Evaluation of Desi Type Chickpea (*Cicer artinum* 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 29 31.5kg/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 (ICRISAT, 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.

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MATERIALS AND METHOD

The experiment was conducted in the northeastern part of Amhara National Regional State at four locations, namely; Srinika, 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 Srinika. Only twelve genotypes were advanced to regional variety trial and tested with varieties Kutaye and Minjar as checks at Srinika, 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 9.6m². 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 (GYi) 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:

\[ \text{GSI} = \frac{\text{RASVi} + \text{RYi}}{2} \]

**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 kgs/ha) whereas, the lowest seed yield performance was recorded for genotype ICCV-08104 (1992kgs/ha) (Table 2). The standard checks, variety Kutaye and Minjar, recorded 2150kg/ha and 2093.5kg/ha respectively, under the total grand mean of seed yield (2230.3kg/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 (93days) 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 23.3g and 23g, 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 3685.7kg/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.

| 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°04’5”| 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| 1.2d| 42.1a-d| 33.5a| 2151.2de |
| 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| 2053.9gf |
| 6    | DO62      | 44gh| 94ef| 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    | DO47      | 44h | 93g| 46a| 1.6ab| 36.3g| 25.8e| 2731.6b |
| 10   | ICCV-03203| 50a | 98a| 32g| 1.7a| 40.1ef| 27.2e| 2057.9gf |
| 11   | DZ-2012-CK-0027| 47bc| 96bc| 37cde| 1.3cde| 43.3ab| 29.9cd| 2235.3cd |
| 12   | DZ-2012-CK-0033| 47b | 96c| 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| 23.9| 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.
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 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).

**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 |
|---------------------|-----|--------------|
| Genotype (Gen)      | 13  | 12982.68**   |
| Location (Loc)      | 3   | 309955.9**   |
| Year (Yr)           | 1   | 400292.4*    |
| Gen x Loc           | 39  | 294393.3**   |
| Gen x Yr            | 13  | 328754.3**   |
| Gen x Loc x Yr      | 42  | 130950.7**   |

*, **-Significant at 5%; AYKGHA-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 | 2086.0 |
| 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 | 1194  | 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  | 2284 | 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.
Evaluation of Desi Type Chickpea (*Cicer aritinum* L.) Genotypes for Yield and Yield Components in Eastern Amhara, Ethiopia (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 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-00104 (6.21) > ICCV-08104 (6.01) > ICCV-00104 (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 IPCA1 (interaction principal component analysis axis 1) scores against IPCA2 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 IPCA1 and IPCA2 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

| 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        |
| Environments| 7  | 121956368 | 17422338 | 71.8        |
| Block       | 16 | 2478855   | 154928   | 1.5         |
| Interactions| 91 | 28434623  | 312468   | 16.7        |
| IPCA 1      | 19 | 12585700  | 662405   | 44.3        |
| IPCA 2      | 17 | 6032355   | 354844   | 21.2        |
| IPCA 3      | 15 | 3263288   | 1043894  | 65.5        |
| IPCA 4      | 13 | 2726283   | 209714   | 86.6        |
| Residuals   | 27 | 3826998   | 141741   | 50780       |
| 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 | -5.30252 | 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 | Mean | 1  | 2  | 3  | 4  |
|-------------|------|----|----|----|----|
| 8           | 2072 | G8 | G9 | G14| G7 |
| 3           | 3668 | G8 | G14| G7 | G11|
| 6           | 1659 | G10| G4 | G1 | G8 |
| 1           | 2097 | G10| G8 | G3 | G13|
| 2           | 1599 | G8 | G5 | G1 | G10|
| 5           | 2475 | G10| G8 | G4 | G3 |
| 7           | 2289 | G8 | G10| G4 | G1 |
| 4           | 2210 | G8 | G10| G11| G13|

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.

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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