ORIGINAL ARTICLE

AMMI- and GGE biplot analysis of taro (*Colocasia esculenta* (L.) Schott) genotypes in Southern Ethiopia

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ABSTRACT

Taro *(Colocasia esculenta* (L.) Schott) is becoming an important food security crop for millions of smallholder farmers, particularly in some parts of southern Ethiopia as a result of release of a few high yielding varieties. In the process of release of the improved varieties, emphasis has been mainly given on the superiority of corm and cormel yield of the released varieties over the existing cultivars, neglecting the importance of genotype x environment interaction and yield stability analysis. In this study, eleven taro genotypes, designed with RCBD with three replications, were investigated at six locations under rain-fed condition during the 2014/15 cropping season. The objective was to assess the genotype x environment interaction (GEI) and corm and cormel yield stability of the genotypes. Genotype attributed higher proportion of the variation in the data (37.29%), while location contributed 35.78% with their interaction contributing 17.6% of the total variation. The 'which-won-where' analysis grouped the six test locations into a single mega-environment, which resulted in a non-crossover GEI, with *Boloso*-1 (G6) being an overall best yielding and specially adapted variety to all test environments. Thus, it could be selected for broad adaptation across the test locations and elsewhere in similar agro-ecologies. G2 (ARC/012/96) was identified as the most stable though low yielder genotype. This study further revealed that E2 (Areka) was an 'ideal' environment for evaluating superior taro genotypes.

Keywords: AMMI- and GGE biplot, GEI, Mega-environment, Stability, Taro

INTRODUCTION

In Ethiopia, taro (*Colocasia esculenta* (L.) Schott) is one of the underutilized crops predominantly grown as a staple or co-staple food crop in the wetter parts of South and Southwestern parts of the country mainly for its edible corms and cormels since time immemorial (Simon, 1992; Asfaw, 2011). The cultivars were reported to show substantial phenotypic variations for most of morphologic and agronomic traits of the foliar and subterranean organs (Simon, 1992; Fujimato, 2009). Taro contributes significantly to food security, agricultural diversification and income generation in numerous developing countries, especially in the context of climate change (Pe et al., 2015; Mukherjee et al., 2016). Ecologically it is a unique crop in that most cultivars are well adapted to difficult environmental extremes including flooded/swampy and dry conditions, making various physiological adjustments.

Nutritionally, taro is one of the cheapest sources of dietary carbohydrate-derived energy. Starch derived from the taro corm is unique because of its very small (1 to 5 µg) granular sizes. Its digestibility is estimated at 98.8% (Jane et al., 1999). The combination of small granules and high soluble dietary fiber content makes taro corm and cormel a good source of carbohydrate to process special products such as the diets of infant (Huang, et al., 2007) and taro has been food of first choice for people allergic to cereals and to children sensitive to milk (Benesi et al., 2004). In addition, taro is an excellent source of minerals, vitamins and essential amino acids (Onwueme, 1978). In the current test locations, several constraints including loss of genetic diversity, poor pre-and postharvest management and culinary practices had been observed in the production systems of the crop. As part of initial phase of genetic improvement effort, taro germplasm collection was made from major growing parts of the region and over 144 germplasm collections have been maintained in Areka Agricultural Research Center (AARC) since 1997 (Asfaw et al, 2011). Collections are also available in Jimma Agricultural Research Center (JARC). Up to now, three varieties have been released in both research centers (one, from AARC and two, from JARC) by direct selections (Asfaw et al, 2011). Some initial research works had also been done on morphological characterization (Asfaw, 2006) and nutritional experiments (Adane et al., 2013), among others.

To ensure food and nutrition security to the alarmingly increasing population in the region and to exploit its numerous useful non-food values, productivity of taro needs to be augmented with further breeding efforts. To this effect, multi-location testing of new cultivars plays an important role in breeding program (Rakshit et al., 2012). However, research on corm and cormel yield stability and GEI of taro genotypes across diverse environments at the whole country level had not been carried out. Consequently, its expansion and utilization has been confined to limited environments. According to Yan and Kang (2003), better understanding of GEI and yield stability in crops was used as a decision tool to determine the recommendation domains for released varieties.

Zobel et al. (1988) proposed additive main effects and multiplicative interaction (AMMI) model by integrating additive and multiplicative components into an integrated, powerful least squares analysis, which can explain GEI much effectively. Further advent and propagation of biplot methodology has greatly addressed the complex GEI in much simplistic graphical manner (Gabriel, 1971). AMMI and GGE biplot analyses have been carried out in understanding GEI in many crop species including potato (Bai et al., 2014), bread wheat (Shitaye, 2015), sesame (Chemeda et al., 2015), sunflower (Cherinet et al., 2016), taro (Eze et al., 2016), maize (Legesse et al., 2018) and many others. Regardless of several reports on usefulness of GEI analysis in deciding stable and superior genotypes and/or test environments in many crops, application of such techniques in taro multi location trials in Ethiopia has not yet been implemented. Thus, the present study was carried out to assess the GEI and corm and cormel yield stability of taro across multi-locations.

MATERIALS AND METHODS

The present study was carried out between March, 2014 and January, 2015 cropping season under a rain-fed condition using one released and ten top best performing genotypes selected from the germplasm collection maintained in Areka Agricultural Research Center. The pedigree and some distinguishing foliar and subterranean qualitative morphological traits of the 11 taro genotypes selected for the GEI analysis are explained in Table 1.

The experiment, except at Areka, where it was carried out at the experimental site of Areka Agricultural Research Center, was executed on farmers` fields under the investigators` close follow up and farmers' perception. In all test locations, rain fall distribution is bimodal with slight variations occurring on the onset and wide variation in the amount and pattern of distribution. The dry season in all locations stretches from December to February as opposed to the wet season, which occurs between May and August. As taro is a biennial crop, its life cycle extends across both modes of the rainfall systems. The geographic positions and respective climatic conditions of the experimental locations are explained in Table 2.

Table 1. Pedigree and some distinguishing foliar and subterranean morphological traits of 11 taro genotypes selected for GXE analysis in Southern Ethiopia during 2014/15

G	Pedigree/AC#	LBC	LSC	LSEV	SSA	CCC
G1	ARC/008/95	Yellow green	Light green	Absent	Clustered	White
G2	ARC/012/96	Dark green	Red purple	Present	Clustered	Purple
G3	ARC/016/96	Dark green	Red purple	Present	Dispersed	White
G4	ARC/027/96	Yellow green	Light green	Absent	Clustered	White
G5	ARC/034/96	Dark green	Red purple	Present	emerged sucker	White
G6	ARC/047/96	Yellow green	Light green	Absent	Intermediate	Pink
G7	ARC/065/96	Dark green	Brownish	Absent	Clustered	Yellowish
G8	ARC/074/96	Yellowish	Light green	Absent	Clustered	Yellowish
G9	ARC/080/96	Dark green	Brownish	Absent	Clustered	Yellowish
G10	ARC/082/96	Dark green	Brownish	Absent	Clustered	Yellowish
G11	ARC/085/96	purple	Red purple	Present	Dispersed	White

G=genotype code; AC#= accession number; LBC=leaf blade color; LSC= Leaf sheath color; LSEV=leaf sheath edge variegation; sucker spatial arrangement; CCC= corm and cormel cortex color

Table 2. Geographic positions and, respective climatic and edaphic conditions of the experimental locations

Location (Environment)	Geographic position			ARF (mm)*	AE
	Altitude	Latitude	Longitude		
Angacha	2395	7 º 19′37"	37 º50′59"	1650	Highland
Areka	1781	7 º 4′9"	37 º41′22"	1494	Mid altitude
Bele	1143	6º55′34"	37 º28′51"	NA	Lowland
Bombe	1514	7 º 9′23"	37 º34′20"	900	Lowland
Gununo	1942	6º53′51"	37 º42′35"	1335	Mid altitude
Himbecho	1708	7 º 8′16"	37 º41′8"	1494	Mid altitude

*ARF= average annual rainfall; AE= agro-ecology

All testing locations were distributed between two administrative zones of southern Ethiopia (one, in Kambata-Tambaro and five, in Wolaita).

Agronomic practices and experimental design

Experimental fields were plowed frequently to bring the land to fine tilth using oxen-drown plows, except at Areka where a tractor was used for plowing and harrowing. The recommended depth of planting of 30 cm at all locations was maintained by further digging the planting holes manually during planting. For each of the cultivars, large cormels (>100 g) of uniform size and age were used for planting. The experiment was arranged in Randomized Complete Block Design (RCBD) with three replications in all test locations. The experimental plots consisted of 5 rows with 3m length each. Row-to-row and plant-to-plant distances were maintained at 60 and 50 cm, respectively. The recommended dose of fertilizers i.e., 124.8: 39: 0 kg NP per hectare was applied in the form of urea, and Diamonium Phosphate (DAP), respectively. Full dose of phosphorus and 35.1 kg N ha^{-1} were applied during planting time in the form of DAP. The crop was top dressed with the remaining 89.7 kg N ha^{-1} four months of planting in the form of urea. Plots were kept free from weeds by hoeing whenever necessary.

Data collection

Fresh yield of corm and cormel of total population of the three middle rows in each plot was harvested for data collection. Data were recorded in respective experimental locations just after harvesting and only fresh yield of corm and cormel was used to analyze the GEI of taro since corms and cormels are the main economic and the most widely used parts of taro in the case of Ethiopia. Time of planting and harvesting in each location varied based on the agro-ecological differences.

Analysis of variance

Analysis of variance was first computed for each location separately after the homogeneity of individual variances were verified using Bartlett`s test (Bartlett, 1937). The corm and cormel yield data across test locations (environments) were used to perform combined analysis of variance (ANOVA), to determine the effects of environment (E), genotype (G) and their interactions, considering locations and genotypes as fixed. The linear model equations applicable to RCBD as outlined by Gomez and Gomez (1984) were used for the analysis of variances as denoted by the model equations:

(1) $\mathbf{Y_{ij} = \mu + g_i + b_j + e_{ij}}$,

where, Y_{ij}= yield of genotype i in block j; μ=g rand mean; g_i= effect of genotype i; bj= effect of block j and e_{ij}= error effect, and

(2) $\mathbf{Y_{ijk} = \mu + G_i + L_j + GL_{ij} + B_{kj} + E_{ijk}}$ for combined yield data analysis

where Y_{ijk} = yield of genotype i in block k and location j; μ = grand mean of the experiment; G_i = effect of genotype i; L = effect of location j; $(GL)_{ij}$ = the interaction effect of genotype i with location j and B_{kj} = effect of block k in location j and E_{ijk} = error effect.

Existences of significant genotype x environment interaction (GEI) variances justified further partitioning of variance components. These variance components (genotype, environment and genotype by environment interaction) were also estimated from their respective mean squares obtained from the analysis of variance table (Table 3). Significance of different sources of variances was tested following the standard procedures of F-tests at 5% levels of significance.

AMMI analysis

After detecting the significance of GEI, stability analysis was done using the AMMI- biplot model, which combines standard analysis of variance with PC analysis (Zobel et al., 1988), subjecting the corm and cormel yield data to GenStat-17 software program (GenStat, 2009). The AMMI model equation used was:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^{N} \lambda n \gamma_{gn} \delta_{en} + \rho_{ge} \quad ,$$

where γ_{ge}= yield of the genotype (g) in the environment (e); μ= grand mean; a_e=genotype mean deviation; β_e= environment mean deviation; N = No. of IPCAs (Interaction Principal Component Axes) retained in the model; λ_n= singular value for IPCA axis n; γ_{gn}= genotype eigenvector values for IPCA axis n; δ_{en}= environment eigenvector values for IPCA axis n and ρ_{ge}= the residuals. AMMI analysis was also used to determine stability of the genotypes across locations using the PCA scores (IPCA1 and IPCA2).

AMMI stability value (ASV)

ASV is the distance from the coordinate point to the origin in a two-dimensional of IPCA1 scores against IPCA2 scores in the AMMI model (Purchase et al., 2000). Because the IPCA1 score contributes more to the GEI sum of square, a weighted value is needed. This weight was calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2 to the interaction sum of squares as follows:

$$\mathbf{ASV} = \sqrt{\left[\frac{\mathrm{SSIPCA1}}{\mathrm{SSIPCA2}}(\mathrm{IPCA1\ score})\right]^2 + (\mathrm{IPCA2\ score})^2} \quad ,$$

Where: SS= sum of squares against IPCA2 es; IPCA1= Interaction principal component analysis axis one; IPCA2= Interaction principal component analysis axis two. Least ASV indicates wide adaptation of specific genotypes for certain environments and vice-versa. The larger IPC score, either negative or positive, the more specifically adapted a genotype is to certain environments. Smaller ASV scores indicate a more stable genotype across environments.

GGE Analysis

The GGE refers to the genotype main effect (G) and the genotype x environment interaction (GE), which are the two most important sources of variation for cultivar evaluation in a multi environment trials (Yan et al., 2007). A GGE biplot displays the genotypic main effect (G) and genotype by environment interaction (GE) of a genotype-by-environment dataset (Yan et al., 2000). The PBtools software (PB tools for windows, 2014) was used to generate graphs showing (i) "which-won-where" pattern, (ii) ranking of genotypes on the basis of yield and stability, (iii) comparison of genotypes to an 'ideal' genotype, (iv) identification of environments relative to the 'ideal' environment and, (v) ranking of genotypes relative to the test environment with highest yielding performance. The GGE biplot model used to generate the graphs was:

$$\boldsymbol{Y_{ij} = \mu + \beta_j + \sum_{n=1}^{k} \lambda_n \xi_{in} \eta_{in} + \varepsilon_{ij}}$$

where Y_{ij} is the mean of genotype I in environment j; μ is the grand mean; β_j is the environment j main effect; n is the singular value; λ_n, ζ_{in} and η_{in} are, respectively, singular value, genotype eigenvectors, and environment eigenvectors for n^{th} interaction principal component; and ε_{ij} is the residual effect.

RESULTS AND DISCUSSION

Analysis of variance

Table 3 presents the combined **a**nalysis of variance for fresh corm and cormel yield of 11 taro genotypes grown at six environments. Genotype (G), environment (E) and their interactions (GEI) showed highly significant (P<0.01) variations. The highly significant G × E effects suggest that genotypes may be selected for adaptation to specific environments, which is in harmony with the findings reported by Eze and Nwofia (2016) who evaluated the yield performance and stability of taro using AMMI and GGE Biplot Models in Nigeria. Table 3 also depicts the relative contribution of each source to the total variation (Genotype + Location + Genotype x Location interaction). Genotype and location captured 37.29% and 35.78% of the variation, respectively. The significant effects of genotypes and environments exhibited the phenotypic appearance of variability in genotypes and diversity of growing conditions at different environments, which is in line with the finding reported by Sharifi et al. (2017) in rice multi- location trial in Iran. In the present study, the genotype sum of squares was slightly larger (69.28) than that of the environments (66.49), which resulted from best performance of one of the genotypes (G6) across all test locations as a consequence of which formation of a non-crossover type of GEI and a single mega environment was resulted. In this study, the GEI sum of squares, which accounted for 17.6% of the variation was further partitioned into four highly significant (P< 0.01) Interaction Principal Component Axes (IPCAs) and a residual term (Table 3).

The sum of squares for the first two IPCAs cumulatively contributed to 81.34% of the total GEI,

which is sufficient, since 70% is considered the minimum amount of variability for the model to be relatively reliable (Zobel et al., 1988). Thus the first two principal components (IPCA1 and IPCA2) were used to plot a 2-dimensional GGE biplot, avoiding IPCA3 and IPCA4 from further analysis to maintain the simplicity of the two-dimensional analysis and thereby to ensure effective interpretation of the biplots as effective graphical representation of the variability in the Multi Location Trial data (Rakshit et al., 2012). In the present study, the significant effects of GEI reflected on the differential response of genotypes in various environments demonstrated the possibility to calculate stability parameters.

Table 3. Combined **a**nalysis of variance for fresh corm and cormel yield of 11 taro genotypes grown at six environments in southern Ethiopia, 2014/15

Source of variation	DF	SS	MS	F value	P	TVE (%)	GEI (%)	Cumulative (%)
Environments	5	66.49	13.298	36.14	<0.001	35.78		
Genotypes	10	69.28	6.928	64.44	<0.001	37.29		
Interactions	50	32.71	0.654	6.09	<0.001	17.60		
IPCA1	14	19.91	1.422	13.23	<0.001		60.86	60.86
IPCA2	12	6.7	0.558	5.19	<0.001		20.48	81.34
IPCA3	10	2.73	0.273	2.54	0.0082		4.50	85.84
IPCA4	8	2.31	0.289	2.69	0.0094		7.06	92.90
Residuals	6	1.07	0.178	1.65	0.1388		18.7	
Error	120	12.9	0.107					
Total	197	185.8	0.943					

IPCA= Interaction principal component analysis; DF= degree of freedom; SS= sum of square; MS= mean squares; P= probability; TVE=total variation explained; GEI= genotype x environment interaction; %= percentage

Evaluation of environments and genotypes around overall mean Value

Table 4 summarizes mean fresh corm and cormel yields (t ha^{-1}) of 11 taro genotypes (G1 to G11) tested at six locations (E1 to E6) and respective genetic and environmental indices (GI and EI). The combined environmental corm and cormel yield for genotypes ranged from 8.79 t ha^{-1} at E1 (Angacha) to 22.45 t ha^{-1} at E2 (Areka) whereas, the average genotype corm and cormel yield across environments ranged from 11.72 t ha^{-1} for genotype G11 to 34.18 t ha^{-1} for genotype G6, with an overall mean corm and cormel yield of 16.58 t ha^{-1} (Table 4). Accordingly, different genotypes showed specific yield performances across the test environments. On the basis of environmental index (EI) values, the six locations were grouped into two favorable/rich and unfavorable/poor. Accordingly, environments E1, E5 and E6 were poor, recording negative EI values and E2, E3 and E4, with positive EI values were rich environments. In this regard, similar finding was reported by Sharifi et al. (2017) for sorghum yield trial in India.

In the view of the genotypic index (GI) values, the 11 genotypes were also grouped into two clusters. Correspondingly, 63.64% of the genotypes, i.e., G1, G2, G3, G4, G7, G10 and G11 showed negative genotypic index values with genotypes G5, G6, G8, and G9 indicating positive values. Mean yield performance of the genotypes characterized by negative index values were below the overall mean yield across environments or genotypes. In environment E1 (Angacha), yield performance of all genotypes was inferior to the overall mean yield with only one genotype, G6 surpassing the overall mean yield, which demonstrated that E1 was the poorest environment for multiplication of taro genotypes. Conversely, in E6 (Himbecho), genotypes G5, G6, G8 and G9 gave higher average yields with positive genotypic index (GI) values, which indicated that these genotypes were adapted to favorable environments, while genotypes G5 and G6 adapted in poor environments. Genotype G6, however was the top performer (34.18 t ha^{-1}), exhibiting above the overall average yield across all test locations, whilst G5 (16.96), G8 (16.74) and G9 (17.36 t ha^{-1}) were moderate. On the other hand, G1 (12.43), G2 (13.68), G3 (14.69), G4 (15.49), G7 (15.92), and G10 (13.19 t ha^{-1}) were the poorest yielders since their yield performance was below the overall mean yield. On the contrary, G1, G10 and G11 yielded consistently below average yield across all test environments.

Nevertheless, it should be noted that poorly performed genotypes in terms of corm and cormel yield might appear superior in one or more agronomic traits or socioeconomic characteristics in the same or different environments. In line with this, Sharifi, et al. (2012) in their sorghum yield trial observed high fodder yield than grain yield for same genotypes in different locations and vice versa. As suggested by the same authors, this might be explained by the fact that each trait is governed by different set of genes and influence of environment on the cumulative expression of different set of genes will vary considerably. Correspondingly, some taro genotypes might be superior for one or more desirable traits, for instance, for better cooking/eating quality because of less content of mucilage or for vertebrate pest resistance as a result of high content of acridity. Thus, taro producers need to pay due attention not to discard such valuable genotypes when they appear to be poor for a single or more traits across diverse environments, which otherwise, would lead to taro genetic erosion.

AMMI stability value (ASV)

The AMMI stability values (ASV) of 11 taro genotypes (G1 to G11) tested at six locations (E1 to E6) in Southern Ethiopia are presented in Table 4. In present investigation, AMMI stability values (ASV) evidently revealed variations in fresh corm and cormel yield stability among genotypes. Accordingly, G2 was the most stable though low yielder, followed by G4, G1, G5 and G7 in decreasing order (Table 4). The results of ASV further confirmed that G6 was the most unstable but the best high yielding genotype in all test environments, followed by G10, G11 and G9 in decreasing order. According to Purchase (1997), a genotype with low ASV is considered more stable than a genotype with a high ASV. A stable genotype is the one possessing a constant performance irrespective of any changes in environmental conditions (Fasahat et al., 2014). Following similar approaches, several authors have identified high performing and stable genotypes in different crop species including bread wheat-barley lines (Farshadfar, 2012), sesame (Chemeda et al., 2015), yellow passion (Oliveira et al., 2018), and others. The greater the IPCA scores (positive or negative) as it is a relative value, the more specifically adapted a genotype is to certain environments. Jeberson et al. (2017) while analyzing the stability and adaptability of elite genotypes of bread wheat in India observed that the more IPCA scores approximate to zero, the more stable the genotype were across environments. Phenotypic performance of the stable genotype remains constant while the environmental conditions change.

AMMI analysis

AMMI biplot with the genotype and environment main effects for corm and cormel yield on the X-axis and PC1 scores on the Y-axis for 11 taro genotypes tested at six locations showing 61% fitness in the model is shown in Fig 1. Based on the result of the AMMI biplot analysis, genotypes and environments represented by respective codes on the right-hand side of the Y-axis recorded higher yields than those positioned at the left-hand side of the Y-axis. Environments characterized by low yielding performance (E1, E5, and E6) were grouped in the quadrants of low yielding genotypes (G1, G2, G3, G4, G7, G10 and G11) as opposed to favorable environments (E2, E3, and E4) being grouped in quadrants of high yielding genotypes (G6, G9, G8 and G5). Out of these genotypes that showed high yield performance, G6 and G9 had higher IPCA1 scores in which G6 being the overall best genotype. Hence, G6 was identified as specially adapted and the high yielding genotype to the corresponding environments (Fig.1). Conversely, genotypes G1, G2, G4, G8 and G5 were with near zero IPCA1 scores exhibiting more stability and relatively less interaction with the environments. Furthermore, among the test environments, those marked with E3, E4, and E5 also exhibited near zero IPCA1 score and hence had small interaction effects indicating that all genotypes performed well in these locations. Environments E2, E3 and E4 were most favorable for most genotypes, while E1 and E6 were good for only a few genotypes. Similar findings was reported by Erdemci (2018). Generally, genotypes closer to the origin of the axis (IPCA1) provided a smaller contribution to the interaction than those that are farther away and they showed better general adaptation than specific adaptation and vice versa.

Table 4. Genotype and environment mean fresh corm and cormel yield (t ha^{-1}) of 11 taro genotypes (G1 to G11) tested at six locations (E1 to E6) in Southern Ethiopia during 2014/15 and respective IPCA1, IPCA2, ASV, and genetic (GI) and environmental (EI) indices

G	Test Environments						GOM	GI	IPCA1	IPCA2	ASV	ASV Rank
	E1	E2	E3	E4	E5	E6						
G1	6.45	16.54	15.12	15.24	12.06	9.17	12.43	-4.15	-0.08	0.08	0.24	3
G2	5.77	19.07	16.60	15.80	13.95	10.87	13.68	-2.90	0.05	0.12	0.19	1
G3	7.59	22.90	17.35	17.84	13.92	8.52	14.69	-1.89	0.31	-0.05	0.93	7
G4	10.28	22.62	18.70	14.69	15.80	10.86	15.49	-1.09	0.06	0.12	0.21	2
G5	8.40	21.24	16.97	21.70	17.96	15.49	16.96	0.38	-0.13	0.38	0.53	4
G6	13.80	61.73	36.23	37.29	33.49	22.53	34.18	17.60	1.11	0.40	3.33	11
G7	9.10	16.17	20.37	23.83	14.44	11.60	15.92	-0.66	-0.25	-0.42	0.85	5
G8	7.90	18.21	28.64	21.11	14.88	9.69	16.74	0.16	0.04	-0.85	0.86	6
G9	10.74	26.24	22.78	20.19	14.38	9.81	17.36	0.78	0.32	-0.30	0.99	8
G10	8.67	10.19	14.81	13.95	18.70	12.84	13.19	-3.39	-0.79	0.18	2.36	10
G11	8.03	12.04	12.65	12.90	9.88	14.81	11.72	-4.86	-0.65	0.35	1.96	9
EOM	8.79	22.45	20.02	19.50	16.31	12.38	16.58					
EI	-7.79	5.87	3.44	2.92	-0.27	-4.2						

G=genotype; E= environment (location); GOM and EOM=fresh corm and cormel yield of overall mean values of original data of taro genotypes and test environments, respectively; IPCA= interaction principal component analysis; GI and EI, genotypic and environmental indices, respectively; ASV= AMMI stability value

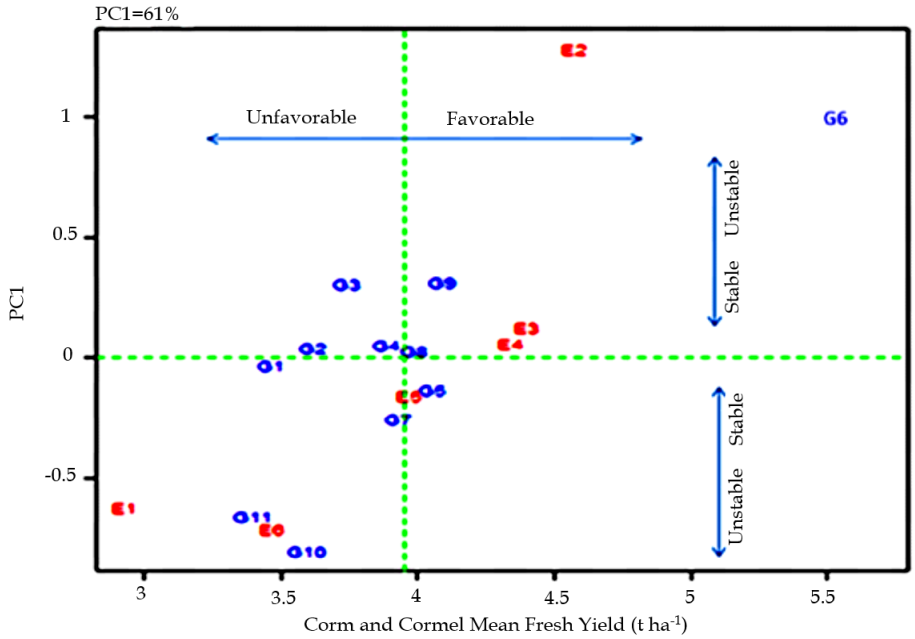

Figure 1. AMMI-1 model biplot for Corm and Cormel fresh mean yield (t ha^{-1}) of 11 taro genotypes evaluated at six locations in Southern Ethiopia in 2014/15 cropping season. **Key: PC**, Principal Component Axis; **E**, Environment; **G**, Genotype

Identification of genotypes based on the 'ideal' genotype

In the present experiment, the GGE biplot analysis identified genotype G6, followed by G9 and G5 as an 'ideal' genotype since it was in a very close proximity to the center of the first concentric circle in the GGE biplot graph in terms of high corm and cormel yield performance among all genotypes. According to Mitrovic et al. (2012), the genotype closer to the concentric circle is more desirable than others. Although 'ideal' genotype may not exist in real world, these may be used as references for selecting genotype in multi-environmental data (Mitroic et al., 2012). Therefore, genotype G6 could be used as a reference for genotype evaluation or could be selected for broad adaptation across the test multi-locations. Other genotypes including G1, G2, G3, G4, G6, G7, G8 and G11 were located far from the concentric circle in the GGE biplot and may not be regarded as desirable (Fig. 2). This is consistent with Rakshit et al. (2012) and Oral et al. (2019) who found similar results in different crops.

Identification of environments relative to the 'ideal' environment

Although, ideal environment may not exist in real world (Yan and Tinker, 2006), location E2 (Areka) in current investigation is the `ideal` environment since it is closer to the center of concentric circles as illustrated by graphic representation (Fig.3) and it may be considered as the best representative among all test locations for evaluating superior taro genotypes. In the present study, environment E2 (Areka) was very stable and suitable for all genotypes (Table 4). E4, followed by E3 and E5 was a moderate location with respect to relative position from the center of the concentric circles on the Average Environmental Axis (AEA). However, E1, followed by E6 was the farthest location from the center of the concentric circles and might not be used in selecting superior genotypes, but could be useful in discarding unstable genotypes. Environments E1 and E6 were the least representative as they were located far from the average environment coordinate. Similar studies in several traits were also conducted by Rakshit et al. (2012) and Akter et al. (2015).

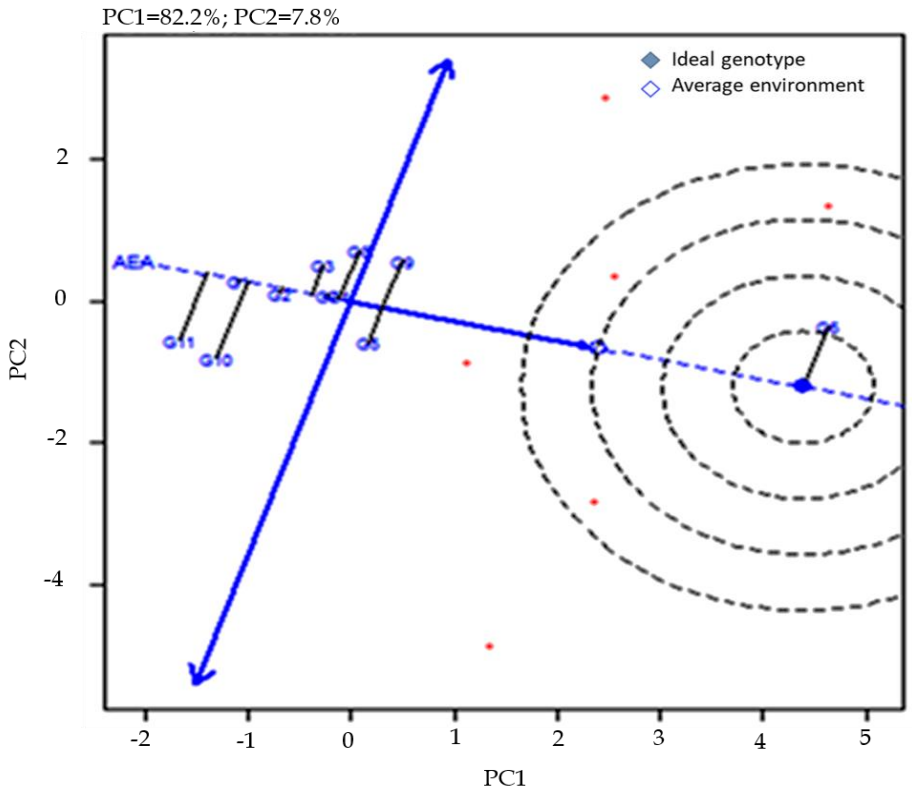

Figure 2. GGE biplot showing the two main axes of interaction (IPCA2 vs. IPCA1) of 11 taro genotypes tested at six locations in south Ethiopia relative to an 'ideal' genotype. Key: **PC**, Principal Component Axis; **G**, Genotype; E, Environment; AEA, Average Environmental Axis

Which-won-where and mega-environment identification

A GGE biplot for 11 taro genotypes tested at six locations in southern Ethiopia (Fig 4) was constructed by plotting the first principal component (PC1) scores of the genotypes and the environments against their respective scores for the second principal component (PC2) (Table 4). In the present investigation, based on the biplot sketch, the pentagon was constructed by connecting the markers of five vertex genotypes (G6, G10, G11, G1 and G8) which are located farthest away from the biplot origin in different directions. Consequently, four perpendicular equality lines denoted by L1, L2, L3 and L4 originating from the center of the biplot dissected the straight lines at right angles connecting between adjacent vertices of marker genotypes on the polygon. Genotypes at the vertices of the pentagon are either the best or poorest in one or more environments (Rakshit et al, 2012). In this experiment, the biplot was divided into four sectors (S1, S2, S3 and S4), with each marker of one genotype at each vertex of the pentagon. L1, the equality line that separated between genotypes G10 and G6 revealed that G6 showed better yield performance than G10 at all test environments. In the same way, L4 delineated G8 and G6 demonstrating that G8 was surpassed by G6 at all locations in terms of same parameters. L2 also explained that G10 was beaten by G11. In general, the GGE biplot analyses clearly defined that genotypes either at the vertices or inside the sectors of the polygon at the left hand side of the equality lines always remained inferior to those genotypes located at the right hand side in terms of the test traits.

Genotypes characterized by shorter vectors inside the polygon, mainly those located close to the biplot origin such as G4, G7, and G2 were less responsive and not the best in any environment comparing with the vertex genotypes. such genotypes are considered more stable while genotypes with longer vector are unstable, which is in line with the finding reported by Bai et al. (2014) in potato multi location trial in China. Genotype G6, which formed the vertex of sector 1 (S1) was considered as a winning genotype across all test environments (Fig 4). G6 shown at the peak vertex of the pentagon (Fig. 4) gave inconsistently the highest corm and cormel yield across all test locations. Based on this analysis, the test locations were grouped into a single mega-environment that indicated the existence of the non-crossover type of GEI (Fig 5). In contrast, 90.9% of the test genotypes (G1, G2, G3, G4, G5, G7, G8, G9, G10, and G11) in this study remained without environment, which explained that none of them outdid G6 in any of the test locations explaining a non-cross over type of GEI.

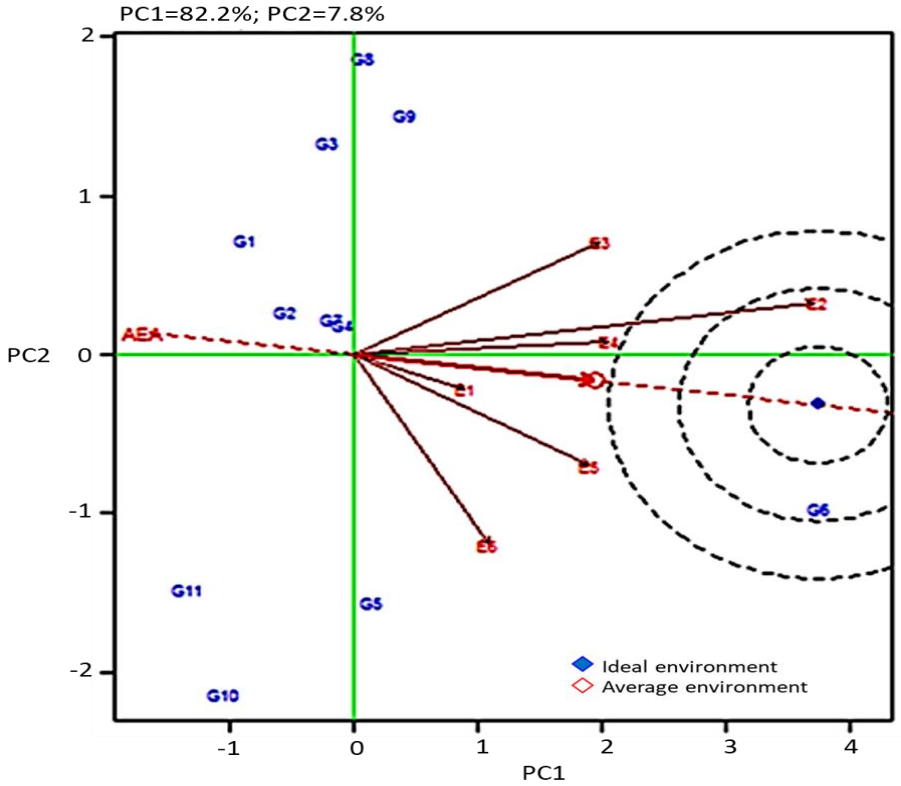

Figure 3. GGE biplot showing the two main axes of interaction (IPCA2 vs.IPCA1) of 11 taro genotypes tested at six locations in south Ethiopia relative to an 'ideal' environment. Key: **PC**, Principal Component Axis; **E**, Environment; **G**, Genotype; AEA, Average Environmental Axis

Although no other genotype outdid G6 in any of the test environments, some genotypes won each other interchangeably in a small number of environments indicating that the GEI was also crossover type (Fig. 5), which is in line with the finding reported by Shitaye (2015) in durum wheat multi location variety trial in Ethiopia. But such kind of crossover type of GEI cannot warrant formation of multiple mega environments as formation of multiple mega-environments is only possible under conditions of a cross-over type of GEI (Chemeda et al., 2015). In the present study, genotypes G9, G8, G7, G10, and G5 exhibited highest yield performances at locations E1, E2, E3, E4, E5, and E6, respectively. Therefore, the current investigation clearly illustrated the existence of a mixture of crossover and non-crossover types of GEIs (Fig. 5). According to Sharifi et al. (2017), it is very common for mega-environment trials data to embody a mixture of crossover and non-crossover types of GEI. Mega environments are environments that consistently share the same best genotypes for a given trait. In this experiment, 'which-won-where' analysis has demonstrated existence of single mega-environments and many of the locations though geographically located far apart may generate similar information. Hence, to conduct the MET effectively with limited resources, discriminative locations encompassing representative locations may be included, rather than extending the trials extensively over related locations. In the given situation, smaller zonation of testing locations and focusing breeding efforts in a location-specific manner holds more importance. Thus the cost of testing may be reduced significantly (Sharifi et al. 2017).

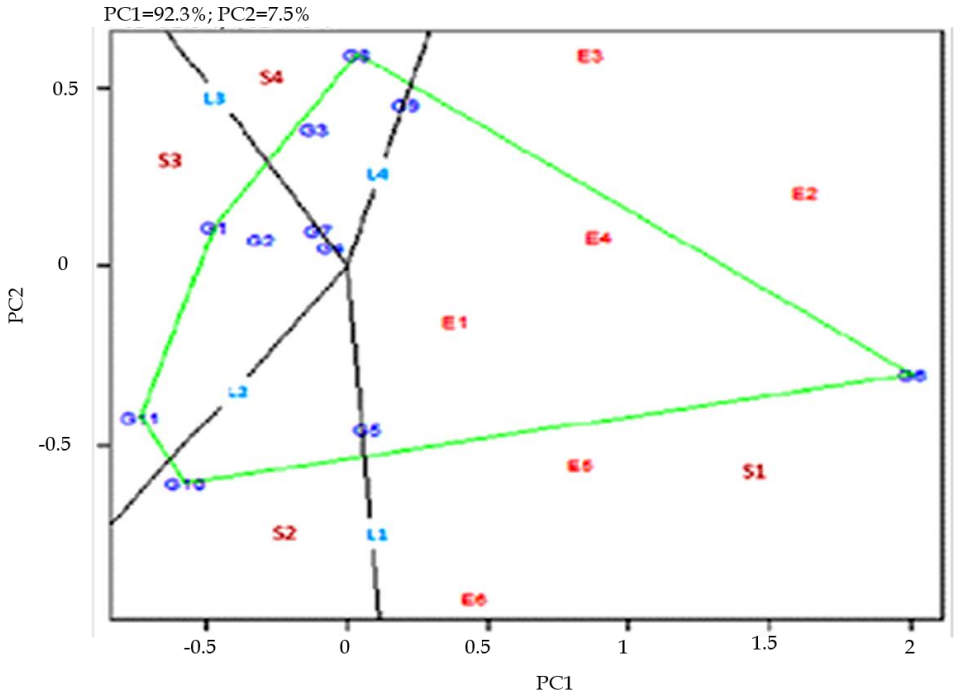

Figure 4. Polygon view of GGE biplot (which–won–where) showing the (G+G×E) interaction effect for grain yield of 11 taro genotypes in six environments. Key: **PC**, Principal Component Axis; **E**, Environment; **G**, Genotype; S, Sector; L, Equality Line

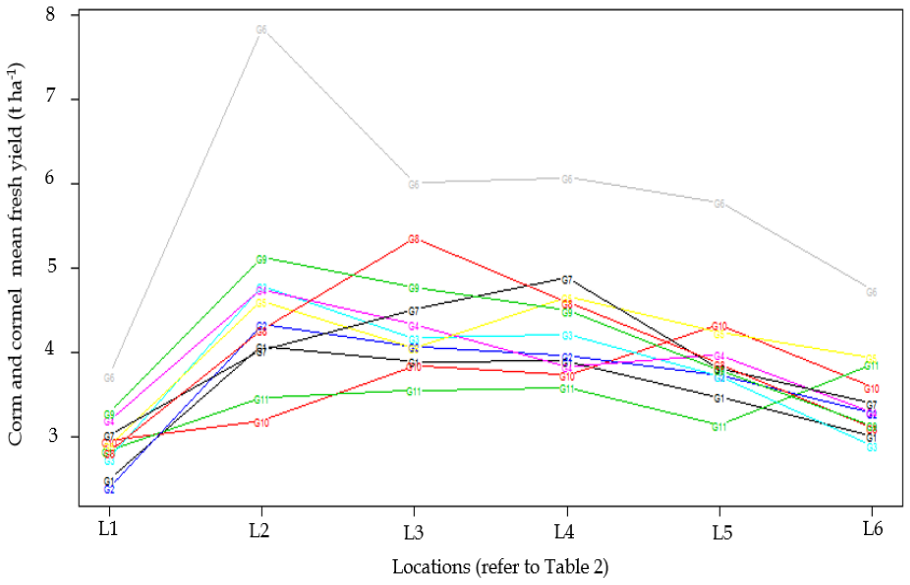

Figure 5. Graph showing a mixture of crossover and non-crossover types of GEI for corm and cormel mean fresh yield of 11 taro genotypes in six environments. Key: G, Genotype; L= Locations (environments)

CONCLUSION

G6 (*Boloso* 1) was the winning genotype over the entire set of test locations and led to the formation of a single mega-environment, showing a non-cross over type of GEI. It showed wider adaptation and could be multiplied in and recommended to all test locations. Analysis of ASV conveniently facilitated categorization of the set of the test genotypes into stable and unstable classes. Though G6 was inconsistently a high yielding genotype across all test locations, it was found to be the most unstable. Majority of the genotypes displayed low yield performance across all test locations and couldn't respond to the changing environmental conditions (stable). On the basis of environmental index (EI) values, the six locations were categorized into favorable/rich and unfavorable/poor environments. E1 (Angacha) was identified as the poorest

environment but E2 (Areka) was the most favorable for multiplication and testing of taro genotypes relative to corm and cormel yield. G6 (*Boloso*-1) was identified as a desirable/'ideal' genotype and hence could be used as a reference for genotype evaluation across the test multi-locations. Similarly, E2 (Areka) was identified as an 'ideal' environment which may be considered as the best discriminating and representative among all test locations for evaluating superior taro genotypes.

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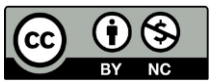

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