



The performance profile of *Dioscorea rotundata* cultivar Dorban genotypes in Ghana using GGE biplot analysis

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Abstract

Twenty-two genotypes of *D. rotundata* cultivar Dorban consisting of 19 botanically developed seeds and 3 vegetative checks were evaluated in 15 environments from 2000 to 2004 using CRD to assess the effect of genotype and genotype x environment interaction on the tuber yield of 22 white yam (*D. rotundata* L. cv. Dorban) genotypes via GGE (genotype plus genotype x environment) biplot methodology. The GGE biplot procedure was used to determine the yield potential and stability of the genotypes. Significant differences ($p < 0.001$) were observed in all cultivars with respect to genotype, environment and genotype by environment interactions. Biplot analysis identified three mega-environments corresponding to the three agroecologies - Fumesua (Forest) was the most representative and discriminating environment followed by Bodwease (Coastal Savannah) and Wenchi (Forest-Savannah Transition). Genotypes Gdo02, Gdo03, Gdo20 and Gdo01 including the three checks were identified as superior. Genotype Gdo016 was the worst genotype.

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

Introduction

In Ghana there are many cultivated species of *Dioscorea rotundata*, of which Pona, Laribako and Dente are the main cultivars of importance. There are other important cultivars which are not as sweet and floury as the aforementioned cultivars, yet occupy very important niche in the yam market dynamics ensuring that there is yam all year round. Amongst these cultivars are Dorban, Lillee, Serwa, Muchumudu, Afebetua, Mmowea and others. These other cultivars have received no research attention. Dorban, for instance, is good for boil and eat and fufu (pounded yam) making, the main forms of yam consumption in Ghana, and can be grown in almost all the agroecologies in Ghana. It also has good tolerance to pest and disease, good yield potential, matures in 8-10 months and stores better than 'Pona' and 'Laribako' ¹¹ and set seed profusely, however, its full potential is yet to be exploited by research. To explore the yield potential and stability in these cultivars, a total of 22 genotypes of *Dioscorea rotundata* 'Dorban' consisting of 19 true botanically-developed genotypes and 3 vegetative-propagated counterparts as checks were assessed. Studies were conducted in Ghana in Crops Research Institute's outstations in 15 environments (3 locations in 5 years). The three locations were Bodwease (Coastal Savanna), Fumesua (Forest) and Wenchi (Forest-Savanna Transition) from 2001-2004.

Cultivar evaluation and mega-environment identification are among the most important objectives of multi-environment trials (MET) ⁵. 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 ⁶. 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 ¹⁷. 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 ⁷ 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 ^{13, 14, 17}.

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 ¹⁵. 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 ^{4, 16, 17, 21}.

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 visualized¹⁵. 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 identification²¹. 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 data²¹. GGE biplot has been successfully used in evaluating cultivar and investigating mega-environment in *D. cayenensis* in Ghana¹⁰.

The objectives of this study were to identify best test environments (representative, discriminating and unique environments) and superior genotypes among the cultivars (high-yielding and stable genotypes).

Materials and Methods

Data for this study consisted of data collected from 19 genotypes true botanically developed seeds of *D. rotundata* cultivar Dorban respectively with three vegetatively developed checks (Table 1). The genotypes were evaluated in 15 environments consisting of 3 locations in 5 years, 2000 to 2004. The experimental design used was CRD with 3 blocks. The three locations were Bodwease (Coastal Savanna), Fumesua (Forest) and Wenchi (Forest-Savanna Transition). Table 2 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 sets 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

Table 1. Source and code of genotypes.

Source	Genotype	Code
CRI	WSD00/015	Gdo01
CRI	CRIDORBAN	Gdo02
CRI	WSD00/002	Gdo03
IITA	GH00D/058	Gdo04
IITA	GH00D/014	Gdo05
IITA	GH00D/072	Gdo06
IITA	GH00D/075	Gdo07
IITA	GH00D/037	Gdo08
IITA	GH00D/023	Gdo09
IITA	GH00D/033	Gdo10
IITA	GH00D/001	Gdo11
IITA	GH00D/009	Gdo12
IITA	GH00D/111	Gdo13
IITA	GH00D/049	Gdo14
IITA	GH00D/052	Gdo15
IITA	GH00D/099	Gdo16
IITA	GH00D/034	Gdo17
IITA	GH00D/008	Gdo18
IITA	GH00D/044	Gdo19
IITA	GH00D/005	Gdo20
IITA	GH00D/018	Gdo21
IITA	GH00D/068	Gdo22

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

fertilizer or any other agro-chemical application. The crop was weeded manually 3-5 times in a season. The crop was 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 method²¹ was employed to study the genotype by environment interaction of yield. It is based on the formula:

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

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); λ_1 and λ_2 are the singular values for the first and second principal components, PC1 and PC2 respectively; ξ_{i1} and ξ_{i2} are the PC1 and PC2 scores, respectively, for genotype i ; η_{j1} and η_{j2} are the PC1 and PC2 scores, respectively, for environment j ; and ϵ_{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 λ 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⁻¹ in terms of yield), although other methods of scaling are equally valid.

A GGE biplot is generated by plotting ξ_{i1}^* and ξ_{i2}^* against η_{j1}^* and η_{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 Yan¹² and Yan *et al.*²¹.

Results and Discussion

The ANOVA shows significant differences ($p < 0.001$) in the genotypes with respect to genotype, environment and genotype by environment interactions (Table 3). The GGE biplot model accounted for 90% of the total variation of the standardized data, consisting of 67 and 23% of variance attributable to PC1 and PC2 respectively, suggesting that meaningful deductions can be made from the data using the GGE biplot methodology¹⁵. This result can be attributed to the study sites which differ in edaphic and climatic conditions (Table 4) and the cultivar genotypes similarly 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 trial²¹. The closer the YREM value to 1, the better the performance of the genotype. The performance of the genotypes was extremely good since 95.5% (21 genotypes) achieved more than 50% of their potential, with as much as 68.2% (15 genotypes) achieving 70% or more of their yield potential. GD002 was the best performer and GD016 was the poorest performer. The checks, G1, G2 and G3 had 0.93, 0.90 and 0.89 YREM scores corresponding to 1st, 3rd and 4th positions respectively (Table 5). The relatively good yield potential achieved by the checks can be attributed to their relative adaptation to the test sites.

Relationships among environments: Fig. 1 shows the GGE biplot for yield data of 20 genotypes of *D. rotundata* cv. Dorban evaluated 15 environments. The GGE biplot explained 90% 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 them¹⁸. When the biplot explains a greater portion of the total variation, for example >50%, (90% 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

Table 4. Analysis of variance (ANOVA) of 20 *D. rotundata* cv. Dorban genotypes in 15 environments.

Source	Dorban		
	DF	SS	%
Genotype (G)	21	2803	38.4
Environment (E)	14	3034	41.5
G x E	294	1472	20.1
	PC	Lambda	% of total SS
	1	53.52	67
	2	31.06	23
	3	16.26	6
	4	5.97	1
	5	5.26	1
	6	5.15	1

Table 5. Yield relative to environment maximum (YREM) of 22 genotypes of *D. rotundata* cultivar Dorban in 15 environments.

Genotype	YREM
Gdo02	0.93
Gdo20	0.91
Gdo01	0.90
Gdo03	0.89
Gdo10	0.84
Gdo09	0.83
Gdo14	0.80
Gdo19	0.79
Gdo11	0.76
Gdo15	0.75
Gdo08	0.72
Gdo06	0.70
Gdo21	0.70
Gdo22	0.69
Gdo12	0.69
Gdo05	0.68
Gdo13	0.67
Gdo17	0.65
Gdo04	0.61
Gdo18	0.61
Gdo07	0.58
Gdo16	0.36

Table 3. Agroecological characteristics of the test sites.

Characteristic	Location		
	Fumesua	Wenchi	Bodwease
Coordinates	6°41'N, 1°28'W	7°44'N 2°07'W	5°35'N 0°35'W
Agroecological zone	Humid Forest Ferric Acrisol [#] Asuansi series with c. 5 cm thick top layer of dark grey gritty loam to gritty clay loam	Forest-Guinea Savannah transition Ferric Lixisol [#] 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 ^{##} 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
Soil type			
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 1125 mm/year

[#]FAO/UNESCO classes; Asiamah *et al.*³, ^{##}FAO/UNESCO classes; Asiamah and Adu².

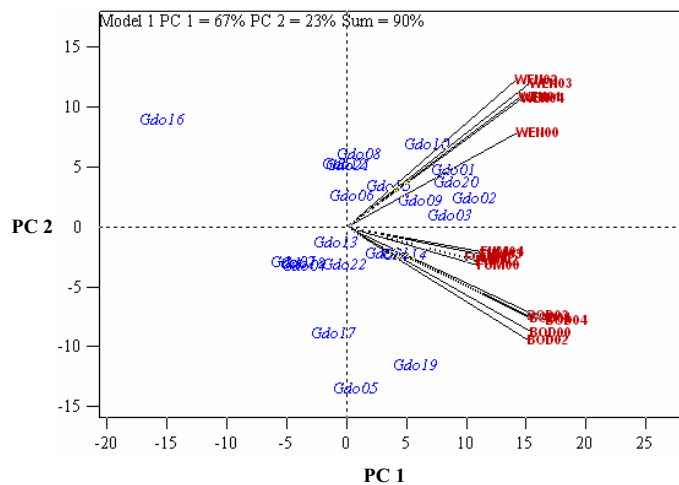


Figure 1. Biplot of relationships of 15 environments based on 22 genotypes of *D. rotundata* cv. Dorban.

discriminative at all. The cosine of the angle between the vectors of two environments therefore approximates the correlation between them. Environments within an agroecology seemed to cluster together, suggesting the existence of three mega-environments corresponding to the agroecologies. For instance, all the Wenchi environments (WEN00-WEN04) were positively correlated to each other. Similarly, Fumesua and Bodwease environments were positively correlated to each other. Amongst the environments, all the environments seemed to be positively correlated, even though WEN02 and BOD02 seemed to be of each other (angle between them is 90). The distance between two environments measures their similarity in discriminating the genotypes. Thus the 15 environments fell into two apparent groups: WEN00, WEN01, WEN02, WEN03, WEN04 and WEN04 were similar whereas the other environments were also similar.

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 environments¹⁵. Wenchi and Bodwease environments seemed to have almost equal environmental vectors and hence were the best (most informative) environments for *D. rotundata* cv. Dorban genotypes (Fig. 2). Wenchi was the least discriminating environment, suggesting 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 biplot¹³. 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. Results from Fig. 2, the average environment coordinate (AEC) view of the GGE biplot based on the genotype focused scaling, showing the 22 genotypes of *D. rotundata* cv. Dorban genotypes in 15 environments, shows

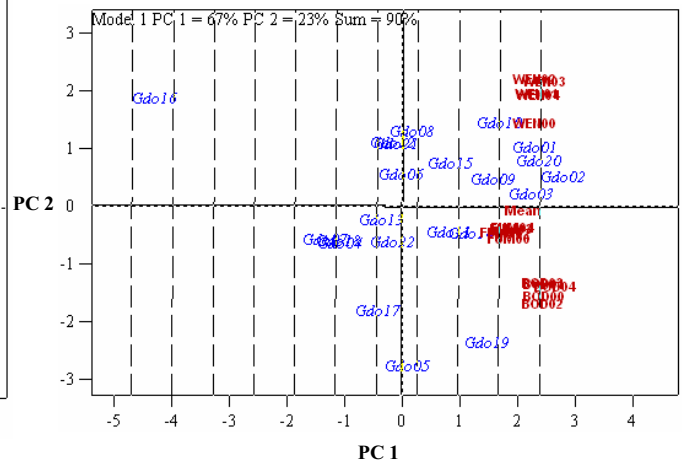


Figure 2. The average environment coordinate (AEC) view of the GGE biplot based on the genotype focused scaling, showing the mean yield and stability of 22 genotypes of *D. rotundata* cv. Dorban in 15 environments.

that the Fumesua environments were more representative of the test environments for *D. rotundata* cv. Dorban evaluation (Fig. 3). Wenchi and Bodwease environments were independent of each other, and can be considered as separate mega-environments. They will be useful for identifying genotypes of specific adaptation.

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 22 *D. rotundata* cv. Dorban genotypes, which is the center of the concentric circles. Fumesua environments were closest to the ideal environment, whereas Wenchi was least ideal, among all test environments, for selecting cultivars adapted to the whole region.

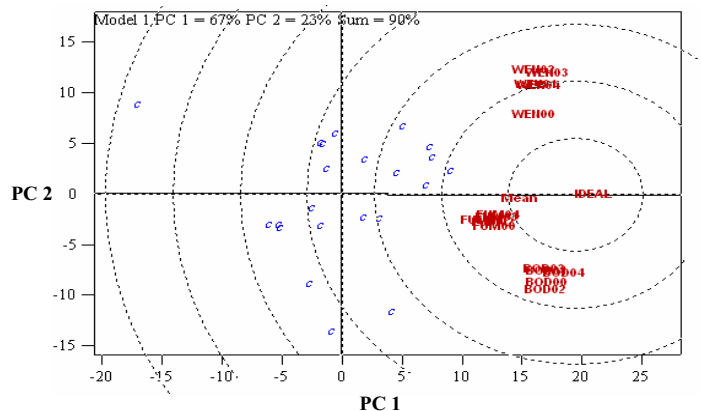


Figure 3. Biplot of rankings of 15 environments using 22 genotypes of *D. rotundata* cv. Dorban based on both discriminating ability and representativeness.

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 mean¹⁵. Genotypes with long vectors are either the best (e.g., Gdo02) or poorest (e.g., Gdo16) 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, Gdo16 and Gdo02 were the poorest and the best genotypes of *D. rotundata* cv. Dorban, respectively.

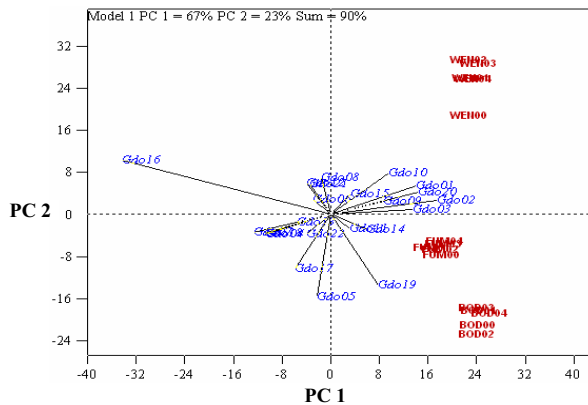


Figure 4. Biplot of rankings (relationships) of 22 genotypes of *D. rotundata* cv. Dorban in 15 environments based on both mean and stability.

Mean performance and stability of the genotypes: In a single mega-environment, genotypes should be evaluated on both mean performance and stability across environments¹⁵. Fig. 5 is the average-environment coordination (AEC) view of the GGE biplot for 22 genotypes of *D. rotundata* cv. Dorban in 15 environments based on both mean and stability. The AEA (the single-angled line) points to higher average yield. Thus Gdo03 had the highest mean yield, followed by Gdo02, Gdo10 and Gdo01 in that order. The double-angled line is the AEC ordinate; it points to greater variability (smaller stability) in either direction. Thus, Gdo03 was highly stable whereas Gdo05 was highly unstable. Gdo05 was

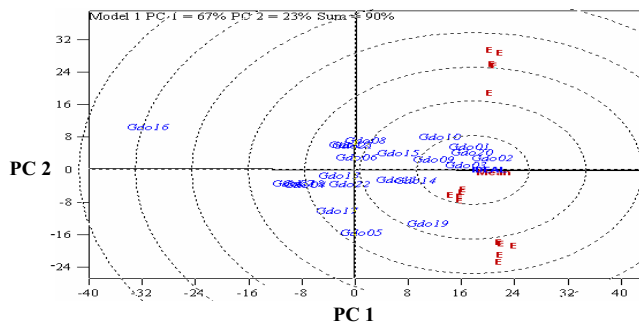


Figure 5. Biplot of rankings of 22 genotypes of *D. rotundata* cv. Dorban in 15 environments in reference to an “ideal genotype” based on both mean and stability.

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. 5 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 Gdo02, Gdo03, Gdo20 and Gdo01 were the ideal genotypes with respect to *D. rotundata* cv. Dorban.

Which-won-where analysis: In which-won-where analysis of the GGE biplot analysis, 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. 6). 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. Dorban genotypes, three mega-environments were identified corresponding to the three agroecologies. Gdo019 was the winning genotype in Bodwease environments, Gdo02 in Fumesua and Gdo10 in Wenchi environments.

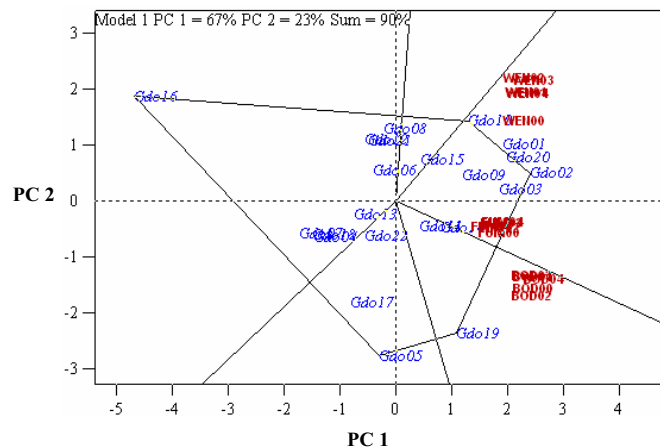


Figure 6. Biplot of winning genotype of *D. rotundata* cv. Dorban genotypes in 15 environments using the “which wins where or which is best for what” approach.

Conclusions

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. Three mega-environments corresponding to the three agroecologies were identified by GGE biplot analysis for evaluation of *D. rotundata* cv. Dorban. Fumesua environments were the ideal environments, whereas Wenchi was least ideal, among all test environments, for selecting cultivars adapted to the whole region. Genotypes Gdo02, Gdo03, Gdo20 and Gdo01 were identified as superior. Genotype Gdo016 was the worst genotype.

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