

## Stability studies of hybrid yam (*Dioscorea rotundata* Poir.) genotypes in Ghana

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### Abstract

Seven white yam (*Dioscorea rotundata* Poir.) genotypes (1 local and 6 hybrids from IITA) were evaluated in 13 environments using randomised complete block design (RCBD) with 3 replications. The environments were Fumesua (forest) from 2000 to 2004 and Wenchi (forest Guinea savannah transition) from 2000 to 2003 and Bodwease (forest-coastal savannah transition) from 2000-2004. The yield data were analysed using the Mixed Model version of the additive main effects multiplicative interaction (AMMI) with one multiplicative term (AMMI1) statistical model in SAS version 8. Highly significant ( $P < 0.001$ ) genotype (G), environments (E) and G x E effects were observed on yield of the tested genotypes. Genotype accounted for 8.9, environment 30.8 and G x E 43.7% of the total sum of squares. The Akaike's Information Criterion (AIC) value was -817.6 indicating a high degree of statistical fit of the yield data. Using the Additive Main Effects and Multiplicative Interaction (AMMI) model with one multiplicative term (AMMI1), four groupings were identified: low yielding and highly unstable (Dorban and TDr 95/18944); low yielding but very stable (TDr 95/19158); high and stable yielding (TDr 89/02665 and TDr 95/19177) and high but unstable yielding genotypes, (TDr 95/18949 and TDr 89/18894). TDr 89/02665 has therefore been formally released as a new variety (Mankrong Pona) in Ghana in 2005. Bodwease, Wenchi and Fumesua were identified as most favourable and stable environments for yam improvement studies in that order of importance. Bodwease generally had lower leaf spot disease pressure compared with locations that exhibited unstable yields such as Fumesua with higher temperature and relative humidity. Yam improvement therefore should be focused on multiple disease and pest resistance, which would guarantee stability of crop performance.

**Key words:** AMMI1, Ghana, G X E, hybrid, yams.

### Introduction

One of the aims of yam (*Dioscorea* spp.) improvement programmes is to improve fresh tuber yields. Yams are grown in many agroecologies and it is important to assess adaptation and yield stability of promising genotypes across environments<sup>1</sup>. In Ghana, yam cultivation spans from the northern Guinea savannah agroecological zone through forest-Guinea savannah transition and forest zones to coastal savannah zones of the south. Its cultivation covers 34 out of the 43 agricultural districts in Ghana. These zones differ in their environmental conditions and hence performance of yams<sup>2</sup>. High yields of yam depend on good planting material and husbandry, particularly weed control to establish a reasonable crop leaf area, adequate water and near optimum temperatures (25-30°C) during the period of maximum potential growth at 14-20 weeks after planting<sup>3</sup>. Deep, well drained and friable soils are also key factors that are needed for growing yam<sup>3</sup>. A friable soil is particularly important since while other root crops such as cassava initially penetrate the soil with relatively thin roots which later expand, the yam tuber penetrates the soil as it expands<sup>4</sup>.

Success of any genotype depends not only on its good performance with respect to yield and pest and disease tolerance but also its consistency in an ever-changing environment. A genotype by environment (G x E) interaction is said to exist if changes are observed in relative performance of genotypes across environments. Genotype by environment interactions are of great

interest when evaluating the stability of breeding clones under different environmental conditions. Several methods have been proposed for statistical analysis of G x E and to predict the phenotypic response to changes in the environment<sup>5</sup>. The success of identifying high yielding genotypes from yield trials depends on the effectiveness of the statistical analysis used to evaluate patterns in the data and estimated yields<sup>6</sup>.

A significant G x E interaction for a quantitative trait reduces the usefulness of the genotype means over all locations or environments for selecting and advancing superior genotypes to the next stage of selection<sup>7</sup>. This implies that a significant G x E interaction reduces the correlation between phenotypic and genotypic values and confounds yield evaluations of clones<sup>8</sup>. Very little work has been done in yams except<sup>1</sup> with respect to identifying means of selecting stable and high yielding yam clones. A lot of work has however been done in a related crop, cassava but few in yams. Again, to use many of the published stability parameters<sup>9</sup> will require expensive and sophisticated computers and softwares, often beyond the reach of most researchers in the developing countries<sup>10</sup>.

The Additive Main Effects and Multiplicative Interaction (AMMI) model<sup>11</sup> which combines regular analysis of variance for additive main effects with principal component analysis for multiplicative structure within the interaction has been identified by several workers including<sup>1</sup> as the most efficient in determining

**Table 1.** Legends for environments and genotypes used in the trial.

Environment		<i>D. rotundata</i>	
		Genotype	Source
E1= Fumesua 2000	E8 = Wenchi 2002	G1= 'Dorban'	Ghana
E2 = Fumesua 2001	E9 = Wenchi 2003	G2= TDr 89/02665	IITA
E3 = Fumesua 2002	E10= Bodwease 2001	G3= TDr 95/18894	IITA
E4 = Fumesua 2003	E11= Bodwease 2002	G4= TDr 95/18944	IITA
E5 = Fumesua 2004	E12= Bodwease 2003	G5= TDr 95/18949	IITA
E6 = Wenchi 2000	E13= Bodwease 2004	G6= TDr 95/19158	IITA
E7 = Wenchi 2001		G7= TDr 95/19177	IITA

the most stable and high yielding yam genotypes in multi-environment trials compared to earlier procedures<sup>12,13</sup>. Using the "Proc Mixed" facility of SAS software, the stability of the genotypes could be assessed by using AMMI model with one multiplicative term (AMMI1)<sup>14</sup>. This could be achieved by augmenting the SAS code of Finlay-Wilkinson by environmental main effect.

The object of this study was to determine the level of adaptation (broad or specific) of IITA-developed hybrid yams to the agroecological zones in Ghana using AMMI1 procedure to analyse the yield data of seven yam (*D. rotundata*) genotypes in 13 environments.

### Materials and Methods

A multilocational trial was carried out in 13 environments using seven *D. rotundata* genotypes (Table 1) consisting of six hybrid yam genotypes introduced from International Institute of Tropical Agriculture (IITA) and one local landrace (a check). These were evaluated in the forest Guinea savannah transition (Wenchi) from 2000 to 2003, forest (Fumesua) from 2000 to 2004 and coastal savannah (Bodwease) from 2001 to 2004. Experimental design used

**Table 2.** Agroecological characteristics of the test sites.

Characteristics	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	Forest-Guinea savannah transition	Forest-coastal savannah transition
Soil type	Ferric Acrisol* Asuansi series with c. 5cm thick top layer of dark grey gritty loam to gritty clay loam	Ferric Lixisol* Damongo series with 20-50cm of dark brown to brown, 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 March- July; -major peak in June -minor Sep - Nov; peak in Oct	Bimodal rainfall pattern March - July; peak in June Sep - Nov; peak in Oct	Bimodal rainfall pattern March - 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<sup>19,20</sup>.

was RCBD with 3 replications. The trials were conducted under rain-fed conditions with no fertilizer or any other agro-chemicals application. Weeding was manually done 3-5 times in a cropping season. The yam setts were planted in mounds and individually staked with a bamboo of 2-3 m height. The yam setts were planted at the onset of rains (March-April) with setts weighing 300 g. Each plot consisted of 40 plants spaced 1 m apart with 10 plants per row and 4 rows per plot.

Both leafspot and virus severity were scored on a scale of 1-5, where 1 = tolerant and 5 = highly susceptible. Disease was scored at three and six months after planting (MAP). The crop was harvested at 9 MAP and fresh tuber yields recorded. The genotypes, tests sites and years of testing, and the agro-ecological characteristics of the test sites are presented in Tables 1 and 2, respectively.

Analyses of variance for diseases were conducted using Mixed Model procedure as per SAS version 8<sup>15</sup>. The yield data was analysed using the Mixed Model version of the additive main effects interaction (AMMI) with one multiplicative term (AMMI1) statistical model in SAS version 8<sup>15</sup> as per<sup>14</sup>. The AMMI1 model for replicative data is  $\hat{y}_{ijk} = \mu + g_i + r_{jk} + \mu_j + \lambda_i w_j + d_{ij} + e_{ijk}$  where  $\hat{y}_{ijk}$  ( $i = 1, \dots, I; j = 1, \dots, J; k = 1, \dots, K$ ) is the yield of the  $k$ th replicate of the  $i$ th genotype in the  $j$ th environment,  $r_{jk}$  is the  $k$ th block effect in the  $j$ th environment;  $\mu$  is a general mean,  $g_i$  is the  $i$ th genotype main effect,  $\mu_j$  is the  $j$ th environment main effect,  $\lambda_i$  is the sensitivity of the  $i$ th genotype to a latent environmental variable  $w_j$ ,  $d_{ij}$  is a random deviation (unexplained interaction), and  $e_{ijk}$  is an experimental error term corresponding to  $\hat{y}_{ijk}$ . The AMMI1 model for means is  $\bar{y}_{ijk} = \mu + g_i + \mu_j + \lambda_i w_j + f_{ij}$  where  $f_{ij} = (\text{gu})_{ij} + \sum e_{ijk}/K$ .

The F-tests and significance of the various main effects and interactions were determined using the appropriate error terms and degrees of freedom. The proportions of total sum of squares contributed by each source of variation were computed.

The stability of the genotypes and environments were assessed by plotting the means of the genotype and the environments against the singular PCA values (FA1 (1)).

### Results and Discussion

Highly significant ( $P < 0.001$ ) genotype (G), environment (E) and G x E effects were observed on yield of the tested genotypes. Genotype accounted for 8.9, environment 30.8 and G x E 43.7% of the total sum of squares (Table 3). The Akaike's Information Criterion (AIC) value was -817.6 indicating a high degree of statistical fit of the yield data. The postdictive success of AMMI1 using all data in all replicates, indicated that the treatment sum of squares was partitioned into two components: 61% due to the model or pattern (including main effects for genotypes and the singular PCA) with 29 degrees of freedom; and 39% due to residual or random variation (noise)

with 61 degrees of freedom. The model-validation procedure, therefore, identifies that 39% of the treatment sum of squares as allocated to the residual term was a predictive value.

The AMMI analysis gives a graphical representation or biplot to summarize information on the main effects and the first principal component scores of the interactions (IPCA1) of both genotypes and environments simultaneously<sup>1, 16</sup>. The AMMI1 analysis similarly gives a biplot (Fig. 1) to summarize information on the main effects and the singular PC scores of the interactions (FA1(1)) of both genotypes and environments simultaneously<sup>14</sup>. Displacement along the abscissa reflected differences in main effects, whereas displacement along the ordinate exhibited differences in interaction effects. The additive AMMI0 which is part of the AMMI1 model is the sum of genotype and environment means minus the grand mean, while the interaction part is the genotype PCA scores times the environment PCA score. These two parts added to produce the expected AMMI1 model. The biplot captured 61% of the treatment sum of squares.

Genotypes or environments on the same parallel line, relative to the ordinate, have similar yields (Fig. 1), and a genotype or environment on the right side of the midpoint of this axis has greater yields than those on the left hand side. Consequently, the genotypes TDr 89/02665, TDr 95/18894, TDr 95/18949 and TDr 95/19177, were generally high yielding with TDr 95/19177 being the greatest yielder. In contrast, Dorban, TDr 95/19158 and TDr 95/18944 were low yielding genotypes with Dorban being the worst. The Bodwease locations (E10-E13) were always on the right hand side of the midpoint of the main axis, seemed to be very favourable for the yam genotypes evaluated; Wenchi (E6-E9) was moderately favourable, whilst Fumesua was the least favourable environment except in 2000 where very high yields were obtained.

In AMMI0 analysis, genotypes with IPCA1 scores near zero had little interaction across environments and vice versa<sup>17</sup>. Similarly, in AMMI1 analysis genotypes with FA1(1) scores near zero had little interaction across environments and vice versa. For such genotypes, overall mean ranking is a reliable measure<sup>1</sup>.

**Table 3.** AMMI1 analysis<sup>a</sup> for seven *Dioscorea rotundata* genotypes grown in 13 environments<sup>b</sup> (3 locations in 5 years) in Ghana.

Source	df	SS	MS	Probability
Total	271	14334.25	-	-
Treatment	90	11981.81	133.13	***
Genotype (G)	6	1274.12	212.35	***
Environment (E)	12	4416.51	368.04	***
G x E	72	6270.58	87.09	***
FA1(1) <sup>c</sup>	11	1617.25	147.02	***
Residual	61	4653.33	76.28	***
Error	181	2352.40	13.00	***

<sup>a</sup>Grand mean of fresh tuber yield = 15.2 (tha<sup>-1</sup>), Akaike's Information Criterion (AIC) = -817.6.

\*\*\*Significant at P<0.001.

<sup>b</sup>Planting at Forest zone was for 5 years instead of the 4 for coastal savannah and forest-savannah transition.

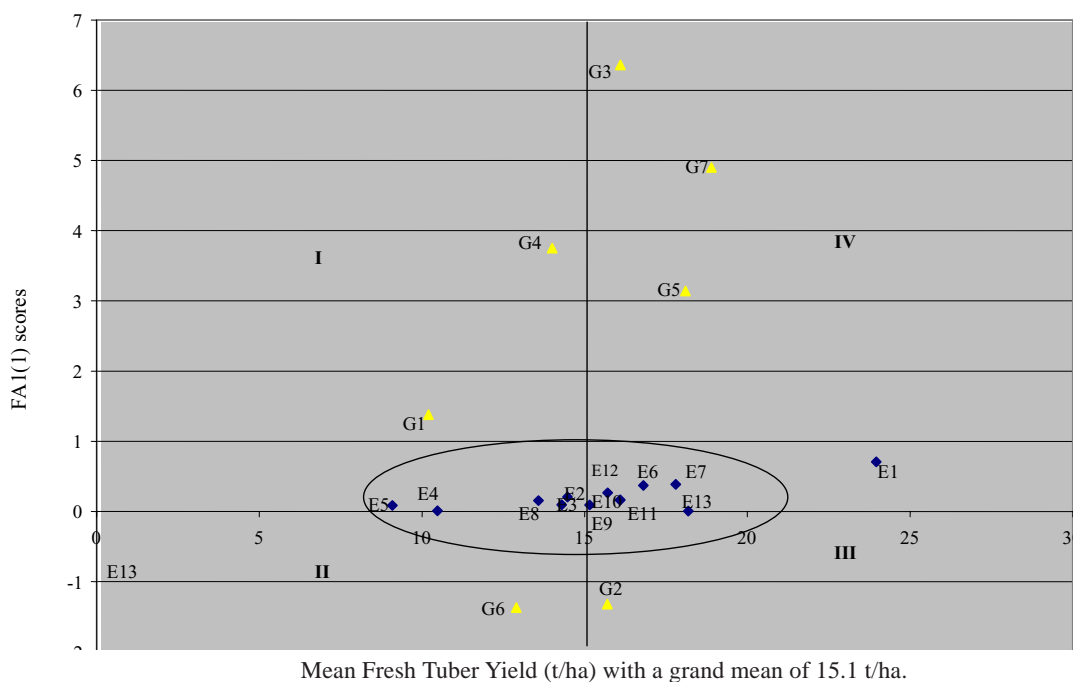
<sup>c</sup>Singular PCA values.

Genotype and environment combinations with FA1(1) scores of the same sign produced positive specific interaction effects, whereas combinations of opposite signs had negative specific interactions.

Genotypes TDr 89/02665 and TDr 95/19158 had negligible interactions with the environments, indicating their broad adaptations with TDr 89/02665 being the most stable genotype across environments. Although Dorban was fairly stable, it was not very productive. Genotypes, TDr95/18894, TDr 95/18944 TDr 95/18949 and TDr 95/19177 were highly unstable and generally poorly adapted to the environments.

Generally, all the environments except E1 (Fumesua 2000) had FA1(1) scores close to zero, indicating relatively low genotype by environments interaction. Environment 1 had no correlation whatsoever with any of the other environments where the studies were conducted (Table 4).

This indicates that its response pattern differs from the remaining environment. Wenchi had moderate G x E interaction (average FA1(1) scores). However, all the Bodwease environments (E10-



**Figure 1.** Biplot of the unadjusted mean fresh tuber yield (t/ha) and the singular AMMI1 (FA1(1)) scores for 7 genotypes in 13 environments in Ghana.

**Table 4.** Correlation matrix of yield of 7 yam genotypes in 13 environments in Ghana.

	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	E13
E1	0.106 <sup>a</sup>	0.069	0.379	-0.051	0.440	0.617	0.477	0.304	0.599	0.507	0.301	-0.263
	<i>0.821<sup>b</sup></i>	<i>0.883</i>	<i>0.402</i>	<i>0.914</i>	<i>0.323</i>	<i>0.140</i>	<i>0.279</i>	<i>0.508</i>	<i>0.155</i>	<i>0.246</i>	<i>0.512</i>	<i>0.568</i>
E2		0.014	0.010	0.106	0.000	0.203	0.872	0.504	0.289	-0.102	-0.496	-0.042
		<i>0.976</i>	<i>0.983</i>	<i>0.821</i>	<i>0.999</i>	<i>0.662</i>	<b>0.011</b>	<i>0.249</i>	<i>0.530</i>	<i>0.827</i>	<i>0.258</i>	<i>0.929</i>
E3		1.000	-0.862	0.549	0.696	-0.271	0.284	0.728	0.710	0.867	0.687	0.636
			<b>0.013<sup>c</sup></b>	<i>0.202</i>	<i>0.082</i>	<i>0.556</i>	<i>0.537</i>	<i>0.064</i>	<i>0.074</i>	<b>0.012</b>	<i>0.088</i>	<i>0.125</i>
E4			1.000	-0.672	-0.514	0.365	-0.098	-0.534	-0.408	-0.517	-0.515	-0.783
				<i>0.099</i>	<i>0.238</i>	<i>0.421</i>	<i>0.835</i>	<i>0.217</i>	<i>0.364</i>	<i>0.235</i>	<i>0.237</i>	<b>0.037</b>
E5				1.000	0.364	0.389	0.237	0.271	0.310	0.372	0.331	0.905
					<i>0.423</i>	<i>0.389</i>	<i>0.609</i>	<i>0.557</i>	<i>0.499</i>	<i>0.411</i>	<i>0.468</i>	<b>0.005</b>
E6					1.000	0.099	0.429	0.624	0.759	0.706	0.838	0.188
						<i>0.833</i>	<i>0.337</i>	<i>0.134</i>	<b>0.048</b>	<i>0.076</i>	<b>0.019</b>	<i>0.686</i>
E7						1.000	0.370	-0.073	0.173	-0.019	-0.066	0.080
							<i>0.414</i>	<i>0.877</i>	<i>0.711</i>	<i>0.967</i>	<i>0.889</i>	<i>0.864</i>
E8							1.000	0.739	0.673	0.294	-0.079	0.020
								<i>0.058</i>	<i>0.097</i>	<i>0.522</i>	<i>0.867</i>	<i>0.967</i>
E9								1.000	0.917	0.663	0.275	0.289
									<i>0.004</i>	<i>0.104</i>	<i>0.551</i>	<i>0.530</i>
E10									1.000	0.812	0.889	0.889
										<b>0.027</b>	<b>0.031</b>	<b>0.031</b>
E11										1.000	0.889	0.891
											<b>0.031</b>	<b>0.029</b>
E12												0.874
												<b>0.034</b>

a Correlation coefficients; b Probability; c Bold text are significant correlations

**Table 5.** Disease (yam leaf spot and yam viral disease) severity ratings (1= no symptom and 5= very severe symptoms) and unadjusted mean yield (tha<sup>-1</sup>) of 7 *Dioscorea rotundata* genotypes in 13 environments in Ghana.

Main effect	Leaf spot		Virus		Yield (t ha <sup>-1</sup> )					
	3 MAP	6 MAP	3 MAP	6 MAP	2000	2001	2002	2003	2004	Mean
<b>Genotype</b>										
DORBAN	1.0	3.0	1.0	1.8	10.1	7.8	10.1	11.0	12.4	10.3
TDr89/02665	1.2	1.8	1.3	1.7	19.7	11.6	13.3	18.4	17.1	16.0
TDr95/18894	1.1	2.2	1.2	2.8	24.6	11.4	19.5	12.7	14.8	16.6
TDr95/18944	1.2	2.4	1.2	2.1	16.9	10.7	16.5	12.0	15.4	14.3
TDr95/18949	1.3	2.1	1.3	2.3	16.8	15.9	18.7	19.7	23.1	18.8
TDr95/19158	1.2	1.4	1.3	1.8	13.8	11.8	11.3	12.1	17.3	13.2
TDr95/19177	1.2	1.5	1.2	1.5	32.7	10.7	20.8	19.0	13.2	19.3
Mean	1.2	2.1	1.2	2.0	19.2	11.4	15.9	15.0	16.2	15.5
SE	0.02	0.08	0.03	0.04	1.4	2.1	1.2	1.4	1.3	1.2
F-test (P<0.001)	***	***	***	***	***	***	***	***	***	***
<b>Location</b>										
Fumesua	1.8	2.6	1.4	2.9	24.0	14.2	16.0	16.1	14.2	16.9
Wenchi	1.1	2.2	1.5	2.4	14.5	10.3	18.1	14.7	-	11.5
Bodwease	1.2	1.8	1.0	2.5	-	9.6	13.6	14.1	18.2	13.9
Mean	1.4	2.2	1.3	2.6	19.2	11.4	15.9	15.0	10.8	14.1
SE	0.04	0.05	0.03	0.08	2.3	1.3	1.3	1.4	1.8	1.1
F-test (P<0.001)	***	***	***	***	***	***	***	***	***	***

MAP= Months after planting. \*\*\* Significant at P<0.001.

E13) were in the third quadrant indicating a very favourable site for breeding yams for broad adaptation. This was reflected in the significant (P<0.05) correlations between environments 10-13 (Table 4). This could be attributed to extremely good rainfall pattern and high soil fertility in Bodwease and its environs (Table 2).

The biplot (Fig. 1) therefore identified four groupings among the genotypes evaluated: Dorban and TDr 95/18944 in quadrant I, were low yielding and highly unstable (high positive FA1(1) score); TDr 95/19158 was low yielding but very stable (in quadrant II, negative low FA1(1) score); TDr 89/02665 was high and stable

yielding (quadrant III, and negative and low FA1(1) score) and TDr 95/19177, TDr 95/18949 and TDr 89/18894 were high but unstable yielding genotypes (high and positive FA1(1), quadrant IV).

Stability in the field performance of genotypes is influenced by prevailing biotic and abiotic stresses<sup>18</sup>. Resistance to biotic stresses in addition to tolerance of common abiotic factors in the environment would ensure good varietal performance<sup>1</sup>. In this study, the most stable genotypes (TDr 89/02665) generally had moderate disease ratings (Table 5).

Conversely, TDr 95/18944 (the most unstable and low yielding genotypes) had the largest scores for yam leafspot disease. Environments that exhibited stable yields for genotype especially Bodwease, generally had lower leaf spot disease pressure compared with locations that exhibited unstable yields such as Fumesua with higher temperature and relative humidity.

The long growing period and diverse agroecologies, in which yams are cultivated, expose cultivars to numerous biotic stresses with some being very devastating in cases of complex stress interactions<sup>1</sup>. During the wet season, yam leaf spot diseases can be very prevalent. They cause serious yield losses due to their destructive effects on the photosynthetic machinery of the plants. Yam improvement should be focused on multiple disease and pest resistance, which would guarantee stability of crop performance<sup>1</sup>.

### Conclusions

Four groupings were identified in the genotypes evaluated: Dorban and TDr 95/18944 were low yielding and highly unstable; TDr 95/19158 was low yielding but very stable; TDr 89/02665 was high and stable yielding and TDr 95/19177, TDr 95/18949 and TDr 89/18894 were high but unstable yielding genotypes. TDr 89/02665 has therefore being formally released as a new variety (Mankrong Pona) in Ghana in 2005.

Bodwease, Wenchi and Fumesua were identified as most favourable and stable environments for yam improvement studies in that order of importance.

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