



## GGE biplot analysis of *Dioscorea rotundata* cultivar Tela genotypes in Ghana

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### Abstract

A five-year study involving 38 genotypes of *D. rotundata* cultivar Tela was evaluated in 15 environments from 2000 to 2004 using CRD. The three locations were Bodwease (Coastal Savanna), Fumesua (Forest) and Wenchi (Forest-Savanna Transition). The objective was to assess the effect of genotype and genotype x environment interaction on the tuber yield of 38 white yam (*D. rotundata* L. cv. Tela) genotypes via GGE (genotype plus genotype x environment) biplot methodology. Significant differences ( $p < 0.005$ ) were observed among the genotypes with respect to genotype, environment and genotype by environment interactions. Biplot analysis identified three mega-environments corresponding to three agroecologies. Fumesua environments were most representative and discriminating. Bodwease environments except BOD04 were most discriminating but most non-representative and Wenchi least discriminating and least representative. Three winning genotypes, G10, G18 and G1, were the winning genotypes in Bodwease, Fumesua and Wenchi respectively, with G18 as the most stable and high yielding *D. rotundata* cv. Tela genotype.

**Key crops:** *D. rotundata*, agroecologies, genotypes, genotype x environment interaction.

### Introduction

Even though Ghana has been a major exporter of yams in the world for a long time, the cultivation and utilization of yams in Ghana have not benefited from research and development efforts in a manner commensurate with the relative importance of the crop. Several species of yams are indigenous to West Africa. These varieties have been cultivated from time immemorial in Ghana with little or no improvement to the crop from the formal sector. In 2005, the Crops Research Institute released three improved genotypes of *D. rotundata* in Ghana, the first-ever yam release in the country. In West and Central Africa in general, and Ghana, in particular, *D. rotundata* is the most widely cultivated yam species followed by *D. alata*, and then *D. cayenensis* Poir. *D. rotundata* and *D. cayenensis* Lam. (both known as Guinea yams) are the most important yams and are indigenous to West and Central Africa <sup>10</sup>. Even though, there are many *D. rotundata* cultivars differing in pest and disease tolerance, yield potential, maturity period, storability and culinary qualities <sup>11</sup>, research and development efforts failed to fully exploit this unique diversity. *D. rotundata* cultivar Tela is among the preferred cultivars in Ghana. It matures in 8-10 months, has good taste, good texture and high yielding and is good for boil and eat and fufu (pounded yam), the main forms of yam consumption in Ghana, and can be grown in almost all the agroecologies in Ghana.

Many cultivated varieties of *Dioscorea* species produce seeds, yet no direct use of these seeds by farmers have been reported. *D. rotundata* cultivar Tela fruits profusely and set seed. The need to explore the diversity in this cultivar therefore cannot be over-emphasized. It is important to evaluate new genotypes at a number of relevant locations over a period of time to determine stability of their performance before they can be recommended for release to

farmers. Differential responses of genotypes to varied environmental conditions (genotype by environment interactions) are often observed in such multi-environment trials.

Cultivar evaluation and mega-environment identification are among the most important objectives of multi-environment trials (MET) <sup>5</sup>. 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. More recently, the GGE biplot is used in identifying genetic regions associated with a particular trait quantitative trait loci (QTL) mapping and in displaying QTL by environment interactions (called QQE biplots), which has long been a challenge to geneticists <sup>6</sup>. Biplot analysis is the novel approach for analyzing such data. A biplot is a scatter plot that approximates and graphically displays a two-way table by both its row and column factors in a way that relationships among row factors, relationships among column factors, and interactions between row and column factors can be simultaneously visualized <sup>17</sup>. For MET data, a biplot will simultaneously display both the genotypes and the environments (or in more general terms, both the row and the column factors). It was first employed by Gabriel <sup>7</sup> and has in recent times gained acceptability and being used in GGE analysis of MET data. GGE biplot analysis has evolved into a comprehensive biplot analysis system whereby most questions that may be asked of a genotype by environment table can be graphically addressed <sup>13, 14, 17</sup>.

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 they must be

considered simultaneously, not alone or separately, for appropriate genotype evaluation<sup>15</sup>. In yield trials, when a significant GE interaction exists, selection should not be based solely on the genotype (G) effect or on the GE effect; rather it should be based on both G and GE simultaneously. The GGE is a contraction of G and GE. The GGE biplot methodology of analyzing multi-environment trial (MET) data has been well documented<sup>4, 16, 17, 21</sup>.

A biplot is 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 among column factors and interactions between row and column factors can be simultaneously visualized<sup>15</sup>. GGE biplot is therefore biplot that displays the GGE, i.e. the environment-centered or standardized data of a genotype by environment two-way table. Although the measured yield is a combined result of effects of genotype (G), environment (E) and genotype by environment interaction (GE), only G and GE are relevant to cultivar evaluation and mega-environment identification<sup>21</sup>. GGE biplots graphically display G plus GE of a MET in a way that facilitates visual cultivar evaluation and mega-environment identification. It also has a unique merit of graphically showing the which-won-where patterns of the data<sup>21</sup>.

GGE biplot has been successfully used in evaluating cultivar and investigating mega-environment in *D. cayenensis* in Ghana<sup>10</sup>. There are no published reports on *D. rotundata*. The objective of this study was to identify best test environments (representative, discriminating and unique environments) and superior genotypes among the cultivar (high-yielding and stable genotypes) for *D. rotundata* cv. Tela.

### Materials and Methods

A total 38 genotypes of *Dioscorea rotundata* cv. Tela consisting of 35 botanically-developed genotypes and three each of vegetative-propagated counterparts (Table 1) were studied in Ghana in Crops Research Institute's outstation in 15 environments-3 locations in 5 years, from 2000 to 2004 (Table 2). The three locations were Bodwease (Coastal Savanna), Fumesua (Forest) and Wenchi (Forest-Savanna Transition). The experimental design used was CRD. Table 3 shows the characteristics of the agroecologies.

The crop was 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. Each plot consisted of 10 stands planted at a spacing of 1 m x 1 m. Data was taken from all the 10 plants in a plot. The trials were conducted under rain-fed conditions with no fertilizer or any other agro-chemical application. The crop was weeded manually 3-5 times in a season and harvested at 10 months after planting (MAP) and fresh tuber yields recorded.

**Statistical analysis:** The mean yield data was analyzed using Model 1 biplot procedure of GGE computer software. This model generates biplots based on singular value decomposition of tester-centered data. It is used for dataset in which all testers use the same unit, such as a genotype-by-environment table of a single trait. The GGE biplot method<sup>21</sup> was employed to study the genotype by environment interaction of yield. It is based on the formula:

$$Y_{ij} - \bar{y}_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \epsilon_{ij}$$

**Table 1.** Source and code of genotypes.

Source	Genotype	Code
IITA	GH00T/0332	G1
CRI	WTELA	G2
IITA	GH00T/0328	G3
IITA	GH00T/0329	G4
IITA	GH00T/0330	G5
IITA	GH00T/0331	G6
IITA	GH00T/0332	G7
IITA	GH00T/0333	G8
IITA	GH00T/0334	G9
IITA	GH00T/0335	G10
IITA	GH00T/0336	G11
IITA	GH00T/0337	G12
IITA	GH00T/0338	G13
IITA	GH00T/0339	G14
IITA	GH00T/0340	G15
IITA	GH00T/0341	G16
CRI	FTELA	G17
CRI	KTELA	G18
IITA	GH00T/0340	G19
IITA	GH00T/0341	G20
IITA	GH00T/0342	G21
IITA	GH00T/0343	G22
IITA	GH00T/0344	G23
IITA	GH00T/0345	G24
IITA	GH00T/0346	G25
IITA	GH00T/0347	G26
IITA	GH00T/0348	G27
IITA	GH00T/0349	G28
IITA	GH00T/0350	G29
IITA	GH00T/0351	G30
IITA	GH00T/0352	G31
IITA	GH00T/0353	G32
IITA	GH00T/0354	G33
IITA	GH00T/0355	G34
IITA	GH00T/0356	G35
IITA	GH00T/0357	G36
IITA	GH00T/0358	G37
IITA	GH00T/0359	G38

**Table 2.** Code for studied environments.

Code	Environment
FUM00	Fumesua 2000
FUM01	Fumesua 2001
FUM02	Fumesua 2002
FUM03	Fumesua 2003
FUM04	Fumesua 2004
BOD00	Bodwease 2000
BOD01	Bodwease 2001
BOD02	Bodwease 2002
BOD03	Bodwease 2003
BOD04	Bodwease 2004
WEN00	Wenchi 2000
WEN01	Wenchi 2001
WEN02	Wenchi 2002
WEN03	Wenchi 2003
WEN04	Wenchi 2004

where  $Y_{ij}$  is the average yield of genotype  $i$  in environment  $j$ ;  $\bar{y}_j$  is the average yield over all genotypes in environment  $j$ ; and  $\lambda_1 \xi_{i1} \eta_{j1}$  and  $\lambda_2 \xi_{i2} \eta_{j2}$  are collectively called the first principal component (PC1) and the second principal component (PC2);  $\lambda_1$  and  $\lambda_2$  are the singular values for the first and second principal components, PC1 and PC2 respectively;  $\xi_{i1}$  and  $\xi_{i2}$  are the PC1 and PC2 scores, respectively, for genotype  $i$ ;  $\eta_{j1}$  and  $\eta_{j2}$  are the PC1 and PC2 scores, respectively, for environment  $j$ ; and  $\epsilon_{ij}$  is the residual of the model associated with the genotype  $i$  in environment  $j$ .

To display the PC1 and PC2 in a biplot, the  $\lambda$  values are absorbed into the genotype and environment scores so that the equation is written as:

$$Y_{ij} - \bar{y}_j = \xi_{i1}^* \eta_{j1}^* + \xi_{i2}^* \eta_{j2}^* + \epsilon_{ij}$$

where  $\xi_{in}^* = \lambda^{1/2} \xi_{in}$  and  $\eta_{jn}^* = \lambda^{1/2} \eta_{jn} = n \eta_{jn}$ , with  $n = 1, 2$ . This scaling method has the advantage that PC1 and PC2 have the same unit (square root of original unit Mg ha<sup>-1</sup> in terms of yield), although other methods of scaling are equally valid.

A GGE biplot is generated by plotting  $\xi_{i1}^*$  and  $\xi_{i2}^*$  against  $\eta_{j1}^*$  and  $\eta_{j2}^*$ , respectively, so that each genotype or environment is represented by a marker in the biplot. The interpretation of a GGE biplot was first described in Yan<sup>12</sup> and Yan *et al.*<sup>21</sup>.

**Table 3.** Agroecological characteristics of the test sites.

Characteristic	Location		
	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 Ferric Acrisol <sup>ff</sup> Asuansi series with c. 5 cm thick top layer of dark grey gritty loam to gritty clay loam	Forest-Guinea Savannah transition Ferric Lixisol <sup>ff</sup> Damongo series with 20-50 cm of dark brown to brown, slightly loose, porous, loamy sand topsoil grading into homogenous red, friable and porous sandy clay loam to clay loam.	Forest-coastal savannah transition Haplic lixisol <sup>fff</sup> Bodwease series with 10cm thick top layer of dark reddish brown, humus; 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 -major Mar – July; peak in June -minor Sep – Nov; peak in Oct	Bimodal rainfall pattern Mar – July; peak in June Sep – Nov; peak in Oct	Bimodal rainfall pattern Mar – July; peak in June Sep – Nov; peak in Oct
Total annual rainfall (mm)	1000-1800 mm averaging 1500 mm/year	1000-1500 mm averaging 1300 mm/year	1050-1200 mm averaging 1125mm/year

<sup>ff</sup>FAO/UNESCO classes; Asiamah *et al.* <sup>3</sup>, <sup>fff</sup>FAO/UNESCO classes; Asiamah and Adu <sup>2</sup>.

### Results and Discussion

Significant differences ( $p < 0.005$ ) were observed among the genotypes with respect to genotype, environment and genotype by environment interactions (Table 4). The GGE biplot model accounted for 86% of the total variation of the standardized data, consisting of 77 and 9% of variance attributable to PC1 and PC2 respectively, suggesting that meaningful deductions can be made from the data using the GGE biplot methodology <sup>15</sup>. This result was expected since the study sites had different edaphic and climatic conditions (Table 3) and the cultivar genotypes differ in source and genetic composition (Table 2).

**Yield relative to environmental maximum (YREM):** Yield relative to environmental maximum (YREM) also known as the superiority index is an important parameter for assessing the yield potential of a genotype. The yield ability of a genotype in a given environment can therefore be expressed as the YREM. Each genotype therefore has an YREM in each environment. In GGE biplot analysis, however, the YREM used is the averaged YREM across all environments in a multi-environment trial <sup>21</sup>. The closer the YREM value to 1, the better the performance of the genotype. The performance of the studied genotypes was extremely good since 82.7% (31 genotypes) achieved more than 50% of their potential, with as much as 39.5% (15 genotypes) achieving 70% or more of their yield potential. G23 was the poorest performer. The checks, G2, G17 and G18 had 0.84, 0.61 and 0.91 YREM scores corresponding to 4<sup>th</sup>, 21<sup>st</sup> and 1<sup>st</sup> positions respectively (Table 5). The relatively good yield potential achieved by the checks can be attributed to their relative good adaptation to the test sites since they have been planted in these environments from time immemorial.

**Table 4.** Analysis of variance (ANOVA) of 38 *D. rotundata* cultivar “Tela” genotypes in 15 environments.

Source	DF	SS	%
Genotype (G)	37	12,200	59.5
Environment (E)	14	3,594	17.5
G x E	518	4,724	23.0

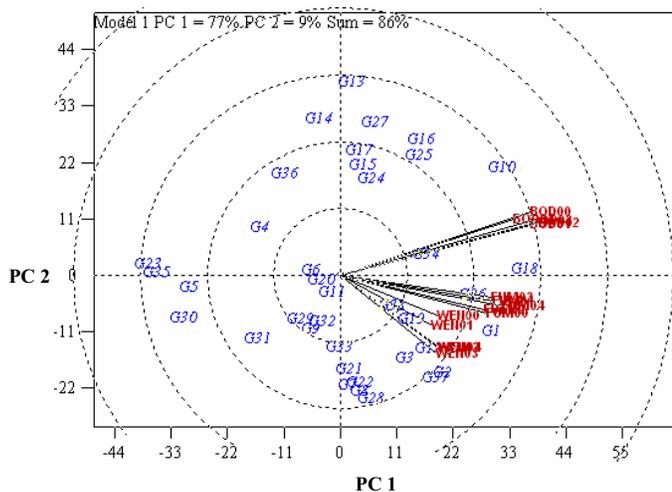
**Table 5.** Yield relative to environmental maximum averaged across environments (YREM) of 38 *D. rotundata* cv. Tela genotypes in 15 environments.

Genotype	YREM
G18	0.91
G1	0.88
G10	0.88
G2	0.84
G37	0.81
G12	0.80
G3	0.76
G34	0.76
G19	0.75
G26	0.72
G38	0.71
G25	0.71
G16	0.70
G28	0.69
G8	0.69
G22	0.66
G21	0.66
G24	0.65
G7	0.63
G15	0.61
G17	0.61
G11	0.59
G27	0.58
G9	0.58
G13	0.57
G33	0.56
G32	0.55
G29	0.54
G20	0.53
G6	0.53
G14	0.51
G36	0.45
G31	0.43
G4	0.42
G5	0.32
G30	0.31
G35	0.24
G23	0.23

**Relationships among environments:** Fig. 1 shows the GGE biplot for yield data of 38 genotypes of *D. rotundata* cv. Tela evaluated 15 environments. The GGE biplot explained 86% of the G plus GE data. When the data is sufficiently approximated by the biplot, the cosine of the angle between the vectors of two environments approximates the correlation coefficients between them<sup>19</sup>. When the biplot explains a greater portion of the total variation, for example >50%, (86% in this case) the angles exactly reflect the correlations among the testers. Two environments are positively correlated if the angle between their vectors is <90; two environments are negatively correlated if the angle between their vectors is >90; two environments are independent if the angle between them is 90. Zero means regression coefficient ( $r$ ) = 1. 180 means  $r = -1$  and environments with longer vectors are more discriminative of the entries; those with short vectors are less discriminative; those located at the biplot origin are not discriminative at all. The cosine of the angle between the vectors of two environments therefore approximates the correlation between them. For example, all the Bodwease environments (BOD00-BOD04) were positively correlated to each other. Similarly all the Wenchi environments (WEN00-WEN04) and Fumesua environments (FUM00-FUM04) were all positively correlated to each other. Even 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* cv. Tela genotypes, hence no strong crossover GE.

The distance between two environments measures the similarity in discriminating the genotypes. Thus the 15 environments fell into three apparent groups: all Bodwease environments were similar and Fumesua and Wenchi environments were also similar. This suggests possible existence of mega-environments justifying why the study was conducted for more years (5 years) to access for repeatability of the observed patterns.

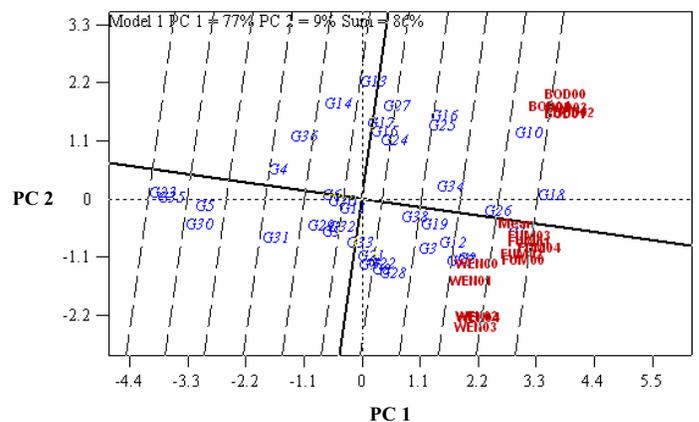
Since, if two test environments are closely correlated consistently across years, removing one of them would not lead to any loss of information, the *D. rotundata* cv. Tela genotypes could have been evaluated in Bodwease and Fumesua environments.



**Figure 1.** Biplot of relationships of 15 environments based with respect to 38 genotypes of *D. rotundata* cv. Tela.

**Discriminateness of test environments:** 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<sup>15</sup>. Bodwease had relatively longer environmental vectors followed by Fumesua and Wenchi, suggesting that Bodwease was best (most discriminative) for *D. rotundata* cv. Tela. The difference in environmental vectors for the three agroecologies also suggests the possible existence of mega-environments, which can be unraveled by further studies.

**Representativeness of the test environments:** The representativeness of the test environment can be assessed using “Average-Environment Axis” (AEA, or average-tester-axis,) view of the GGE biplot<sup>13</sup>. 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. A test environment that has a smaller angle with the AEA is more representative of the target environment. The average environment coordinate (AEC) view of the GGE biplot based on the genotype focused scaling, showing the 38 genotypes of *D. rotundata* cv. Tela in 15 environments (Fig. 2), shows that generally the Fumesua environments were more representative than the other environments, with Bodwease environment generally being the least representative even though, the performance of environment BOD04 was close to that of Fumesua environment. Discriminating and representative test environments are good test environments for selecting generally adapted genotypes hence for *D. rotundata* cv. Tela genotypes; BOD04 which was discriminating and representative environment can be used for genotypes with wide adaptation. Discriminating but non-representative test environments (e.g., BOD00, BOD01, BOD02 and BOD03) 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. Three mega environments were identified corresponding to the three agroecologies: Bodwease, Fumesua and Wenchi. Hence, for *D. rotundata* cv. Tela genotypes, Bodwease environments can be used for selecting specifically adapted genotypes and Fumesua for widely adapted genotypes.



**Figure 2.** The average environment coordinate (AEC) view of the GGE biplot based on the genotype focused scaling, showing the mean yield and stability of 38 genotypes of *D. rotundata* cv. Tela in 15 environments.

Since, non-discriminating test environments are useless, Wenchi environments can be considered useless with respect to the evaluation of *D. rotundata* cv. Tela genotypes.

**Ideal test environments for selecting high mean performance genotypes:** The ideal test environment should be most discriminating (informative) and most representative. Fig. 3 defines an “ideal test environment” for 38 *D. rotundata* cv. Tela genotypes, which is the center of the concentric circles. Fumesua environments were closest to the ideal environment, whereas Bodwease was least ideal, among all test environments, for selecting cultivars adapted to the whole region.

**Similarity among genotypes:** 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<sup>15</sup>. Genotypes with long vectors are either the best (e.g., G18) or poorest (e.g., G21) in one or more environments (Fig. 4); genotypes located near the biplot origin are close to average in all environments.

The cosine of the angle between the vectors of two genotypes also measures their similarity in response to (interaction with) the environments, i.e., in specific adaptations. The distance between two genotypes also measures their dissimilarity. For example, G10 and G31 are very different whereas G10 and G18 are quite similar.

**Mean performance and stability of the genotypes:** In a single mega-environment, genotypes should be evaluated on both mean performance and stability across environments<sup>15</sup>. Fig. 5 is the average-environment coordination (AEC) view of the GGE biplot for 38 genotypes of *D. rotundata* cv. Tela in 15 environments based on both mean and stability. The AEA (the single-angled line) points to higher average yield. Thus G18 had the highest mean yield, followed by G10, G1 and G26 in that order. The double-angled line is the AEC ordinate; it points to greater variability (smaller stability) in either direction. Thus, genotypes G4, G6, G11, G38 and G19 were highly stable whereas G13 was highly unstable. G13 was highly unstable because it had lower than expected yield in environments in Bodwease, but higher than expected yield in Wenchi. Its yield in Fumesua was just as expected from its average yield. An ideal genotype should have both high mean performance and high stability. Fig. 6 also defines an ‘ideal’ genotype (the center of the concentric circles), which has the highest yield in all environments. So genotypes located closer to it are more ideal than others. Genotypes G1, G26 and G18 were the ideal genotypes with respect to *D. rotundata* cv. Tela.

**Which-won-where analysis:** In the which-won-where analysis GGE biplot procedure, 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 (Fig. 7). These perpendicular lines divide the biplot into sectors, and the winning genotype for each sector is the one located on the respective vertex. For *D. rotundata* cv. Tela genotypes, genotype G10 was the winning genotype in environments BOD00, BOD01, BOD02 and BOD03. For environments FUM00, FUM01, FUM02, FUM03, FUM04, BOD04 and WEN00, G18 was the winning genotype. G1 was the winning genotype in WEN00 and WEN01.

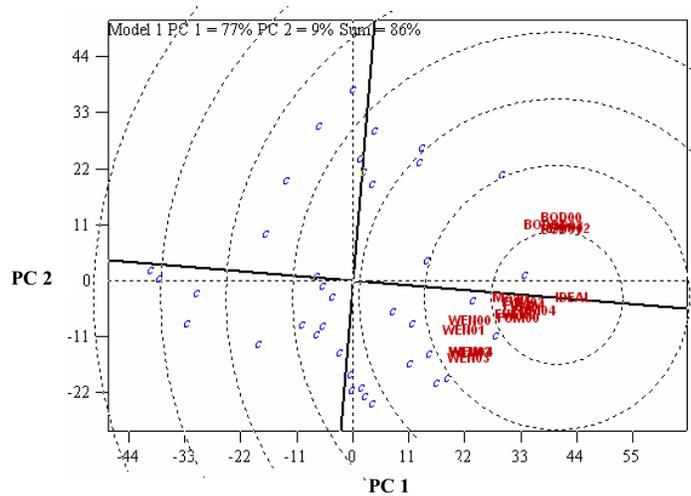


Figure 3. Biplot of rankings of 15 environments using 38 genotypes of *D. rotundata* cv. Tela based on both discriminating ability and representativeness.

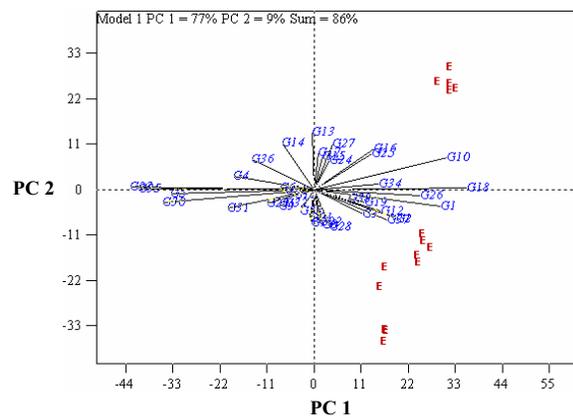


Figure 4. Biplot of rankings (relationships) of 38 genotypes of *D. rotundata* cv. Tela in 15 environments based on both mean and stability.

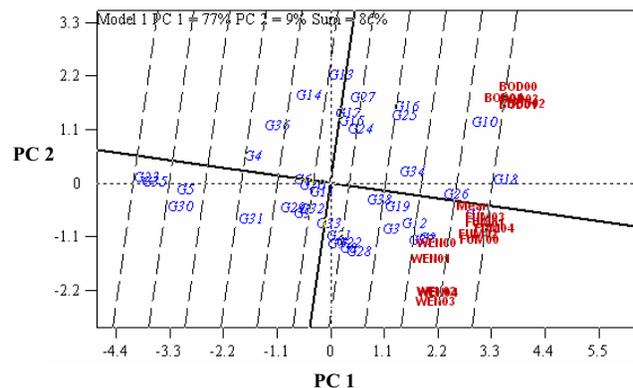
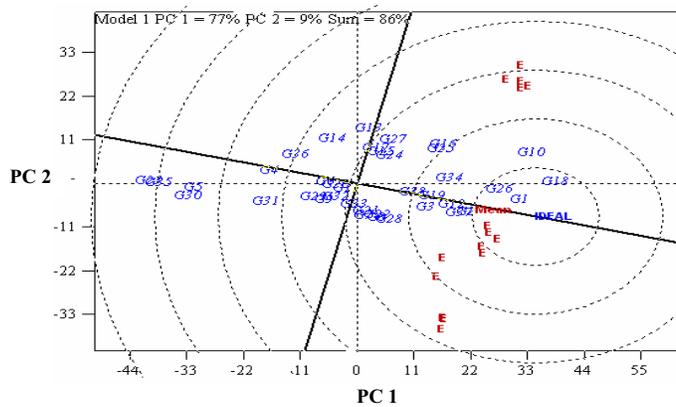


Figure 5. The average environment coordinate (AEC) view of the GGE biplot based on the genotype focused scaling, showing the mean yield and stability of 38 genotypes of *D. rotundata* cv. Tela in 15 environments.



**Figure 6.** Ranking of 38 genotypes of *D. rotundata* cv. Tela in reference to an “ideal genotype” based on both mean and stability.

### Conclusions

Generally, 3 mega-environments were identified for evaluation of *D. rotundata* cv. Tela, namely, Fumesua, Bodwease and Wenchi in that order of discriminating ability. Fumesua environments were more representative than the other environments, with Bodwease environment generally being the least representative even though, the performance of environment BOD04 was close to that of Fumesua environment. Bodwease environments can therefore be used for selecting specifically adapted genotypes and Fumesua for widely adapted genotypes. Wenchi environments due to its non-discriminating nature were useless with respect to the evaluation of *D. rotundata* cv. Tela genotypes. GGE biplot model effectively interpreted variation existing in this dataset and provided an easy-to-do means of studying the interrelationships between both the genotypes and environments. It also identified mega-environments and representative genotypes and environments.

### References

<sup>1</sup>Akwaag, A.A., Berchie, J.N., Echavez, M.L., Dapaah, H.K., Kebede, T., Njue, S.W., Paraoan, I. and Labrada, H.R. 2000. Sustainable Farming Practices - Towards Reducing the Expansion of the Forest Savanna Transition Zone of the Sekyere-West and Ejura-Sekyedumase Districts of the Ashanti Region of Ghana. International Centre for Development Oriented Research in Agriculture and Crops Research Institute, Working Document Series 86, Ghana.

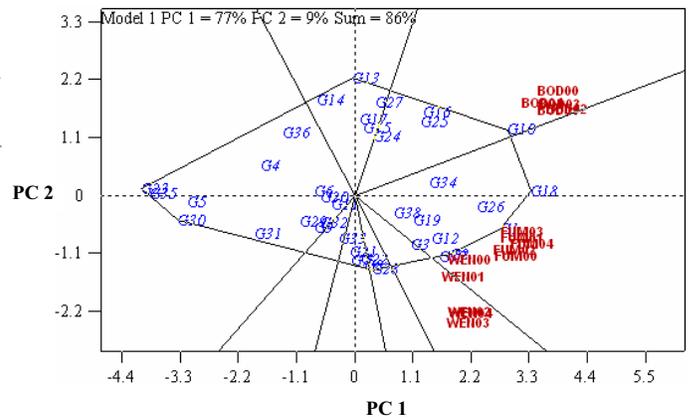
<sup>2</sup>Asiamah, R.D. and Adu, S.V. 1992. Soils of the Ayensu-Densu Basin, Central, Eastern and Greater Accra Regions of Ghana. Council for Scientific and Industrial Research (CSIR) - Soil Research Institute Memoir No. 9.

<sup>3</sup>Asiamah, R.D., Mensah, C.A. and Nyantakyi, P.O. 1993. Report of the detailed soil survey and land evaluation of Wenchi Agricultural Research Station, Brong Ahafo Region, Ghana. Technical Report No. 171.

<sup>4</sup>Bhan, M.K., Pal, S., Rao, B.L., Dhar, A.K. and Kang, M.S. 2005. GGE biplot analysis of oil yield in lemongrass (*Cymbopogon* spp.). *Journal of New Seeds* 7(2).

<sup>5</sup>Dehghani, H., Ebadi, A. and Yousefi, A. 2006. Biplot analysis of genotype by environment interaction for barley yield in Iran. *Agron. J.* 98:388-393.

<sup>6</sup>Dixon, A.G.O. 2003. Crop Improvement and New Tools for Managing Genotype by Environment Interactions, Parental Selection, and Participatory Breeding in Africa. Report of International Institute for



**Figure 7.** Polygon view of GGE biplot indicating winning genotypes of 38 *D. rotundata* cv. Tela genotypes in 15 environments using the “which wins where or which is best for what” approach.

Tropical Agriculture, Planning Week, pp. 11-12.

<sup>7</sup>Gabriel, K.R. 1971. The biplot graphic display of matrices with application to principal component analysis. *Biometrika* 58:453-467.

<sup>8</sup>GYPEA 2000. Ghana yam exports surge ahead. Ghana Yam Producers and Exporters Association. SPORE No.87, pp. 8.

<sup>9</sup>Rubio, J., Cubero, J.I., Martin, L.M., Suso, M.J. and Flores, F. 2004. Biplot analysis of trait relations of white lupin in Spain. *Euphytica* 135:217-224.

<sup>10</sup>Otoo, E. and Asiedu, R. 2006. Cultivar evaluation and mega-environment investigation of *D. cayenensis* cultivars in Ghana based on the GGE biplot analysis. *Journal of Food, Agriculture & Environment (JFAE)* 4(3&4):162-166.

<sup>11</sup>Otoo, E. 2001. Yam production in Ghana: A food security enhancer or an environmental degrader. In Akoroda, M. (ed.). Proceedings of the 8<sup>th</sup> Symposium of the International Society for Tropical Root Crops - Africa Branch Triennial Workshop, Ibadan, Nigeria, November 12-16, 2001, pp. 387-391.

<sup>12</sup>Yan, W. 1999. A Study on the Methodology of Yield Trial Data Analysis - with Special Reference to Winter Wheat in Ontario. PhD. diss., University of Guelph, Guelph, Ontario, Canada.

<sup>13</sup>Yan, W. 2001. TGGE biplot - Windows application for graphical analysis of multi-environment trial data and other types of two-way data. *Agron. J.* 93(5):1111-1118.

<sup>14</sup>Yan, W. 2002. Singular value partitioning for biplot analysis of multi-environment trial data. *Agron. J.* 94:990-996.

<sup>15</sup>Yan, W. 2005. Use of biplot analysis in crop breeding. Proceedings of the Eastern Wheat Workers and Southern Small Grain Workers Conference, May 9-12, 2005. Bowling Green, KY, pp. 7-30.

<sup>16</sup>Yan, W. and Hunt, L.A. 2002. Biplot analysis of diallel data. *Crop Sci.* 42(1):21-30.

<sup>17</sup>Yan, W. and Kang, M.S. 2003. GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists and Agronomists. CRC Press, Boca Raton, FL.

<sup>18</sup>Yan, W. and Rajcan, I. 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. *Crop Sci.* 42:11-20.

<sup>19</sup>Yan, W. and Rajcan, I. 2003. Prediction of cultivar performance based on single vs. multiple year trials. *Crop Sci.* 43:549-555.

<sup>20</sup>Yan, W., Cornelius, P.L., Crossa, J. and Hunt, L.A. 2001. Two types of GGE biplots for analyzing multi-environment trial data. *Crop Sci.* 41:656-663.

<sup>21</sup>Yan, W., Hunt, L.A., Sheng, Q. and Szlavnic, Z. 2000. Cultivar evaluation and mega-environment investigation based on the GGE Biplot. *Crop Science* 40:597-605.