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Agronomic Performance and Yield Stability of Sixteen Elite White Yam Genotypes (*Dioscorea rotundata*) Across Three Agro-ecologies in Nigeria

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Abstract

Yam is an important staple in Africa, but the availability is constrained by the gradual decline in varietal productivity due to repeated cycle of cultivation. To improve yam productivity, breeders have developed several new varieties of yam, however, their adaptability and resistance to major yam diseases needs to be assessed in different location to select the best stable varieties. This study thus evaluated the agronomic performance and yield stability of sixteen elite white yam (*D. rotundata*) genotypes across three locations in Southern Nigeria. A randomized complete block design with two replications was used at each location. Data were collected on total tuber yield, dry matter content (DMC), stems per plant, Yam Mosaic Disease (YMV), and Yam Anthracnose Disease (YAD). Combined ANOVA revealed significant ($p<0.05$) environmental effects for all traits, with Ibadan location producing 3.1 times higher yield (31.5 t/ha) than other locations. Genotypic effects were significant for all traits, while genotype × environment interaction (G×E) was non-significant for yield ($p=0.157$), DMC ($p=0.326$), and stems per plant ($p=0.167$), but significant for average_YMV ($p=0.0039$) and average_YAD ($p<0.0001$). TDr19153013 ranked highest for yield (25.6 t/ha) with good DMC (29.8%), while TDr19153001 had highest DMC (30.5%). AMMI analysis showed IPCA1 explained 82.6% of G×E variance for yield and 78.4% for DMC. The study identified and recommended TDr19153013, TDr19162008, and TDr19171003 as superior genotypes to farmers for adoption in the study area.

Keywords: *Dioscorea rotundata*, Yam Breeding, Phenotypic Evaluation, Disease Evaluation

Introduction

White yam (*Dioscorea rotundata*) is a vital, indigenous tuber crop that forms the bedrock of food security, economic livelihood, and cultural identity for millions across West Africa, a region historically termed the "yam belt" (Akakpo *et al*., 2024; Mondo *et al*., 2021) [3, 7]. As the most preferred and economically significant species among cultivated yams, *D. rotundata* contributes substantially to dietary energy intake and serves as a critical source of income for smallholder farmers, particularly in Nigeria, Ghana, Côte d'Ivoire, and Benin (Agre *et al*., 2021; Norman *et al*., 2018) [2, 10]. Recent genomic and ethnobotanical research has solidified the narrative of its independent domestication in the forest-savanna transition zone of the Niger River basin, distinguishing it evolutionarily from the Asian water yam (*Dioscorea alata*) and underscoring its deep anthropogenic selection for desirable traits like large tuber size and storability (Scarcelli *et al*., 2019; Siadjeu *et al*., 2020) [13, 14].

Despite its socio-agronomic primacy, yam production systems are besieged by a nexus of biophysical and anthropogenic constraints that perpetuate significant yield gaps. The crop's inherent low multiplication ratio, prolonged growth cycle, and high labour demands are compounded by intensifying biotic stresses, including yam mosaic virus (YMV), nematodes (*Scutellonema bradys*), and anthracnose disease, which collectively cause substantial pre- and post-harvest losses (Darkwa *et al*., 2020; Nkansah *et al*., 2023) [5, 9]. Furthermore, climate-change-induced variability in rainfall patterns and temperatures exacerbates these challenges, threatening the stability of production in traditional yam-growing ecologies (Otoo *et al.*, 2021) [12]. These persistent constraints highlight an urgent need for a genetic enhancement strategy to develop and deploy high-yielding, resilient, and adaptable cultivars that can sustainably bridge the productivity gap.

Central to this breeding objective is the comprehensive evaluation of elite genotypes across diverse agro-ecologies. The phenotypic expression of yield and associated agronomic traits is a complex function of genetic makeup (G), environment (E), and their interaction (GEI) (Mukherjee *et al.*, 2022; Yan, 2021) [8, 15]. GEI is particularly pronounced in clonally propagated crops like yam and often leads to inconsistent cultivar performance, thereby complicating selection and recommendation processes (Asfaw *et al.*, 2019) [4]. Consequently, conducting multi-environment trials (METs) and applying advanced stability models are indispensable for discriminating genotypes with either broad adaptability across variable conditions or specific adaptability to targeted niches—a prerequisite for informed varietal release and effective breeding (Adjei *et al.*, 2022; Oladosu *et al.*, 2019) [1, 11].

Despite the acknowledgement of previous studies on the existence of GEI in yam, there remains a critical paucity of contemporary, systematic assessments that integrate modern stability analysis tools to evaluate recently developed elite *D. rotundata* breeding lines. Many evaluations are either localized or rely on parametric models that may not fully capture the complexity of genotype-environment dynamics (Loko *et al.*, 2021) [6]. This gap impedes the identification of superior, stable genotypes ready for dissemination to farmers. To address this, the present study was conducted with aim of evaluating the agronomic performance, yield potential, and stability of sixteen elite *D. rotundata* genotypes across three key agroecological zones in Nigeria to quantify the pattern of GEI using the additive gene effects, multiplicative interaction (AMMI) and genotype-by-environment interaction (GGE) for yield stability and disease parameters.

Materials and Methods

Experimental Locations: The experiments were carried out at Agunrege located at latitude 8° 41′ longitude 3° 36″, Ibadan located at latitude 7° 50′ Longitude 3° 90′, and Abraka located at latitude 5° 80′ longitude 6° 13′ in southern part of Nigeria for one growing season.

Plant materials and trial establishment:

Sixteen elite white yam genotype: fourteen test clone genotypes newly developed breeding lines with potential for high yield and disease resistance (*D. rotundata)* (TDr19153013, TDr19162008, TDr19162038, TDr19150030, TDr19151011, TDr19171003, TDr19153001, TDr19150017, TDr19179005, TDr19149004, TDr19174013, TDr1000048, TDr19153008, TDr19151003) bred at the International Institute of Tropical Agriculture (IITA) Ibadan, Nigeria, yam breeding program and two local check genotypes serving as controls for performance comparison (Ojulyawo, TDr19180005) were used in this study. The genotypes were chosen based on their attributes, which include dry matter content, fresh tuber yield, and disease resistance.

Each plot consisted of 10 plant stands spacing standard of 1m × 1m between plants. Land preparation, staking, weeding, and pest control applied uniformly across locations. The trial was established in April coinciding with the onset of rainy season as a rain fed. The trial was staked at 2 m high and proper weeding was performed manually with hoes to ensure that the field was kept clean and free of weeds. NPK 15-15-15 (15% Nitrogen, 15% Phosphorus, 15% potassium) fertilizer was applied at the rate of 200 kg ha−1 at 8 weeks after planting. All agronomic management practices were carried out equally and properly at the three locations.

Experimental design: The experiment involved 16 varieties evaluated across 3 locations. At each location, the experiment was established using a 4 x4 simple lattice design with two replications.

Data collection and statistical analysis: Agronomic data were collected on the following growth and yield parameters: average number of stems per plant at maturity, total fresh weight of tubers, yam mosaic virus, yam anthracnose disease, and dry matter content (DMC %). All data were subjected to a two-way ANOVA using RCBD to assess genotype, environment, and genotype × environment (G×E) interaction effects was conducted using R statistical software with lme4 and agricolae packages and significance tested at $\alpha = 0.05$, Student-Newman-Keuls (SNK) test for mean separation at $\alpha = 0.05$ was used to group genotypes that are not significantly different within each trait. AMMI (Additive Main Effects and Multiplicative Interaction) Analysis was used for partitioning of G×E interaction effects, IPCA (Interaction Principal Component Axis) scores calculated, biplots generated for visualization. Stability Indices was used for regression approach for stability assessment. Multi-Environment Data Analysis was used to combined analysis across three locations, calculation of overall means and location-specific means, and ranking of genotypes based on performance.

Results

Table 1 shows that based on the stem_per_plant, the environmental effect was significant ($P \leq 0.05$), the genotype was also significant ($P \leq 0.05$). The prevalence of yam mosaic virus (YMV) was significant based on the environment ($P \leq 0.05$), the genotypic effect ($P \leq 0.05$), and the genotype x environment interaction. The average yam anthracnose disease (YAD); the prevalence of yam anthracnose disease was significant ($P \leq 0.05$) based on the environment, was significant ($P \leq 0.05$) based on the genotype and also significant ($P \leq 0.05$) based on the genotype x environment interaction. For total tuber field, the environmental effect was significant ($P \leq 0.05$). The genotype effect was significant ($P \leq 0.05$). Furthermore, the dry matter contact (DMC) was significant ($P \leq 0.05$) based on the environment and also significant ($P \leq 0.05$) based on the genotype.

The highest tuber yield was recorded in TDr19153013 (25.60t/ha) which was not significantly higher than TDr19152008 (23.00t/ha) but was significantly higher than the rest genotypes (Table 2). The highest Dry Matter Content (DMC) was observed in Ijuiyawo (35.20) which was not significantly different from TDr19153001 (30.50) and TDr1000048 (30.9), TDr19151003 (29.80) and TDr19174013 (30.00), but was significantly higher than the rest genotypes. The highest value for the stem_per_plant was observed in TDr19162038 (2.36) which was not significantly higher than TDr19152008 (2.01), but was significantly higher than the rest genotypes. The highest average yam mosaic virus (YMV) was observed in TDr19180005 (2.79) but was not significantly higher than TDr19153001 (2.78) but was significantly higher than the rest genotypes. Lastly, the highest average yam anthracnose disease (YAD) was observed in TDr19153001 (2.00) which was not significantly higher than TDr19180005 (1.93), but was significantly higher than the rest genotypes.

Table 1: Combined Analysis of Variance (ANOVA) For Evaluated 5 yam traits

Trait	Source	Df	Sum Sq	Mean Sq	F value	P value
Stem_per_plant	ENV	2	3.57	1.79	8.6	0.000658
	GEN	15	6.89	0.459	2.21	0.0197
	GEN:ENV	30	8.5	0.283	1.36	0.167
	RESIDUAL	47	9.77	0.208	-	-
Average YMV	ENV	2	3.74	1.87	115	0.0001
	GEN	15	0.736	0.0491	3.02	0.0019
	GEN:ENV	30	1.15	0.0384	2.37	0.0039
	RESIDUAL	47	0.763	0.0162	-	-
Average YAD	ENV	2	14.5	7.25	21.42	<0.0001
	GEN	15	1.21	0.0808	23.9	<0.0001
	GEN:ENV	30	1.24	0.0414	12.2	<0.0001
	RESIDUAL	47	0.159	0.00339	-	-
Total Tuber Yield	ENV	2	9698	4849	169	<0.0001
	GEN	15	1435	95.7	3.34	0.000788
	GEN:ENV	30	1188	39.6	1.38	0.157
	RESIDUAL	45	1347	28.7	-	-
Dry Matter Content	ENV	2	94.7	47.4	3.57	0.036
	GEN	15	520	34.7	2.61	0.0062
	GEN:ENV	30	458	15.3	1.15	0.326
	RESIDUAL	47	623	13.3	-	-

ENV: Environment, GEN: Genotype, GEN:ENV: Genotype x Environment, YMV: Yam Mosaic Virus, YAD: Yam Anthracnose Disease.

Table 2: Overall Genotype Means and SNK Mean Separation (α = 0.05) For 5 Traits Across Three Location

GENOTYPES	TOTAL TUBER YIELD	DRY MATTER CONTENT	STEM_PER_PLANT	AVERAGE YMV	AVERAGE YAD
TDr19153013	25.60a	29.80ab	1.66abc	2.61bc	1.53d
TDr19162008	23.00ab	27.50cd	2.01cd	2.55c	1.67bcd
TDr19162038	20.10bc	28.90bc	2.36a	2.59bc	1.61cd
TDr19150030	19.40bcd	28.40bcd	1.72abc	2.65abc	1.68bcd
TDr19151011	19.10bcd	26.20de	1.62abc	2.67abc	1.69bcd
TDr19171003	18.80cd	28.80bc	1.65abc	2.69abc	1.79bcd
TDr19153001	17.00de	30.50a	1.47bc	2.78a	2.00a
TDr19150017	16.80de	26.50de	1.36c	2.43d	1.67bcd
TDr19179005	16.40de	26.90de	1.60abc	2.64abc	1.68bcd
TDr19149004	16.20.de	27.40cd	1.53bc	2.53c	1.68bcd
TDr19174013	15.00ef	30.00ab	1.71abc	2.60bc	1.62cd
TDr1000048	14.60ef	30.90a	1.68abc	2.65abc	1.72bcd
TDr19153008	13.50fg	28.80bc	1.39c	2.69abc	1.67bcd
TDr19151003	13.20fg	29.00bc	1.42bc	2.70ab	1.82ab
Ojuiyawo	11.60gh	35.20e	1.19c	2.60bc	1.69bcd
TDr19180005	10.70h	24.70f	1.39c	2.79a	1.93a

Means with the same alphabet down the group are not significantly different from each other at 5% level of significance.

At Abraka location, the highest value for stem_per_plant was observed in TDr19162038 (2.06), which was not significantly higher than TDr19153013 (1.61) but was significantly higher than the rest genotypes (Table 3). At Ibadan, TDr19162038 (4.4) also performed highest, which was not significantly higher than TDr19162008 (3.05) but was significantly higher than the rest genotypes. There were no significant differences amongst the varieties in each of the locations with respect to the yam mosaic virus and yam anthracnose disease. However, at Ibadan, the highest incidence of yam anthracnose disease was observed in TDr19153001 (1.71) which was significantly than the rest varieties with the lowest incidence recorded in TDr19153013 (0.8).

In evaluating the total tuber yield, the highest tuber yield at Abraka was observed in TDr19153013 (16.96 t/ha) which was not significantly higher than TDr19152008 (13.72 t/ha) but was significantly higher than the rest genotypes. The highest total tuber yield at Ibadan was observed in TDr19153013 (42.83 t/ha), which was not significantly different from TDr19162008 (42.35 t/ha), TDr19171003 (41.06 t/ha) TDr19162038 (38.55 t/ha) and TDr19151011 (37.48 t/ha) but was significantly higher than the rest genotypes. At Agunrege, the highest total tuber yield was observed in TDr19153013 (16.96 t/ha) and TDr19153001 (16.96 t/ha) which was not significantly different from TDr19150030 (13.6 t/ha) and TDr19162008 (13.02 t/ha) but was significantly higher than the rest genotypes. Subsequently, the highest dry matter content of the genotypes at Abraka was observed in Ojuiyawo (34.33%) which was not significantly different from TDr19171003 (33.3%).and TDr19174013 (31.33%) but was significantly different from the rest of the genotypes. The highest dry matter content at Ibadan was observed in TDr1000048 (35.33%) which was not significantly different from TDr19151003 (33.67%) but was significantly different from the rest. Finally, at Agunrege location, the highest dry matter content was observed in the genotype Ojuiyawo (39.26%) which was not significantly different from TDr19171003 (30%) but was significantly higher than the rest elite genotypes.

Table 3: Growth, yield and disease resistance performances of 16 yam varieties across three agroecologies

GENOTYPES	STEM_PER_PLANT			YMV			YAD			TUBER YIELD t/ha			DMC %		
	ABK	IBD	AGJ	ABK	IBD	AGJ	ABK	IBD	AGJ	ABK	IBD	AGJ	ABK	IBD	AGJ
TDr19153013	1.61b	1.75b	1.61a	2.63a	2.56a	2.63a	1.71a	2.08a	0.8c	16.96b	42.83a	16.96b	28.71b	32a	28.71b
TDr19162008	1.38c	3.05a	1.61a	2.57a	2.88a	2.2a	1.8a	2a	1.2b	13.72b	42.35a	13.02c	27.67b	29a	25.77c
TDr19162038	2.06a	3.4a	1.61a	2.67a	2.79a	2.3a	1.6a	2.04a	1.2b	9.71c	38.55a	12.08c	29.33a	31.33a	26c
TDr19150030	1.36c	2.2a	1.61a	2.69a	2.97a	2.3a	1.8a	2.03a	1.2b	11.19c	33.4a	13.6c	27.67b	30a	27.67b
TDr19151011	1.50c	1.75b	1.61a	2.81a	2.85a	2.35a	1.8a	2.08a	1.2b	10c	37.48a	9.81c	26c	26.33c	26.39c
TDr19171003	1.27c	2.05a	1.61a	2.81a	2.95a	2.3a	1.8a	2.13a	1.2b	8.11c	41.06a	7.35c	33.33a	23c	30a
TDr19153001	1.25c	1.55b	1.61a	2.76a	2.93a	2.63a	1.8a	2.5a	1.71a	7.26c	26.81a	16.96b	29.67a	33a	28.71b
TDr19150017	1.21c	1.25c	1.61a	2.46a	2.82a	2a	1.8a	2.01a	1.2b	9.69c	31.65a	9.12c	25c	30.67a	23.91c
TDr19179005	1.30c	1.9b	1.61a	2.83a	2.68a	2.4a	1.8a	2.03a	1.2b	12.58b	24.94a	11.75c	27b	27b	26.85c
TDr19149004	1.38c	1.6b	1.61a	2.46a	2.83a	2.3a	1.8a	2.05a	1.2b	11.31c	31.58a	5.56c	26.67c	31.67a	23.74c
TDr19174013	1.38c	2.6a	1.61a	2.72a	2.51a	2.52a	1.8a	2.09a	1.2b	12.46b	34.85a	7.55c	31.33a	29.33a	29.1a
TDr1000048	1.33c	2.1a	1.61a	2.72a	2.92a	2.3a	1.8a	2.17a	1.2b	4.03c	33.33a	6.58c	31a	35.33a	26.44c
TDr19153008	1.21c	1.35c	1.61a	2.61a	2.92a	2.52a	1.8a	2.02a	1.2b	10.38c	25.69a	4.42c	29a	29a	28.5b
TDr19151003	1.1c	1.55b	1.61a	2.88a	2.92a	2.3	1.8a	2.46a	1.2b	8.55c	24.42a	6.5c	24.67c	33.67a	28.71b
Ojuiyawo	1.17c	0.8c	1.61a	2.73a	2.73a	2.3a	1.8a	2.05a	1.2b	7.38c	19.79a	7.58c	34.33a	32a	39.26a
TDr19180005	1.5c	1.05c	1.61a	2.74a	3.1a	2.52a	1.8a	2.78a	1.2b	8.02c	16.79b	7.31c	25.67c	26.33c	21.98c

Means with the same alphabet down the group are not significantly different from each other at 5% level of significance.

Table 4 shows the top ten elite genotypes ranked by total tuber yield (overall mean across the three locations). The yield per variety ranges from 16.4t/ha (TDr19179005) to 25.6t/ha (TDr19153013). The dry matter content for the top 10 elite genotypes ranges from 26.2% (TDr19151011) to 30.5% (TDr19153001). The stem_per_plant ranges from 1.36(TDR19150017) to 2.36(TDr19162038). Table 5 shows the trait performance across the three locations. The highest stem_per_plant was observed at Ibadan (1.85) which was not significantly higher than Agunrege (1.61) but was significantly higher than the average stem_per_plant at Abraka (1.38). The highest average yam mosaic virus was observed at Ibadan (2.84) which was not significantly higher than that of Abraka (2.69) but was significantly higher than that of Agunrege (2.37). The highest average yam anthracnose disease was observed at Ibadan (2.16) which was not significantly higher than that of Abraka (1.78) but was significantly higher than that of Agunrege (1.21).

The top five yield performing (t/ha) genotypes in each location (Table 6). The yield per variety at Abraka ranges from 11.19t/ha (TDrr19150030 to 16.96t/ha (TDr19153013). At Agunrege, the yield per variety ranges from 12.08t/ha (TDr19162038) to 16.96t/ha (TDr19153001). While at Ibadan, the yield per variety ranges from 37:-SS 48t/ha (TDr19151011) to 42.83t/ha (TDr19153013).

Table 4: Top 10 Genotypes Ranked by Total Tuber Yield (Overall Mean Across Locations)

RANKED	GENOTYPES	STEM_PER_PLANT	AVE_YMV	AVE_YAD	TOTAL TUBER YIELD	DRY MATTER CONTENT
1	TDr19153013	1.66	2.61	1.53	25.6	29.8
2	TDr19162008	2.01	2.55	1.67	23	27.5
3	TDr19162038	2.36	2.59	1.61	20.1	28.9
4	TDr19150030	1.72	2.65	1.68	19.4	28.4
5	TDr19151011	1.62	2.67	1.69	19.1	26.2
6	TDr19171003	1.65	2.69	1.71	18.8	28.8
7	TDr19153001	1.47	2.78	2	17	30.5
8	TDr19150017	1.36	2.43	1.67	16.8	26.5
9	TDr19179005	1.6	2.64	1.68	16.4	26.9
10	TDr19174013	1.86	2.58	1.7	18.29	29.92

Table 5: Trait Performance across the 3 Locations.

TRAITS	ABRAKA	AGUNREGE	IBADAN
STEM_PER_PLANT	1.38c	1.61b	1.85a
AVERAGE YMV	2.69b	2.37c	2.84a
AVERAGE YAD	1.78b	1.21c	2.16a
TOTAL TUBER YIELD	10.1b	9.76c	31.5a
DRY MATTER CONTENT	28.6b	27.6c	30.0a

Table 6: Top 5 yield performing (t/ha) genotypes in each location.

RANKED	ABRAKA	AGUNREGE	IBADAN
1	TDr19153013	TDr19153001	TDr19153013
	-16.96	-16.96	-42.83
2	TDr19162008	TDr19153013	TDr19162008
	-13.72	-16.96	-42.35
3	TDr19174013	TDr19150030	TDr19171003
	-12.46	-13.6	-41.06
4	TDr19149004	TDr19162008	TDr19162038
	-11.31	-13.02	-38.55
5	TDr19150030	TDr19162038	TDr19151011
	-11.19	-12.08	-37.48

Figure 1 shows the genotype x environment biplot for yield. At Abraka, TDr19153008 performed best as it was closest to Abraka from the biplot chart. Also, at Agunrege, TDr19153001 performed better compared to the other genotypes. TDr19171003 performed better at Ibadan as it was closest to Ibadan from the biplot chart. Other genotypes that are scattered at the center of the biplot chart performed generally equal at all the locations. The genotype x environment biplot for dry matter content (figure 2). From the chart, Ojuiyawo have the highest DMC at Agunrege. TDr19171003 have the highest DMC at Abraka. While TDr1000048 and TDr19149004 have the highest DMC at Ibadan respectively.

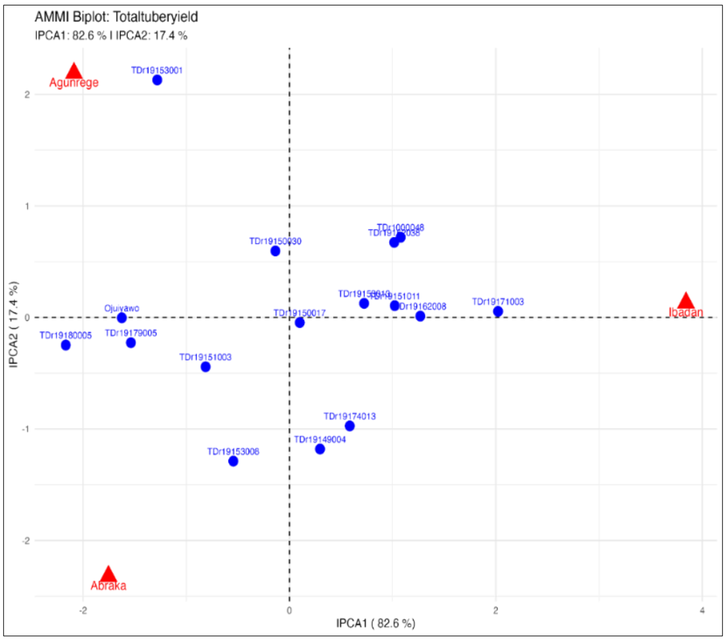

Fig 1: Genotype x environment biplot for yield

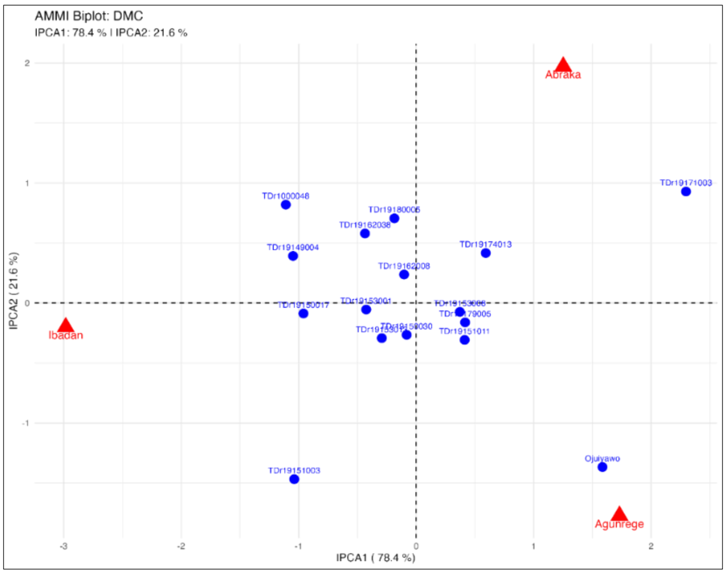

Fig 2: Genotype x environment biplot for dry matter content

Discussion

The present study evaluated the performance and stability of sixteen elite *Dioscorea rotundata* genotypes across three contrasting agro-ecologies in Southern Nigeria. The results confirm the profound influence of environment on yam productivity, reveal significant genetic potential for improvement, and delineate the complex nature of genotype-by-environment interactions (GEI) for key traits. These findings align with and extend the contemporary body of knowledge on yam breeding and adaptation.

The overwhelming environmental effect, particularly on tuber yield, where the Ibadan location yielded 3.1 times more than other sites, underscores a fundamental challenge in tropical root crop production. This finding resonates with studies by Otoo *et al*. (2021) [12], who emphasized that climate variability and soil quality are primary determinants of yield gaps in West African yam systems. The superior performance at Ibadan can be attributed to its optimal research station conditions—fertile soil, assured moisture, and intensive management—highlighting the significant yield potential that can be unlocked with improved agronomic inputs. This echoes the work of Asfaw *et al*. (2019) [4], who noted that environmental main effects often overshadow genetic differences in multi-environment trials (METs) for clonally propagated crops, necessitating careful site selection for effective selection.

Despite the strong environmental influence, significant genotypic variation was observed for all measured traits. The 2.5-fold range in yield (10.7 to 25.6 t/ha) among genotypes indicates substantial genetic diversity upon which selection can act. This aligns with the findings of Agre *et al*. (2021) [2], who reported considerable genetic variability in yield and quality traits within *D. rotundata* breeding lines, providing a robust foundation for genetic gain. The identification of high-performing genotypes like TDr19153013 (25.6 t/ha) and TDr19162008 (23.0 t/ha) demonstrates the success of modern yam breeding programs in developing superior genetic material, a progress also documented by Darkwa *et al*. (2020) [5].

A critical insight from this study is the differential nature of GEI across traits. The non-significant GEI for key agronomic traits—tuber yield, dry matter content (DMC), and stems per plant—is particularly noteworthy. This suggests that these traits are primarily under additive genetic control and exhibit relatively stable performance across the tested environments. Consequently, selection for high yield and good DMC in one representative environment is likely to result in superior performance across a broad range of similar agro-ecologies. This finding supports the breeding strategy proposed by Oladosu *et al*. (2019) [11], who advocated for identifying broadly adapted genotypes as the most efficient approach for staple crop improvement in sub-Saharan Africa. It implies that resources can be focused on maximizing genetic gain for these traits without excessive concern for complex crossover interactions in the target regions.

In contrast, the highly significant GEI for disease scores (average_YMV and average_YAD) reveals a different genetic architecture for disease resistance. This indicates that the expression of resistance to Yam Mosaic Virus and Yam Anthracnose is highly context-dependent, influenced by specific environmental pressures such as pathogen load, humidity, and temperature. This aligns with the observations of Nkansah *et al*. (2023) [9], who reported that disease resistance in yam is often quantitative and sensitive to environmental conditions. Therefore, breeding for durable disease resistance necessitates selection under diverse disease pressures and potentially requires location-specific breeding pipelines or the deployment of varieties with specific adaptation, as suggested by Adjei *et al*. (2022) [1].

The AMMI analysis, which captured a high percentage of the interaction sum of squares in the first interaction principal component axis (IPCA1), provided a visual and statistical tool to interpret the non-crossover interactions for yield and DMC. The biplots helped identify genotypes with specific adaptation, such as the superior performance of certain genotypes in specific locations. This methodological application is consistent with the recommendations of Yan (2021) [15] and Mukherjee *et al*. (2022) [8], who emphasized the utility of AMMI and GGE biplots in MET analysis for uncovering patterns of adaptation and stability.

The study successfully identified genotypes with desirable combinations of traits. TDr19153013 stands out as a superior candidate, combining the highest yield with good DMC (29.8%) and stable performance. This lack of a severe yield-quality trade-off is encouraging for breeding programs aimed at delivering both productivity and consumer-preferred traits, a dual objective also highlighted by Mondo *et al*. (2021) [7]. The high DMC of genotypes like TDr19153001 (30.5%) and TDr1000048 (30.9%) is particularly valuable, as DMC is a key determinant of texture, storability, and economic value, traits prioritized by both farmers and consumers (Akakpo *et al*., 2024) [3].

Conclusion

This research successfully used AMMI stability analysis to distinguish broadly adapted from specifically adapted varieties, providing a model for future yam breeding programs with the varieties TDr19153013, TDr19162008, and TDr19171003 showing broader adaptability and tolerance to yam anthracnose and mosaic diseases relative to the rest varieties. It also demonstrated that optimal growing conditions can yield 3.1 times more than challenging environments, highlighting that improving agronomic practices is as crucial as developing new varieties.

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