 pp.

Hongyu K, Garc M (2014) Statistical analysis of yield trials by AMMI analysis of genotype x environment interaction. Biometrical Letters. 51(2): 89–102.

Kanouni H, Farayedi Y, Saeid A, Sabaghpour SH (2015) Stability analyses for seed yield of chickpea (*Cicer arietinum* L.) genotypes in the Western cold zone of Iran. J Agr Sci. 7(5):219-230.

Kempton RA (1984) The use of biplots in interpreting variety by environment interactions. The J Agri Sci. 103(01): 123-135.

Farshadfar E, Mahmodi N, Yaghotipoor A (2011) AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (*Triticum aestivum* L.). Aust J Crop Sci. 5(13):1837-1844.

Osiru MO, Olanya OM, Adipala E, Kapinga R, Lemaga B (2009) Yield stability analysis of *Ipomoea batatus* L. cultivars in diverse environments. Aust J Crop Sci. 3(4): 213-220

Padi FK (2007) Genotype × environment interaction and yield stability in a cowpea-based cropping system. Euphytica 158(1-2): 11-25.

Purchase JL, Hatting H, Vandeventer CS (2000) Genotype × environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: Π. Stability analysis of yield performance. South Afric J Plant Soil 17: 101-107

Purchase JL (1997) Parametric analysis to describe genotype x environment interaction and yield stability in winter wheat: 1997 (Doctoral dissertation, University of the Orange Free State).

Rashidi M, Farshadfar E, Jowkar MM (2013) AMMI analysis of phenotypic stability in chickpea genotypes over stress and non-stress environments. Int J of Agri Crop Sci. 5: 253-260.

Samonte SOPB, Wilson LT, McClung AM, Medley JC (2005) Targeting cultivar onto rice growing environments using AMMI and SREG GGE biplot analyses. Crop Sci. 45:2414-2424.

Tai GCC (1979) Analysis of genotype-environment interactions of potato yield. Crop Sci. 19(4): 434-438.

Thangavel P, Anandan A, Eswaran R (2011) AMMI analysis to comprehend genotype-by-environment (G × E) interactions in rainfed grown mungbean (*Vigna radiata* L.). Aust J Crop Sci. 5(13): 1767-1775.

Yan W, Istvan R (2002) Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Sci 42(1):11-20.

Yan W and Kang MS (2003) Biplot analysis: A graphical tool for breeders, geneticists and agronomists. CRC Press, Boca Raton, FL 631.52/Y921.

Yan W, and Kang MS (2002) GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. CRC press.

Yan W, Hunt LA, Sheng Q, Szlavnics Z (2000) Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci. 40(3): 597-605.