# AMMI and GGE-Biplot Analyses of Taro (*Colocasia esculenta* (L.) Schott) Genotypes in Southwest Ethiopia

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## Abstract

*The study was conducted in major taro growing areas of Jimma, Agaro, Gera and Metu for two consecutive cropping seasons (20219-2021). Nine genotypes and one standard check were evaluated to identify high yielding and stable genotypes for further breeding works. The experiment was established by using a Randomized Complete Block Design (RCBD) with three replications. Data for yield and yield related traits were collected and analyzed using the additive main effect and multiplicative interaction (AMMI) and genotype main effect plus genotype by environment interaction (GGE) bi-plot analyses. The result of the combined analysis of variance revealed significant differences ($p<0.01$) for genotype, environment and genotype by environment interaction effects for all the traits considered except for root length. The average total storage root yield of the genotypes across the eight environments was 25.69 t/ha. Genotypes 053, 133 and Kiyaq gave the highest yield of 29.17 t/ha, 26.36 t/ha and 25.99 t/ha root yield, respectively. Genotype 165 was the lowest performing genotype and it produced average storage root yield of 24.1 t/ha. AMMI and GGE bi-plot analyses revealed that genotypes 053 and 133 were the ideal genotypes with high yield and wider adaptability. On the other hand, genotypes 165, 130, 023 and 032 were found to be unstable genotypes. Furthermore, AMMI and GGE bi-plot exhibited Agaro-2 and Gera-2 were the most discriminating and representative environment for the evaluation of taro genotypes for yield and yield components. Genotypes 053 and 133 were found to be widely adaptable and had yield stability across environments.* Therefore, the two genotypes are recommended for release for production in southwest Ethiopia

**Keywords:** AMMI, Genotype by environment interaction, GGE bi-plot, Root yield and Taro

## Introduction

Taro (*Colocasiaesculenta* (L.) Schott) is one of the oldest cultivated crops in the world serving as food for mankind for over 9000 years (Adelekan, 2012; Esther *et al.*, 2020). It is an important root crop and potentially produced for reasonable yield under conditions where most crops fail, making it a food security crop (Singh *et al*. 2008; Tewodros and Getachew, 2013; Yared *et al*., 2014). In most producing areas, taro production is usually carried out by smallholder farmers with little reliance on external support and plays important economic and nutritional roles in the livelihood of many poor

farmers in developing countries (Singh *et al*., 2012; Singh *et al*., 2012; Banjaw, 2017). The leaves and petioles of taro also serve as rich source of protein, carbohydrate, fiber, minerals, vitamins and micronutrients and consumed as vegetables in Africa (Esther *et al*., 2020).

In Ethiopia, taro is cultivated at subsistence level due to the unavailability of high yielding varieties which are stable and adaptable to different environments (Tewodros and Getachew. 2013; Yared *et al*., 2014; Asfaw *et al.,* 2020). The most effective way of producing more stable and high yielding varieties is through evaluation of genotypes in multi-location trials (MET) (Fan *et al*., 2007; Esther *et al.,* 2020). The success of genetic enhancement programme hinges on identification of best genotypes adapted to a specific time in a year with the conducive rainy season, frost-free time, drought spell that made stable performance for harnessing maximum gains from the selection. The yield of each genotype in each test environment is a measure of an environment main effect (E), a genotype main effect (G), and the genotype × environment (GE) interaction (Yan and Tinker, 2006). Typically, environmental effect elucidates 80% or higher of the total yield variation in many crops; however, it is genotype and genotype × environment interaction that are relevant to genotype evaluation (Yan and Rajcan, 2002). The GE interaction has been extensively studied on taro by different researchers, and several methods have been proposed to analyze it. For instance, Sing *et al*.,(2006) reported that the evaluation of multi-location trial on taro genotypes collected from New Zealand; Asfaw *et al.,* (2020) described the additive main effect and multiplicative interaction (AMMI) and genotype plus genotype × environment (GGE) bi-plot study of taro from Southern Ethiopia, Further, Eze *et al.* (2016) reported the evaluation of taro genotypes based on AMMI and GGE from Nigeria. Esther *et al.,* (2020) reported the estimation of GxE and the yield stability performance of taro genotypes from Ghana. Frequently, a large number of genotypes are tested across a number of environments, seasons and years, and it is often difficult to determine the pattern of genotypic response across locations or seasons without the help of graphical display of the data (Yan *et al.* 2001). Bi-plot analysis provides solution to the aforementioned problem as it displays the two-way data and allows visualization of the interrelationship among environments, genotypes, and interactions between genotypes and environments (Owusu *et al.,* 2018). Two types of bi-plots, the AMMI bi-plot (Gauch, 1988; Gauch and Zobel, 1997) and the GGE bi-plot (Yan and Rajcan, 2002; Aina *et al*. 2007) have been used widely to visualize genotype × environment interaction.

AMMI is a statistical model that combines analysis of variance with principal component analysis to adjust

the main effects and G×E interaction effects (Gauch and Zobel, 1996; Aian *et al*. 2007; Gauch, 2013). The GGE bi-plot analysis was developed by Yan *et al*. (2000) to determine the relationship between genotypes and test environments graphically. These models are providing valuable insights in assessing the extent of G×E interactions in multiple environments and also to classify the environments of taro (Badu-Apraku and Oyekunle, 2012). Understanding the nature and magnitude of GxE are important to identify the most discriminating and representative environments for taro production in Ethiopia. Therefore, the objectives of the current study were (i) to determine the effect of GEI on yield and yield related traits of taro genotypes in major growing areas of southwest Ethiopia, (ii) to select stable and high yielding taro genotypes for the yield and yield related traits for further breeding works and (iii) to determine the most discriminating and representative environment for the root yield and yield related traits of taro in Southwest Ethiopia.

# Materials and Methods

## Study areas

The field experiments were conducted at Jimma Agricultural Research Center, and Agaro, Gera and Metu Sub-centers, which are considered as representative taro growing areas of southwest Ethiopia. The experiment was conducted for two consecutive cropping seasons (2019/20 and 2020/21) in all the four locations. This made a total of eight environments considering one location and one cropping season as one environment. The detail descriptions of all test sites are presented in Table 1.

Table 1. Description of the study sites

| Location | Altitude (m.a.s.l.) | Latitude | Longitude | Rainfall (mm) | Temperature ($^0$C) | |
|---|---|---|---|---|---|---|
| | | | | | Maximum | Minimum |
| Jimma | 1753 | 7$^o$ 40.00' N | 36$^o$ 47'.00' E | 1521 | 26.2 | 12.1 |
| Agaro | 1560 | 7°51' .00' N | 36°51' 35' E | 1520 | 23.3 | 12.6 |
| Gera | 1970 | 7$^o$ 31.60' N | 36$^o$ 15'.00' E | 1877 | 18.6 | 12.0 |
| Metu | 1550 | 8°18' .00' N | 35°35' .00' E | 1520 | 28.0 | 12.2 |

Source: JARC, 2010

## Plant materials, experimental design and management

Nine taro genotypes which were collected from major growing areas of Southwest Ethiopia and one released variety (Kiyaq) were used for this study. The genotypes were evaluated using a randomized complete block design (RCBD) with three replications. The gross plot size for

each treatment was 9 $m^2$ (3 m x 3 m), using inter-row spacing of 0.75 m and intra-rows spacing of 0.5 m. Corms of the same size and age were used as planting material. One month after planting, seedlings were earthed up followed by frequent weeding. All other agronomic practices were applied according to the recommendations.

## Data collection

Data were collected from eight middle plants from each plot and the average values were used for data analysis. The traits used for data collection were : number of tillers per plant, storage root length (cm), storage root diameter (cm), marketable storage root number per plant (number of marketable or saleable roots represents the number of roots that were more than or equal to 100 g or with diameters at the widest point >25mm roots) (Levette, 1993), total number of storage root number $plant^{-1}$, weight of marketable storage root (t/ha), and weight of total storage root (t/ha).

## Data analysis

Homogeneity of residual variance was tested prior to combined analysis over locations in each year as well as over locations and years (for the combined data) using Bartlet's test (Steel and Torrie, 1980). Accordingly, the data collected indicated homogenous variance. Normality test was also conducted and all data showed normal distribution. The collected data were subjected to analysis of variance (ANOVA) for each location and combined over environments following the standard procedure using SAS software (SAS, 2000) and GenStat software (Payne *et al*., 2011). Treatment means were separated by using the Fisher's protected least significant difference (LSD) test at 1% and 5% probability levels.

## AMMI analysis

The total root yield was subjected to the combined analysis of variance and AMMI analysis, which is a combination of analysis of variance and multiplication effect analysis. The analysis of variance was used to partition variance into three components: genotype deviations from the grand mean, environment deviations from the grand mean, and G×E deviations from the grand mean. Subsequently, multiplication effect analysis was used to partition G×E deviations into different interaction principal component axes (IPCA), which were tested for statistical significance through ANOVA. To determine the G × E interaction for yield parameters, AMMI and GGE bi-plot analyses were performed. The following AMMI model was used (Gauch, 2013). Genotypic stability for each genotype was computed using GenStat software, as prescribed by Malhotra *et al*., (2007). The additive main effects and multiplicative interactions (AMMI) statistical model reported by Gauch and Zobel (1996), was used to analyze yield data to obtain AMMI analysis of variance and AMMI mean estimates as follows:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum \Lambda_n y_{gn} \delta_{en} + \rho_{ge} + E_{ger}$$

Where: $Y_{ger}$ = yield of genotype g in environment e for replicate r, $\mu$ = grand mean, $\alpha_g$ = genotype mean deviation (genotype means minus grand mean), $\beta_e$ = environment mean deviation, n = number of principal component analysis (PCA) axes retained in the model, $\Lambda_n$ singular value for PCA axis n,$y_{gn}$ = genotype eigenvector values for PCA axis n $\delta_{en}$ = environment eigenvector values for PCA axis n, $\rho_{ge}$ = residuals, $E_{ger}$ = error term.

The GGE bi-plot model was also used to determine the influence of GEI on total storage root yield, storage root length and marketable storage root number per plant across test environments. The model for the GGE bi-plot based on singular value decomposition (SVD) of first two principal components were calculated by using the model developed by Yan *et al*, (2007) as follows:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where: $Y_{ij}$= measured mean of genotype i in environment j, $\mu$= grand mean, $\beta_j$ = main effects of environment j, $\mu + \beta_j$ = the mean yield across all genotypes in environment j, $\lambda_1$ and $\lambda_2$= are the singular values (SV) for the first and second principle components (PCA-1 and PCA-2) respectively. $\xi_{i1}$and$\xi_{i2}$ = are eigenvectors of genotype i for PCA-1 and PCA-2, respectively, $\eta_{j1}$ and$\eta_{j2}$ = eigenvectors for environment j for PCA-1 and PCA-2, respectively.$\varepsilon_{ij}$= residual associated with genotype i in environment j.

# Results and Discussion

## Analysis of variance for the storage root yield and yield related traits of taro genotypes

The results from the combined analysis of variance revealed that the genotype and environment components showed highly significant variations ($p<0.01$) for all agronomic traits. Except storage root length and girth, the other traits also showed significant variations ($p<0.01$) for genotype x environment interaction GEI (Table 2). The results further revealed that, the response of the genotypes were varied and fluctuated in their trait expression with change in the environments. These all phenomena clearly confirm the existence of GEI in this study.

**Table 2**. Mean squares for yield and related traits of taro genotypes across the test locations

| Sources of variation | DF | Mean squares | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | TSRW | NTPH | SRL | SRG | MSRN | TSRNP | MSRW |
| Block | 16 | 13.12 | 17.39 | 3.43 | 3.51 | 4.94 | 19.11 | 12.72 |
| Genotype (G) | 9 | 30.34** | 47.40*** | 1.97* | 3.15*** | 19.77*** | 38.14*** | 43.98*** |
| Environment (E) | 7 | 81.88*** | 647.77*** | 32.37*** | 32.54*** | 116.74*** | 655.74*** | 154.04*** |
| G*E | 63 | 10.88* | 17.14** | 1.19 | 1.12 | 4.44*** | 19.92*** | 21.57* |
| Residual | 35 | 6.43 | 6.04 | 0.50 | 0.66 | 1.21 | 6.39 | 6.98 |

**, **, *** significant at 0.05, 0.01 and 0.001 % of probability level. DF= Degree of freedom, TSRW= Total storage root weight (t/ha), NPTH= Number of tillers per hill, SRL= Storage root length (cm), SRG= Storage root girth (cm), MSRN= Marketable storage root number, TSRW= Total storage root number and, MSRW= Marketable storage root weight (t/ha)*

For most of the traits, the contribution of environment for the overall variance varied from 16.83% for total storage root weight to 57.74% for total storage root number followed by genotype x environment interaction and genotype, respectively (Table 3). Similar results were reported by Sing *et al* (2006) and Tewodros and Getachew (2013). With respect to total storage root weight, the greatest source of variance was mainly the inherent genetic component, meaning genotypic effect (8.02%) (Table 3), which is similar to the results reported by Asfaw *et al.*, (2020).

## The agronomic performance of taro genotypes

The average total storage root yield of ten tested taro genotypes over the eight environments was 25.69 t/ha. Genotype 053 had the highest average total storage root yield of 29.17 t/ha, followed by genotype 133 (26.36 t/ha) and Kiyaq (25.99 t/ha), respectively, while, genotype 165 was the lowest yielding genotype with average yield of 24.15 t/ha (Table 4).

Genotype Kiyaq had the highest average storage root length and girth (18.02 and 33.02 cm), and marketable and total storage root numbers (6.65 and 12.13). While, genotype 9/75 produced the lowest storage length and girth of 16.83 and 31.83 cm and genotype 183 produced the lowest marketable and total storage roots numbers of 3.74 and 7.76, respectively (Table 4).

Table 3. Combined sum of squares for yield and related traits of taro genotypes evaluated during 2019/20-2020/21 cropping season

| Sources of Variation | DF | TSRW | NTPH | SRL | SRG | MSRN | TSRN | MSRW |
|---|---|---|---|---|---|---|---|---|
| Block | 16 | 210(6.17) | 278(3.5) | 54.9(10.47) | 56.2(10.62) | 79.0(4.75) | 306(3.85) | 203(4.85) |
| Gen | 9 | 273.1(8.02) | 427(5.37) | 17.7(3.38) | 28.4(5.37) | 177.9(10.69) | 343(4.31) | 396(9.46) |
| Env | 7 | 573.2(16.83) | 4534(57.02) | 226.6(43.22) | 227.8(43.04) | 817.2(49.10) | 4590(57.74) | 1078(25.75) |
| Gen*Env | 63 | 685.5(20.13) | 1080(13.58) | 75.1(14.32) | 70.9(13.40) | 279.8(16.81) | 1255(15.79) | 729(17.42) |
| Residual | 35 | 224.9(6.60) | 212(2.67) | 17.8(3.40) | 23.1(4.36) | 42.5(2.55) | 224(2.82) | 244(5.83) |
| Total | 239 | 3405.8 | 7952 | 524.3 | 529.3 | 1664.2 | 7950 | 4186 |

**Note:** Number inside and outside parentheses are SS and % of SS of traits, respectively. DF= Degree of freedom, Gen= Genotype, Env= Environment, TSRW= Total storage root weight (t/ha), NPTH= Number of tillers per hill, SRL= Storage root length (cm), SRG= Storage root girth (cm), MSRN= Marketable storage root number, TSRW= Total storage root number and, MSRW= Marketable storage root weight (t/ha)

Table 4. Combined mean yield and yield related traits of taro genotypes across all test environments

| Genotypes | TSRW | NTPH | SRL | SRG | MSRN | TSRN | MSRW |
|---|---|---|---|---|---|---|---|
| 44/75 | 24.63bc | 6.55 bcd | 17.34bc | 32.34bc | 4.13de | 8.59de | 20.7cde |
| 133 | 26.36bc | 5.93d | 17.19bc | 32.19bc | 4.45cde | 8.88cde | 22.98b |
| Kiyaq | 25.99bc | 6.23 bcd | 18.02a | 33.02a | 6.65a | 12.13a | 22.56bc |
| 165 | 24.15c | 6.87bc | 17.07bc | 32.07bc | 4.98cd | 10.35abcd | 19.83e |
| 130 | 25.92bc | 6.88bc | 16.90c | 31.90c | 5.17bc | 11.45ab | 22.18cde |
| 023 | 24.64bc | 7.03b | 17.04bc | 32.04bc | 4.99cd | 11.25ab | 22.18bcd |
| 9/75 | 24.99bc | 8.04a | 16.83c | 31.83c | 4.65cde | 10.56abc | 20.89cde |
| 183 | 25.36bc | 6.07cd | 17.29bc | 32.29bc | 3.74e | 7.76e | 21.3bcde |
| 032 | 25.65bc | 6.75bc | 17.03bc | 32.03bc | 4.47cde | 10.08bcd | 21.1bcde |
| 053 | 29.17a | 6.17cd | 17.63ab | 32.63ab | 5.99ab | 11.15ab | 25.04a |
| Mean | **25.69** | **6.65** | **17.23** | **32.23** | **4.92** | **10.22** | **21.70** |
| LSD | **1.91** | **0.81** | **0.63** | **0.63** | **0.97** | **1.97** | **2.00** |
| CV(%) | **13.06** | **21.53** | **6.50** | **3.47** | **34.63** | **33.80** | **16.20** |

*Means followed by the same letter are not statistically different from each other DF= Degree of freedom, TSRW= Total storage root weight (t/ha), NTPH= Number of tillers per hill, SRL= Storage root length (cm), SRG= Storage root girth (cm), MSRN= Marketable storage root number, TSRW= Total storage root number and, MSRW= Marketable storage root weight (t/ha)*

## Variance estimate for total storage root yield and related traits of taro genotypes

The combined analyses of variance (ANOVA) of the agronomic traits evaluated in eight environments revealed that there were highly significant variations ($p<0.01$) among the genotypes, environments (year, location, year x location) and genotype by environment interaction (genotype x year, genotype x location and genotype x year x location) (Table 5). These significant variations of the genotypes, environments and the genotype by environment interaction indicated that the response of the genotypes were variable and varied in their total storage root yield with change in environment and these phenomena clearly declared the presence of GEI in this study.

The storage root yields of the ten taro genotypes were highly variable over the eight environments, showing a cross-over interaction from environment to environment. Among the environments the highest total storage root yield (25.04 t/ha) was obtained from genotype 053 and Metu-2 was the best environment. While, the lowest root yield (19.83 t/ha) was recorded from genotype 165 and Jimma-1 was the least suitable environment for taro production (Table 6).

Table 5. Combined analysis of variance and significant tests for taro yield and related traits of ten genotypes tested at four locations for two years.

| Sources of variation | DF | Mean squares | | | | | |
|---|---|---|---|---|---|---|---|
| | | TSRW | NTPH | SRL | MSRNP | TSRNP | MSRW |
| Environment (E) | 3 | 47.85*** | 337.07*** | 45.80*** | 159.9*** | 501.8*** | 128.6*** |
| Genotype (G) | 9 | 47.48*** | 9.17*** | 3.15** | 17.90*** | 47.4*** | 55.97*** |
| Year (Y) | 1 | 353.12*** | 161.04*** | 4.69* | 71.38*** | 136.1*** | 563.6*** |
| Y*E | 3 | 4.53 | 15.23*** | 28.57*** | 82.91*** | 964.3*** | 24.0 |
| G*E | 27 | 20.14* | 4.90*** | 1.09 | 2.55 | 12.63 | 21.65* |
| G*Y | 9 | 9.15 | 1.14 | 0.29 | 2.36 | 34.83** | 16.11 |
| G*Y*E | 27 | 14.05 | 1.50 | 1.43 | 4.44* | 15.74 | 11.52 |
| Error | 158 | 11.26 | 2.05 | 1.25 | 2.91 | 11.94 | 12.38 |

**, **, *** significant at 0.05, 0.01 and 0.001 % of probability level.*

**Table 6.** Mean total storage root yield (t/ha) performance of ten taro genotypes tested across eight environments

| Genotypes | Environments | | | | | | | | Over all mean |
|---|---|---|---|---|---|---|---|---|---|
| | Jimma-1 | Agaro -1 | Gera-1 | Metu -1 | Jimma-2 | Agaro-2 | Gera-2 | Metu -2 | |
| 44/75 | 17.50 | 15.33 | 18.09 | 22.95 | 22.11 | 20.73 | 22.81 | 26.22 | 24.63 |
| 133 | 22.35 | 20.33 | 22.54 | 24.57 | 24.44 | 23.04 | 22.98 | 23.59 | 26.36 |
| Kiyaq | 23.74 | 15.50 | 24.44 | 24.59 | 24.00 | 21.33 | 24.52 | 22.40 | 25.99 |
| 165 | 13.18 | 17.67 | 16.67 | 18.81 | 23.78 | 22.54 | 22.27 | 23.73 | 24.15 |
| 130 | 19.67 | 17.67 | 22.57 | 18.57 | 23.55 | 19.96 | 23.17 | 25.24 | 25.36 |
| 023 | 15.71 | 17.50 | 18.51 | 23.81 | 24.51 | 17.82 | 21.03 | 24.62 | 24.64 |
| 9/75 | 17.46 | 18.16 | 18.41 | 23.67 | 23.55 | 19.67 | 21.92 | 24.26 | 24.99 |
| 183 | 18.09 | 24.33 | 18.73 | 22.14 | 26.44 | 21.48 | 22.45 | 23.82 | 25.92 |
| 032 | 20.77 | 19.78 | 18.57 | 18.09 | 26.06 | 10.90 | 21.47 | 24.27 | 25.65 |
| 053 | 25.08 | 20.50 | 23.81 | 27.09 | 24.55 | 25.51 | 25.96 | 27.82 | 29.17 |
| **Mean** | **19.35** | **18.67** | **20.23** | **22.43** | **24.30** | **21.20** | **22.85** | **24.59** | **25.69** |
| **LSD** | **5.69** | **5.43** | **5.9** | **5.94** | **6.19** | **5.98** | **4.73** | **2.49** | **5.29** |
| **CV(%)** | **17.15** | **25.07** | **17.01** | **15.44** | **14.85** | **16.45** | **12.09** | **5.90** | **15.50** |

**Table 7.** Mean storage root length (cm) performance of ten taro genotypes tested across eight environments

| Genotypes | Environments | | | | | | | | Over all mean |
|---|---|---|---|---|---|---|---|---|---|
| | Jimma-1 | Agaro -1 | Gera-1 | Metu -1 | Jimma-2 | Agaro-2 | Gera-2 | Metu -2 | |
| **44/75** | **19.14** | **19.49** | **16.90** | **17.75** | **14.80** | **17.65** | **18.13** | **14.92** | **17.35** |
| 133 | 18.81 | 18.08 | 16.65 | 18.12 | 16.21 | 17.63 | 16.97 | 15.96 | 17.30 |
| **Kiyaq** | **18.90** | **18.02** | **17.12** | **18.84** | **16.93** | **17.73** | **17.08** | **16.69** | **17.66** |
| 165 | 19.21 | 18.52 | 16.16 | 17.23 | 15.54 | 18.08 | 17.09 | 15.20 | 17.13 |
| 130 | 18.22 | 17.50 | 16.37 | 17.97 | 15.94 | 17.01 | 16.50 | 15.74 | 16.91 |
| 023 | 18.72 | 18.03 | 16.27 | 17.60 | 15.73 | 17.55 | 16.81 | 15.47 | 17.02 |
| 9/75 | 18.16 | 17.63 | 16.35 | 17.87 | 15.63 | 16.89 | 16.61 | 15.51 | 16.83 |
| 183 | 18.26 | 18.08 | 17.21 | 18.72 | 15.93 | 16.83 | 17.23 | 16.02 | 17.29 |
| 032 | 19.24 | 17.76 | 15.86 | 17.23 | 16.45 | 18.38 | 16.35 | 15.78 | 17.13 |
| 053 | 18.25 | 17.86 | 17.69 | 19.67 | 16.89 | 16.83 | 17.27 | 16.99 | **17.68** |
| **Mean** | 18.69 | 18.10 | 16.66 | 18.10 | 16.01 | 17.46 | 17.00 | 15.83 | 17.23 |
| **LSD** | 1.34 | **1.83** | **1.95** | **1.59** | **1.36** | **3.29** | **2.03** | **3.71** | **2.14** |
| **CV(%)** | **15.16** | **14.41** | **14.04** | **16.58** | **25.14** | **22.95** | **18.55** | **40.12** | **20.87** |

**Table 8.** Mean marketable number of root per plant performance of ten taro genotypes tested across eight environments

| Genotypes | Environments | | | | | | | | Over all mean |
|---|---|---|---|---|---|---|---|---|---|
| | Jimma-1 | Agaro -1 | Gera-1 | Metu -1 | Jimma-2 | Agaro-2 | Gera-2 | Metu -2 | |
| 44/75 | 3.845 | 4.966 | 7.254 | 4.514 | 3.157 | 2.044 | 4.203 | 3.108 | 4.136 |
| 133 | 3.613 | 5.461 | 8.928 | 4.527 | 3.496 | 1.919 | 4.510 | 3.179 | 4.454 |
| Kiyaq | 4.209 | 12.175 | 14.30 | 6.200 | 4.815 | 2.516 | 6.141 | 4.333 | **6.836** |
| 165 | 4.285 | 7.433 | 7.949 | 5.195 | 3.355 | 2.378 | 4.573 | 3.498 | 4.833 |
| 130 | 5.120 | 5.303 | 7.957 | 5.638 | 4.380 | 3.332 | 5.369 | 4.326 | 5.178 |
| 023 | 4.636 | 4.529 | 7.677 | 5.141 | 4.017 | 2.882 | 4.970 | 3.892 | 4.718 |
| 9/75 | 4.419 | 6.296 | 7.330 | 5.127 | 3.426 | 2.531 | 4.556 | 3.559 | 4.656 |
| 183 | 3.709 | 4.865 | 6.122 | 4.295 | 2.654 | 1.826 | 3.754 | 2.794 | 3.752 |
| 032 | 4.521 | 5.063 | 7.036 | 5.050 | 3.605 | 2.685 | 4.644 | 3.653 | 4.532 |
| 053 | 4.125 | 8.219 | 14.38 | 5.713 | 5.429 | 2.686 | 6.393 | 4.459 | **6.426** |
| **Mean** | 4.248 | 6.431 | **8.893** | **5.140** | 3.833 | 2.480 | **4.911** | **3.680** | 4.952 |
| **LSD** | **1.48** | **1.33** | **1.60** | **1.42** | **2.00** | **1.43** | **2.09** | **1.16** | **1.56** |
| **CV(%)** | **2.76** | **3.42** | **2.95** | **2.59** | **3.60** | **2.52** | **3.69** | **2.20** | **2.97** |

## Additive main effect and multiplicative interaction (AMMI 2) bi-plot analysis

The performance of a genotype in the environment is considered better than the average performance in that environment if the angle between its vector and the environment is less than acute angle ($90^0$); near average if the angle is $90^0$ (right angle) and below average if the angle is greater than $90^0$ (obtuse angle) (Yan *et al.* 2007). The AMMI-2 bi-plot analyses of total storage root weight (TSRW), storage root length (SRL) and marketable number of roots per plant (MSRNP) of the ten genotypes evaluated in eight environments are shown in Figures 1-3. For TSRW, the percentage of variation accounted by the IPCA-1 and IPCA-2 axes was 45.86% and 21.33%, respectively (Figure 1). Genotypes 2 (133), 1 (44/75), and 7 (9/75) had broad adaptability as they were located closer to the center of the bi-plot. Genotypes 9 (032), 8(183), 3 (Kiyaq), 5 (130) and 4 (165) were placed furthest from the point of origin, showing specific adaptation to the environments within their proximity on the bi-plot.

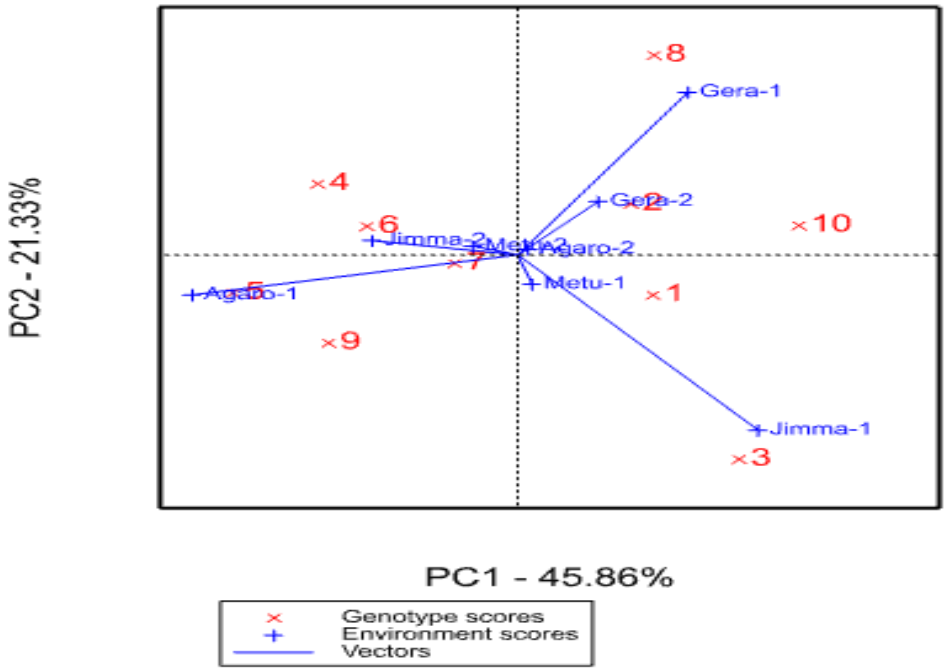


Figure 1. AMMI 2 bi-plot for IPCA 1 against IPCA 2 scores for 10 taro genotypes and eight environments on total storage root weight

Furthermore, genotypes 8 (183), 2 (133), and 10 (053) had above-average yields and were located on the acute angle of PC-1. Genotypes located on the right-hand side of the bi-plot were positively associated with the environments on the same side. Based on this analysis, environment Gera-1 was considered highly discriminating and had similar discriminating ability of the site since it had longer vector. Environments Gera-2 and Agaro-2 were highly positively correlated, indicating that genotypes ranked similarly with respect to total storage root weight in these environments. This suggested that these environments might form part of the same mega-environment.

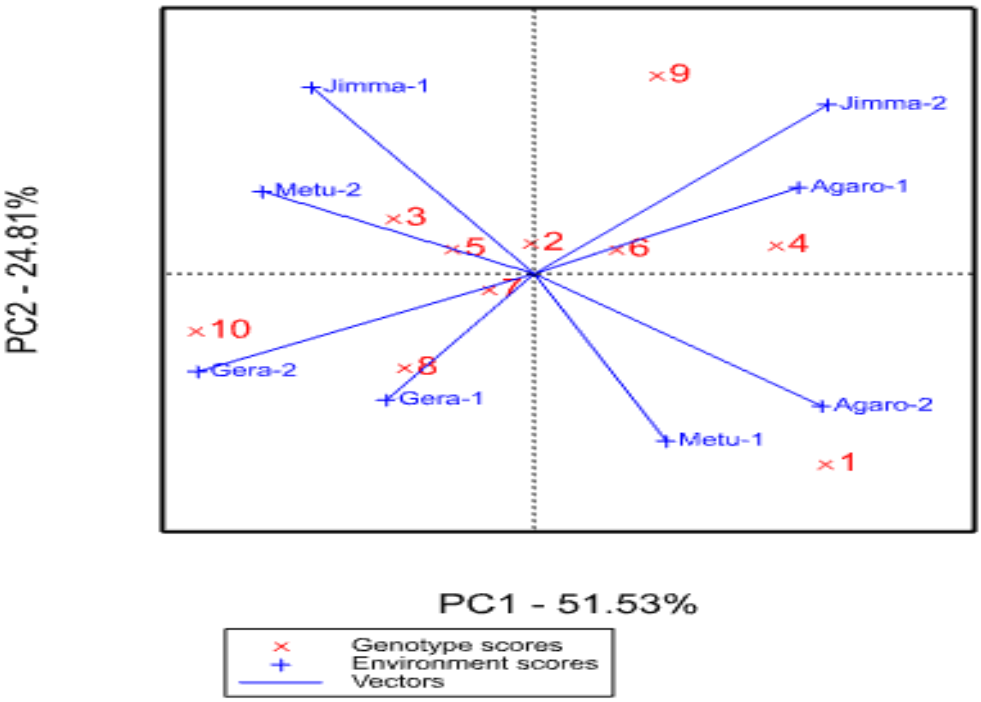


Figure 2. AMMI 2 bi-plot for IPCA-1 against IPCA-2 scores for 10 taro genotypes and eight environments on storage root length

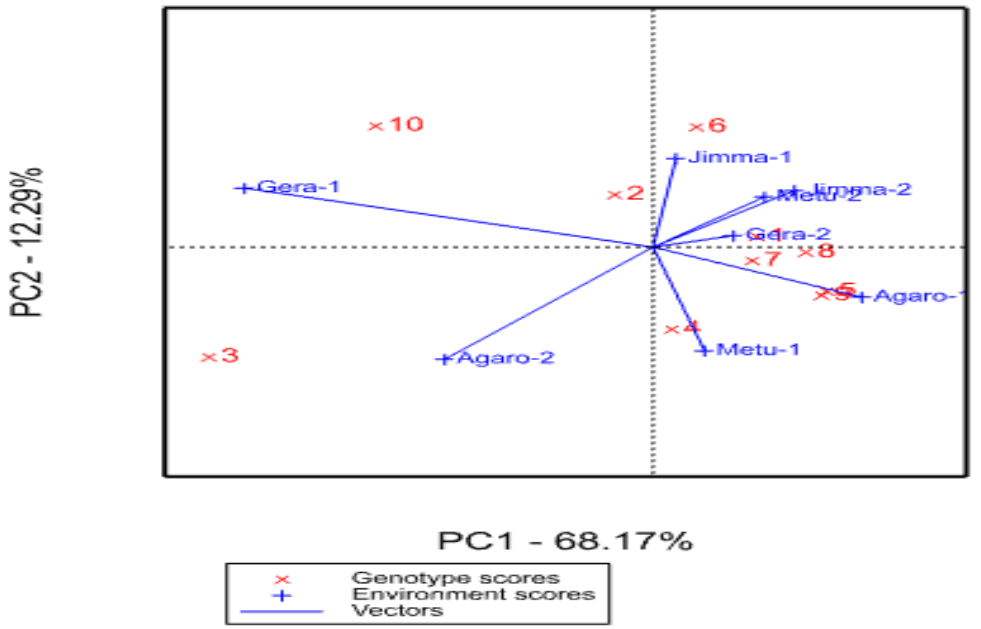


Figure 3. AMMI 2 bi-plot for IPCA 1 against IPCA 2 scores for 10 taro genotypes and eight environments on marketable number of root per plant

Regarding storage root length, the AMMI 2 bi-plot explained 76.34% of the total GEI (Figure 2). The percentage of variation accounted for by IPCA-1 and IPCA-2 was 51.53% and 24.81%, respectively. Genotypes 2 (133), 6 (023), 7 (9/75) and 5 (130) were close to the bi-plot origin; these genotypes had yields close to the overall mean yield. The following genotypes were positively correlated with environments closer to them: 032 (Jimma-2), 023 and 165 (Agaro-1), Kiyaq and 130 (Metu-2) and 053 (Gera-2). Genotypes located on the right-hand side of the bi-plot were positively correlated with the environments found on that side. Thus, all environments had similar discriminating ability of the site at different right angles. Environments Gera-1 and Metu-2 had the shortest vector, suggesting poor genotype discriminating ability.

The percentage of variation of AMMI-2 bi-plot for marketable storage root number accounted for by IPCA-1 and IPCA-2 was 68.17% and 12.29%, respectively (Figure 3). Genotypes 1(44/75), 7 (9/75) and 8 (183) were much closer to the bi-plot center, showing broader adaptability across the environments and had positively correlated with environments located on the right-hand side of the bi-plot. Genotypes 1 (44/75), 7 (9/75) and 8 (183) were positively correlated with environment Gera-2, and genotype 5 (130) and 9 (032) suggesting specific adaptation to this environment. In this investigation, except environments Gera-1, Agaro-2 and Agaro-1, all environments had shorter vectors, which implied the low discriminating ability of the sites. Most environments in this study had positive correlations. The positive correlation obtained between test environments also suggests that indirect selection for total storage root yields and related traits can be applied across the sites. Combining these environments into a single test environment can give similar genotypic responses, thus reducing unnecessary costs and improving breeding efficiency.

## Genotype yield and stability using GGE bi-plots

The average environment coordinate (AEC) view based on genotype-focused singular value partitioning (SVP = 1) can be referred as the "mean vs. stability" view of GGE bi-plot (Yan *et al.,* 2007). That view facilitates genotype comparisons based on mean performance and stability across environments within a mega-environment. The genotype stability view of GGE bi-plot explained 88.24, 68.98 and 86.03% of genotypic and genotype by environment variation for the total storage root weight, storage root length and marketable root number per plant, respectively (Figure 7: Panel A, B, and C). The arrow shows on the AEC abscissa points in the direction of higher trait performance of genotypes and ranks the genotypes with respect to trait performance. Thus, genotype 10 (053)

had the highest total storage root yield and marketable yield and genotype 1 (44/75) had the lowest (Figure 7: Panel A). Similarly, genotypes 3 (Kiyaq) and 10 (053), had the highest storage root length and marketable storage root per plant, respectively. Genotype 9 (032) and 4 (165) had the shortest storage root length and genotype 8 (183) had the lowest marketable storage root count (Figure. 7: Panel B, C, D, and E). The stability of each genotype was explored by its projection onto the AEC vertical axis. The most stable genotype was located almost on the AEC abscissa (horizontal axis) and had a near-zero projection onto the AEC (vertical axis). Thus, genotypes 10 (053) and 2 (133) were the most stable and 1 (44/75) and 4 (165) were the least stable for total storage root yield (Figure. 7: Panel A). According to Yan and Tinker, (2006), stability is meaningful only when associated with high trait mean. Therefore, an ideal genotype has both high trait mean and stable performance. An ideal genotype is represented on the head of arrow on the AEC abscissa (horizontal axis) (Figure. 7: Panel A, B and C). For storage root length, genotypes 3 (Kiyaq) and 10 (053) could be regarded as the best genotypes (Fig. 7: Panel B). Similarly, for marketable number of storage roots per plant these genotypes were the best (Figure. 7: Panel C).

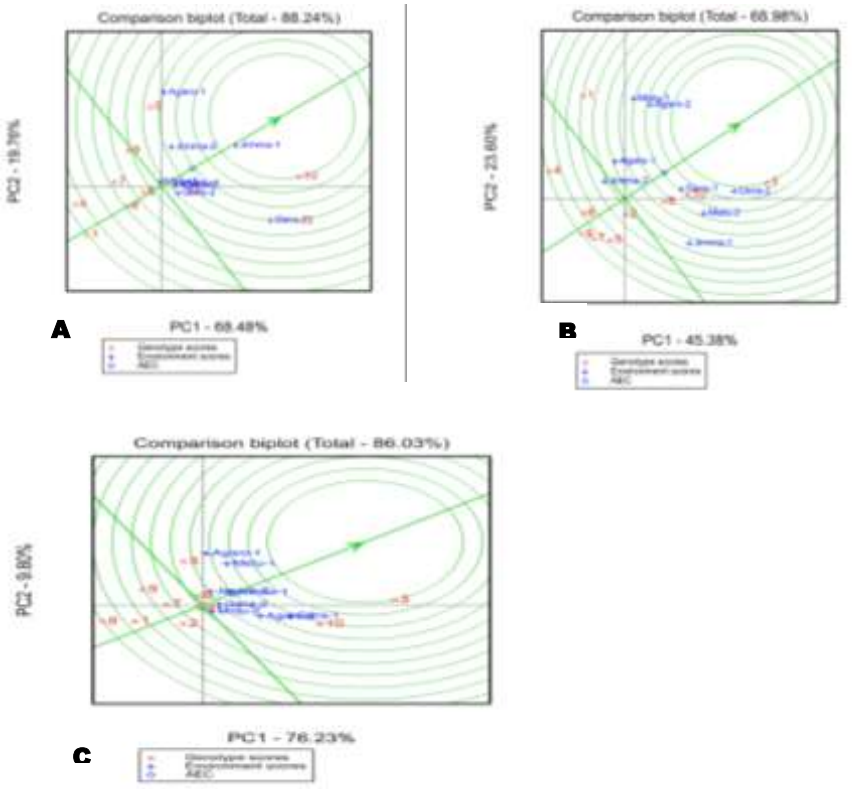

Figure 7a-c. The average environment coordination (AEC) view showing mean performance and stability of 10 taro genotypes tested in eight environments on (Panel A) Total storage root weight, (Panel B) storage root length and (Panel C) marketable number of roots per plant.

## Environment discriminating ability and representativeness using GGE bi-plot:

A similar analysis was applied for environment focused bi-plots for total storage root yield, storage root length and marketable root number per plant, which represented the ideal environment within a mega-environment (Figure 8 a-c). Ideal environment must have high discriminating ability and representativeness. For total storage root yield, the ideal test environment was environment Jimma-1 followed by environment Metu-1 (Figure 8 a); whereas for storage root length and number of marketable root per plant, environments Gera-1 and Agaro-2 were the best environments, owing to their closeness to the ideal environment (Figure 8 b and c). Test environments that had close proximity to the ideal environment on the AEC axis were positively correlated with genotypes closer to them.

Environments that had less interaction with the genotypes were environments Agaro-2 and Gera-2 (for total storage root weight and root length) (Figure 8a and b) and environment Agaro-1 (for number of marketable root per plant) (Figure 8c). The purpose of validation of test-environment is to identify idea environments that effectively identify superior genotypes for a mega-environment. The ideal test environment should be highly discriminating of the genotypes and representatives of the mega-environment. The result of this study showed that environment Jimma-1 and Metu-1 had a high discriminating ability and representativeness for genotype evaluation for total storage root weight and Gera-1 and Agaro-2, storage root length and number of marketable root per plant, respectively.

The positive correlation existing between the genotypes and environments indicated that these genotypes possessed a specific adaptation. However, when test environment markers fall close to the bi-plot origin, as of their short vectors, it means that all genotypes performed similarly in those environments. This provides little or no information about the genotype differences, since the genotypes show broad adaptability. In this case, breeders find it difficult to select higher yielding and more stable taro genotypes.

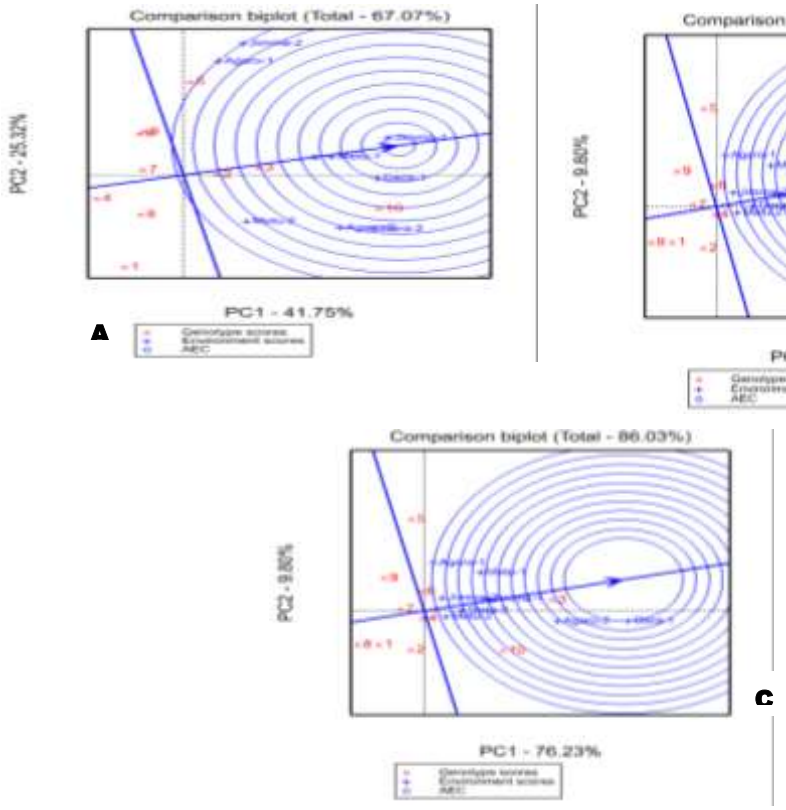


Figure 8a-c. The bi-plot for comparison of all environments with the ideal environment for (Panel A) total storage root weight, (Panel B) storage root length and (Panel C) marketable number of roots per plant

# Discussion

Variation in the performance of genotypes in different environments is a great constraint to the breeding and selection of genotypes for narrow and wide adaptations (Owusu *et al.*, 2017). The significant differences ($p<0.01$) among the environments for all the traits considered reveals that the tested environments were distinctive. The environments had different influences on the performance genotypes due to the different climatic conditions that prevailed at the experimental locations during the research period. This finding agrees with the reports of (Eze *et al.*, 2016; Asfaw *et al.*, 2020) who found significant differences among environments during their multi-environment trials. Understanding the effect of GEI on traits enables breeders to identify locations which are efficient in distinguishing ideal genotypes across sites as well as environments which are good representatives of target regions of interest (Lin *et al.*, 1986). The significant GEI observed for all the traits except for storage root length and girth (cm) suggests that the expression of these traits by the genotypes was inconsistent across the eight environments. A genotypes that

performed better in one environment, performed poorly in another environment. A higher magnitude of the mean square for environment than for genotypes and GEI for all the traits suggests that environmental influence played a major role in the expression of the traits. The higher magnitude of the mean square of the environment reveals the diversity among the environments and large variation amongst the environments over genotypes (Purchase *et.al*, 2020; Asfaw *et.al*, 2020). The genotype ranked differently at different environments also suggests the existence of GEI and the environmental conditions at the environments were variable during the execution of the experiment. This therefore suggests that environment-specific genotypes of taro should be selected for different agro ecological zones and environmental conditions as reported by (Waki *et al.*, 2018; Gerrano *et al*., 2019).

In the present study, the mean storage root yield showed highly significant differences ($p<0.01$) among taro genotypes from southwest Ethiopia, this suggested, the presence of high degree of genetic variability in the materials evaluated and the existence of considerable genetic diversity among taro genotypes for selection. The result of this study is similar with the finding of Tewodros and Yared, (2014) who reported taro genotypes collected from southern Ethiopia had significant difference for storage tuber yield and related traits. Similarly, Yared *et.al*, (2014) also reported highly significant ($p<0.01$) differences among taro genotypes in south Ethiopia. The storage root length was also varied significantly ($p<0.01$) among tested taro genotypes. The longest root length was obtained from genotypes 053, Kiyaq and 44/75 with values of 17.68, 17.66 and 17.35cm, respectively. The length of tuber was highly affected by the soil texture of taro grown. This result is supported by the finding of Tewodros and Yared, (2015), who reported the storage tuber length of taro grown in clay soil and high moisture stress areas of southern Ethiopia were reduced significantly. Further, Esther *et al*, (2020) reported significantly different corm length among 25 genotypes grown in Dormah Ahenkro, Bunso and Tano Dumasi districts of Ghana. However, in this study the storage tuber length obtained from Jimma (48.90) and Metu (53.10 cm) was higher than the report of Asfaw *et al*, (2020).

In the present study, taro genotypes 053, 133 and Kiyaq produced the highest total storage root yields with values of 25.04, 22.98 and 22.57 tons/ha, respectively. The result obtained from this study was lower than the report of Esther *et al.*, (2020), who reported, the corm weight of taro ranged from 8.62-440 t/ha of taro collected from different areas of Ghana. On contrarily, the result obtained from this study was higher than the report of Tewodros and

Getachew, (2013) for taro genotypes collected from southwest Ethiopia. Similarly, the mean marketable storage root number of taro genotypes ranged from 2-14. The lowest marketable storage root number was obtained from genotype 183 at Agaro-2 and the highest mean marketable storage root number was collected from genotype Kiyaq at Gera-1. The result obtained from this study was similar with the report of Tewodros and Yared, (2015) who reported the marketable storage root number ranged from 3-22. Similarly, the starch content obtained was almost similar with the study of Tewodros and Getachew, (2013) who found the marketable storage root number of taro genotypes from southwest Ethiopia ranged from 2-16.

# Conclusion and Recommendation

The result of the study indicated that the yield of taro was highly affected by genotype and location (environment) and that GEI contributed to the variation among the genotypes studied. This also further indicated the yields and related traits studied were varying across the eight environments. Genotypes 053, 133 and Kiyaq were found to be widely adaptable and had yield stability across environments. Therefore, genotypes 053 and 133 are recommended for release for production in southwest Ethiopia.

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