Stability Analysis in Chickpea Genotype Sets as Tool for Breeding Germplasm Structuring Strategy and Adaptability Scoping

***Asnake Fikre[1,2], Assefa Funga[2], Lijalem Korbu[2], Million Eshete[2], Niguse Girma[2], Asrat Zewdie[2], Dagnachew Bekele[2], Redwan Muhamed[2], Ketema Daba[3] and Chris Ojiewo[2]**

[1] International Crops Research Institute for the Semi-Arid Tropics (ICRISAT-Ethiopia)
E-mail: A.Fikre@CGIAR.org, Addis-Ababa, Ethiopia;
[2] Ethiopian Institute of Agricultural Research; [3] University of Saskatoon

Abstract

Chickpea research program has come across realizing the importance of restructuring the working germplasm pool in Ethiopia where we have 39 divergent agroecological zones (AEZ). Though chickpea is not suit to all, it adapts in more than 30% of the agroecologies having different scale of responses. Hence, as show case we have tried to scan the agroecologies discrimination power based on crop using three sets of bred-crop responses. Evidently enough, germplasms in all the sets have revealed differential responses for economical yield and associated traits, from the three set of 57 entries put under 47 environments. The AMMI stability value and stability index have been able to discriminate genotypes with designated position; and supposed the breeding program would signify values by attempting both environment and genetics still as key considerable factors.

Keywords: Adaptability, Agro-ecology, Breeding, Genotype, stability

Introduction

Chickpea (*Cicer arietnum* L) in Ethiopia is crop on a high moment of development and transformed from simple precursor to principal crop of the producing households. Ethiopia as secondary center of diversity (van-der-Maesen, 1987) is making advantage in developing the chickpea industry faster and bolder by time. Unlike the altitudinal range (1400-2800 m asl) suggested by Anbessa and Bejiga (2002), the crop adaptation range has verified to expand further to thermal zones where the altitude goes down to 600m asl with reasonable yield in Afar (Semera and Werer) and South Ethiopia (Woito) demonstrating high yield of more than 2 tons/ha (Shimelis, 2017). This would at least double the command area of suitability of the crop in magnitude of multimillion hectares.

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). This make Ethiopia one of the high productive geography as it demonstrated doubling value of the global average. However, the yield potential of chickpea in Ethiopia still is verified to hit 6t/ha (Asnake, 2016) of course under optimal genetics x management x environment combination.

Classical breeding programs extensively employ the effect of genetics and environment as drivers of genotypic responses and eventually determines their outcome of characterization and evaluation. Response traits could be varying in the germplasm resources, that breeding programs employ structuring depending on the objectives of the study. Genotype evaluation for traits of interest using multiple locations and years often pose complication of selection as the interaction of G x E could leads to unpredicted outcome (Farshadfar *et al*., 2012). The yield stability evaluation based on genotype by year or genotype by location by year interaction (G x E x Y) is a good selection parameter (Annicchiarico, 1997); and would lead to stratification of the genotypes on narrow base adaptability or wider adaptability. In Ethiopian chickpea some 25% of the released varieties have been developed for specific regional adaptation, as they are released by the RARIs. 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 Russell, 1966; Tai, 1979). The other commonest 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 genotypes 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 managing GxE interaction in which its applicability depends on the experimental data, the number of environments, and the accuracy of collected data and environmental information. In this study, we used The Additive Main effects and Multiplicative Interaction (AMMI) a widely applicable model that combines analysis of variance (AOV) to partition the genotype main effects, environment and their interaction in yield stability analysis as its reliability recently been forwarded (Hongyu and Garc, 2014). Moreover, AMMI provides an initial diagnosis of the model and is well-suited for data analysis with many environmental influences. It also allows greater unfolding of the G×E interaction and summarizes the patterns and relationships between genotypes and environments, and improves the

accuracy of trait estimates (Gauch, 1988; Zobel et al., 1988; Crossa et al., 1990). Using AMMI stability value and mean yield, YSI incorporates both mean yield and stability in a single criterion. Low value of this parameter shows desirable genotypes with high mean yield and stability. The objectives of this study were (i) to identify genotypes in the three sets that have both high mean yield and stable yield performance across different environments, (ii) to study the relationships, similarities and dissimilarities among yield–stability statistics that is implicated on genotypes structuring

Materials and Methods

Description of eco-location and genotypes

A study was undertaken by the national chickpea research program using germplasms of different genetic background to determine their level of stability and consistency in their biological yield responses. Fifty-seven advanced breeding genotypes in three sets (Table 2) together with appropriate checks were evaluated each over three seasons between 2008 and 2010 at eight diverse elevations (1500's m asl to 2400's m asl) eco-locations (Table 1). In the three years a total of 47 environments, however, some locations shared among the three sets have been considered. The experiments were put under three independent sets (desi types set (A), kabuli type early set (B), late set (C)) using Randomized Complete Block Design (RCBD) with independent and combined analysis for each set of genotypes. Each genotype was planted in 30cm by 10cm inter and intra row spacing in three replications. Production was all under rain fed condition. The eco-climatic characteristics of the research locations are presented in Table 1.

Table 1: Characteristic features of test eco-locations

Research Location	Altitude /m asl/	Rainfall mean /mm/	Temp. mean /^{0}C/ min and max	Soil
Debre Zeit /DZ/	1900	851	8.9-28.3	Vertisol
Alem Tena /AT/	1575	728	12.9-29.8	Sandy-loam/light
Chefe Donsa /CD/	2450	750-1200	7-26	vertisol
Sinana /Sin/	2400	1150	9-21	Nitosol
Minjar/Min/	1810	600-1000	10-28	Light vertisol
Akaki/Ak/	2200	1025	7-26	vertisol
Arsi Negele /AN/	1913	915	17.7	Sandy-loam
Dhera/Dh/	1650	680	14-27.8	Silty loam/andosol/
Arsi Robe /AR/	2420	890	6-22.1	Heavy clay/vertisol/
Adet /Ad/	2240	1270.5	8-25	Nitosol
Ambo /Am/	2175	1018.29	10.02-26.89	vertisol
Hawassa /Haw/	1700	1141	13.1-27.1	Light soil

Table 2. Over location performance of set genotypes over test year1, year 2 and year 3 of 2008, 2009 and 2010 respectively [eco-locations suffix 1, 2, 3 indicates the test year]

	Over location yield performance test Desi late= Set A [DZ1-AK1-CD1-Sin1-DZ2-AK2-CD2-AR2-Ad2-DZ3-AK3-CD3-AM3]	**Over location yield performance test kabuli early=Set B** [Min1-AT1-DZ1-AN1-DH1-Min2-AT2-DZ2-Haw2-DZ3-Min3-AN3]	**Over location yield performance test kabuli =Set C** [AK1-CD1-DZ1-Min1-Sin1-AK2-CD2-DZ2-AN2-Ad2-AM2-AR2-HaW2-AK3-CD3-DZ3-AN3-Min3]
1	Akaki	Chefe	Chefe
2	ICC-3195	DZ-10-4	DZ-10-4
3	ICCV-00104	FLIP 00-60C	FLIP 01-12C
4	ICCV-00110	FLIP 00-73C	FLIP 01-21C
5	ICCV-00202	FLIP 01-16C	FLIP 01-40C
6	ICCV-03103	FLIP 01-29C	FLIP 01-45C
7	ICCV-03107	FLIP 01-2C	FLIP 01-46C
8	ICCV-03203	FLIP 01-56C	FLIP 01-52C
9	ICCV-04111	FLIP 02-25C	FLIP 01-57C
10	ICCV-92219	FLIP 02-39C	FLIP 01-58C
11	ICCV-95138	FLIP 02-46C	FLIP 01-60C
12	ICCV-97030	Teji	FLIP 01-7C
13	ICCX-910121-5	X96TH-52-14/2000	FLIP 01-8C
14	ICCX-910144-4	X98TH-51-1-3	FLIP 02-02C
15	ICCX-940002-F5-242P-1-1-1	X98TH-81-2	FLIP 02-11C
16	ICCX-940002-F5-294P-1-1-1	X98TH-82-4	FLIP 02-22C
17	ICCX-940002-F5-335P-1-1-1	X98TH-82-7	FLIP 98-218C
18	ICCX-940002-F5-6P-1-1-1		Habru
19	ICCX-940002-F5-88P-1-1-1		ICCV-04305
20			ICCV-04307

Statistical analysis

AMMI analysis

The grain yield data were subjected to combined analysis of variance and AMMI analysis which is a combination of analysis of variance and multiplication effect analysis. AMMI analysis of variance was used to partition total sum of squares into its components: genotype and environment main effects, GxE interaction and the residual term. Subsequently, multiplication effect analysis is used to partition GxE deviations into different interaction principal component axes (IPCA), which can be tested for statistical significance through ANOVA.

The AMMI model equation for i^{th} genotype in j^{th} environment in r blocks (replication) formulated by Gauch, (1992) was used to analyze G x E interactions as;

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

Where $Yijr$ is the yield of genotype (i) in environment (j) for replicate (r), μ is the total yield mean, Gi is the main effect of genotype or the genotype (i) mean deviation (genotype mean minus

total yield mean), Ej is the main effect of environment or the environment (j) mean deviation, Br (Ej) is the effect of the block r within the environment j, r is the number of blocks, k is the singular value for IPCA axis k (k is the number of remain IPCA axis in AMMI model) γjk and jk are the genotype (i) environment (j) Eigen vector value (i.e. the left and right singular vectors) for IPCA axis k, Pij 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 εij is the experimental error, assumed independent with identical distribution

We considered stability parameters based on Farshadfar *et al*. (2011), which affirmed that Yield stability index (YSI) which incorporate AMMI stability value (ASV) and mean grain yield in a single non-parametric index, and Rank sum as explained by sum of rank mean (R) plus standard deviation of ranks (SDR), were found the most desirable indices for discriminating the most stable genotypes with high grain yield.

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

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}}\left(IPCA1_{score}\right)\right]^2 + \left(IPCA2_{score}\right)^2}$$

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, IPCA1i= IPCA1 score of the i^{th} genotype and IPCA2i = 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

AMMI 2 biplot for demonstrating the magnitude of GxE

Genotypes and environments, in the three sets, were overlaid on the biplot and their responsiveness was drawn

based on their distance from the reference origin on the AMMI 2 biplot. Genotypes which are close to the origin are considered non-sensitive to environmental interaction.

The relationships among and between environments and genotypes on the graph of AMMI 2 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). 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 et al., 2000; Yan and Kang, 2002; Yan and Kang, 2003).Thus, genotypes in the current study were judged based on their discriminative environments for adaptation or suitability.

Results and Discussion

Adaptive response of yield by environment

Three analytical evidences ANOVA, AMMI biplot ASV (AMMI Stability Value) and YSI (Yield Stability Index) have been done across the three experimental sets and used as support of the discussion. Combined analysis of variance (Table 3) of environment (year + location) by genotypes resulted in highly significant differences ($P \leq 0.01$) in their interaction for the three sets. The significant interactions of genotypes × environments (locations and years) suggest that grain yield of genotypes varied across environments. Similarly, there are differential responses of the genetic constituents. Significant differences for genotypes, environments and GE interaction indicated the effect of environments in the GE interaction, genetic variability among the entries and the possibility of selection for narrow base or wider based adaptability genotypes. It was reported that GE interaction in multi-locations within a year is more important than GE interaction with year (Chandra *et al*., 1974). As GE interaction was significant, therefore we can further proceed and estimate phenotypic stability (Farshadfar and Sutka, 2006).

Table 3: ANOVA Table for National Variety Trial of Desi, early Kabuli and late Kabuli chickpea sets evaluated across diverse agro ecologies.

Set A (D)	Df	Sum Sq	Mean Sq value	F	Pr(>F)	Remark
ENV	17	2548388156	149905186	121.8507	< 2.2e-16 ***	
REP(ENV)	53	65202523	1230236	5.9941	< 2.2e-16 ***	Coeff var: 17.5
GEN	19	62856597	3308242	16.1187	< 2.2e-16 ***	Mean YLD: 2595.2
ENV:GEN	323	322211444	997559	4.8604	< 2.2e-16 ***	
Residuals	1647	338035059	205243			
Set B (KE)						
ENV	11	956889433	86989948	194.9231	< 2.2e-16 ***	Coeff var: 19.4
REP(ENV)	24	10710677	446278	2.8248	7.816e-06 ***	Mean YLD: 2054.0
GEN	16	39774570	2485911	15.7349	< 2.2e-16 ***	
ENV:GEN	176	209204374	1188661	7.5238	< 2.2e-16 ***	
Residuals	996	157355455	157987			
Set C (KL)						
ENV	12	1076408410	89700701	68.0685	< 2.2e-16 ***	Coeff var: 14.8
REP(ENV)	39	51394199	1317800	7.5436	< 2.2e-16 ***	Mean YLD: 2830.1
GEN	19	109856180	5781904	33.0979	< 2.2e-16 ***	
ENV:GEN	228	227028264	995738	5.7000	< 2.2e-16 ***	
Residuals	1461	255223890	174691			

Key: ENV= environment, rep= replication, gen= genotypes, df= degree of freedom, pr= probability

Mean grain yield of the three sets of genotypes ranged from 1327 kg/ha in set B to 3057kg/ha in Set C (Table 4) clearly demonstrating the high productivity differences in the Sets for yield scale. Genotypes of annual crops evaluated for grain yield on a multi-locational, multi-year basis frequently show GE interaction that complicates the selection or recommendation of materials. Coping with genotype-year or genotype-location-year interaction effects is possible only by selection for yield stability across environments defined as location-year combinations (Annicchiarico, 1997). If the deriving interest is to get low G x E, interaction as is the case with many programs, the two possibility are either to follow homogeneous environmental cluster, which is difficult to realize (Tai, 1979), or to go for reducing GxE interaction by selecting genotypes with a better stability across a wide range of environments in order to better predict behavior (Yaghotipoor and Farshadfar, 2007), which is the dominant practice of breeding programs. Calculating the account of the total Sum of Squares/TSS/, in all the three sets A, B and C, environment was dominant factor accounting for 76%, 70% and 63%, respectively and followed by the interaction effect as the next high for all, but Set B. This would suggest the existence of the different environment groups conditioned by complex and easily unpredictable parameters. From this parallel analysis of the three sets, interestingly enough, environment is universally dominating factor that highly influences the system with its unpredictability outcomes.

Table 4. AMMI stability value based rankings of genotypes with average yield performances in the three sets.

Set A (D)						Set B (KE)						Set C (KL)					
	ASV	YSI	rASV	rYSI	means		ASV	YSI	rASV	rYSI	means		ASV	YSI	rASV	rYSI	means
G15	9.7	4.0	3.0	1.0	2715.6	G1	19.8	6.0	5.0	1.0	2256.1	G18	8.54	8.00	7.00	1.00	3057.4
G20	27.8	19.0	17.0	2.0	2625.4	G13	17.5	5.0	3.0	2.0	2110.5	G1	7.28	5.00	3.00	2.00	2909.5
G13	26.3	19.0	16.0	3.0	2618.2	G10	41.0	19.0	16.0	3.0	2066.7	G17	13.98	16.00	13.00	3.00	2888.8
G8	22.9	18.0	14.0	4.0	2597.5	G12	25.4	13.0	9.0	4.0	2045.4	G3	3.11	5.00	1.00	4.00	2836.4
G16	21.2	18.0	13.0	5.0	2563.7	G8	18.8	9.0	4.0	5.0	2037.2	G13	6.14	7.00	2.00	5.00	2812.0
G18	3.9	7.0	1.0	6.0	2523.5	G14	31.6	18.0	12.0	6.0	2003.9	G10	15.14	20.00	14.00	6.00	2767.7
G17	12.4	11.0	4.0	7.0	2482.1	G17	23.2	14.0	7.0	7.0	1986.7	G9	16.50	22.00	15.00	7.00	2757.3
G19	20.1	19.0	11.0	8.0	2477.4	G7	24.5	16.0	8.0	8.0	1983.6	G8	11.57	18.00	10.00	8.00	2745.4
G10	20.5	21.0	12.0	9.0	2450.1	G16	38.6	24.0	15.0	9.0	1972.4	G7	10.04	18.00	9.00	9.00	2733.3
G5	16.2	18.0	8.0	10.0	2449.5	G15	28.3	21.0	11.0	10.0	1909.4	G5	7.32	14.00	4.00	10.00	2691.3
G11	9.5	13.0	2.0	11.0	2419.4	G6	22.2	17.0	6.0	11.0	1908.5	G6	12.00	22.00	11.00	11.00	2647.9
G3	18.5	21.0	9.0	12.0	2353.4	G3	5.6	13.0	1.0	12.0	1882.8	G12	27.03	30.00	18.00	12.00	2638.5
G14	23.8	28.0	15.0	13.0	2351.7	G11	25.8	23.0	10.0	13.0	1850.7	G11	8.34	19.00	6.00	13.00	2608.0
G1	15.8	21.0	7.0	14.0	2331.4	G4	33.1	27.0	13.0	14.0	1833.1	G15	13.04	26.00	12.00	14.00	2583.2
G12	29.2	33.0	18.0	15.0	2303.9	G5	17.5	17.0	2.0	15.0	1787.8	G4	21.61	31.00	16.00	15.00	2558.6
G2	19.8	26.0	10.0	16.0	2303.0	G9	37.7	30.0	14.0	16.0	1766.9	G14	9.88	24.00	8.00	16.00	2557.1
G9	14.7	23.0	6.0	17.0	2297.1	G2	48.9	34.0	17.0	17.0	1327.0	G16	7.47	22.00	5.00	17.00	2517.2
G6	30.7	38.0	20.0	18.0	2290.3							G19	41.03	37.00	19.00	18.00	2480.7
G4	14.6	24.0	5.0	19.0	2245.6							G20	26.85	36.00	17.00	19.00	2470.8
G7	30.0	39.0	19.0	20.0	2202.8							G2	42.56	40.00	20.00	20.00	1941.6
												G2	42.56	40.00	20.00	20.00	1941.6

Key: ASV= AMMY stability value, YSI= yield stability index, r= rank

AMMI stability values (ASV) and bi-plot analysis

ASV measure was proposed by Purchase *et al*. (2000) in looking provision for a quantitative stability measure, such a measure is essential in order to quantify and rank genotypes according to their yield stability. In fact, ASV is the distance from zero in a two-dimensional scatter-gram of IPCA1 (interaction principal component analysis axis 1) scores against IPCA2 scores. The distance from zero is then determined using the theorem of Pythagoras (Purchase *et al*., 2000). In ASV method, a genotype with least ASV score is the most stable, accordingly, G18 followed by G11of set A i.e., Desi type, G3 followed by G5 of set B i.e., kabuli early, and G3 followed by G5 of set C i.e., Kabuli late, were the most stable genotypes. In general the importance of AMMI model is in reduction of noise even if principal components do not cover much of the GE sum square (Gauch, 1992; Gauch and Zobel, 1996).

G18, G3, G3, despite being the most stable genotypes of set A, set B and set C, respectively, their respective yield compromise of 7.6%, 19.7%, 7.8% compared with the first rank of YSI, is of particular interest. 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 poorly competent variety.

As far as stability is concerned G18>G11> G15 from experiment set A (Figure 1 and Table 4 set A); genotypes G1, G13 and G10 from experiment set B (Figure 2 and Table 4 set B); genotypes G3, G1 and G13 from experiment set C (Figure 3 and Table 4 set C) were the first three genotypes that were located to the right side of AMMI 1 biplot in decreasing order of the stability value. However, in terms of yield stability index, with some alteration in stability order genotype G15>G18> G17 from set A; from experiment set B genotype G13> G1> G8; and also genotypes from experiment set C G3>G1>G13 had the most desirable trait of high yielding and stability as well.

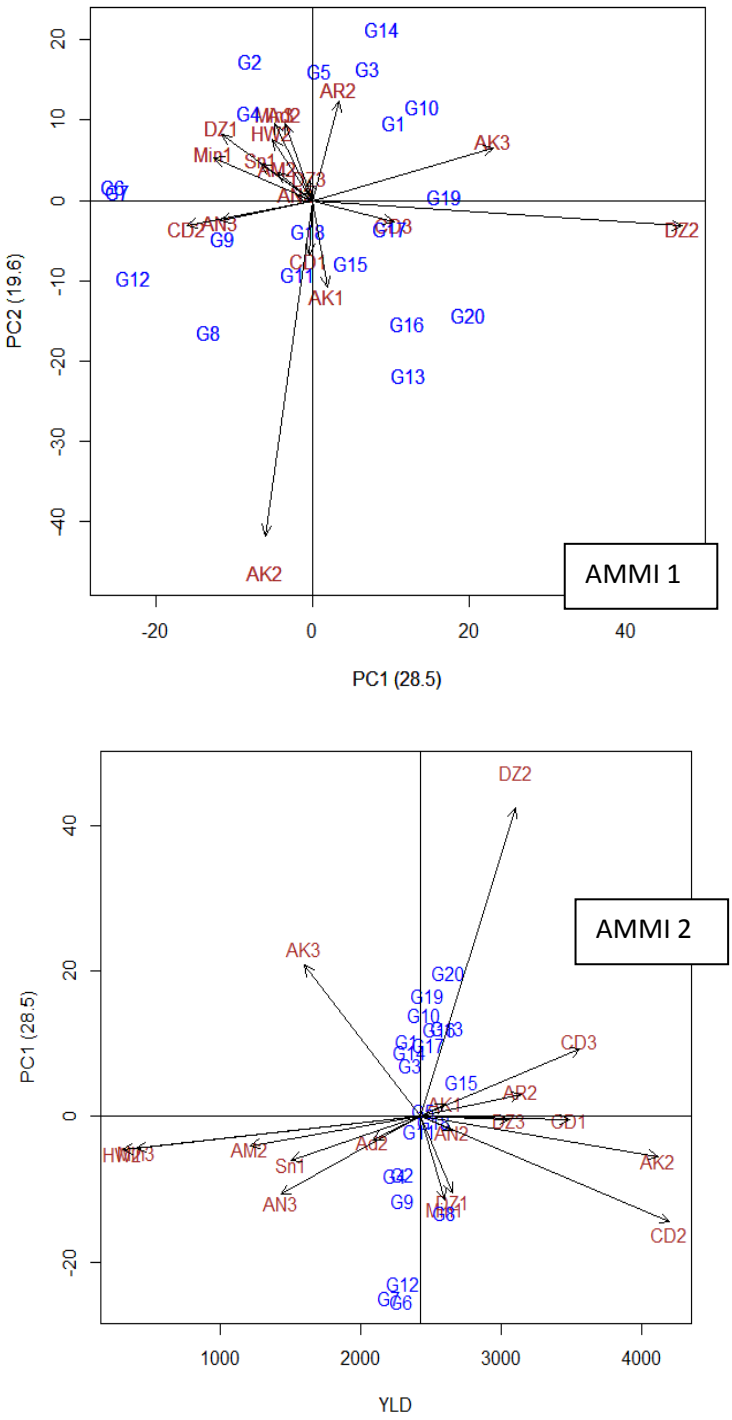

Figure 1. AMMI Biplot for desi chickpea genotypes

Graphical representation of the AMMI 1 biplot for additive and interaction effects

The adaptation habit for most of genotypes of the experiment set A (Desi type late) in figure 1 of AMMI 1 biplot, could be categorized mainly into two with exclusion of the three stable genotypes. The first genotype category comprises of nine genotypes which had positive IPCA1 scores namely G3, G14, G1, G17, G16, G13, G10, G19 and G20 according to increasing order of their interactive nature with environment. The second genotype category consisted of seven genotypes having negative IPCA1 score. Except G8 which had higher yield performance, the remaining six genotypes (G2, G4, G9, G12, G7 and G6) had low yield performance and hence had nothing to be retained in the breeding scheme. Similarly, environments had shown variation in main effect as well as in interaction effect (Figure 1).

According to Duarte and Vencovsky (1999), stability is evaluated in the y-axis (IPCA1) by AMMI1, whereas AMMI2 analysis revealed stable environments and genotypes located near the origin, with low scores for the two axes of the interaction (IPCA1 and IPCA2). On this basis of their effect on yield performance of genotypes; environments were grouped into two groups as high and low yielding. Environments Akaki 2008, Arsi Negelle in year 2009, Minjar in year 2008, Debre Zeit in year 2008, Debre Zeit in year 2010, Debre Zeit in year 2009, Arsi Robe in year 2009, Chefe Donsa in year 2008, Chefe Donsa in year 2010, Akaki in year 2009 and Chefe Donsa in year 2009 were identified as high yielder out of which Akaki in year 2008, Arsi Negelle in year 2009, Debre Zeit in year 2010 and Chefe Donsa in year 2008 were found to be stable environments. Those environments were closely located on the x-axis indicating that they were stable. The second environment group was those environments located on the left side of the Y-axis having low yield performance. Environments Hawassa in year 2009 and Minjar in year 2010 were locations identified with poor yield performance of the genotypes.

On biplot of AMMI 2(Figure 1) genotypes in experiment set A (Desi type) G6, G7, G14, G20, G13, G8 and G12 and environments Debre Zeit in year 2010, Akaki in year 2009, Chefe Donsa in year 2009, Debre Zeit in year 2008, Arsi Robe in year 2009 and Akaki in year 2010 were identified as the most responsive/interactive since they were located far from the origin (0, 0) (Purchase, 1997). On the other hand, genotypes G8, G11 and G15 which were located close to the origin and hence were considered non-sensitive to environmental interaction (Figure 1). The distribution of environments on AMMI 2 biplot were concentrated on quadrate II forming a cluster of environments which most likely influence the performance of genotypes distributed in quadrant II and quadrant IV. It is worth to note that extending vectors formed by

environments to their opposite directions help see the relationships among and between environments and genotypes (Mcdermott & Centre, 2012) . Accordingly, genotypes in quadrant IV (G13, G16, G17and G20) and also genotypes in quadrant II (G2, G4, G6, G7) were influenced by environments AN3, DZ3, AM2,Sn1, Min1, DZ1, HW2, Min2 and Ad2.

AMMI1 biplot presentation (Figure 2) of seventeen chickpea genotype in an experiment set B revealed that two of the genotypes (G5 and G3) were identified as stable lines, though were poor in yield performance. There were only three genotypes (G1, G13 and G10) that performed higher yield over grand mean (2054kg/ha) of all observation. G1 (2256 kg/ha) with the highest yield performance was released variety named Chefe confirming that breeders' capability in developing cultivars with better yield trait, and since none of the genotypes could surpass the check the breeding program need to see into more vigor of genetic combination and recombination. Similarly, yield of the genotypes (in experiment set B) in most of environments (seven out of twelve) was also found to be low (Figure 2).

In contrary to this, environments Debre Zeit in year 2009, Debre Zeit in year 2008, Minjar in year 2009, Debre Zeit in year 2010, and Minjar in year 2008 were high yielding environments among which Debre Zeit in year 2010 was found to be most stable environment. It is important to notice the seasonal influence on physically same location to behave as distinct environment. It is also worth to note that the definition of environment in the current study was referred to as combination of physical attributes of a location and the climatic and other attributes of a specific season (i.e. soil type, fertility, topography, temperature, rainfall, pest/disease challenge) that affect the plant growth (Mcdermott & Centre, 2012).

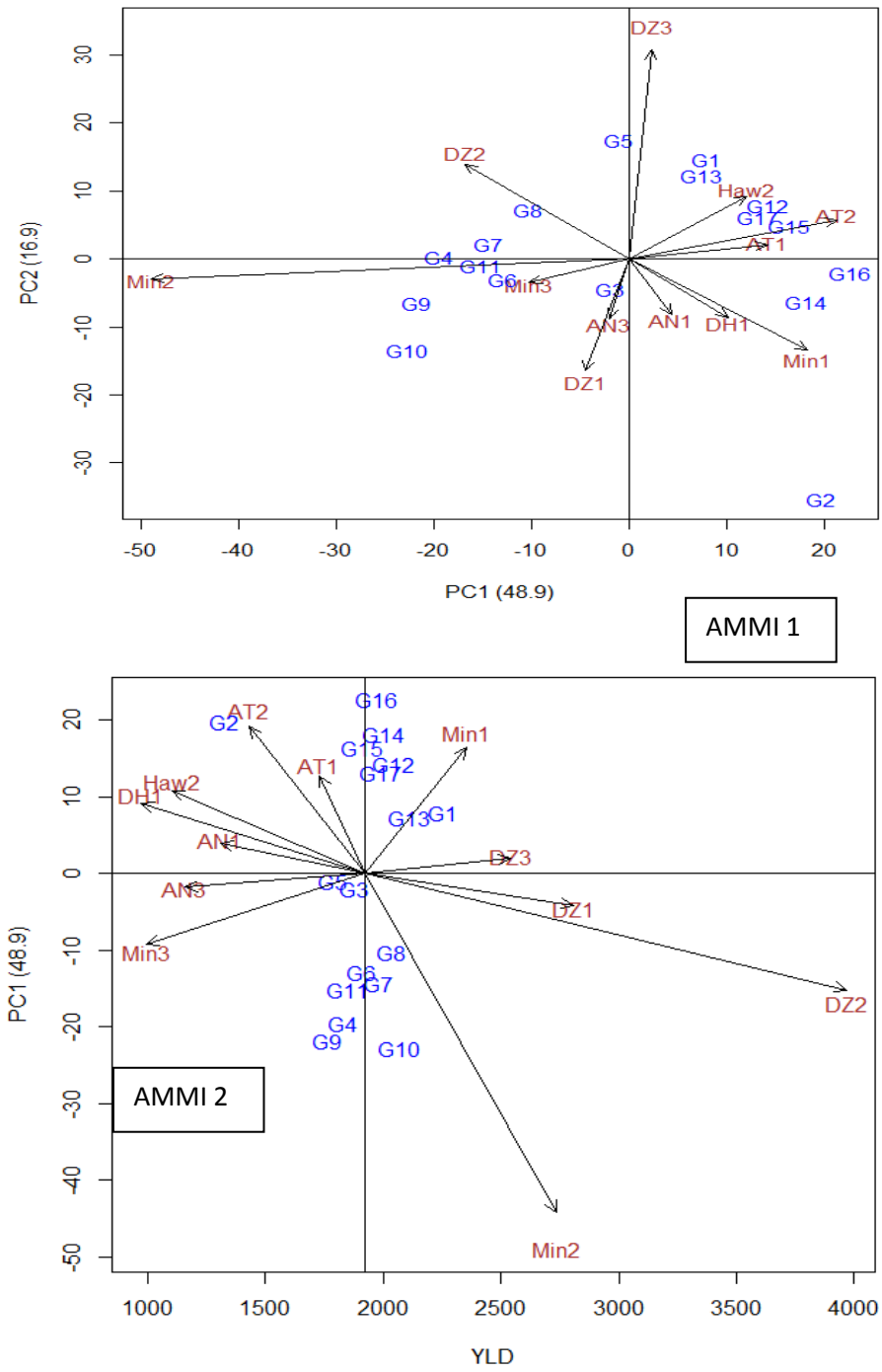

Figure 2. AMMI Bi-plot f or early maturity kabuli chickpea genotypes

Discriminative nature of the environments that would be exerted on genotypes can be determined from the magnitude of IPCA scores (Figure 2). Environments with large IPCA score had more discriminative of genotypes, while environments with IPCA scores near zero exhibit little interaction across genotypes and less discrimination among genotypes (Thangavel *et al*. 2011; Funga *et al*., 2017) . Accordingly, Debre Zeit and Minjar in year 2009 were most discriminative environments as indicated by long distance from the origin of the biplot graph (Figure 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 as stated elsewhere (Samonte *et al.*, 2005).

The AMMI1 biplot (figure 2) revealed that genotypes G1, G13, G17, G12, G15, G14, G16 and, G2 with positive IPCA1 scores responded positively to the environments distributed on the first and second quadrant of AMMI1 biplot regardless of the merit of genotypes. Similarly, genotypes distributed over the third and fourth quadrants of AMMI1 biplot has negative IPCA-1 scores and hence respond positively to the environments located in the same quadrants. For instance, genotypes G8, G6, G7, G11, G4, G9 and G10 respond positively to environments Arsi Negelle in year 2010, Minjar in year 2010, Minjar in year 2009, Debre Zeit in year 2009 and Debre Zeit in year 2008.

Predicting the relative performance of a given genotype in a given environment for this study had no use since there were no new genotypes performing better than the already registered chickpea variety Chefe (G1) (Figure 1 and Figure 2), however, it gives clues on breeding genotypes development and competence. It could also be a case where the genetic composition of the commercial varieties are well constructed, that new approaches need be sought.

There were ten genotypes in experiment set C (Kabuli late type) such as G18, G1, G17, G3, G13, G10, G7, G8, G9 and G5 that performed higher yield than grand mean (2830.1kg/ha) with different stability habit (Figure 3). According to the value of IPCA1 score and ASV score G3 was the most stable line followed by G13. However, the mean yield performance of these two genotypes were at par amount to grand mean (2830kg/ha) which expelled us to find other high yielding genotype using yield stability index (YSI). Accordingly, Genotypes G18, G1, G17 and G3 were identified as high yielding lines in a decreasing order. As a matter of chance, the first two high yielding genotypes (G18 and G1) are released varieties and registered in the Official Varieties Catalogue of Ethiopia as ‘Habru’ and ‘Chefe’. As a result of this, it is not important discussing on the remaining genotypes

because of their poor yield performance instability nature.

However, it is possible to predict the relative performance of a given genotype in a given environment according to the procedure given by Yan and Kang, (2003), Yan and Kang (2002) and Yan et al. (2000). Hence, genotypes in the current study were assigned to their adaptive environments as follow. On segment formed by G2 and G12 on AMMI 2 biplot (Figure 3) the two genotypes (G2, G12) at the vertex had a capacity to give equal yield at Ambo in year 2010 and the other genotypes performed better at environments close in the either side of the dotted line. Similarity, on segment formed by G12 and G19 seven genotypes such as G7, G13, G1, G14, G6, G10 and G12 won at Akaki in year 2009, while G5, G18, G16, G17 and G20 performed better at Debre Zeit in year 2008, Akaki and Debre Zeit in year 2010. On third segment formed by G19 and G2, genotypes G19 and G2 perform at equal magnitude at Akaki and Chefe Donsa in year 2008 since both environments were located on red dotted line. Likewise, G3, G15, and G4 showed specific adaptation at Adet in year 2009, Sinana in year 2008 and Arsi Robe in year 2009 (Figure 3)

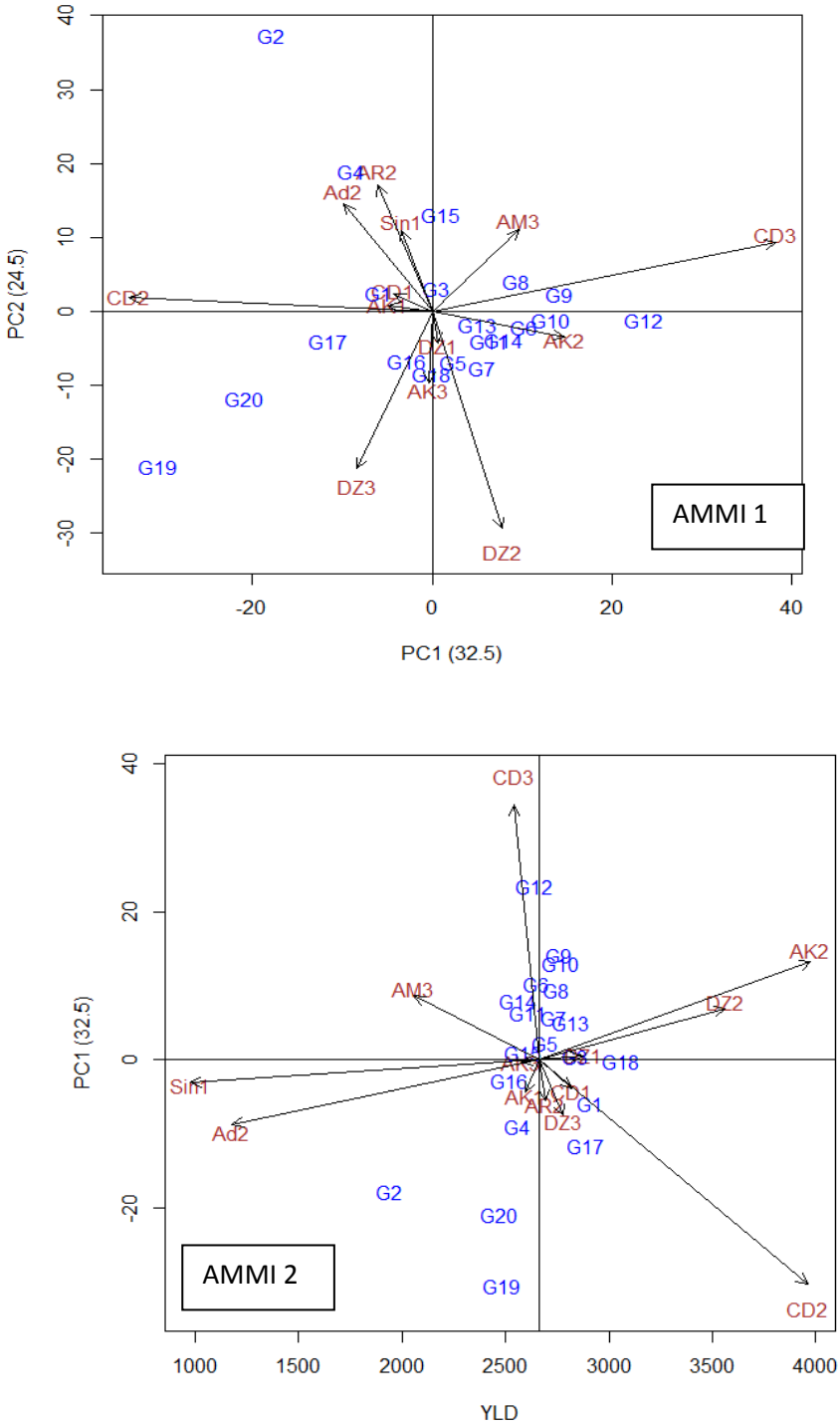

Figure 3. AMMI bi-plot for kabuli late maturing genotypes of chickpea

Conclusions and Implications

In the current study with exclusion of the released variety Chefe seven new test genotypes were identified from the three sets of experiments as stable genotype with comparable yield performance. Genotype G15(ICCX-940002-F5-242P-1-1-1), G18 (ICCX-940002-F5-6P-1-1-1)> G17 (ICCX-940002-F5-335P-1-1-1) from set A; genotype G13(X96TH-52-14/2000), G8 (FLIP 01-56C) from experiment set B and genotypes G3 (FLIP 01-12C), and G13(FLIP 01-8C) from experiment set C were genotypes identified having both high mean yield and stable yield performance across different environments.

From computing the ASV and presentation of AMMI 1 biplot, genotype with low IPCA 1 and AMMI stability value associated parameters, witness that decision making could be supported for the breeding and evaluation programs before getting into the final steps. Evidently, the analysis has demonstrated that the breeding genotypes in test seem to bounce with highest point, where we had non-surpassing the standard check. This could come from two perspectives; 1/ the germplasm enhancement program need be improved with innovative approach 2/ the right environment of potential expression is not well matched. Agro-eco-environments have different capacity set ups in discriminating genotypes which critical processes of the breeding. In dealing with the three sets, the tool of analysis clearly demonstrated scenario of breeding considerations like stability, high yield, seed market quality (not considered here) or a combination of them to make the forward decision.

It is important to underline such type of studies are key informants of both in forward and back ward germplasm management in the breeding program. It is also important this analysis is subject to time bound (periodic functionality) and changes in time as environmental changes are experiencing in due course.

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