



Evaluation of Desi Type Chickpea (*Cicer arinum* L.) Genotypes for Yield and Yield Components in Eastern Amhara, Ethiopia

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ABSTRACT

Background: Chickpea is the second most important legumes next to faba bean in Ethiopia. The productivity of chickpea in the country is below 2 t/ha but its yield potential reaches 5-6 t/ha. The major reasons attributed to non-availability of widely adaptable and high yielding varieties. Therefore; the objective of this experiment was to identify and recommend a widely adaptable and high yielding variety.

Methods: Forty genotypes with checks were evaluated in RCB design with three replications at four locations for two years. Phenological and Agronomical data collected and analyzed by using SAS software 9.0 version.

Result: The combined analysis of variance revealed significant differences among the genotypes. Based on ANOVA and GEI analysis result three promising genotypes namely ICCV-93954, DO47 and ICC-07108 with average seed yield of 2931.5kg/ha, 2731.6kg/ha and 2335.4kg/ha respectively, were selected and verified. Among the verified genotypes ICCV- 93954 has been officially released and recommended in the name of Mitik, for production in the tested and similar areas of chickpea growing in the region.

Key words: Chickpea, Genotypes, Genotype-environment interaction, Seed yield.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is categorized in *Fabaceae* (*Leguminosae*) family, one of the oldest and most widely consumed legumes in the world and it is a staple food crop particularly in tropical and subtropical areas (Asnake and Dagnachew, 2020). It is produced in more than 60 countries. India is the largest chickpea producing country accounting for 72% of the global production. Ethiopia is the largest producer, consumer and exporter of chickpea in Africa and shares some 4.5% of global chickpea market and more than 60% of Africa's global chickpea market (Tebkew and Ojiewo, 2016).

Chickpea is very important due to its good nutritional value having an average of 22% protein, 63% carbohydrate, 4.5% fat, 8% crude fiber and 2.7% ash (Shafique *et al.*, 2016). Besides being an important source of human food and animal feed, it is also an important contributor to soil fertility as it provides nitrogen to soil through fixation of atmospheric nitrogen (Gul *et al.*, 2011).

In Ethiopia, chickpea is grown by subsistence farmers in several regions of the country under rain fed conditions with residual moisture. According to CSA (2019), productivity of chickpea is 1.9 tons per hectare but the yield potential of chickpea is as high as 6 t/ha (Gaur *et al.*, 2010). The major reason for this gap comes due to non-availability of widely adaptable and relatively high yielding varieties especially in chickpea growing areas of eastern Amhara region. Therefore; the objective of this experiment was to evaluate, identify and recommend early maturing, widely adaptable and relatively high yielding genotypes.

MATERIALS AND METHODS

The experiment was conducted in the northeastern part of Amhara National Regional State at four locations, namely;

Srinka and Sekota Agricultural Research Center, P. O. Box 74, Woldia, Ethiopia.

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Sirinka, Kobo, Chefa and Weleh. These four locations represent various agro-ecologies where chickpea is widely grown in the region. All these locations' environmental condition listed in Table 1.

The experiment was started in 2013 as observation trial with 150 desi type chickpea genotypes, which were received from ICRISAT and passing through observation and preliminary variety trial for one year at Sirinka. Only twelve genotypes were advanced to regional variety trial and tested with varieties Kutaye and Minjar as checks at Sirinka, Kobo, Chefa and Weleh for two years (2015 and 2016). The trial was laid out in a randomized complete block design with three replications on a plot size of 9.6 m². The spacing between rows was 40 cm apart and 10 cm between plants within the rows. All agronomic practices were done uniformly for all treatments as required.

The data of days to flowering and maturity, number of pods per plant, number of seeds per pod, plant height, hundred seed weight and grain yield recorded and analyzed

by SAS 9.0 (SAS, 2004). AMMI analysis was done to assess the genotype and environment interaction to identify relatively wide adaptable genotype (Mukherjee *et al.*, 2013). The AMMI stability value (ASV) as described by Purchase *et al.*, (2000) was calculated. (GSI): Based on the rank of mean grain yield of genotypes (RYi) across environments and rank of AMMI stability value (RASVi) a selection index called Genotype selection index. It was calculated for each genotype (Bavandpori, 2015), which incorporates both mean grain yield and stability index in single criteria:

$$GSI_i = RASVi + RYi$$

RESULTS AND DISCUSSION

The combined analysis of variance showed significant differences ($P < 0.01$) among the genotypes for all of the studied traits (Table 2 and 3). The mean seed yield performance ranged from 1992 - 2914 kgs/ha. According to the analysis of variance result, genotype ICCV-93954 scored the highest seed yield performance (2931.5 kgs/ha) followed by genotype DO47 (2731.6 kgs/ha) and ICC-07108 (2335.4 kg/ha) whereas, the lowest seed yield performance was recorded for genotype ICCV-08104 (1992 kg/ha) (Table 2). The standard checks, variety Kutaye and Minjar, recorded 2150kg/ha and 2093.5 kg/ha respectively, under the total grand mean of seed yield (2230.3 kg/ha). The range of variability for maturity (when 90% of plants from the plot

reached at physiological maturity stage) was 93 to 98 days this indicates all the genotypes including the checks can group under early type of chickpea. Genotype DO47 the earliest genotype (93 days) followed by genotype ICCV-93954 and ICC-07108 which took 94 days to mature (Table 2). The maximum hundred seed weight of 34.2 gram was recorded in the genotype ICC-07108 this indicates the genotype is bold seeded whereas the smallest seed weight was recorded for the standard checks variety Kutaye and Minjar with 23.3 g and 23 g, respectively. The highest number of pods per plant was recorded 47 pods for genotype ICCV-93954 and the lowest 32 pods for ICCV-03203.

Environmental mean seed yield performance ranged from 1373.5kg/ha for Kobo-15 to 3685.7 kg/ha for Chefa-15 (Table 4). The highest environmental mean seed yield at Chefa-15 was attributed to uniform distribution and adequate rainfall during the growing season. On the other hand, inadequate and early cessation of rainfall contributed to the low mean seed yield at Kobo-15. The mean seed yield averaged over environments and genotypes was 2229.8 kg/ha. Both checks scored below overall environmental seed yield mean.

The genotype-environment interaction (GEI) was highly significant to contribute the variability between the genotypes (Table 5). As GEI is significant, it was further proceeded to estimate phenotypic stability (Farshadfar, 2011) using

Table 1: Experimental site description.

Location	Altitude (m.a.s.l.)	Temp./min and max	Rain fall average (mm)	Soil type	Latitude	Longitude
Sirinka	1850	13.6-26.7°C	1006.3	Vertisol	11°45'	39°36'
Chefa	1465	11.6-30.4°C	850	Vertisol	10°57'	39°47'
Kobo	1470	15.8-29.1°C	637	Vertisol	11°08'21"	39°18'21"
Weleh	2081	14-26°C	600	Vertisol	12°11'06"	39°00'53"

Table 2: Mean and Standard deviation of Chickpea genotypes for seed yield and yield related traits across eight environments.

GN	Genotypes	DF	DM	NPP	NSP	PH	HSW	AYKGHA
1	ICC-07108	45fg	94d-f	37c-f	1.2e	40.8c-f	34.2a	2335.4c
2	DO51	47bc	95c-f	35d-g	1.2de	42.1a-d	33.5a	2151.2def
3	ICCX-90000-2-F5-	46def	96bc	37cde	1.4b-e	42.4abc	31.2bc	2195.5c-f
4	ICCV-04101	45ef	96bc	39bc	1.3cde	42.1a-d	31.5b	2288.3cd
5	ICCV-00104	46cd	96bcd	33fg	1.4b-e	43.8a	27.9e	2053.9fg
6	DO62	44gh	94efg	35efg	1.5abc	36.9g	25f	2154.3def
7	ICCV-08104	46cde	97ab	40bc	1.4bc	40.6def	30.1cd	1992.8g
8	ICCV-93954	44hg	94d-f	47a	1.2de	39.3f	25.6e	2931.5a
9	ICCV-03203	50a	98a	32g	1.7a	40.1ef	27.2e	2057.9fg
10	DO47	44h	93g	46a	1.6ab	36.3g	25.8e	2731.6b
11	DZ-2012-CK-0027	47bc	96bc	37cde	1.3cde	43.3ab	29.9cd	2235.3cde
12	DZ-2012-CK-0033	47b	96bc	42b	1.3cde	40.4def	29.5d	2071.1fg
13	Kutaye	47bc	95bcd	39bcd	1.4bcd	39.9f	23.3g	2150edf
14	Minjar	46bcd	94g	36c-f	1.6ab	41.7b-e	23.g	2093.5efg
	GM	45.9	95	38.2	1.4	40.7	28.4	2230.3
	CV%	4.8	3.5	17.3	15.2	7.8	8.2	19.3

Note: GN- Genotype number, GM- Grand mean; CV- Coefficient of variance; DF- Days to flowering; DM- Days maturity, NPP- Number of pods per plant, NSP- Number of seeds per pod, PH- Plant height in cm, HSW- Hundred seed weight, AYKGHA- Adjusted yield in kg per ha.

Additive Main-effect and Multiplicative Interaction (AMMI) model. The results of AMMI analysis of grain yield data for twelve genotypes along with two checks over 8 environments (Table 5) revealed that the genotypes accounted for 11.4% of the total treatment sum of squares (SS), the environmental effect explained 71.8% and the GEI effect captured 16.7%, were all significant ($P < 0.001$) (Table 5). A large SS for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield, indicating that environment has a strong influence on grain yield (Alam *et al.*, 2015).

Based on this, the trial result was highly affected by environmental contribution. The magnitude of the GEI sum of squares was higher than that for genotypes (Table 5), indicating that there were substantial differences in genotypic response across environments, in agreement with previous reports (Tonk *et al.*, 2011, Alam *et al.*, 2015, Vaezi *et al.*, 2017).

Thus, only about 28.1% of the variation was relevant for identifying highest yielding genotypes in different

environments as only G and GE interaction affect the ranking. The presence of GEI complicates the selection process as GEI reduces the usefulness of genotypes by confounding their yield performance through minimizing the association between genotypic and phenotypic values (Farshadfar, 2011). Based on this, GEI was partitioned into IPCA-1, IPCA-2, IPCA-3 and IPCA-4 (Table 5). Similar findings were also obtained by Tarakanovas and Ruzgas, (2006) and Bavandpori, (2015) on the additive main-effect and multiplicative interaction variance of the sum of squares due to GEI was partitioned into IPCA-1, IPCA-2, IPCA-3 and IPCA-4.

The first principal component axis (PCA-1) of the interaction captured 44.3% of the interaction sum of square in 20.9% of the interaction degrees of freedom. Similarly, the second principal component axis explained further 21.2% of the GEI sum of square while IPCA3 and IPCA4 explained 11.5 and 9.6% respectively.

According to Kadhem and Baktash (2016), in AMMI the first two interaction principal component axis best predictive model explains the interaction sum of squares. Thus, interaction of the 14 genotypes with 8 environments was predicted by the first two principal components of GEI (Table 6).

The score and sign of IPCA1 reflect the magnitude of the contribution of both genotypes and environments to GEI, where scores near zero are characteristic of stability, whereas higher score (absolute value) considered as unstable and specific adapted to certain environment (Kadhem and Baktash 2016). Based on this concept, G4, G6 and G12 placed relatively close to zero IPCA1 score line that means they performed and adapted to all environments where as G8, G14 and G10 were furthest away from zero due to this they adapted certain environments (Table 6). In overall, the genotypes adaptability/stability

Table 3: The combined analysis of variance for seed yield traits for 14 chickpea genotypes over eight environments.

Source of variation	d.f.	Mean squares ASYKGH
Genotype (Gen)	13	12982.68**
Location (Loc)	3	309955.9**
Year (Yr)	1	400292.4*
Gen × Loc	39	294393.3**
Gen × Yr	13	328754.3**
Gen × Loc × Yr	42	130950.7**

*, ** - Significant at 5%; ASYKGH-Adjusted yield in kg per ha.

Table 4: Mean seed yield (kg/ha) of fourteen chickpea genotypes at individual environment.

GN	Genotypes	Testing environments								Over all mean
		SR 15	KB 15	CH 15	WH 15	SR 16	KB 16	CH16	WH16	
1	ICC-07108	2041	1946	3865	1869	2684	1837	2668	2005	2364.4
2	DO51	1866	1251	3790	1939	2295	1589	2131	1893	2094.3
3	ICCX-90000-2-F5-	1940	401	3588	1840	2716	1788	2100	1900	2034.1
4	ICCV-04101	1579	693	3837	2045	2676	2223	2771	1907	2216.4
5	ICCV-00104	2131	1367	3541	1824	1938	1872	1986	1885	2068.0
6	DO62	2277	1262	3926	2169	1933	1490	1895	2011	2120.4
7	ICCV-08104	1522	1354	3715	2168	2312	1158	1665	2210	2013.0
8	ICCV-93954	2496	2249	4281	3219	3373	2078	3672	2184	2931.5
9	ICCV-03203	2311	1220	3445	2207	2154	1524	1541	2220	2077.8
10	DO47	2530	1937	3681	3041	3005	2047	3289	2323	2731.6
11	DZ-2012-CK-0027	1871	1897	3609	2459	2255	1451	2573	2115	2278.8
12	DZ-2012-CK-0033	2235	1149	3160	2142	2397	1297	2144	2050	2071.8
13	Kutaye	2432	1204	3554	2127	2537	1222	1988	1909	2121.6
14	Minjar	2070	1299	3608	1329	2178	1656	2264	2397	2093.1
	EM	2093	1374	3686	2169	2461	1659	2335	2072	2229.8

Note: GN-Genotype number, SR-15- Sirinka 2015, KB 15- Kobo 2015; CH15- Chefa 2015, WH-15- Weleh 2015; SR-16- Sirinka 2016, KB 16- Kobo 2016, CH 16- Chefa 2016, WH-16- Weleh 2016.

ranking for seed yield performance based on lower absolute IPCA1 scores was ICCV-04101 (0.48) > DO62 (0.52) > DZ-2012-CK-0033 (1.89) > Kutaye (3.68) > DO51 (4.25) > ICCV-03203 (4.41) > DZ-2012-CK-0027 (4.54) > ICC-07108 (5.88) > ICCV-08104 (6.01) > ICCV-00104 (6.21) > ICCX-90000-2-F5- (7.65) > DO47 (14.9) > Minjar (17.8) > ICCV-93954 (35.57) (Table 6).

AMMI stability value (ASV)

AMMI stability value was also computed to determine stability of the genotypes (Table 6). In fact, ASV is the distance from zero in a two-dimensional scatter of IPCA 1 (interaction principal component analysis axis 1) scores against IPCA 2 scores (Kadhem and Baktash, 2016). Since the IPCA1 score contributes more to GE sum of scores, it has to be weighted by the proportional difference between IPCA 1 and IPCA 2 scores to compensate for the relative contribution of IPCA 1 and IPCA 2 total GE sum of squares. 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 considered as the most stable. Accordingly, genotypes G12, G2, G3, G5, G11 and G8 had general adaptation, while genotypes G4, G9, G13 and G1 were the

most unstable. This was in agreement with Farshadfar (2008) who has used ASV as one method of evaluating grain yield stability of bread wheat varieties. Similar reports were also observed by Fereny *et al.* (2007) who has studied adaptability and stability pattern of spring wheat using ASV and other stability parameters.

Genotype selection index (GSI)

Stability information about a genotype is very important however not be the only parameter for selection, because the most stable genotypes would not necessarily give the best yield performance (Mohammadi *et al.*, 2007), hence there is a need for approaches that incorporate both seed yield mean and stability in a single criterion. In this regard, as ASV takes into account both IPCA1 and IPCA2 that justify most of the variation of GE interaction, therefore the rank of ASVi and rank of mean are incorporated in a single selection index namely Genotype Selection Index (GSI). The least GSI is considered as the most stable (Table 6) in that regard the G8, G11, G10 and G3 were considered as most stable genotypes, whereas, G9, G7, G14, G13 and G4 are the least stable genotypes.

Table 5: ANOVA table for AMMI model.

Source	df	TSS	m.s	TSS%	GE explained %	Cumulative %	MS
Total	335	182864099	545863				545863
Treatment	111	169822989	1529937				1529937**
Genotypes	13	19431998	1494769	11.4			1494769**
Environments	7	121956368	17422338	71.8			17422338**
Block	16	2478855	154928	1.5			154928
Interactions	91	28434623	312468	16.7			312468**
IPCA 1	19	12585700	662405		44.3	44.3	662405**
IPCA 2	17	6032355	354844		21.2	65.5	354844**
IPCA 3	15	3263288	217553		11.5	77	217553**
IPCA 4	13	2726283	209714		9.6	86.6	209714**
Residuals	27	3826998	141741				141741
Error	208	10562254	50780				50780

NB: The block source of variation refers to blocks within environments.

Table 6: genotype means, scores and AMMI stability value (ASV).

Genotype	Mean	ASV	Seed yield rank	Stability rank	GSI	IPCAg1	IPCAg2	IPCAg3	IPCAg4
G1	2384	10.42	3	11	14	5.88232	9.81864	7.45821	9.27151
G2	2114	3.63	9	2	11	4.24549	2.56128	-5.25593	1.84280
G3	2217	4.11	7	3	10	7.65135	-0.95332	10.43894	-7.47326
G4	2249	23.47	4	14	18	0.48593	23.45240	-8.43406	-12.80773
G5	2162	4.35	8	4	12	6.21169	2.43681	7.64620	18.61241
G6	2104	9.35	11	7	18	0.52215	-9.29048	3.60377	0.06764
G7	2006	9.36	14	8	22	6.00542	-8.66521	-18.33663	0.48607
G8	2914	8.89	1	6	7	-35.57276	-2.20163	-5.53025	4.60170
G9	2111	16.28	10	13	23	4.40646	-15.99101	-1.35555	-6.48957
G10	2665	10.33	2	10	12	-14.90098	8.70152	13.32077	-4.50512
G11	2246	5.33	5	5	10	-4.54483	2.78492	-9.48354	6.51561
G12	2077	3.42	13	1	14	-1.88744	-8.64693	7.06050	-12.84473
G13	2244	11.56	6	12	18	3.68424	-11.22211	2.72216	2.51230
G14	2103	9.45	12	9	21	17.81095	7.21514	-3.85459	0.21037

Note: ASV- AMMI stability value; GSI- Genotype selection index.

Table 7: the first four AMMI selections per environment.

Environment	Environment	Mean	1	2	3	4
8	WLH2016	2072	G8	G9	G14	G7
3	CH2015	3668	G8	G14	G7	G11
6	KB2016	1659	G10	G4	G1	G8
1	SR2015	2097	G10	G8	G3	G13
2	KB2015	1599	G8	G5	G1	G10
5	SR2016	2475	G10	G8	G4	G3
7	CH2016	2289	G8	G10	G4	G1
4	WLH2015	2210	G8	G10	G11	G13

According to the first four AMMI selections per environment, G8 (genotype ICCV-93954) selected five times under first class and two times under second class this indicates G8 was the best performed overall the genotypes (Table 5). Depending on its performance this genotype was the best genotype to release as variety with G10 (genotype DO47) which was selected once under first and fourth class and six times under second class. G1 (genotype ICCV-08104) was selected twice under first class and once under third class. This genotype was also selected three times under fourth class. Based on this, G8 the most stable genotype followed by G10 and G1 (Table 5).

The best performs and stable genotype ICCV-93954 (G8) has 36.3 and 40% yield advantage over the standard checks (Table 6). The second-best genotype DO47 (G10) has 27.1 and 31.4% yield advantage over the checks. The genotype ICCV-07108 (G1) is the third best performed compare to others genotype including the checks.

CONCLUSION AND RECOMMENDATION

The development of varieties, which are adapted to a wide range of diversified environments, is ultimate aim of breeders in crop improvement programs. The adaptability of genotypes over diverse environments is commonly evaluated by the degree of its interaction with different environments in which it is grown. The combined analysis of variance revealed significant differences among the genotypes for all of the studied traits. According to the variance and genotype by environment interaction analysis result three promising genotypes namely ICCV-93954, DO47 and ICC-07108 with average seed yield of 2931.5kg/ha, 2731.6kg/ha and 2335.4kg/ha respectively, were selected and promoted for identification. Therefore, these three genotypes evaluated by National variety release committee to release as a variety. Among the identified genotypes ICCV-93954 has been officially released and recommended for production with its name Mitik for the tested and other similar agro-ecologies of chickpea growing areas in the northeastern part of Amhara National Regional State.

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