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Genotype, Environment, and GXE Interaction Effect on Some Selected Traits of Taro (*Colocasia esculenta* (L.) Schott)

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Abstract: The experiment was conducted to evaluate the nature and the extent of the genotype and environment interactions, to select stable and high yielding taro genotypes for fresh storage corm yield, and related traits to identify the most representative and discriminating environment in southwest Ethiopian regions. The study was tested across four environments (Jimma, Agaro, Gera, and Metu) for two cropping seasons in southwest Ethiopia. Nine selected and promising genotypes and one standard check (Denu) were evaluated by using RCBD that replicated three times. The important data were collected from all tested location and analyzed using different statistical software's. The analyzed result showed significant differences ($p<0.01$) for genotype, environment, and genotype by environment interactions (GEI) effects for all the traits evaluated exceptions to the root length. It also revealed that the extent of the mean square of the environment was more than those of the genotype and GEI for all traits targeted and indicated the uniqueness of the test environment. The genotypes 053 and 133 were identified as an ideal genotypes being high yield and wider adaptability hence nominated for release and then for production. The GGE bi-plot also identified Agaro-2 and Gera-2 were the most ideal environment for the evaluated of taro genotypes for their important useable traits. Four mega-environments (MGE) were identified for taro breeding; where environments Agaro-22, Gera-2, and Gera-1 combined into MGE-1, environments Metu-1, and Jimma-1 fell into a separate MGE-2, and environments Jimma-2 and Agaro-1 pooled into MGE-3, and Metu-2 separated into MGE-4, respectively.

Keywords: AMMI, Genotype by Environment Interaction, GGE Bi-plot, Taro and Yield

1. Introduction

Taro (*Colocasia esculenta* (L.) Schott) is the oldest cultivated crops in the world serving as food for human being for over 900 [1, 2]. It is one of the most important among root crops and typically and potentially produced for the due of its yield in conditions where and when most the crops were/will/ fail to serve for food security [3-5]. In most producing areas, the production of taro is usually done by smallholder farmers with little depend on eternal support and plays vital role in economy and nutrition in the lively hoods of many poor farmers in the nations of developing countries [6, 7]. The petioles and the leaves of taro can also a source of different food compositions and rich in protein, carbohydrate, fiber minerals, vitamins, and micro nutrients which are consumed as vegetable in most African countries [2].

In most cases, in Ethiopia taro is cultivated in the subsistent level due to less close to high yielding varieties which adapted to the cultivating area? [4, 5, 8] The most effective way of producing more stable and high-yielding varieties is through the evaluation of genotypes/varieties at different location trials (MET) [2, 9]. The achievement of a genetic enhancement program relies on the selection of the best cultivar/genotypes/fit to the specific growing time having constant/stable outcome. The corm yield of each genotype in the each testing environment is a major of an

environment main effect (E), a genotype main effect (G), and, and the genotype x environment (GE) interactions [10]. Mainly, environmental effect elucidate 80% or higher of the total yield variance in many crops; however the genotype and genotype × environment interaction which is relevant to evaluation of genotypes [11]. Regarding to this many researches were done on Taro. For example, Singh *et al*. [12] reported an evaluation of a multi-location trial on taro genotypes collected from New Zealand, Kifle *et al.* [8] described the additive main effect and Multiplicative interaction (AMMI), the genotype plus the Genotype x environment (GGE) bi-plots study of taro from Southern Ethiopia, Further, Eze *et al.* [13] reported the evaluation taro genotypes based on AMMI and GGE from Nigeria. Donkor *et al.* [2] reported the estimation of G x E and the yield stability performance of taro genotypes from Ghana. Frequently large number of genotypes/cultivar had been evaluated across seasons and years. It also difficulty to determine the genotypic responses across locations/ years without the aid of graphical display of the data [14]. Therefore; the bi-plot analysis provides a solution to such happened problem. It also displays the two-way data and allows the visualization of the interrelationships with the environments, genotypes and interaction between them [15]. The two commonly used bi-plots are: the AMMI [16] and GGE bi-plot [11, 17].

AMMI is a statistical model that combines the analysis variance with the principal components to adjust the main effect and G x E interaction effect [18, 19].

The GGE bi-plot that developed by Yan *et al.* [17] is used to determine the relationship between test environment and genotypes graphically. These models are giving valuable insights in to assessing the extent of G x E interaction in many environments and also classifying the environment for the evaluated crop [20]. Through understand of the nature and extent of G x E are important to identify the most representatives and discriminating environment for taro production. The objectives of the study is: (i) to determine the influence of GEI on yield and yield related traits of Taro (ii) to select the stable and high yielding taro genotypes for yield and yield related traits for release (iii) To determine the representative and discriminating environment to yield and yield related traits for release.

2. Materials and Methods

2.1. Study Site Descriptions

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

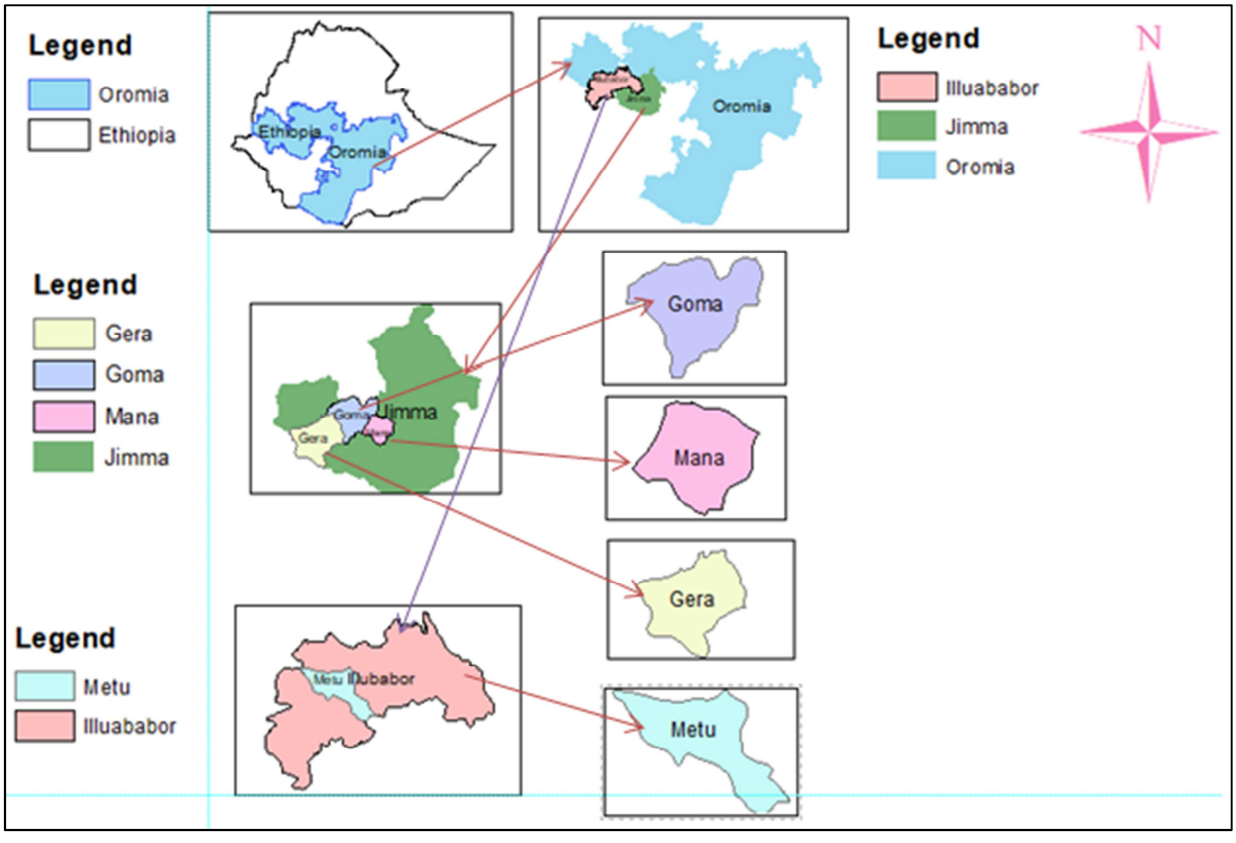

Figure 1. *Map of the study sites.*

Table 1. *The geographical descriptions of the study sites.*

Location	Altitude (m.a.s.l.)	Latitude	Longitude	Rainfall (mm)	Temperature (°C)	
					Maximum	Minimum
Jimma	1753	7°40.00' N	36°47'.00' E	1521.1	26.2	12.1
Agaro	1560	7°51′.00' N	36°51′ 35' E	1520	23.3	12.6
Gera	1970	7°31.60' N	36°15'.00' E	1877.8	18.6	12.0
Metu	1550	8°18′.00' N	35°35′.00' E	1520	28.0	12.2

Source: JARC, 2010.

2.2. Plant Materials, Experimental Design, and Management

Nine taro genotypes which were collected from major growing areas of Southwest Ethiopia and one released variety (Denu) 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 $9m^2$ (3m x 3m), using an inter-row spacing of 0.75 cm and intra-rows spacing of 0.5 cm. 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 followed according to the recommendations.

2.3. Data Collection

Data were collected from eight middle plants from each plot and the average values were used for data analysis. The traits that are used for data collection were: storage root length (cm), storage root diameter (cm), marketable storage root number numbers plant (more than or equal to 100 g or with diameters at the widest point >25mm according to Levette, [22], the total number of storage root number per plant, the weight of marketable storage root ton ha^{-1}, and weight of total storage root ton ha^{-1}.

2.4. Data Analysis

Homogeneity of residual variance was tested before combined analysis over locations in each year as well as over locations and years (for the combined data) using Bartlett's test [23]. Accordingly, the data collected indicated homogenous variance. A 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 [24] and Gen Stat software [25]. Treatment means were separated by using the Fisher's protected least significant difference (LSD) test at 1% and 5% probability levels.

2.5. 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 as stated by Gauch, [26]. Genotypic stability for each genotype will be computed using GenStat software, as prescribed by Malhotra *et al*. [27]) The additive main effects and multiplicative interactions (AMMI) statistical model reported by Gauch and Zobel, [18] was used to analyze yield data to obtain (AMMI) analysis of variance and (AMMI) mean estimates as follows.

$$Y_{ger} = \mu + \alpha_g + \beta_e + \Sigma\lambda_n Y_{gn} \delta_{en} + \rho_{ge} + E_{ger}$$

Where: Y_{ger} = yield of genotype g in environment e for replicate r, μ = grand mean, α_g = genotype mean deviation (genotype means minus grand mean), β_e = environment mean deviation, n = number of principal component analysis (PCA) axes retained in the model, λ_n singular value for PCA axis n, y_{gn} = genotype eigenvector values for PCA axis n δ_{en} = environment eigenvector values for PCA axis n, ρ_{ge} = residuals, E_{ger} = error term.

Another important point was further reported by Yan *et al*. [28]); Duma, *et al*. [29] that genotype and genotype-by-environment effects must be considered simultaneously to make a meaningful decision in selection. Significant genotype by environment interaction was also analyzed by a GGE bi-plot which was also useful in ranking genotypes based on their average performance and stability for best traits in taro [28, 29]. 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 the first two principal components was calculated by using the model:

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

Where: Y_{ij}= measured mean of genotype i in environment j, μ= grand mean, β_j = main effects of environment j, $\mu + \beta_j$ = the mean yield across all genotypes in environment j, λ_1 and λ_2= are the singular values (SV) for the first and second principle components (PCA-1 and PCA-2) respectively.ξ_{i1} and ξ_{i2} = are eigenvectors of genotype i for PCA-1 and PCA-2, respectively, η_{j1} and η_{j2} = eigenvectors for environment j for PCA-1 and PCA-2, respectively.ε_{ij}= residual associated with genotype i in environment j.

3. Results and Discussions

3.1. Analysis of Variance for the Storage Root Yield and Yield-Related Traits of Taro Genotypes

The result of the combined analysis of variance revealed that the genotypes and environmental component showed the highest significant variation ($p<0.01$) for most of the agronomic variables exception to storage root length and girth. The other traits also showed significant variation ($p<0.01$) for G x E interaction. From the genetic variability point of view, the analysis of variance revealed that the environments were differing for one trait to another for the tested genotypes (Table 2). The results further revealed that the genotypes responded varies and fluctuated in their variable trait genetic expression with varied in environment that confirms the existence of GEI in this experiment result.

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

Sources of variation	DF	Mean square						
		TSRW	NVPH	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 ton ha^{-1}, NVPH= Number of verticals 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 ton ha^{-1}.

For most of the variables, the contribution of the environment for the overall variance varied from 16.83% for total storage root weight to 57.74% for total storage root number and then followed by GEI and genotypes respectively (Table 3). Anonymous results were reported by Singh *et al.* [12]; Mulualem *et al.* [4]. Concerning total storage root weight, the most source of variance was typically the inherent genetic component means that the genotypic effect (8.02%) (Table 3), which was a similarity with the result reported by Kifle *et al.* [8].

Table 3. *The combined sum of squares for yield and related traits of taro genotypes evaluated during the 2019-2020 cropping season.*

Sources of Variation	DF	TSRW	NVPH	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

*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 ton ha^{-1}, NVPH= Number of verticals 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 ton ha^{-1}.

3.2. The Agronomic Performance of Taro Genotypes

The average total storage root yield of ten evaluated taro genotypes under eight different environments was 25.69 ton ha^{-1}. Genotype 053 had had the highest average total and the highest average total storage corm yield (29.17 ton ha^{-1}), followed by 133 (26.36 ton ha^{-1}) and Denu (25.99 ton ha^{-1}), respectively, while, genotype 165 was the lowest yielding (24.15 ton ha^{-1}) (Table 4). Similarly, genotype Denu had the highest average storage root length and girth (18.02 and 33.02 cm), and marketable and total storage root number (6.65 and 12.13) While genotype 9/75 produced the lowest storage length and girth (16.83 and 31.83 cm) and genotype and 183 produced the lowest marketable and total storage roots number (3.74 and 7.76), respectively (Table 4).

Table 4. *Combined mean yield and yield-related traits of taro genotypes across all tested environments.*

Genotypes	TSRW	NVPH	SRL	SRG	MSRN	TSRN	MSRW
44/75	24.63^{bc}	6.55^{bcd}	17.34^{bc}	32.34^{bc}	4.13^{de}	8.59^{de}	20.7^{cde}
133	26.36^{bc}	5.93^{d}	17.19^{bc}	32.19^{bc}	4.45^{cde}	8.88^{cde}	22.98^{b}
Denu	25.99^{bc}	6.23^{bcd}	18.02^{a}	33.02^{a}	6.65^{a}	12.13^{a}	22.56^{bc}
165	24.15^{c}	6.87^{bc}	17.07^{bc}	32.07^{bc}	4.98^{cd}	10.35^{abcd}	19.83^{e}
130	25.92^{bc}	6.88^{bc}	16.90^{c}	31.90^{c}	5.17^{bc}	11.45^{ab}	22.18^{cde}
023	24.64^{bc}	7.03^{b}	17.04^{bc}	32.04^{bc}	4.99^{cd}	11.25^{ab}	22.18^{bcd}
9/75	24.99^{bc}	8.04^{a}	16.83^{c}	31.83^{c}	4.65^{cde}	10.56^{abc}	20.89^{cde}
183	25.36^{bc}	6.07^{cd}	17.29^{bc}	32.29^{bc}	3.74^{e}	7.76^{e}	21.3^{bcde}
032	25.65^{bc}	6.75^{bc}	17.03^{bc}	32.03^{bc}	4.47^{cde}	10.08^{bcd}	21.1^{bcde}
053	29.17^{a}	6.17^{cd}	17.63^{ab}	32.63^{ab}	5.99^{ab}	11.15^{ab}	25.04^{a}

Genotypes	TSRW	NVPH	SRL	SRG	MSRN	TSRN	MSRW
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 ton ha^{-1}, NVPH= Number of verticals 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 ton ha^{-1}.

3.3. Variance Estimate for Total Storage Root Yield and Related Traits of Taro Genotypes

The combined analysis of variance of the agronomic traits evaluated at eight different environment revealed that there were a high significant variations among the genotypes, environment, year, environment x year, genotype x year and GEI, at ($p<0.01$) probability level (Table 5). Thus, these significant variations indicated that the responses of the genotypes were varied in their total storage com/root yield with the change in environment. Such kinds of phenomenon clearly notified the presence of interactions in genotype and environments declared the presence of GEI in this study.

The storage corm/ root yield of 10 taro genotypes were highly variable over the eight environments in which they evaluated. They showed that the highest storage corm yield in the interaction. Of all environments, the highest total storage corm yield of (25.04 ton ha^{-1}) was observed in the genotype 053 at Metu-2 is the best environment. The lowest root yield (19.83 ton ha^{-1} was recorded from genotype 165 and Jimma-1 is 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 in two years and four locations.*

Sources of variation	DF	Mean squares					
		TSRW	NVPH	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 respectively.

Table 6. *Mean total storage root yield ton ha^{-1} performance of ten taro genotypes tested across eight environments.*

Genotypes	Environments								Over all
	Jimma-1	Agaro -1	Gera-1	Metu -1	Jimma-2	Agaro-2	Gera-2	Metu -2	mean
44/75	17.50	15.33	18.09	22.95	22.11	20.73	22.81	26.22	20.72
133	22.35	20.33	22.54	24.57	24.44	23.04	22.98	23.59	22.98
Denu	23.74	15.50	24.44	24.59	24.00	21.33	24.52	22.40	22.57
165	13.18	17.67	16.67	18.81	23.78	22.54	22.27	23.73	19.83
130	18.09	24.33	18.73	22.14	26.44	21.48	22.45	23.82	22.19
023	15.71	17.50	18.51	23.81	24.51	17.82	21.03	24.62	20.44
9/75	17.46	18.16	18.41	23.67	23.55	19.67	21.92	24.26	20.89
183	19.67	17.67	22.57	18.57	23.55	19.96	23.17	25.24	21.30
032	20.77	19.78	18.57	18.09	26.06	10.90	21.47	24.27	19.99
053	25.08	20.50	23.81	27.09	24.55	25.51	25.96	27.82	25.04
Mean	19.35	18.67	20.23	22.43	24.30	21.20	22.85	24.59	21.59
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
	Jimma-1	Agaro -1	Gera-1	Metu -1	Jimma-2	Agaro-2	Gera-2	Metu -2	mean
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
Denu	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

Genotypes	Environments								Over all mean
	Jimma-1	Agaro -1	Gera-1	Metu -1	Jimma-2	Agaro-2	Gera-2	Metu -2	
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
Denu	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

3.4. Additive Main Effect and Multiplicative Interaction (AMMI 2) Bi-plot Analysis

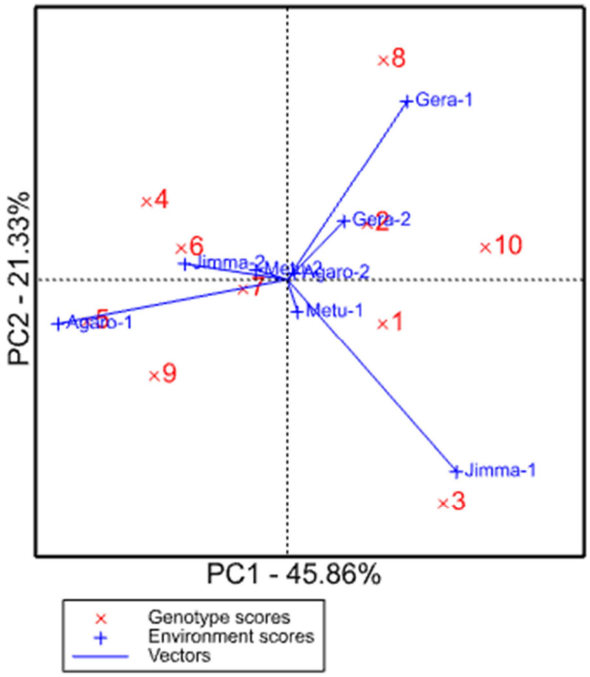

Figure 2. *AMMI 2 bi-plot for IPCA 1 against IPCA 2 scores for 10 taro genotypes and eight environments on total storage root weight.*

The AMMI-2 bi-plot analysis of total storage corm/ root weight (TSRW), storage corm length (SRL), and the marketable number of roots/corm per plant (MSRNP) of the 10 taro genotypes evaluated in eight environments are shown in Figures 2–4, respectively. For TSRW, the variations in percentage by the ICPA-1 and ICPA-2 axes were 45.86% and 21.33%, in their respective way (Figure 2). The genotypes 2 (133), 1 (44/75), and 10 (053) had showed broad adaptability as they were located closer to the center of the bi-plot. The genotypes 9 (032), 8 (183), 3 (Denu), 5 (130), and 4 (165) were placed far away from the origin points. Thus, indicating specific adaptation to the tested environment within their proximity on the bi-plot. Anonymously, Yan *et al.* [28] stated that the performance of the genotypes in the environment are better considered than the average stand in that environment if the angle between its vector and the environment is less than the acute angle (<90^0); near the average if the angle is equal to right angle (90^0) and blew an average if the angle is greater than right angle (>90^0) that means an obtuse angle.

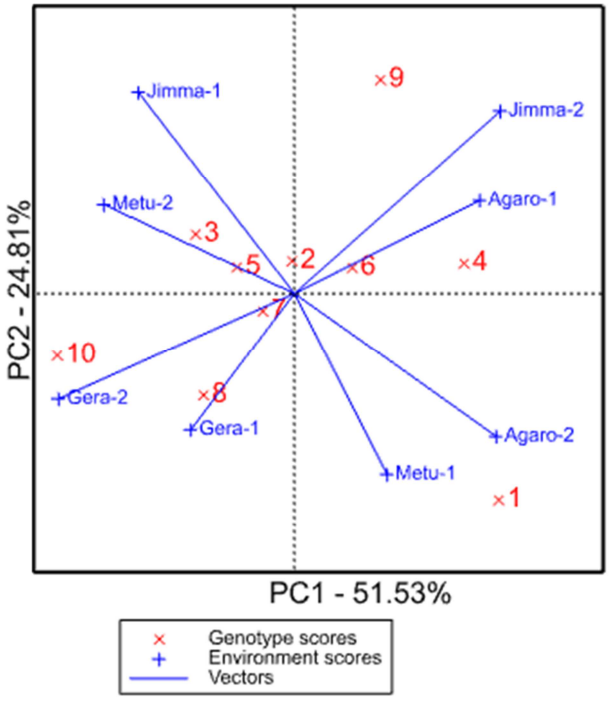

Figure 3. *AMMI 2 bi-plot for IPCA-1 against IPCA-2 scores for 10 taro genotypes and eight environments on storage root length.*

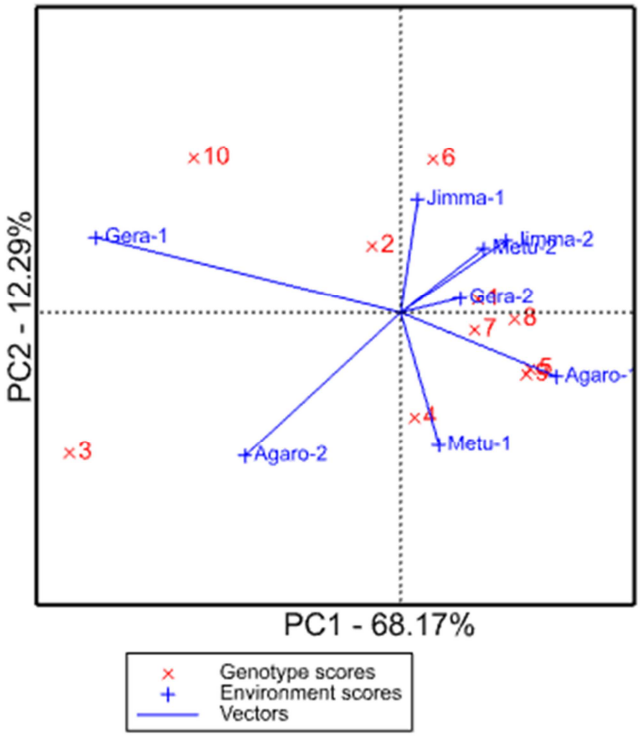

Figure 4. *AMMI 2 bi-plot for IPCA 1 against IPCA 2 scores for 10 taro genotypes and eight environments on a marketable number of roots per plant.*

Furthermore, the genotypes labeled as 8 (183), 2 (133), and 10 (053) average yield hence located on acute angle of PC-1. The genotypes located on the right hand side of the bi-plot were associated positively with the tested environments on the same place. From the analyzed result the environment Gera-1 was considered as a highly discriminating ability as it had along vector. The environment Gera-2 and agaro-2 were positively and highly correlated. This revealed that genotypes ranked similarly to total storage root weight in these environments. From these we can suggested that the environments might be had the same mega environment.

Regarding to the storage corm length, the AMMI-2 bi-plot explained 76.34% of the total GEI (Figure 3). The variation percentage accounted to IPCA-1 and IPCA-2 was 51.53 and 24.81% respectively. The genotypes labeled as 2 (133), 6 (023), 7 (9/75), and 5 (130) were closer to the bi-plot origin and they had the yields close to over all mean yield. The genotypes 032 (Jimma-2), 023 and 165 (Agaro-1), Denu and 130 (Metu-2), and 053 (Gera-2) were positively correlated with the environments close to them. Those genotypes located at the right hand side of the bi-pilot were correlated positively with the environments found on that same side. Therefore, the environments had a similar discriminating ability of at different right angle. The Environments Gera-1 and Metu-2 suggested the poor discriminating ability of the genotypes as they had the shortest vector. The variation in percentage by the AMMI-2 bi-plot for marketable storage root number for the IPCA-1 and IPCA-2 were 68.17% and 12.29%, respectively (Figure 4). The genotypes labeled as 1 (44/75), 7 (9/75), and 8 (183) were too closer to the bi-plot origin/center. Thus why showing wider adaptability over all the environments and correlated positively with stated environments located on the right-hand side the bi-pilots. The genotypes 1 (44/75), 7 (9/75), and 8 (183) were positively correlated with the environment Gera-2, and genotypes 5 (130) and 9 (032) suggested the specific adaptation to this environment. Therefore, in this out-come, except for the environment Gera-1, Agaro-2 and Agaro-1, all environments had a shorter vectors which indicate the less discriminating ability of the site. In this study most of the environments were positively correlated that suggested the indirect selection for total storage corm yield and the related traits can also be applied across these site. The combination of these environmental tests in to a single test site can responded similar to the genotypes. This can reduces the cost and accelerate the breeding efficiency.

3.5. Mega-Environments Analysis Using GGE Bi-plots

The polygon view of the GGE bi-pilot for the total storage corm yield, corm length, and marketable storage corm number per plant depicted in in Figures 5, 6, and 7, in their respective way. In each bi-plot, the different mega environments were grouped in sectors. Those environments within the same MGE were suggested to have similar effect the performance of the genotypes and then considered as the homogenous environment. An anonymously the genotypes in the same MGE were suggested have similar response to the environments in same circles sector or MGE. Those genotypes located at the near vertex of the sector were suggested to the best performing genotypes in the MGE.

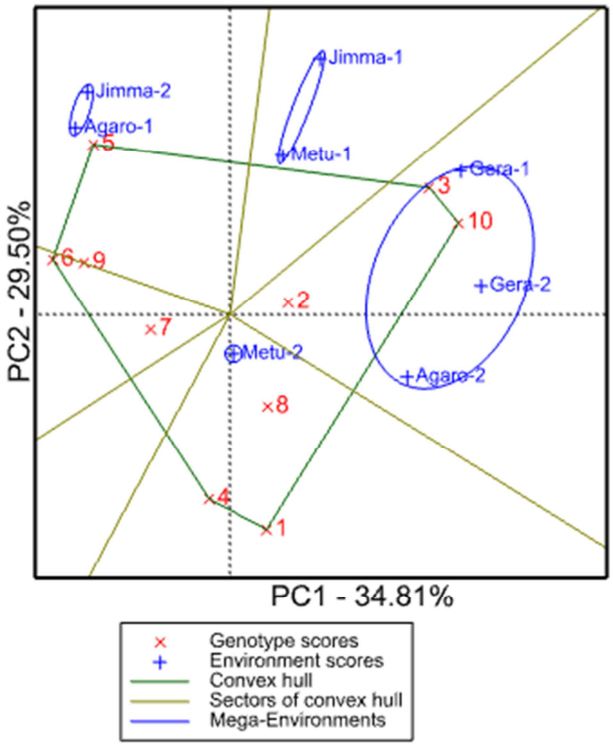

Figure 5. *The "which-won-where" polygon view for total storage root weight of the GGE bi-plot analysis representing the performance of 10 taro genotypes tested across eight environments.*

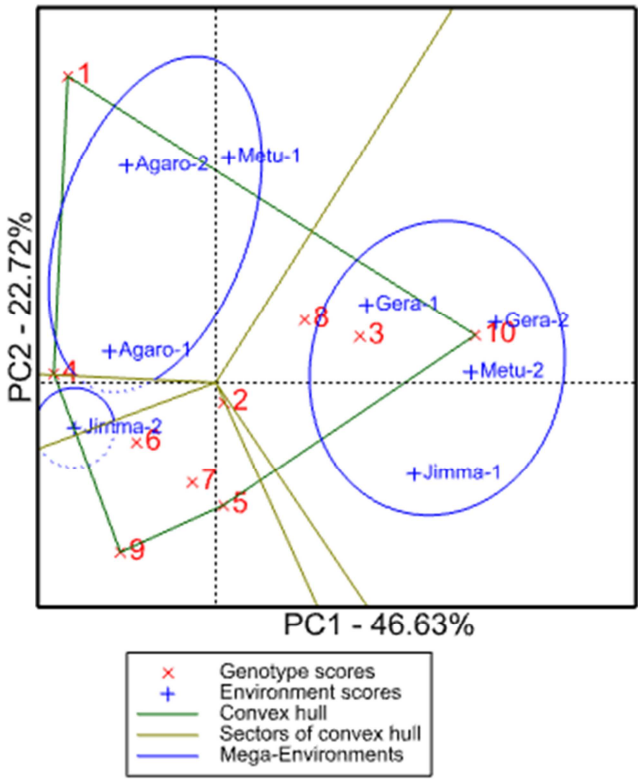

Figure 6. *The "which-won-where" polygon view for storage root length of the GGE bi-plot analysis representing the performance of 10 taro genotypes tested across eight environments.*

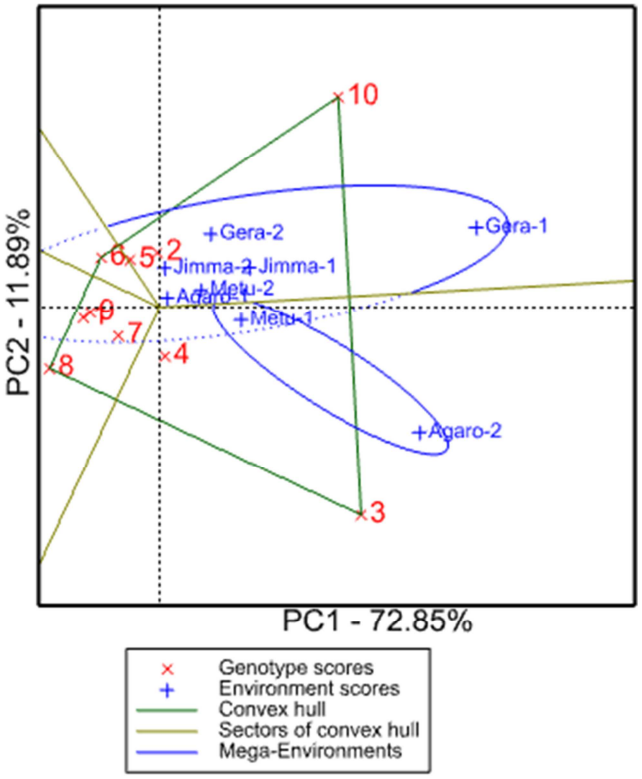

Figure 7. *The "which-won-where" polygon view for marketable storage root number of the GGE bi-plot analysis representing the performance of 10 taro genotypes tested across eight environments.*

For total storage root weight (Figure 5), principal component-1 (PC-1) explained 34.81% of the total difference, whereas PC-2 explained 29.50%, and the both axis accounted 64.31% the total variations. The all perpendicular lines those drawn to each side of the polygon were starting from the bi-pilot origin. In this analysis result, four mega environments were formed. The environments Agaro-1, Gera-2, and Gera-1 combined into MGE-1, environments Metu-1 and Jimma-1 fell into a separate MGE-2; environments Jimma-2 and Agaro-1 pooled in to MGE-3, and Metu-2 separated into MGE-4, respectively. Among the genotypes 3 (Denu) and 10 (053) were the highest-yielding genotypes in MGE-1. The genotype 5 (130) was the winner in the MGE-2. The genotypes 8 (183) was correlated positively to the environment Metu-2 and it was the winner genotype in MGE-4.

3.6. Genotype Yield and Stability Using GGE Bi-plots

The average environment coordinate (AEC) view was based genotype- focused singular value partitioning (SVP=1) can be referred as the "mean vs stability" view of the GGE bi-pilot [28]. This view showed the genotype comparisons on the bases of mean performance and stability across the test environment within the mega environment. The genotype stability view by the GGE bi-pilot explained 82.24%, 68.98%, and 86.03% of the genotypic and genotype x environment variation for the total storage root/corm weight, corm length and Marketable corm number per plant respectively (Figure 8: A, B, and C). The arrow was shown on the AEC abscissa points in the direction of higher variable outstand of the genotypes and ranked the genotypes for their variable/trait outstands. Based on this, the genotype 10 (053) got the highest total marketable corm yield and the genotype 1 (44/75) got the lowest (Figure 8: A). Anonymously the variety coded as number 3 (Denu) and 10 (053) had the highest corm length and marketable corm root per plant respectively. Genotypes 9 (032) and 4 (165) had the shortest storage root length and genotype 8 (183) had the lowest marketable storage root count (Figure 8: Panels B, C, D, and E). The stability of each genotype was shown by its projection on to the AEC vertical axis. The most stable genotype was located on the AEC abscissa (horizontal axis) and had a near zero projection on to the AEC (Vertical axis). Therefore, the genotype 10 (053) and 2 (133) were the most stable, and 1 (44/75) and 4 (165) were the least stable for total corm yield (Figure 8: Panel A). Yan and Tinker,[10] stated that stability is meaningful only when associated with a higher variable mean. Thus, an ideal genotype has both high variable mean and stable performance. According the analyzed result, the ideal genotype was represented on the head the arrow on the AEC abscissa (horizontal axis) (Figure 8: panel A, B, and C). For storage corm length, genotype 3 (Denu) and 10 (053) can be named the best genotype (Figure 8: panel B). For storage root length, genotypes 3 (Denu) and 10 (053) could be regarded as the best genotypes (Figure 8: Panel B). In the same manner marketable storage corm number per plant was the best for these genotypes (Figure 8: Panel C).

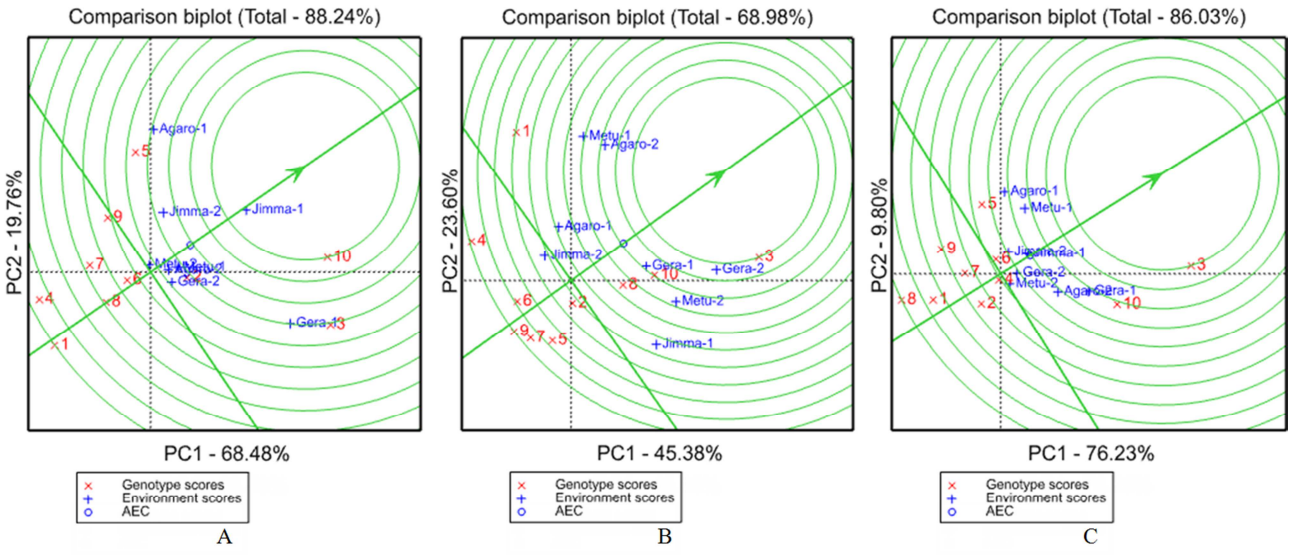

Figure 8. *a - c. The average environment coordination (AEC) view shows the mean performance and stability of 10 taro genotypes tested in six environments on (Panel A), Total storage root weight (Panel B), storage root length, and (Panel C) the marketable number of roots per plant.*

3.7. Environment Discriminating Ability and Representativeness Using GGE Bi-plot

An anonymous analysis was applied for an environment-focused bi-pilot for total storage corm yield, corm length, and marketable corm number per plant which represents the ideal environment within mega-environments (Figure 9: a-c). As to total storage root yield, the ideal test environment was environment Jimma-1 and followed by environment Metu-1 (Figure 9a); whereas for corm length and the number of marketable corm per plant, the, environment Gera-1 and Agaro-2 were the ideal environments, owing to their very closeness to the ideal environment (Figure 9b and c). Based on this, the test environment that had a close proximity to the ideal environment on AEC axis was correlated positively with genotypes closer to them.

Environments that had less interaction with the genotypes were environment Agaro-2 and Gera-2 (for total storage root weight and root length) (Figure 9: a and b) and environment Agaro-1 (for the number of marketable roots per plant) (Figure 9c). The purpose of validation of the 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 the number of marketable roots per plant, respectively.

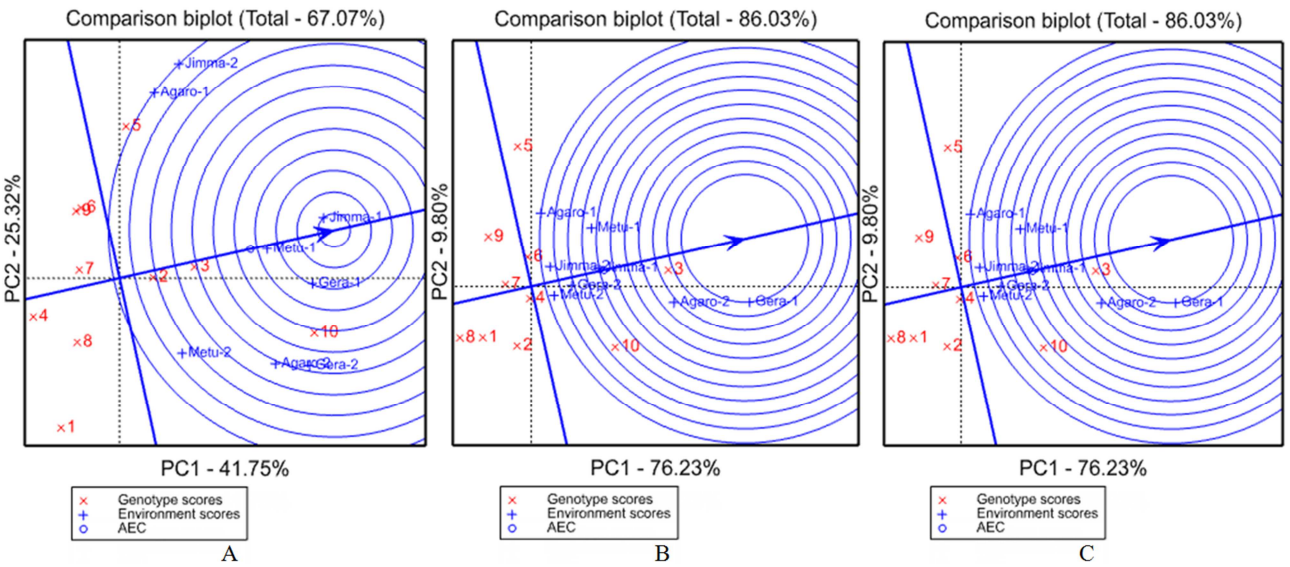

Figure 9. *a-c. The bi-plot for comparison of all environments with the ideal environment for (Panel A) total storage root weight, (Panel B) storage root length, and (Panel C) marketable number of roots per plant.*

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.

4. Conclusion and Recommendation

The result of the study indicated that the yield of taro was highly affected by genotype and location (environment) and that of GEI contributed to the variation among the genotypes studied. The mean storage root yield showed highly significant differences ($p<0.01$) among taro genotypes from southwest Ethiopia, this suggested, the presence of a high degree of genetic variability in the materials evaluated and the existence of considerable genetic diversity among taro genotypes for selection This also further indicated the yields and related traits studied were varying across the eight environments. The genotypes 053, 133, and Denu were found to be widely adaptable and had yield stability across environments. Therefore, they are recommended for verification in order to release for the farmers living in south, southwest and west part of the Ethiopia. In other case farther collection characterization and evaluation of taro genotypes should be done to identify the best genotypes in accordance with different use for food, feed and raw materials for industry.

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References

[1] Adelekan, B. A., 2012. An evaluation of the global potential of cocoyam (Colocasia and Xanthosoma species) as an energy crop. British Journal of Applied Science and Technology, 2 (1), pp. 1-15.

[2] Donkor, E. F., Nyadanu, D., Akromah, R. and Osei, K., 2020. Genotype-by-environment interaction and stability of taro [Colocasia esculenta (l.) Schott.] genotypes for yield and yield components. Ecological Genetics and Genomics, 17, p. 100070.

[3] Singh, D., Mace, E. S., Godwin, I. D., Mathur, P. N., Okpul, T., Taylor, M., Hunter, D., Kambuou, R., Rao, V. R. and Jackson, G., 2008. Assessment and rationalization of genetic diversity of Papua New Guinea taro (Colocasia esculenta) using SSR DNA fingerprinting. Genetic Resources and Crop Evolution, 55 (6), pp. 811-822.

[4] Mulualem, T., WeldeMichael, G. and Belachew, K., 2013. Genetic diversity of Taro (Colocasia esculenta (L.) Schott) genotypes in Ethiopia based on agronomic traits. Time J. Agric. Vet. Sci, 1 (2), pp. 23-30.

[5] Dagne, Y., Mulualem, T. and Kifle, A., 2014. Development of high yielding Taro (Colocacia esculenta L.) Variety for mid altitude growing areas of Southern Ethiopia. Journal of Plant Sciences, 2 (1), pp. 50-54.

[6] Singh, S., Singh, D. R., Faseela, F., Kumar, N., Damodaran, V. and Srivastava, R. C., 2012. Diversity of 21 taro (Colocasia esculenta (L.) Schott) accessions of Andaman Islands. Genetic resources and crop evolution, 59 (5), pp. 821-829.

[7] Banjaw, D. T., 2017. Review of taro (Colocasia esculenta) genetics and breeding. Journal of Horticulture, 4 (1), pp. 1-4.

[8] Kifle, A., Belew, D. and Tesfaye, K., 2020. AMMI-and GGE biplot analysis of taro (Colocasia esculenta (L.) Schott) genotypes in Southern Ethiopia. Ethiopian Journal of Applied Science and Technology, 11 (1), pp. 1-12.

[9] Fan, X. M., Kang, M. S., Chen, H., Zhang, Y., Tan, J. and Xu, C., 2007. Yield stability of maize hybrids evaluated in multi-environment trials in Yunnan, China. Agronomy Journal, 99 (1), pp. 220-228.

[10] Yan, W. and Tinker, N. A., 2006. Bi-plot analysis of multi-environment trial data: Principles and applications. Canadian Journal of plant science, 86 (3), pp. 623-645.

[11] Yan, W. and Rajcan, I., 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Science, 42 (1), pp. 11-20.

[12] Singh D., Guaf J., Okpul T., Wiles G. and Hunter D. 2006. Taro (Colocasia esculenta) variety release recommendations for Papua New Guinea based on multi-location trials, N. Z. J. Crop Hortic. Sci. 34 (2): 163–171.

[13] Eze, C. E., Nwofia, G. E. and Onyeka, J., 2016. An Assessment of Taro yield and stability using Ammi and GGE Biplot Models. J Exper Agr Int, 14 (2): pp. 1-9.

[14] Yan, W., Cornelius, P. L., Crossa, J. and Hunt, L. A., 2001. Two types of GGE biplots for analyzing multi-environment trial data. Crop Science, 41 (3), pp. 656-663.

[15] Owusu, G. A., Nyadanu, D., Owusu-Mensah, P., Amoah, R. A., Amissah, S. and Danso, F. C., 2018. Determining the effect of genotype× environment interactions on grain yield and stability of hybrid maize cultivars under multiple environments in Ghana. Ecological Genetics and Genomics, 9: pp. 7-15.

[16] Gauch Jr, H. G. and Zobel, R. W., 1997. Identifying mega-environments and targeting genotypes. Crop Science, 37 (2): pp. 311-326.

[17] Yan, W., Hunt, L. A., Sheng, Q. and Szlavnics, Z., 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Science, 40 (3): pp. 597-605.

[18] Gauch H. G, and Zobel, R. W. 1996. AMMI analysis of yield trials, in: M. S. Kang, H. G. Gauch Jr. (Eds.), Genotype-by Environment Interaction, CRC Press, Boca Raton, CRE CRC, New York, pp. 85–122.

[19] Aina, O., Dixon, A., and Akinrinde, E. 2007. Additive main effects and multiplicative interaction (AMMI) analysis for the yield of cassava in Nigeria. Journal of biological sciences, 7 (5), 796-800.

[20] Badu-Apraku, B. and Oyekunle, M., 2012. Genetic analysis of grain yield and other traits of extra-early yellow maize inbreds and hybrid performance under contrasting environments. Field Crops Research, 129, pp. 99-110.

[21] JARC (Jimma Agricultural Research Center). 2010. Mean annual Metrogical satation data.

[22] Levett, M. P., 1993. The effects of methods of planting cuttings of sweet potato (Ipomoea batatas (L.) Lam.) on yield. Tropical Agriculture, 70 (2), pp. 110-115.

[23] Steel, R and Torrie, J. 1980. Principle and procedures of statistics a Biometrical Approach. 2nd ed. Mc Graw-Hill, Inc. 471-473.

[24] SAS Institute. 2007. Statistical Analytical Systems SAS/STAT user's guide version 9 (2) Cary NC: SAS institute inc.

[25] Payne, G. T., Moore, C. B., Griffis, S. E. and Autry, C. W., 2011. Multilevel challenges and opportunities in social capital research. Journal of Management, 37 (2), pp. 491-520.

[26] Gauch, HG. 2013. "A simple protocol for AMMI analysis of yield trials." Crop Science 53: 1860–1869.

[27] Malhotra, R. S., Singh, M. and Erskine, W., 2007. Genotype× environment interaction and identification of dual-season cultivars in chickpea. Euphytica, 158 (1), pp. 119-127.

[28] Yan, W., Kang, M. S., Ma, B., Woods, S. and Cornelius, P. L., 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Science, 47 (2), pp. 643-653.

[29] Duma, S. W., Shimelis, H., Ramburan, S. and Shayanowako, A. I., 2019. Genotype-by-region interactions of released sugarcane varieties for cane yield in the South African sugar industry. Journal of Crop Improvement, 33 (4), pp. 478-504.