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Full Length Research Paper

GGE biplot analysis of *Dioscorea rotundata* cultivar "DENTE" in Ghana

Emmanuel Otoo[1]* and Robert Asiedu[2]

[1]Crops Research Institute, P.O. Box 3785, Kumasi, Ghana.
[2]IITA, PMB 5320, Oyo Road, Oyo, Ibadan, Nigeria.

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Yield data of 20 genotypes of *D. rotundata* cultivar "Dente" tested across 15 rain-fed environments during the 2000 to 2004 growing season using Augmented RCBD with 3 blocks were analyzed using the GGE biplot method. The aim of the study was to (i) identify genotypes that combine high yields with stability across environments via GGE (genotype plus genotype x environment) biplot methodology, and (ii) to identify best test environments (representative, discriminating, and unique environments) of improved *D. rotundata* cvr Dente germplasm in Ghana. The environment (E) explained 36.5% of the total (G + E + GE) variation, whereas G and GEI captured 36.1 and 27.4%, respectively. The first 2 principal components (PC1 and PC2), which were used to create a 2-dimensional GGE-biplot and explained 63.8 and 12.0% of GGE sum of squares (SS), respectively. Genotypes Ge1 and Ge28 were the ideal genotypes (desirable in terms of higher yielding ability and stability). Of the 15 environments tested, biplot analysis identified single mega-environment for all environments. Wenchi (Forest-Savannah Transition) was the most representative and discriminating environment.

Key words: *Dioscorea rotun*data, GGE-biplot analysis, multi-environment trials.

INTRODUCTION

Yam (*Dioscorea spp*) is an important crop in West Africa in general and Ghana in particular. This is a multi-species crop. In Ghana the main cultivated species is *Dioscorea rotundata.* There are several cultivars of this species with varying characteristics and end-uses. Among which are Dente, Pona, Larebako, Lilee and others. *Dioscorea rotundata* cvr Dente for instance, is an extremely impor-tant cultivar in Ghana and is third in importance only to Pona and larebarko in terms of tuber quality. It is the best cultivar of yam in terms of storage. It can store up to 6 months- long after pona and larebako are unavailable in the market, and has excellent texture, which makes it an excellent candidate for pounding. Yams are mostly propagated vegetatively hence genetic make-up of the crop remains unchanged from one generation to another. Most yam species do not flower and set seeds, and therefore does not lend themselves readily for genetic improvement via crossing and its attendant benefit of enriching the genetic makeup of the crop. Reverse is the case in *Dioscorea rotundata* cvr Dente. It set seed profusely and can be crossed easily, and has the potential of enriching its genetic makeup from time to time.

Again, yams, generally has benefited very little from research and development and *Dioscorea rotundata* cvr Dente, is no exception. Yield, pest and disease are some of the attributes which need to be improved and are currently receiving attention at Crops Research Institute of Ghana. The germplasm of *Dioscorea rotundata* cvr Dente at Crops Research Institute has been enriched with collection from the entire country and introductions from International Institute for Tropical Agriculture. The need to evaluate these collections in several environments therefore cannot be over-emphasized.

Dente cultivation is also often limited to the Forest-Savannah Transition and Guinea Savannah. The need to evaluate these materials in other environments other than its traditional environments and for that matter in multi-environment cannot also be over-emphasized.

Multi-environment trials (MET) are often done to identify superior genotypes. There are several analytical procedures for analyzing MET and identifying high and stable genotypes. However, most of them require sophisticated and complex analysis of MET data. Biplot analysis is the novel approach for analyzing such data. A biplot is

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*Corresponding author. E-mail: otoo_emmanuel@yahoo.com.

Table 1. Legend for environment used for the trials.

Environment code	Environment
B00	BODWEASE 2000
B01	BODWEASE 2001
B02	BODWEASE 2002
B03	BODWEASE 2003
B04	BODWEASE 2004
W00	WENCHI 2000
W01	WENCHI 2001
W02	WENCHI 2002
W03	WENCHI 2003
W04	WENCHI 2004
F00	FUMESUA 2000
F01	FUMESUA 2001
F02	FUMESUA 2002
F03	FUMESUA 2003
F04	FUMESUA 2004

a scatter plot that approximates and graphically displays a two-way table by both its row and column factors in a way that relationship among row factors, relationships significant GEI interactions can masked the true performance of the individual genotypes. GGE biplot analysis is simple and easy-to-do procedure, which has in recent, times gain acceptability and is being used in GGE analysis of MET data. This procedure has been employed successfully in determining relationship among genotypes, environment and high and stable genotypes of *D. cayenensis* in Ghana (Otoo and Asiedu, 2006).

The objective of this study therefore was to (i) identify genotypes that combine high yields with stability across environments via GGE (genotype plus genotype x environment) biplot methodology and (ii) to identify best test environments (representative, discriminating, and unique environments) of improved *D. rotundata* cvr Dente germplasm in Ghana.

MATERIALS AND METHODS

Data for this study was obtained from 17 improved lines of true botanically developed seeds of *D. rotundata* cultivars of Dente respectively with three vegetatively developed *D. rotundata* cultivars of Dente checks each. The genotypes were evaluated in 15 environments consisting of 3 locations in 5 years, 2000 to 2004. The experimental design used was Augmented RCBD with 3 blocks. Details of the 15 environments, 20 genotypes and characteristics of the environments are given in Tables 1, 2 and 3 respectively. Land was manually prepared. Each plot consisted of 10 stands planted at a spacing of 1 x 1 m. The crop planted in mounds and individually staked with bamboo 2 – 3 m tall at the onset of rains (March-April) with yam setts weighing 300 g. The trials were con-ducted under rain-fed conditions with no fertilizer or any other agro-chemical application. The crop was weeded manually 3 - 5 times in a season. Harvesting was done at 10 months after planting (MAP). Data on fresh tuber yields was collected from all the 10 plants in a plot. Tuber yield was obtained by expressing plot tuber yields on a hectare basis (t ha-1).

Table 2. Legend and source of genotypes used for the trial

Genotype code	Genotype lineage	Genotype source
Ge1	CLONE	TECHIMAN
Ge2	CLONE	WENCHI
Ge3	CLONE	KINTAMPO
Ge5	TBS	IITA
Ge13	TBS	IITA
Ge14	TBS	IITA
Ge15	TBS	IITA
Ge17	TBS	IITA
Ge21	TBS	IITA
Ge22	TBS	IITA
Ge23	TBS	IITA
Ge27	TBS	IITA
Ge28	TBS	IITA
Ge30	TBS	IITA
Ge32	TBS	IITA
Ge34	TBS	IITA
Ge36	TBS	IITA
Ge38	TBS	IITA
Ge39	TBS	IITA
Ge40	TBS	IITA

Statistical analysis

Using SAS version 9.1 for Windows software, the yield data was analyzed using Proc Mixed procedures considering environment and block as random, and genotype (M unreplicated, and C – replicated) as fixed factor. The mean yield data was analyzed using Model 1 biplot procedure of GGE computer software version 5.2.

RESULTS AND DISCUSSIONS

The effects of environment, genotype (M-unreplicated and C–replicated) and their interaction were all significant with respect to the yields of *Dioscorea rotundata cvr dente* lines (Table 4). Generally, the replicated checks

Table 3. Agroecological characteristics of the test sites

	Locations		
Characteristics	**Fumesua**	**Wenchi**	**Bodwease**
Coordinates	**6°41’N, 1°28’W**	**7°44’N 2°7’W**	**5°35’N 0°35’W**
Agroecological zone	**Humid forest**	**Forest-Guinea savannah transition**	**Forest-coastal savannah transition**
Soil types	Ferric Acrisol* Asuansi series with *c.* 5cm thick top layer of dark grey gritty loam to gritty clay loam	Ferric Lixisol* Damongo series with 20-50 cm of dark brown tobrown, slightly loose, porous, loamy sand topsoil grading into homogenous red, friable and porous sandy clay loam to clay loam.	Haplic lixisol** Bodwease series with 10cm thick top layer of dark reddish brown, homous; sandy clay loam; frequent fine rootlets; crumbly; porous; firm with pH of 7.7
Slope	2-6%	0-2%	0-3%
Temperature range (min-max°C)	22-31	21-34	21-34
Wet season	Bimodal rainfall pattern	Bimodal rainfall pattern	Bimodal rainfall pattern
-major	March– July; peak in June	March – July; peak in June	March – July; peak in June
-minor	Sep – Nov; peak in Oct	Sep – Nov; peak in Oct	Sep – Nov; peak in Oct
Total annual rainfall (mm)	1000-1800 mm averaging 1500 mm/year	1000-1500mm averaging 1300 mm/year	1050-1200mm averaging 1125mm/year

*FAO/UNESCO classes (Asiamah and Adu, 1992; **Asiamah et. al., 1993).

(local clones) were higher yielding than the TBS lines (improved genotypes). The mean yield of local clones averaged over all environments had yields ranging from 16.0 t/ha (Ge3) to 25.0 t/ha (Ge1) with a mean of 21.2 t/ha (Table 5) whilst the TBS lines had yields ranging from 8.2 t/ha (Ge40) to 25.0 t/ha (Ge28) and a mean of 16.9 t/ha (Table 6).

These differences in yield between clones and test lines can be attributed to the high level of adaptation of the local clones which have been cultivated in the same prevailing environment from time immemorial. A significant ENV*M, and ENV*C obtained from the SAS analysis (Table 3), necessitating the subjection of the mean yield per environment matrix data to GGE biplot analysis. The results of the combined analysis of variance (Table 7) showed a significant effect of environment. E (environment) explained 36.5% of the total (G + E + GE) variation, whereas G and GEI captured 36.1 and 27.4%, respectively. The first 2 principal components (PC1 and PC2) which were therefore used to create a 2-dimensional GGE-biplot and explained 63.80 and 12.0% of GGE sum of squares (SS), respectively.

GGE stands for genotype main effect (G) plus genotype by environment interaction (GE), and the GGE concept is based on the understanding that genotype main effect (G) and genotype by environment interaction (GE) are the two sources of variation that are relevant to genotype evaluation and that they must be considered simultaneously, not alone or separately, for appropriate genotype evaluation (Yan, 2005).

Choice of genotypes

In this study, different genotypes produced the highest tuber yield in different environments (Table 8). Since, it is very common for multi-environment data to embody a mixture of crossover and non-crossover types of GEI. These differential rankings of genotypes across test environments may or may not reveal that there exists possible crossover GEI. Genotypes Ge1 (best clone) and Ge28 (best improved genotype) had the highest yield in 6 environments each. Ge1 had the highest tuber yield in environments B00, B02, B002, B004 and B005 whilst genotypes Ge28 had its highest tuber yields in environments W01, W03, WO4, B000, B001 and B003. Ge2 won in environments B01 and W00 and genotype Ge21 won in W02.

Table 4. Summary of ANOVA of 20 lines of *D. rotundata* cultivar Dente in 15 environments

Effect	NUM df	Den Df	F value	Pr>F
ENV	14	8	10.76	0.0004
M	16	8	12.50	0.0006
ENV*M	97	8	11.31	0.0005
C	2	8	33.90	0.0001
ENV*C	28	8	11.29	0.0005

NB: M = unreplicated testlines; C = replicated checks

Table 5. Mean yields of 3 clones of D. rotundata cvr Dente replicated checks in 15 environments in Ghana.

	Genotype				
Environment	Ge1	Ge2	Ge3	Mean	SED
F00	22.8	22.3	18.8	21.3	2.2
F01	23.5	25.1	11.6	20.1	7.4
F02	24.9	23.7	13.8	20.8	6.1
F03	28.3	25.1	13.9	22.4	7.6
F04	22.4	23.9	17.6	21.3	3.3
W00	19.1	15.1	15.6	16.6	2.2
W01	17.0	13.0	7.1	12.4	5.0
W02	16.9	14.0	5.4	12.1	6.0
W03	17.8	14.2	4.7	12.2	6.8
W04	19.8	15.9	8.8	14.8	5.6
B00	35.3	28.5	24.9	29.6	5.3
B01	30.7	28.9	25.7	28.4	2.5
B02	32.4	27.6	25.0	28.3	3.8
B03	30.8	29.1	20.5	26.8	5.5
B04	33.1	28.7	26.8	29.5	3.2
MEAN	25.0	22.3	16.0	21.1	4.6
SED	6.3	6.2	7.6	6.4	

This is attributable to the differential edaphic conditions prevailing in the environments (Table 3). Comparison of Ge3 and Ge28 shows a non-significant difference between the best two genotypes across all environments (Figure 1).

Figure 2 shows the average environment coordinate (AEC) view of the GGE biplot based on the genotype focused scaling, showing the mean yield and stability of 20 genotypes of *D. rotundata* cvr Dente in 15 environments. The AEA (the single-arrowed line) points to higher average yield. The double-arrowed line is the AEC ordinate; it points to greater variability (smaller stability) in either direction. Genotypes Ge1 and Ge28 were the highest yielding and stable genotypes; and Ge14 and Ge40 the lowest yielding but stable genotypes. Ge17 though high yielding was highly unstable and Ge34 low yielding and unstable. Genotypes Ge40, Ge14, Ge5 and Ge34 must be culled due to their poor yield performance in all environments.

In GGE biplot analysis, the length of the genotype vectors, which are lines connecting the genotypes to the biplot origin, measures the differences of the genotype from the grand mean (Yan, 2005). Genotypes with long vectors are either the best (e.g. G18) or poorest (e.g. G21) in one or more environments (Figure 3); genotypes located near the biplot origin are close to average in all environments.

Again the cosine of the angle between the vectors of two genotypes also measures their similarity or dissimilarity in response to (interaction with) the environments, that is, in specific adaptations. Therefore, Ge40 and Ge28 (Figure 3) was the poorest and the best lines of *D. rotundata* cvr Dente respectively. The superiority of genotypes Ge1 and Ge28 with respect to their high yield performances were confirmed when the genotypes were compared to an ‘ideal’ genotype (Figure, 4). Genotypes Ge1 and Ge28 were the closest to the ideal genotype followed by genotypes Ge2 and Ge13

Choice of ‘ideal’ test environments for selecting high mean performance genotypes

In multi-environment evaluation, scientists look out for an ‘ideal’ environment where maximum information can be obtained at the minimal cost (both human and resource) from the evaluation. The ideal test environment should be most discriminating (informative) and most representtative, and such a test location or environment can be announced as “ideal” only if it is so across years.

Generally, when the biplot explain a greater portion of the total variation, for example >50%, the angles exactly reflect the correlations among the testers. A positive correlation suggests that one environment can represent the rest of the so correlated environments and vice versa. In this study, the GGE biplot explained 76% of the G plus GE data (Figure 6) suggesting that the angles between the vectors of the environments are good indicators of correlation amongst the environments. For instance, all the Bodwease environments (B00-B04) were positively correlated to each other. So were the Wenchi environments (W00-W04) and Fumesua environments (F00-F04). The cosine of angles between vectors of Bodwease and Wenchi was still less than 90. This means that there were no negative correlations among test environment with respect to the *D. rotundata* cvr Dente lines hence no strong crossover GE. Since, if two test environments are closely correlated consistently across years, removing one of them would not lead to any loss of information, The D. rotundata cvr Dente lines can be evaluated in one better environment such as Wenchi.

Again in biplot analysis, the lines that connect the test environments to the biplot origin are called environment vectors. The length of the vectors approximates the standard deviation within the respective environments, which is a measure of the discriminating ability of the environments (Yan, 2005). Generally, the Bodwease environ-

Table 6. Mean yield data of 17 improved D. rotundata cvr Dente lines in 15 environments in Ghana.

ENV/ GEN	**Ge15**	**Ge17**	**Ge13**	**Ge22**	**Ge28**	**Ge21**	**Ge23**	**Ge27**	**Ge32**	**Ge30**	**Ge34**	**Ge5**	**Ge36**	**Ge14**	**Ge38**	Ge39	Ge40	Mean	SED
F00	20.3	19.9	16.9	14.2	21.2	11.3	14.2	11.8	12.8	14.6	11.8	11.1	17.8	8.9	14.6	18.9	8.2	14.6	4.0
F01	21.6	18.9	19.3	12.0	22.6	15.8	13.4	16.3	13.6	14.4	11.7	16.4	19.2	9.1	16.4	19.2	8.6	15.8	4.1
F02	22.5	22.7	18.9	10.1	23.2	11.5	12.8	13.1	12.7	13.8	10.0	10.7	18.7	8.7	12.7	17.6	10.5	14.7	4.9
F03	22.1	22.9	19.3	13.2	24.8	14.5	10.5	8.6	14.4	16.8	9.6	7.3	18.7	6.2	11.0	17.1	7.2	14.4	5.9
F04	23.1	23.6	18.9	13.8	22.8	18.0	10.1	12.6	18.2	19.4	9.6	15.0	17.3	8.6	12.2	15.7	7.9	15.7	5.1
W00	10.3	11.1	17.6	16.2	17.7	13.0	7.4	6.7	12.9	15.3	16.9	9.9	13.8	8.9	19.0	14.8	8.2	12.9	3.9
W01	15.5	13.2	16.8	17.8	18.2	19.4	13.8	6.3	15.4	17.6	9.1	7.7	18.8	9.2	15.2	14.1	9.0	13.9	4.2
W02	12.2	13.2	16.8	12.6	19.3	15.3	11.6	15.4	16.1	13.9	9.6	6.6	18.4	8.8	15.3	15.7	7.2	13.4	3.7
W03	7.6	11.7	16.8	17.8	18.3	13.6	8.7	6.9	13.2	17.4	5.4	7.6	18.2	5.9	18.4	16.3	6.9	12.4	5.0
W04	11.0	18.1	14.5	15.9	19.9	11.2	10.9	17.3	14.3	16.4	16.6	8.7	14.6	9.5	12.5	15.4	9.2	13.9	3.4
B00	19.1	36.1	31.1	27.9	39.7	21.6	18.6	36.0	19.8	11.6	9.8	9.4	22.8	8.4	19.6	11.2	7.8	20.6	10.4
B01	22.7	19.9	27.8	27.9	30.2	25.2	22.4	22.2	25.3	24.3	30.2	22.2	26.8	9.6	22.7	22.3	9.2	23.0	5.9
B02	16.8	16.3	28.3	22.3	36.5	23.8	23.0	25.7	23.8	20.7	28.3	21.7	22.6	9.3	21.5	22.2	9.3	21.9	6.6
B03	20.1	22.7	28.6	29.5	30.2	27.2	22.1	28.7	22.7	22.1	27.6	23.8	20.0	9.9	22.3	25.5	7.4	23.0	6.3
B04	26.5	23.3	27.8	24.8	30.1	22.4	24.5	26.9	23.4	22.7	25.7	26.2	26.7	6.9	23.0	26.3	6.8	23.2	6.5
MEAN	18.1	19.6	21.3	18.4	25.0	17.6	14.9	17.0	17.2	17.4	15.5	13.6	19.6	8.5	17.1	18.2	8.2	16.9	4.1
SED	5.6	6.34	5.62	6.44	6.86	5.37	5.68	9.09	4.58	3.72	8.33	6.77	3.73	1.22	4.14	4.28	1.06	4.12	

ments had the longest vector and therefore the best (most discriminative) for *D. rotundata* cvr Dente (Figure 5) and Fumesua the least discriminating. It must be noted however that even though Bodwease was the most discriminating it was not the most representative of the environments (Figure 6).

The representativeness of the test environment can be assessed using "Average-Environment Axis" (AEA, or average-tester-axis,) view of the GGE biplot (Yan, 2001). The average environment has the average coordinates of all test environments, and AEA is the line that passes through the average environment and the biplot origin. Generally, a test environment that has a smaller angle with the AEA is more representative of the target environment. Results from Figure 6, the average environment coordinate (AEC) view of the GGE biplot based on the genotype-focused scaling, showing the 20 genotypes of *D. rotundata* cvr Dente in 15 environments. The Wenchi environments (arrowed) were the closest to the ideal environments for Dente evaluation followed by Fumesua and Bodwease environments. This can be attributed to the fact that Dente cultivars are traditional grown mostly in Forest-Savannah Transition (Wenchi and Forest agroecologies (Fume-

Table 7. Analysis of variance (ANOVA) of 20 lines of *D. rotundata* cultivar Dente in 15 environments.

Source	Dente		
	DF	**SS**	**%**
Genotype (G)	19	5359	36.3
Environment (E)	14	5379	36.4
G x E	266	4039	27.4
PC	**Lambda**	**% of Total SS**	
1	77.33	64	
2	33.50	12	
3	29.83	9	
4	24.56	6	
5	14.43	2	
6	12.85	2	

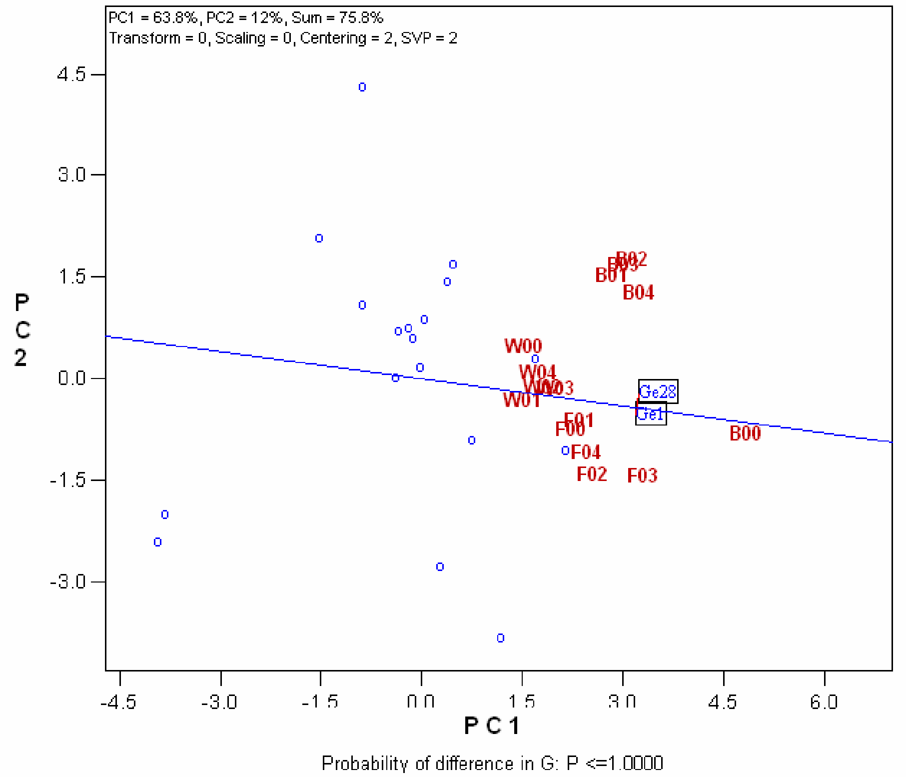

Figure 1. Comparison of best local clone and best improved genotype.

sua), and was an introduction to the Coastal Savannah agroecology, hence the good adaptation to Wenchi followed by Fumesua and Bodwease in that order.

Wenchi environments which were averagely discriminating and most representative environment therefore can be used for genotypes with wide adaptation. Discriminating but non-representative test environments such as B00, B01, B02 and B03 are useful for selecting specifically adapted genotypes if the target environments can be divided into mega-environments and also useful for culling unstable genotypes if the target environment is a single mega-environment. Since, non-discriminating test environments are useless, Fumesua environments can be considered useless with respect to the evaluation of *D. rotundata* cvr Dente lines since their absence will not lead to loss of information.

Suitability of genotypes for particular environment

In the GGE biplot analysis, in assessing an 'ideal' envi-

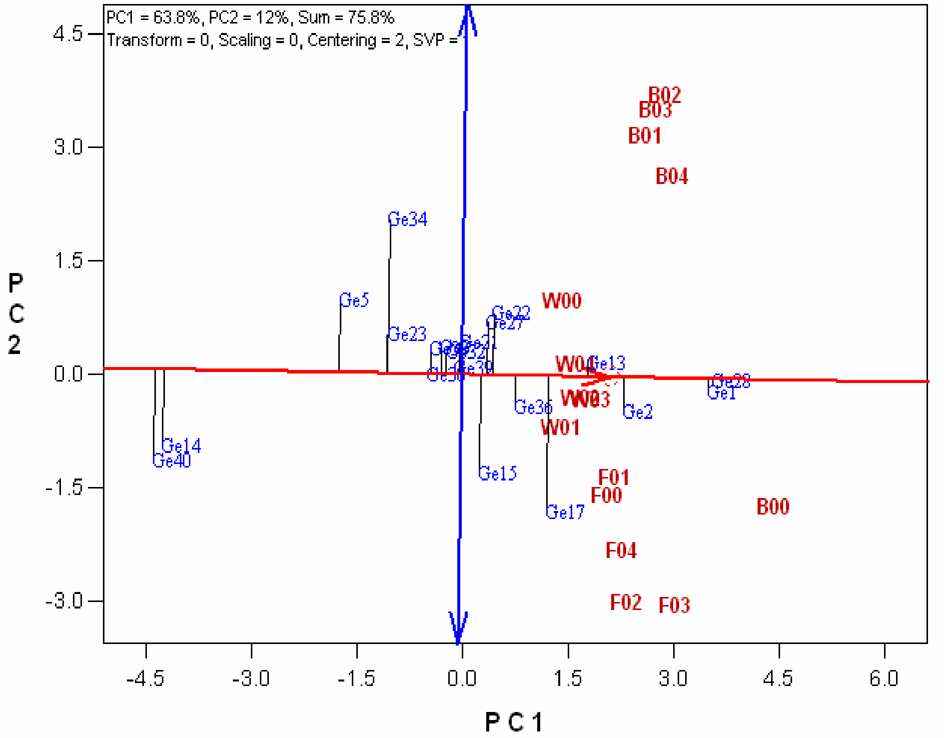

Figure 2. Mean performance and stability of 20 Dioscorea rotundata cvr dente lines.

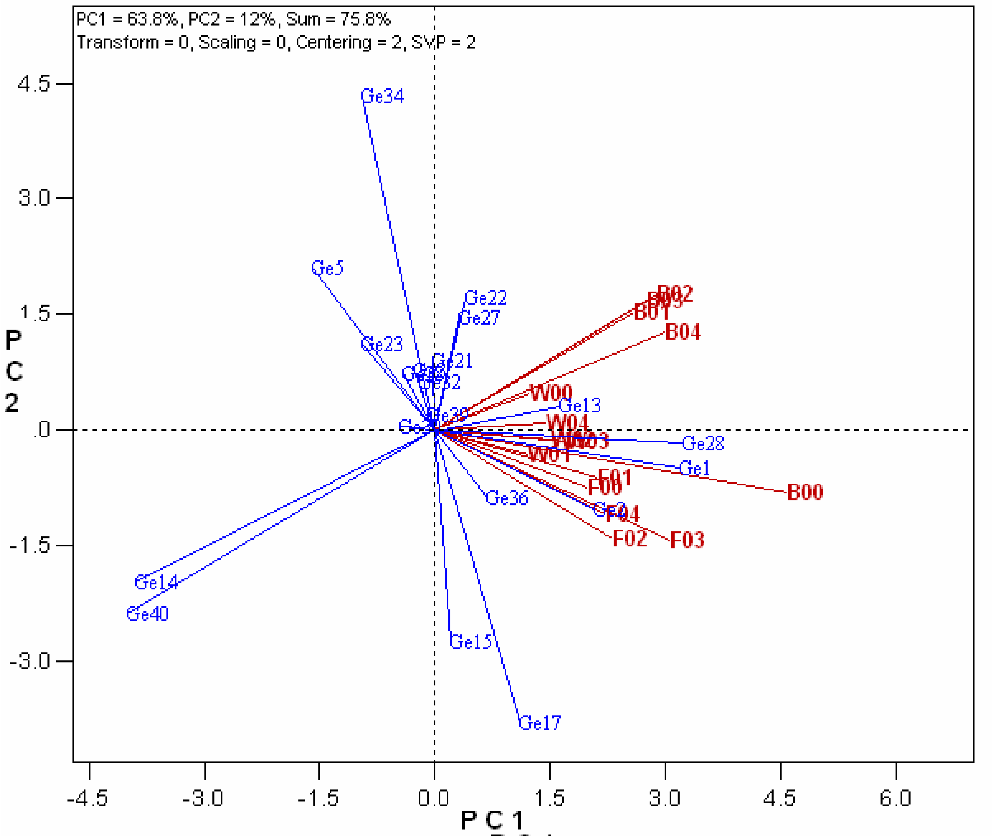

Figure 3. Biplot of relationship between genotypes and environments

Table 8. Mean yield of 20 genotypes of *D. rotundata* cvr Dente in 15 environments in Ghana.

Code	F00	F01	F02	F03	F04	W00	W01	W02	W03	W04	B00	B01	B02	B03	B04	Mean
Ge1	22.8	23.5	24.9	28.3	22.4	19.1	17.0	16.9	17.8	19.8	35.3	30.7	32.4	30.8	33.1	25.0
Ge2	22.3	25.1	23.7	25.1	23.9	15.1	13.0	14.0	14.2	15.9	28.5	28.9	27.6	29.1	28.7	22.3
Ge3	18.8	11.6	13.8	13.9	17.6	15.6	7.1	5.4	4.7	8.8	24.9	25.7	25.0	20.5	26.8	16.0
Ge15	20.3	21.6	22.5	22.1	23.1	10.3	15.5	12.2	7.6	11.0	19.1	22.7	16.8	20.1	26.5	18.1
Ge17	19.9	18.9	22.7	22.9	23.6	11.1	13.2	13.2	11.7	18.1	36.1	19.9	16.3	22.7	23.3	19.6
Ge13	16.9	19.3	18.9	19.3	18.9	17.6	16.8	16.8	16.8	14.5	31.1	27.8	28.3	28.6	27.8	21.3
Ge22	14.2	12.0	10.1	13.2	13.8	16.2	17.8	12.6	17.8	15.9	27.9	27.9	22.3	29.5	24.8	18.4
Ge28	21.2	22.6	23.2	24.8	22.8	17.7	18.2	19.3	18.3	19.9	39.7	30.2	36.5	30.2	30.1	25.0
Ge21	11.3	15.8	11.5	14.5	18.0	13.0	19.4	15.3	13.6	11.2	21.6	25.2	23.8	27.2	22.4	17.6
Ge30	14.2	13.4	12.8	10.5	10.1	7.4	13.8	11.6	8.7	10.9	18.6	22.4	23.0	22.1	24.5	14.9
Ge27	11.8	16.3	13.1	8.6	12.6	6.7	6.3	15.4	6.9	17.3	36.0	22.2	25.7	28.7	26.9	17.0
Ge32	12.8	13.6	12.7	14.4	18.2	12.9	15.4	16.1	13.2	14.3	19.8	25.3	23.8	22.7	23.4	17.2
Ge30	14.6	14.4	13.8	16.8	19.4	15.3	17.6	13.9	17.4	16.4	11.6	24.3	20.7	22.1	22.7	17.4
Ge34	11.8	11.7	10.0	9.6	9.6	16.9	9.1	9.6	5.4	16.6	9.8	30.2	28.3	27.6	25.7	15.5
Ge5	11.1	16.4	10.7	7.3	15.0	9.9	7.7	6.6	7.6	8.7	9.4	22.2	21.7	23.8	26.2	13.6
Ge36	17.8	19.2	18.7	18.7	17.3	13.8	18.8	18.4	18.2	14.6	22.8	26.8	22.6	20.0	26.7	19.6
Ge14	8.9	9.1	8.7	6.2	8.6	8.9	9.2	8.8	5.9	9.5	8.4	9.6	9.3	9.9	6.9	8.5
Ge38	14.6	16.4	12.7	11.0	12.2	19.0	15.2	15.3	18.4	12.5	19.6	22.7	21.5	22.3	23.0	17.1
Ge39	18.9	19.2	17.6	17.1	15.7	14.8	14.1	15.7	16.3	15.4	11.2	22.3	22.2	25.5	26.3	18.2
Ge40	8.2	8.6	10.5	7.2	7.9	8.2	9.0	7.2	6.9	9.2	7.8	9.2	9.3	7.4	6.8	8.2
Mean	15.6	16.4	15.6	15.6	16.5	13.5	13.7	13.2	12.4	14.0	22.0	23.8	22.9	23.5	24.1	17.5
SED	4.5	4.7	5.4	6.6	5.2	3.9	4.2	4.0	5.1	3.6	10.3	5.8	6.6	6.2	6.5	4.3

NB: Winning genotypes in each environment is in bold.

ronment and genotypes, a polygon is first drawn on genotypes that are located away from the biplot origin so that all other genotypes are contained in the polygon.

Perpendicular lines are then drawn, starting from the biplot origin, to each side of the polygon (Figure 7). These perpendicular lines divide the biplot into sectors, and the wining genotype for each sector is the one located on the respective vertex. Ge17 was the winning genotype in F02 and Ge28 and Ge1 were the winners in the rest of the environments.

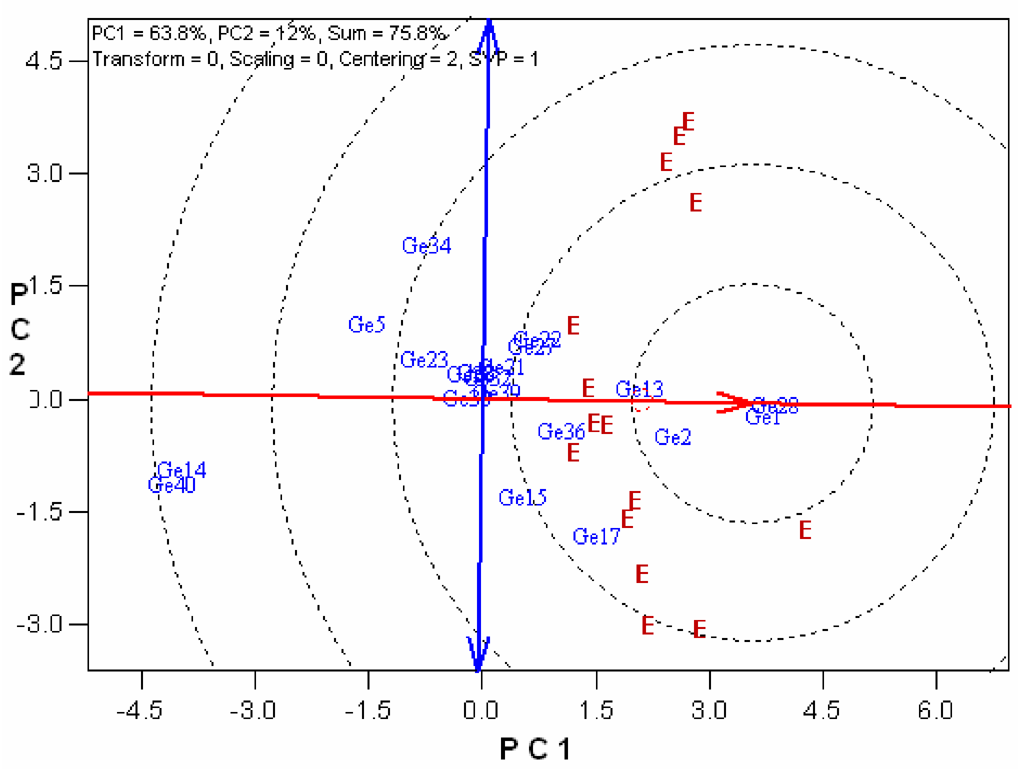

Figure 4. Ranking of genotype based on 'ideal' genotype assessment.

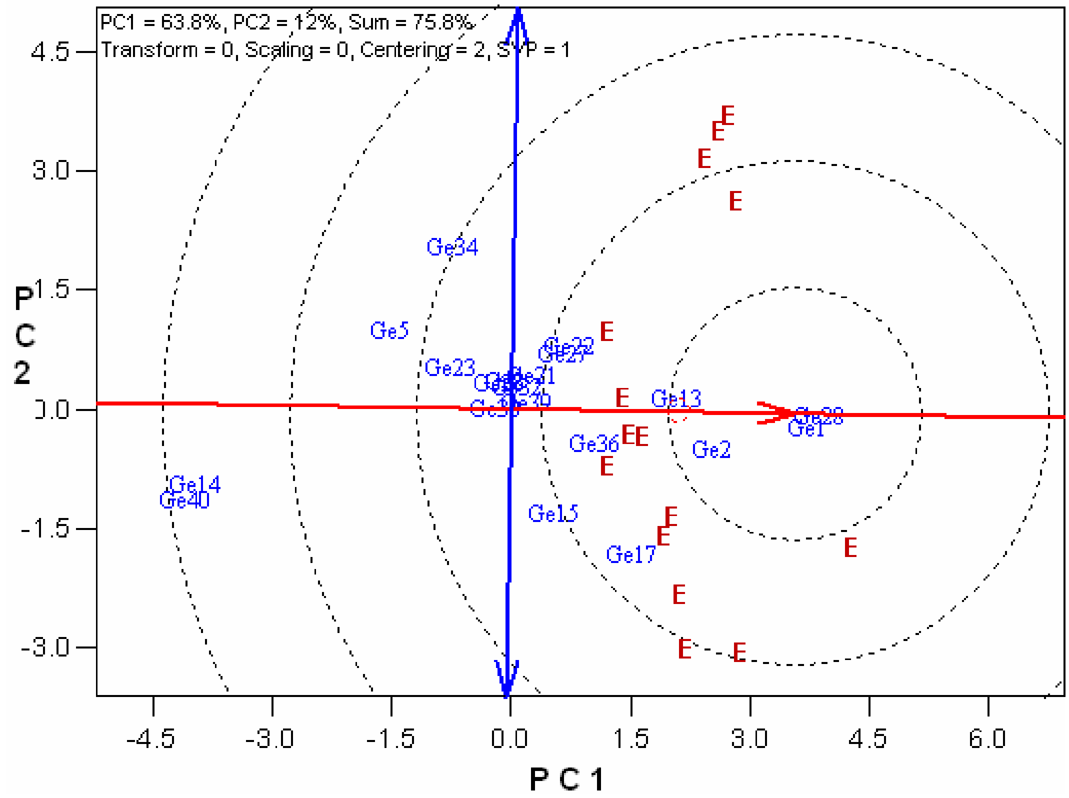

Figure 5. Bioplot of relationships of 15 environment based on 20 genotype of *D. rotundata* cvr Dente.

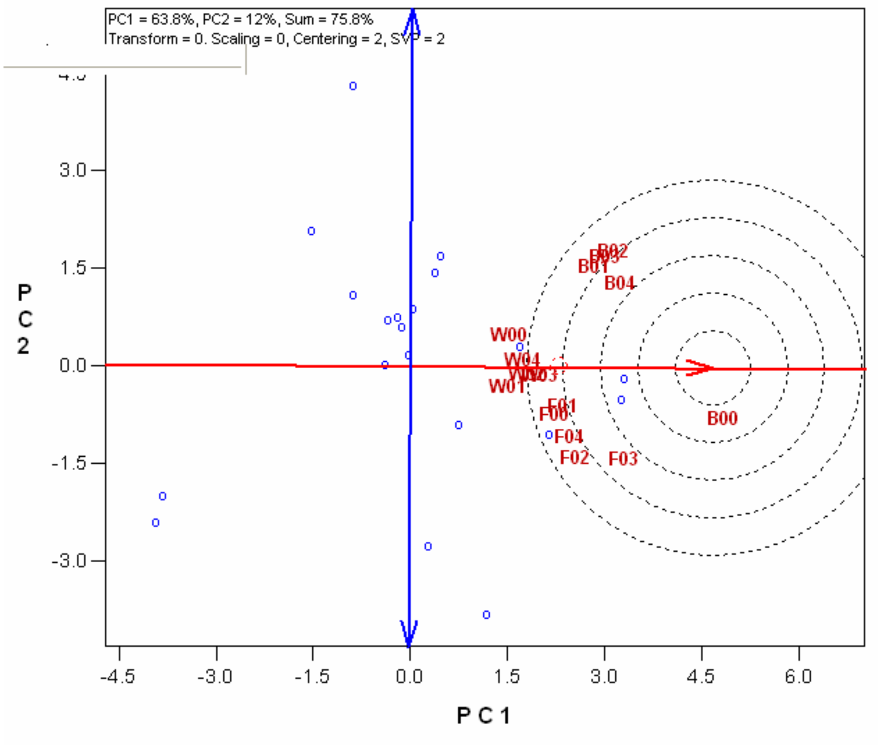

Figure 6. Comparison of environments best in reference to an ideal environment.

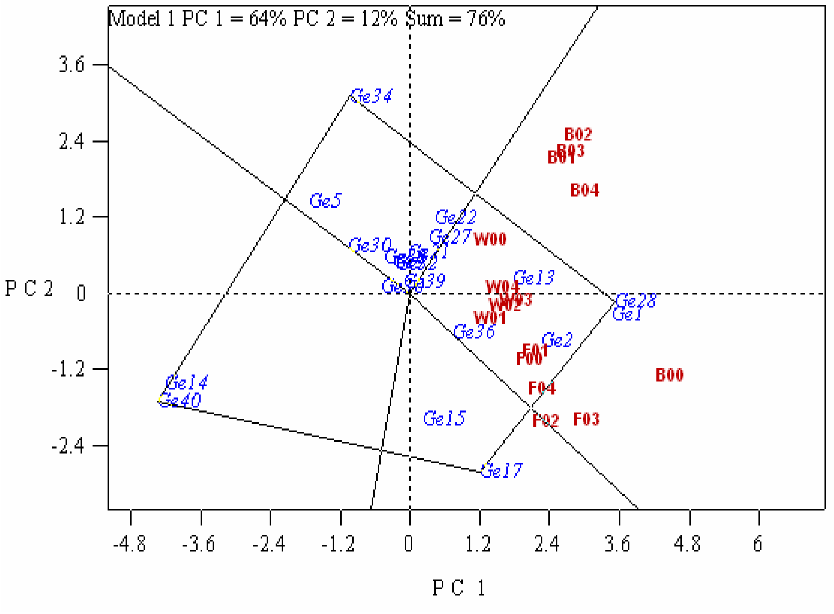

Figure 7. Biplot of winning genotype of 20 *D. rotundata* cvr "Dente" genotypes in 15 environments using the "which wins where or which is best for what" approach.

Conclusion

A local clone, Ge1 and an improved genotype, Ge28 were the best D. rotundata cvr dente genotypes based on mean performance and stability. Wenchi environments were the moderately discriminating than most representatives of the studied environments. Fumesua environments were useless with respect to D. rotundata cvr dente evaluation. Generally, single mega environment was identified for evaluation of *D. rotundata* cvs Dente lines.

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