Abyss. J. Sci. Technol. Vol. 2, No. 2, 2017, 19-29
ISSN 2616 – 4728 (Online); 2616 – 471X (Print)

Abyssinia Journal of Science and Technology

Developing Kabuli Chickpea (*Cicier arietinum* L.) Genotypes for Drought Prone Environment and Utilization and Nutritional Assessment in the Eastern Amahara

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ABSTRACT

Eight promising chickpea genotypes advanced from preliminary yield trial to multi environments trial were evaluated for their yield performance to the moisture stress areas and their utilization from 2009/10 and 2012/13 cropping season. The experiment was conducted at three locations viz, Sirinka, Chefa and Kobo using randomized complete block design with three replications. The additive multiplicative interaction model was used to analyze the data. The combined analysis of variance over years and locations revealed that there were highly significant differences among chickpea genotypes in yield and yield component traits. Based on the analysis of genotype ICC-14808 were better performing in all agronomic and yield parameter. The candidate genotypes were evaluated, validated and verified for release by the National Variety Releasing Committee. The yield potential of the genotype was 3.7 tons ha^{-1} at research station. ICC-14808 genotypes have a 45% of yield advantage over the standard check (Shasho). The candidate genotype has 35gm of 100 seed weight that fulfilled the required standard for export, and it was a drought tolerant that grows in area where all other cool season pulse crops couldn't grow very well. Based on the evaluation and assessment, genotype ICC-14808 was released for farmers in the Eastern Amhara. The breeder designates the variety to be called now and then *Yelbe*. The utilization and quality assessments of the farmers were explained in the papers.

Keywords: Boldness, Chickpea, *Cicier arietinum*, Kabuli, and Yield.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) was classified in the tribe *Cicereae* Alef (Kupicha, 1977). It is one of the first grain legumes to be cultivated in the old world. The crop originated in the present southeastern Turkey and along its boundary with Syria (Vavilov, 1926). Chickpea is the third largest produced food legume globally, after common bean (*Phaseolus vulgaris* L.) and field pea (*Pisum sativum* L.) (Bejiga et al., 1996).The diverse agro-climatic conditions in Ethiopia make it very suitable for growing chickpeas. The country is also considered as the secondary centre of diversity for chickpea (Bejiga et al., 1996). Chickpea has become an important legume, accounting for more than 15% of Ethiopian legumes with about one million households engaged in its production (Central Statistical Agency, 2014). Chickpea area coverage and productivity in Ethiopia have been increasing over a period of time. The last fifteen years data (1995, 2010 and 2014) obtained from the Central Statistics office show that chickpea production area, productivity and production in Ethiopia increased by 60, 100 and 200%, respectively (Central Statistical Agency, 2014). In Ethiopia the average productivity level of 1.7 t/ha is among the highest recorded globally and double the global average. The crop production is mainly concentrated in four regional states Amhara, Oromia, Southern Nations, Nationalities and People's Region (SNNPR) and Tigray with a total of 209020 ha.; Amhara region taking the lead covers 52% area coverage (Central Statistical Agency, 2014). These clearly show the importance of the crop in the country as well as the utilization. Thus, the area coverage and the importance of the crop in the country are expected to increase in the future.

Chickpea serves as a multi-purpose crop where the whole seeds are eaten fresh, cooked or boiled or in the form of dhal which is prepared by splitting the seed in a mill and separating the husk. It is used as a human food and animal feed and in particular, chickpea serves as an important protein

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supplement in the cereal-based diet of most Ethiopians. Yadeta & Geletu (2002) indicated that, it is an excellent source of protein (20-40%), which is approximately three times that of cereals. The protein in chickpea seed is rich in the amino acids, lysine and tryptophan, compared to cereal grains; however, it is deficient in methionine and cystine when compared to animal proteins. Flour made by grinding the seed is one of the chief ingredients of everyday diet for those suffering from uric Acid problem. Besides its food value, chickpea helps in the management of risk aversion where there is crop failure of major cereals due to recurrent drought (Yadeta & Geletu, 2002). It also helps in soil fertility management, particularly in dry land areas, through symbiotic nitrogen fixation. The bulk of the crop variety in the country is dominated by the *Desi* Type and the *Kabuli* type chickpeas are also grown in limited areas (David et al., 2009).

Among the major production constraints that limit the production and wide coverage of chickpea production was low productivity of the crop at farmer's level, absence of *Kabuli* chickpea variety that fulfills the required standard for export to the region (David et al., 2009), farmers preference inclined for the *Desi* type due to the productivity per unit area and lack of awareness for the nutritional and utilization aspect of the crop for home consumptions. To create foods that keep pace with our growing understanding of what constitutes a healthy diet, plant breeders may need to make a significant shift away from traditional selection criteria. Subsidizing crop nutritional value rather than yield could be an important and economical driver for this shift in perspective (Cindy & David, 2006). So the chickpea research should focus on selecting and improving yield potential of the *kabuli* genotype that fulfilled the required standard for export and resistance or tolerance to factors that reduce the yield of chickpea ((Yadeta & Geletu, 2002). In the recent agricultural policy, developing marketable commodity crop is the primary research agenda. Due to the scarcity of genetic variability and partly to the less attention in making crosses, attempted to improve this crop have, therefore, been mostly confined either to the examination of varietal difference or selection from the cultivars improved stocks (Muehlbauer & Singh, 1987). At the early stage of this study 300 genotypes of single seed decent pure lines were evaluated and selected in a single location using preliminary observation and preliminary yield trial. Those genotypes perform better in agronomical, and adaptable traits were advanced for regional variety trial.

Genotypes grown in multi-environment trials react differently to environmental changes. This differential response of genotype from one environment to another is called Genotype Environment Interaction (GEI). The presence of high GEI complicates breeding works, because it make difficult to predict how genotype selected under a given set of condition will perform in a different set of conditions. The GEI limits yield estimates because it is associated with changes in ranks of genotypes, and obscures, the identification of superior and stable genotypes. Besides measuring genotype x environment is important to determine an optimum breeding strategy for releasing genotypes with adequate adaptation to target environments (Zobel et al., 1988). Despite breeders strong interests in interactions and mega-environment analysis, using an adequate statistical tools to exploit GEI and are there any implication for identifying mega-environments and target genotypes are important. One of this model is, the AMMI models (Gauch, 1988) will gain acceptance through better documented it captures a large portion of the genotype by environment sum of square, it cleanly separates main and interaction effects, it provides agricultural researcher with different kind of opportunities and the model often provides agronomical meaningful interpretation of the data (Gauch & Zobel, 1997).

In light of this the present study is aimed to develop and select high yielding, bold seeded chickpea that fulfilled the required standard for export and relatively early maturing genotype that can do well in the terminal moisture stress area of the region over multi-location site. In the second phase of the activity study deals with the nutritional values and utilization of the crop have been studied through the participation of the farmers and food scientists.

MATERIALS AND METHODS

The experiment was conducted at three sites in the major chickpea growing areas of the northeastern part of Ethiopia. It includes North Wollo (Kobo represent lowland altitude and Sirinka represent intermediate altitude) and Oromya Zone (Chefa represent sub-humid lowland) (Table 1) for 2009/10 and 2010/11 cropping season. Eight selected *kabuli* chickpea genotypes advanced from previous preliminary yield trial and two standard varieties (*Sasho and Areti*) were constituted the experimental material of this study. The experiment was carried out in randomized complete block design replicated with three times, on a plot size of 2.4 m wide and 4 m long. A row-to –row distance of 40 cm and plant-to-plant distance of 10 cm were maintained. The material was sown in the first week of September in 2009/10 and 2010/11 cropping season. Data were recorded on nine important phonological, yield and yield component characters. The observations were recorded on ten randomly selected plants for four traits on plant basis (number of pods per plant (NP), number of seeds per pod (NS), 100 seed

weight in gram (SW), plant height (PH)) and rest data were taken from the four harvestable rows on plot basis (days to 50% flowering (DF), days to 90% maturity (DM), seed yield in kg per hectare (SY) and harvest index (HI). Plot means were used to estimate the mean performance of the genotype. Fertilizer was not applied. Seedbed preparation has been done three times; hand weeding was carried out two times.

Table 1. Geographical, climatic and agro- ecological features of the experimental sites.

	Location		
	Kobo	Sirinka	Chefa
Major agro-ecology	SM1-3[2]	M1-7[2]	M1-3[3]
Mean range of temp. (^{0}C)	25-38	21-32	21-36
Mean annual rainfall (mm)	660	876	850
Altitude (masl)	1450	1850	1680
Latitude	12.12	12.11	10.89
Soil type	Sandy loam (Brown)	Black soil	Black soil
Distance from Addis Ababa in km	570	508	355

Source: (*Natural Resource Management and Regulatory Department, MOA, 1998*)

[2]Sub moist hot to warm mountains and plateau

[3]Hot to worm moist vallevs and escarpments

In the 2011/12 cropping season the two promising candidate genotypes were evaluated on both station and on-farmers field with a plot size of 10m by 10m. Farmers' assessment and evaluation such as boldness, pod load, and earliness were included in the data and converted to rank. Seed samples of the candidate varieties were taken to the EBI laboratory for nutrient and quality assessment. In the 2013 utilization and nutritional quality assessment were done through participatory evaluation of 20 women and 20 men farmers from three districts. The utilization assessment includes the flour yield (the flower yield of one kilogram seed, boiling time (the time taken to boil a kilo of chickpea seed), roasting rate (amount of seed count not roasted or boiled with a given time), test (aroma, flavor test when consumed by recipient) and *shiro* color. For the nutritional quality analysis Melkassa ARC food science department and Combolcha agricultural technology institute also involved.

Data Analysis:

The collected Data were subjected to analysis of variance (ANOVA) using GenStat Release 18.1 computer software program. The AMMI model developed by Gauch (1986) was used for the average yield, $\boldsymbol{Y_{ij,}}$ over replicates of the $\boldsymbol{i_{th}}$ genotype in the $\boldsymbol{j_{th}}$ environment was calculated as:

$$Y_{ik} = \mu + \alpha_g + \beta_e + \sum_{n=1}^{N} \lambda_n \zeta g n \acute{\eta}_{en} + \varepsilon_{ij}$$

The least-squares fit to the AMMI model for balanced data (equal replication) is obtained in two steps. The first is the main effect in the additive part of the model grand mean ($\boldsymbol{\mu}$), genotype means, and environment means are analyzed by the ordinary analysis of variance. The second, component the non-additive interaction in the multiplicative part of the model, is analyzed by PCA (Zobel et al., 1988). A convenient scaling for the PCA scores has been selected: genotype and environment PCA scores are expressed as a unit vector times the square root of the eignvalue; that is, $\lambda\zeta g_i \acute{\eta}_{e=} (\lambda^{0.5}\zeta \boldsymbol{g_i})$ $(\lambda^{0.5}\acute{\eta}_{en})$ by (Zobel et al., 1988). The sum, $\sum_{n=1}^{N}\lambda_n\zeta gn\acute{\eta}_{en}$ of the product of genotype interaction scores ($\lambda^{0.5}\zeta \boldsymbol{gn}$) and environment interaction scores ($\lambda^{0.5}\acute{\eta}_{en}$) gives the estimated interaction (Zobel et al., 1988).

The result of AMMI analysis can be presented graphically in the form of biplots (Gabriel, 1971) in which the cultivar and environment scores of the first two or three bilinear (multiplicative terms are represented by vectors in a space with starting points at the origin and end points determined by the scores) (Gauch & Zobel, 1997).

RESULTS

The analysis of vairance for six individual environments revealed that there were significant differences among the genotypes in days to 90% maturity, 100 seed weight in gm, and seed yield in kg per hectare. Despite of the fact that, the Bartlett's test for homogeneity of variances across the six environments showed highly significant variance, could not made any valid inferences, because of the pooled analysis of variance revealed a significant interaction between genotypes, locations and year among the above traits (Table 2). Nevertheless, the additive combined ANOVA showed that the mean range for days to 50% flowering was 35 to 76 days. The earlier genotype mature within (74 days) and the longest mature for (144 days) (Table 2). The smallest 100 seed weight in gm was recorded (18 gm) and the largest was (43 gm). The candidate genotype has 34.6 gram 100 seed weight as compared with the two standard check 25.2 and 32.5 gram, respectively. The lowest seed yield was recorded (0.3 tones ha^{-1}) for genotype *Arerti* and the highest was (3.8 tones ha^{-1}) for genotype *FLIP-93-195C.* At an average the candidate genotypes has (1.8 tones ha^{-1}) compared with the two standard

Table 2. Range, Mean, CV in % of yield and yield component data of tested genotype

Identifier	Minimum	Mean	Maximum	CV %
DF	35	48.63	76	10.31
DM	74	99.61	144	4.08
NP	2	36.87	142	30.46
NS	1	1.2	3	27.9
PH	23	41.98	75	7.54
SW	18	31.93	43	8.66
BI	200	1594	4200	21.79
Seed yield in kg ha^{-1}	31	1352	3782	19
HI	2	26.51	59	17.15

Table 3. Combined means of days to maturity, 100 seed weight and seed yield in kg ha^{-1} of chickpea regional variety trial (Kabuli) across the three locations (Sirinka, Chefa & Kobo) over two years (2010-2011) using conventionally based additive model ANOVA.

Source of variation	d.f.	Days to maturity			100 seed weight			Seed yield in kg/ha		
		SS	MS	F pr.	SS	MS	F pr.	SS	MS	F pr.
REP	2	79.3	39.7		1.4	0.7		400443	200222	
G	9	9324.3	1036.0	<.001	4015.5	446.2	<.001	14329271	1592141	<.001
L	2	40726.1	20363.0	<.001	282.7	141.4	<.001	45905601	22952801	<.001
Y	1	55.6	55.6	0.09	0.04	0.04	0.95	10833460	10833460	<.001
GXL	18	2342.9	130.2	<.001	289.0	16.1	0.02	3490027	193890	<.001
GXY	9	349.4	38.8	0.04	51.9	5.8	0.71	4163804	462645	<.001
LXY	2	2076.5	1038.2	<.001	116.8	58.4	0.00	66406007	33203004	<.001
GXLXY	18	393.9	21.9	0.311	206.6	11.5	0.16	6246764	347042	<.001
Residual	118	2236.7	19.0		982.3	8.3		8124892	68855	
Total	179	57584.6			5946.3			159900270		

Table 4. ANOVA table for AMMI model for days to 90% maturity

Source	df	SS	MS	F	F_prob.
Total	179	57585	322		
Treatments	59	55269	937	50.58	<0.001
Genotypes	9	9324	1036	55.94	<0.001
Environments	5	42858	8572	325.6	<0.001
Block	12	316	26	1.42	0.1671
Interactions	45	3086	69	3.7	<0.001
IPCA 1	13	2348	181	9.75	<0.001
IPCA 2	11	404	37	1.99	0.0367
Residuals	21	334	16	0.86	0.6441
Error	108	2000	19		

check (1.4 tones ha^{-1}) and (0.98 tones ha^{-1}), respectively (Table 8). The minimum harvest index was recorded for *Arerti* variety (2%) this was due to drought, the variety fail to set seed and the maximum was for genotype *FLIP-93-195C* (59%) (Table 2).

As showed on (Table 3) additive ANOVA 71%, 16% and 9% of the total variation for days to maturity was explained by the environments, genotypes and interactions and the rest was residual. This was in agreement that in many of multi-location trial the main contributor sources of variation were come from, due to the changing environmental variables (Table 3).The same kinds of results were observed by the AMMI model for multi-location trial for days to 90% maturity, from the total treatment source of variation 75%, 17%

and 5% was explained by environment, genotype and interaction effect, respectively. The model revealed that the interaction effect was significant (Table 4).

From the total sum square of interaction 76 % was explained by the first IPCA scores. Genotypes FLIP-95-31C, ICC-14808 and FLIP-93-195C were early maturing, whereas Arerti, FLIP-95-39 and *Shaso* were late maturing (Fig. 1). *FLIP-95-31C*, *ICC-14808*, *FLIP-93-22C*, and *FLIP-93-195C* relatively stable keeping their maturity constant over environments where as the rest genotypes show high GEI over environments as revealed by figure distant from the origin (Fig. 1). The

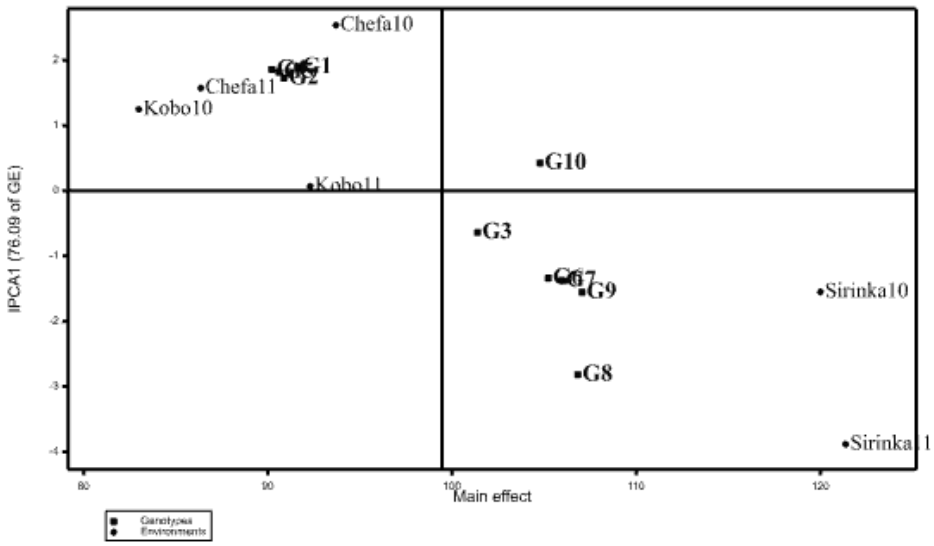

Fig 1. Genotype IPCA 1 scores versus the means performance of the genotype for days to maturity across six environments

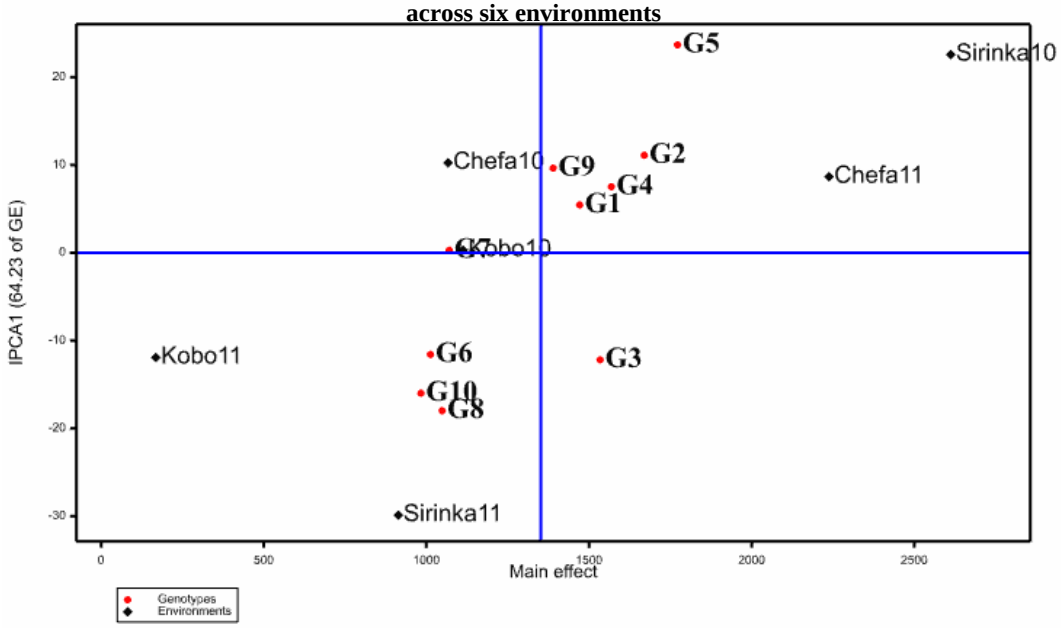

Fig. 2. Genotype and environmental mean against IPCA score using symmetric scaling for seed yield in kilogram per hectare

homogeneity error variance test using Bartlett's test for seed boldness showed that there was no significance difference among the environmental variance. The combined ANOVA using additive model explained 68 % the variation was contributed by the genotypes (Table 5). The two candidate genotypes *ICC-14808* and FLIP-93-22C have the largest 100 seed weight per gram as compared to others; besides they have highly significant variation with the standard check *Arerti* variety (Table 6). The released genotype *ICC-14808* fulfilled the required standard for seed boldness to export. The AMMI model showed that there were significance differences among the genotype for seed yield in kg ha^{-1} across location.

The variation explained by the genotypes, environments, and the interactions effect was 10%, 81 %, 9 %, respectively (Table 7). Of these variation 64% and 22% of the interaction was explained by IPCA 1 and IPCA 2 values, respectively (Table 7). *Arerti* variety was the best stable genotypes associated with low yield. Whereas, the candidate genotype (*ICC-14808*) has the best yielder with a non-cross over GE interaction; IPCA values has same sign with over the (data six environments not shown). AMMI biplot showed that, high yield was recorded at Sirinka and Chefa in 2009/10 and 2010/11 cropping season, respectively (Fig. 2) these showed the irregular nature of the environments from season to season.

In spite of AMMI selection per environments, farmers evaluate genotype in there contextual environment. They considered earliness, pod size, pod load, seed boldness and seed yield as an important selection parameter. In all these criteria's farmer prefer ICC-14808 genotype the first rank over the three locations (Table 10). This candidate variety fulfilled the required standard (32.5 gram 100 seed $weight^{-1}$) for seed boldness for export. Besides in 2011/12 cropping season the candidate genotype out yielded the standard check *Shasho* and *Ararti* by 29.7% and 23.1%, respectively (Table 10).

Utilization and Nutritional Assessment

Table 5. Mean performance of the genotype for days to 90% maturity across locations

	Genotype	Sirinka	Chefa	Kobo	Sirinka	Chefa	Kobo	Grand Mean
1	**FLIP-93-22C**	111	90	78	105	80	85	92
2	**FLIP-93-195C**	111	89	75	105	81	84	91
3	**ICC-12339**	121	97	81	129	90	99	103
4	**FLIP-95-31C**	106	90	77	106	80	82	90
5	**ICC-14808**	106	89	77	107	82	83	91
6	**FLIP-95-39**	131	99	84	132	89	96	105
7	**FLIP-94-119C**	124	96	91	135	90	99	106
8	**FLIP-96805**	133	90	88	138	90	103	107
9	**Arerti**	131	98	89	135	90	100	107
10	**Shaso**	127	98	88	122	91	102	105
	MEAN	120	94	83	121	86	93	100
	CV	7.17	2.06	1.8	2.67	1.05	3.03	4.08
	LSD (5%)	14.76	3.3	2.56	5.55	1.56	4.82	**

Table 6. Combined ANOVA table for AMMI model for 100 seed weight in gram

Source of variation	df	SS	MS	F-calc.	F pr.
Block	2	1.4	0.7	0.08	
Genotype	9	4015.5	446.2	53.6	<.001
Location	2	282.7	141.4	16.98	<.001
Year	1	0.04	0.04	0	0.947
GXL	18	289.0	16.1	1.93	0.02
GXY	9	51.9	5.8	0.69	0.714
LXY	2	116.8	58.4	7.02	0.001
GXLXY	18.0	206.6	11.479	1.38	0.155
Residual	118	982.3	8.3		
Total	179	5946.3			

Farmer's assessment for the nutritional and utilization assessment were displayed on (Table 11, 12 & 13). The assessment of the *nifro* (according to recipe definition chickpea eaten as cooked and boiled seed form*);* such as testing for easiness, easiness for chewing and flavor attractiveness as important criteria for *nifro* quality of the varieties (Table 13). Based on their evaluation most of the farmers are very impressed and attracted in those test parameters. In addition farmers highly preferred dried roasted recipe form commonly called "***Kolo***" and their fast imbibitions of the variety *Yelbe* during roasting with water. The second quality parameter; they considered the flour

Table 7. ANOVA table using AMMI model of the genotype for seed yield in kg hectare^{-1}

Source	df	SS	MS	F	F_prob
Total	179	159900270	893298		
Treatments	59	151374935	2565677	38.63	<0.001
Genotypes	9	14329271	1592141	23.97	<0.001
Environments	5	123145068	24629014	218.63	<0.001
Block	12	1351836	112653	1.7	0.0774
Interactions	45	13900595	308902	4.65	<0.001
IPCA 1	13	8929013	686847	10.34	<0.001
IPCA 2	11	3047050	277005	4.17	<0.001
Residuals	21	1924533	91644	1.38	0.1446
Error	108	7173499	66421		

Table 8: Mean Seed yield in kg per hectare of the genotype across eight environments

	2009			2010			Grand
Genotype	**Sirinka**	**Chefa**	**Kobo**	**Sirinka**	**Chefa**	**Kobo**	**Mean**
FLIP-93-22C	2663	1504.8	1344.8	802	2317.8	196.9	1471.5
FLIP-93-195C	3146.5	1532.4	1646.9	906.8	2551.9	233.3	1669.6
ICC-12339	2317.8	1301.9	1465.6	1572.6	2455.4	91.7	1534.2
FLIP-95-31C	2741.5	1439.7	1338.6	842.2	2807	243.8	1568.8
ICC-14808	3660.1	1831.7	1321.9	685.6	2780.6	354.2	1772.3
FLIP-95-39	1987.4	482.9	767.7	821	1889.8	128.1	1012.8
FLIP-94-119C	2816.3	578.1	539.6	703.6	1625.8	158.3	1070.3
FLIP-96805	1936.8	694.9	497.9	1199.1	1761.9	95.8	1048.5
Arerti	2890.4	854.8	1313.6	632.7	2576.1	71.9	1389.9
Shaso	1964.7	446	582.3	973.5	1613.5	110.4	983.1
MEAN	2612.4	1066.7	1081.9	913.9	2237.98	168.4	1352.117
CV	13.74	20.86	23.01	23.79	15.77	30.82	19
LSD (5%)	615.6	381.7	355.5	372.9	605.5	119.2	**

Table 9: The first four AMMI selections per environment

Number	Environment	Mean	Score	1	2	3	4
1	E1	2612	22.58	G5	G2	G9	G4
2	E2	1067	10.26	G5	G2	G4	G1
5	E5	2238	8.66	G5	G2	G4	G3
3	E3	1113	0.3	G2	G3	G5	G4
6	E6	168	-11.92	G5	G2	G3	G7
4	E4	914	-29.88	G3	G8	G10	G6

Table 10: Kabuli Chickpea Variety Verification Trial Combined Across the Three Locations

CANDIDATE GENOTYPE	DF	DM	NP	NS	SCH	PH	SW	AYKGHA	ADJUSTED with SCH	RANK
FLIP-93-22C	44	100	48	1.3	902.7	45	37	838	2310	2
ICC-14808	47	101	61	1.8	737.7	40	38	934	3003	1
Arerti	59	119	53	1.3	925.4	41	31	837	2440	3
Shaso	57	116	39	1.3	781.1	43	34	725	2316	3
GRAND MEAN	52	109	50	1.4	836.8	42	35	833	2517	
CV%	5.3	3.5	36	23.5	19.7	9.1	6.9	29	30.6	26
LSD	3.1	4.2	NS	NS	NS	NS	2.7	NS	547	

Table 11: Nutritional quality analysis of the candidate varieties

Variety	%Protein	% Carbohydrate	% Fat	% Crude fiber	% Mineral ash	% Moisture
ICC-14808	28.43	50.9	1.1	5.9	3.89	9.66
Arerti	26.12	50.1	1.14	6.83	4.33	9.53
Shaso	27.79	51.96	1.05	5.77	4.01	9.42

Table 12: Roasting and cooking time of chickpea varieties

Varieties	Boiling time at 92^0c	Roasting rate(degree of non-sucker)	Roasting ability
ICC-14808 ***(Yelbe)***	4.10-3.30=0.40	Excellent	1
Shasho	4:25-3:30=0:.55	Very good	1
Local desi variety	4.45-3.30=1.15	Good	2

color of the *shiro* after decorticated. All the three verities have a typical *shiro* that was cream color. Nevertheless, some farmers have commented to adjust the redness of flour color (Table 13). According to the food scientist the color can be adjusted by the amount of spices and pepper added in the flour (Table 13). The other important quality parameter is the roasting ability of the seed, this is because they directly correlated with the amount of fuel (energy) required to boiled the seed. Based on their evaluation variety ICC-14808 relatively boiled within short period of time and has very low number of non-suckers.

DISCUSSION

The analysis of variance for six individual environments revealed that there were significant differences among the genotypes in days to 90% maturity, 100 seed weight in gm, and seed yield in kg per hectare. Despite of the fact that, the Bartlett's test for homogeneity of variances across the six environments showed highly significant variance, could not made any valid inferences, because of the pooled analysis of variance revealed a significant interaction between genotypes, locations and year among the major traits.

Bartlett's test for homogeneity of variances for days to maturity showed a significant variation. The pooled analysis could not show a stable genotype due to higher effect of environment that obscures the identification of superior and stable genotypes. Therefore, the reason for analyzing genotype by environment interactions is to determine the basis for explaining different patterns of response of different genotypes to the varying environments (Girma et al., 2000). The same kinds of results were observed by the AMMI model for multi-location trial for days to 90% maturity, from the total treatment source of variation 75%, 17% and 5% was explained by environment, genotype and interaction effect, respectively. The model revealed that the interaction effect was significant (Table 4). AMMI is effective, because the model partition most of the interaction sum squares (SS) that is rich in pattern, leaving a residual that is rich in noise with most of the degree of freedom but small sum square, thereby affording greater predictive accuracy and statistical efficiency (Gauch, 1988). The additive main effect and multiplicative bi-plot showed that the locations effects were very influential as compared with other sources of variation (Fig.1). Although, the interaction has significant effect but the ranking of the genotypes could not alter over locations. From this we can infer that the interaction effect has quantitative that is, no cross over interaction.

Seed boldness was one of the important traits considered for selection of the candidate genotypes. This is because seed size is largely

determined by the genetic effects. The interaction effect was not as such important, mean effect of the genotypes could be best explained by the additive ANOVA without the need of the PCA score. As indicated by Yan & Hunt (2001), understanding the cause of non-cross over environment interaction would help to develop an understanding of the genetic characteristics seed boldness that contribute to superior cultivar, and the environmental factors that can be manipulated to facilitate selection for such cultivar evaluation.

Bartlett's test for homogeneity of variances showed significant variation for seed yield. The pooled analysis could not show the stable genotype due to genotype by environment interaction. Further advanced analysis was required because the additive ANOVA model, which identifies the interaction as residual source of variation, but does not sub-partition the interaction (Ebdon & Gauch, 2002). Consequently, statistical analysis targeting genotype environment interaction has been largely ignored in genotype evaluation programs and therefore interactions are unable to be exploited fully in crop breeding programs besides the genotype by environment interaction (GEI); it (Ebdon & Gauch, 2002). Therefore, the reason for analyzing genotype by environment interactions is to determine the basis for explaining different patterns of response of different genotypes to the varying environments (Girma et al., 2000). Beside, these understanding of the causes of GEI can be used to formulate recommendation for areas of optimal cultivar adaptation and the environmental factor that can be manipulated to facilitate selection for such genotype (Yan & Hunt, 2001). To allocate target genotype identification and analysis AMMI model were used to get the pattern by excluding the noise.

Regardless of whether the data were from a single year MET or multi-year MET, a universal phenomenon in all regional yield trials is that environment is always the predominant source of yield variation, and genotype and genotype by environment are relatively small (Gauch & Zobel, 1996) that was in agreement with this findings. The large environment main effect, however, is not relevant to cultivar evaluation. Only genotype and genotype by environment are relevant to genotype evaluation. Therefore, for genotype evaluation, it is essential to remove environments from data and

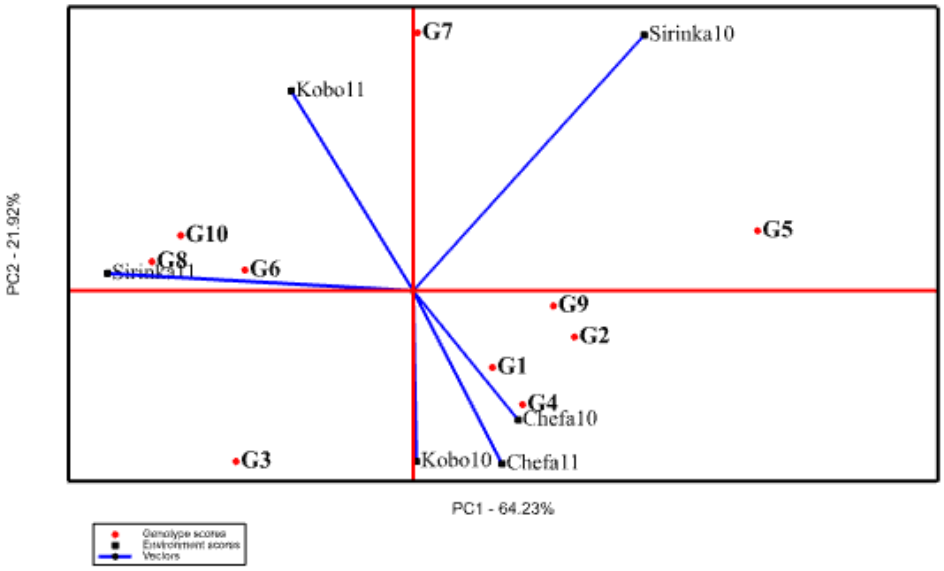

Fig. 3. AMMI bi-plot with (genotype scaling) for seed yield in kilogram per hectare as explained by Genstat software

limits yield estimates because it is associated with changes in ranks of genotypes, and obscures, the identification of superior and stable genotypes focus on genotype and genotype by environment. The genotypes perform linearly across the six

environments, the interaction was quantitative, that is the genotypes have non-cross over interaction.

Most of the genotypes and the environments have a PCA score differ from zero with significant interaction effects well explained by AMMI- 2 model, this finding was in agreement with (Gauch & Zobel, 1997). These also reflected by the largest high opposite IPCA score (22.58) for the year 2010 and (-19.06) for the year 2011 that depart from the origin (Fig. 2). As it has been shown from both analysis the environment showed high variability as reflected by the mean yield, nevertheless at Sirinka (2009/10) and Chefa (2010/11) were found more conducive environment for most genotypes. On average Kobo was a low yielding environment; this was due to severe moisture deficit in the growing season (Table 8). Genotype ICC-14808 has the highest mean yield and the AMMI model selects this genotype, the first rank across four environments and the third ranks in one environment (Fig.3 and Table 9).

The ANOVA for days to flowering, days to maturity, 100 seed weight and seed yield adjusted with optimum stand count showed significant variation whereas non-significant variation was observed on seed yield due to high heterogeneity among block (Table 10). In spite of AMMI selection per environments, farmers evaluate genotype in there contextual environment. They considered earliness, pod size, pod load, seed boldness and seed yield as an important selection parameter. In all these criteria's farmer prefer and made the first rank ICC-14808 genotype over the three locations (Table 10). This candidate variety fulfilled the required standard (32.5 gram/100 seed weight) for seed boldness for export.

The candidate genotype *ICC-14808* has 28.4% protein that is much higher than *Ararti* and *shasho* varieties (Table 11). It can be used an alternative for export and a means for cash income for the farmers, if they scaled up in the farming system. The candidate genotype ICC-14808; released by

Table 13.Consumer evaluation of the *Nifro*, Color of the *Shiro* flour, general acceptance of the varieties after cooking and testing *Shiro wet* of the *kabuli* varieties.

General character	Recipe Criteria	Variety	Total numbers of farmers	Very good %	Good %	Poor %
Consumer evaluation of the Nifro character of the *Kabuli* Chickpea varieties	Testing easiness	ICC-14808 (*Yelbe*)	40	90	10	0
		Shasho	40	87.5	12.5	0
		Local desi variety	40	85	12.5	2.5
	Easiness for chewing	ICC-14808 (*Yelbe*)	40	100	0	0
		Shasho	40	100	0	0
		Local desi variety	40	80	20	0
	Flavor attractiveness	ICC-14808 (*Yelbe*)	40	90	7.5	2.5
		Shasho	40	90	7.5	2.5
		Local desi variety	40	95	5	0
	Preferred *shiro* color	ICC-14808 (*Yelbe*)	40	65	30	5
		Shasho	40	62.5	40	2.5
		Local mixed with all pulses	40	80	20	0
General acceptance of the varieties after cooking and testing Shiro wet	flour yield (*Wuha yanesal*)	ICC-14808 (*Yelbe*)	40	65	30	5
		Shasho	40	62.5	40	2.5
		Local mixed with all pulses	40	80	20	0

the variety releasing committee for Sirinka, Chefa and Kobo and similar agro-ecology and the breeder designates the variety to be called now and then *yelbe*.

In conclusion, the choice of a particular population from the germplasm will depend on the mean performance of the population and the genetic variability within the population. The ANOVA showed significant differences among the genotypes for all the traits considered, signifying the existence of sufficient variability for improvement. AMMI analysis was used to understand the Genotype X Environment interaction pattern. The result exhibited significant environment and genotype main effect and high genotype by environment interaction effect. AMMI analysis showed that genotype ICC-14808 was the first candidate across four environments. ICC-14808 (*Yelbe*) genotype is released by the National Variety Releasing Committee for Sirinka, Chefa, Kobo and similar agro-ecology. Both women and men farmers with food science professional were involved in the evaluation process for food, nutritional values and utilization of the crop. They evaluated the *nifro*, testing for easiness, easiness for chewing, flavor attractiveness, boiling time, roasting rate, test of the *shiro wet*, color of the *shiro* of released *Yelbe variety*. Based on this recommendation the Research and extension division has to demonstrate and popularize the variety within the recommended domains for the end users

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