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GENETIC VARIABILITY AND MULTI-TRAIT SELECTION FOR SUPERIOR TRAITS IN WILD YAM HYBRIDS

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ABSTRACT

The interspecific breeding of yams (*Dioscorea* spp.) for superior traits is hindered by the dioecious nature of their flowers and low flowering frequency, despite the potential of wild yams to improve related cultivated varieties. However, the genetic variability of these wild yam species has yet to be fully explored. This study investigated the genetic variability and heritability estimates for multi-trait selection of hybrids derived from crosses between two wild yam species, *Dioscorea abyssinica* and *Dioscorea praehensilis*. Field experiment was conducted on 65 hybrids using a partially replicated block design. With standard descriptors, data were collected on phenotypic traits, including stem length, internode, plant vigour, tuber length, tuber weight, tuber width, tuber thorniness, and tuber surface cracks. Heritability, genetic advance and variance components were estimated to quantify the genetic contribution to trait variability. Analysis of variance identified significant differences (p=0.00) among hybrids and high genetic variability was observed in phenotypic traits assessed, with tuber weight showing the highest genotypic (104%) and phenotypic (127%) variances. Heritability estimates suggested strong selection potential for stem length (74%), tuber weight (67%) and tuber hairiness (65%), while tuber shape (7%) and tuber width (9%) showed low genetic potential. Multi-trait Genotype Ideotype Distance Index (MGIDI) analysis further identified 8 high-performing wild yam hybrid accessions (TDabp2101010, TDabp2101013, TDabp2101030, TDabp2101042, TDabp2101046, TDabp2101050, TDabp2101052, and TDabp2101055). These findings demonstrate the potential of wild yam hybrids for trait introgression, thereby paving way for the development of new yam cultivars and providing valuable insights for yam improvement programs.

Keywords: *Dioscorea* spp., Hybrid, Genetic variability, Heritability estimate, MGIDI index

INTRODUCTION

Yams (*Dioscorea* spp.), is a tuber crop known for their climbing or twining growth habit, are a type of staple crops with significant agronomic, nutritional, medicinal, and sociocultural value (Andres *et al.*, 2017; Obidiegwu *et al.*, 2020). There are approximately 600 species of *Dioscorea* with *rotundata, alata*, and *cayenensis*, being the most widely cultivated for their edible tubers. Yam plays a vital role in food security in Saharan Africa, especially in Nigeria, Ghana and Benin Republic (Darkwa *et al.*, 2020). The current rapidly growing population in Nigeria, which is projected to be the third largest population globally by 2050, necessitates the demand for yam food and increase in its agricultural productivity to meet future needs (Matemilola, 2017; Oseghale *et al.*, 2024).

Yam breeders face significant challenges in developing improved varieties as a result of the dioecious nature of yam flowers and low flowering frequency, along with their cross-incompatibility (Otoo 2017; Mondo *et al.*, 2020). These factors create barriers to interspecific crossing, hindering genetic improvement efforts for yam crops. There is a need to overcome this barrier with pre-breeding techniques, which involve identifying useful traits in crop wild relatives and transferring them to breeding lines (Kilian *et al*., 2020). It also aims to transfer beneficial traits from wild relatives and landraces into intermediate breeding populations to develop new crop varieties (Sharma, 2017; Kilian *et al*., 2020).

Wild yam species, including *Dioscorea abyssinica* and *Dioscorea praehensilis*, have been identified as progenitors of the domesticated West African yams, *Dioscorea rotundata* and *Dioscorea cayennensis* (Sugihara *et al*., 2020). These wild relatives hold untapped genetic potential for improving cultivated yams, particularly for traits such as disease resistance, drought tolerance, and yield stability (Padhan *et al*., 2019; Adewunmi *et al*., 2023).

The genetic diversity and adaptability of *Dioscorea abyssinica* are critical for addressing breeding challenges (Ousmael *et al*., 2019; Swarup *et al*., 2021). Furthermore, recent studies by Adewunmi *et al*., (2023), highlighted the potential of *Dioscorea praehensilis*, including its high yield potential, resistance to yam mosaic virus (YMV) and desirable tuber quality characteristics, as a valuable genetic resource for improving cultivated yams, particularly white yam (*D. rotundata*). Interestingly, a study reported by Oyedoyin *et al*. (2024), showed that 65 hybrids out of 70 progenies were successfully achieved from a cross between two wild yam species (*D. abyssinica* and *D. praehensilis*) as confirmed by KASP markers. These hybrids although showed some phenotypic potential but their genetic variability is yet to be explored. Identifying their genetic potential will enable yam breeders select superior traits, which are essential for effective trait introgression (Olawuyi *et al*., 2022; Adewumi *et al*., 2023). Therefore, this study assessed the genetic variability and heritability estimates for multi-trait selection in hybrids derived from the interspecific crosses between *D. abyssinica* and *D. praehensilis*.

MATERIALS AND METHODS

Experiment location

The field trial was conducted at the International Institute of Tropical Agriculture (IITA) in Ibadan, Nigeria, which is located on latitude of approximately 7°30'N and longitude of 3°54'E. The site experienced an annual rainfall ranging between 1,200 mm and 1,500 mm, supporting various tropical crops.

Experimental Design

A partially replicated (p-rep) block design was used to optimize the field layout due to the limited availability of plant materials (Cullis & Coombes, 2006; Santos *et al*., 2024). The experimental design comprised 15 rows and 10 columns, with a 1-meter border on each side. This layout optimized resource utilization and enabled effective phenotypic evaluation under field conditions.

Planting materials and planting

In this study, tubers of sixty hybrids from the first filial generation of *D. abyssinica* x *D. praehensilis* (Oyedoyin *et al*., 2024), and control *D. rotundata* (TDr9518544) were utilised. Tubers where directly cultivated on ridges (35-40 cm high) in the fields, with a spacing of 1 m x1 m under rain-fed conditions. Vines were staked three weeks after sprouting, and regular weeding was carried out.

Data collection and statistical analysis

Quantitative and qualitative traits were collected for all the plants according to IITA yam crop ontology (Asfaw, 2016). The data collection was conducted continuously at different intervals throughout the growing season to assess the variability and performance of the hybrids.

The statistical analysis was done using R statistical program. Genotypic Variance (GV) and Phenotypic Variance (PV) were estimated to evaluate the extent of genetic and environmental influences on the observed traits. Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were computed to measure the relative extent of variability present in the traits. Similarly, Genetic Advance as a Percentage of the Mean (GAM) was calculated to assess the potential for selection improvement, and heritability estimates were determined to quantify the proportion of phenotypic variance that could be attributed to genetic factors. ANOVA was conducted to evaluate the extent of variability and determine statistically significant differences among the studied hybrids. Hierarchical clustering was used to group hybrids based on their similarities and differences in trait performance. This method helped in distinguishing the performance of various hybrid and understanding their relationships.

Factor Analysis (FA) was conducted to identify underlying relationships between multiple traits. Additionally, the Multi-Trait Genotype–Ideotype Distance Index (MGIDI) was applied to select superior accessions based on their overall performance across multiple traits, facilitating multi-trait selection of the best-performing hybrids.

RESULTS AND DISCUSSION

Genetic variability of Agro-mophological traits in hybrids

Stem length had the highest genetic variance (4410.26), phenotypic variance (5990.27) and heritability broad sense (73.62%), whereas tuber weight had the highest genotypic coefficient of variance (104.12), phenotypic coefficient of variance (127.43) and genetic advance as a percentage of the mean (175.28%), as shown in Table 1. Moderate genetic potential was observed for traits such as tuber length (GV = 101.51, Hb = 45.27%, GAM = 50.31%) and the number of tubers (GV = 0.71, Hb = 59.41%, GAM = 70.63%). Furthermore, the ANOVA revealed significant and high level of variation among the evaluated traits (P= 0.00) across all hybrids accessed with high F-value of 366.61(Table 2).

Table 1: Genetic advance, variance and heritability estimates for agro-mophological traits among hybrids of *Dioscorea* spp.

Trait	GV	PV	GCV%	PCV%	Hb%	GAM%
Plant_vigour	1.10	2.00	22.78	30.64	55.27	34.88
Stem_length	*4410.26	*5990.27	41.61	48.49	*73.62	73.54
Internode	8.53	63.54	14.09	38.45	13.42	10.63
Tuber weight	0.16	0.27	*104.12	*127.43	66.76	*175.28
Tuber length	101.51	224.24	36.29	53.94	45.27	50.31
Tuber width	1.89	18.95	16.21	51.33	9.97	10.54
No_of_tubers	0.71	1.20	44.48	57.71	59.41	70.63
Tuber_shape	0.02	0.26	4.30	15.51	7.71	2.46
Tuber_thorniness_intensity	3.05	6.19	65.38	93.22	49.2	94.48
Hairiness_of_tuber	0.26	0.40	24.69	30.80	64.23	40.76
Tuber_surface_crack	0.17	0.46	33.79	55.71	36.77	42.21

GV- Genetic Variance, PV- Phenotypic Variance, GCV- Genotypic Coefficient of Variance, PCV- Phenotypic Coefficient of Variance, Hb- Heritability Broad Sense, GAM -Genetic Advance as a percent of Mean at P≤0.05*.

Table 2: Summary of Analysis of Variance (ANOVA) for trait variability among hybrids of *Dioscorea* spp.

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Trait	10	1192445	119245	366.61	*0.00
Error	594	193205	325		
Total	604	1385651			

DF (Degrees of Freedom); Adj SS (Adjusted Sum of Squares); P≤0.05

Performance evaluation of hybrids of *Dioscorea* spp. based on phenotypic traits via cluster analysis

Cluster 1 exhibited the highest mean scores across most phenotypic traits in Table 3, particularly for growth traits (internode length [211. 56 cm], plant vigour [5.43], stem length [214. 44 cm]) and yield traits (tuber length [30.30 cm], tuber weight [0.45kg] and tuber width [8.58 cm]). Among the 60 accessions evaluated, 16 presented a green colour (Figure 1) while Cluster 2 presented yellow colour (Figure 1), which categorized 20 accessions, including the check *D. rotundata* (TDr9518544), and compared with the other clusters, accounted for intermediate values of traits with the highest mean performance in terms of the number of tubers (1.75).

The red colour represent (Figure 1) cluster 3, with 5 accessions, was associated with the lowest tuber length (18.95 cm), tuber weight (0.12 kg), internode height (18.20 cm), plant vigour (3.58), stem length (51.13), tuber thorniness intensity (1.86) and tuber length (18.95 cm), while cluster 4, marked in purple colour in Figure 1, had 19 accessions on the phylogenetic tree which related at a distance to cluster 2. This accession showed high values for several traits, although not as pronounced as those of Cluster 1, with stem length of 160.64 cm and an average tuber weight of 0.39 kg (Table 3).

Table 3: Cluster-based summary of quantitative and qualitative traits in hybrids of *Dioscorea* spp."

Trait	Cluster 1 (Mean ± SD) [Range]	Cluster 2 (Mean ± SD) [Range]	Cluster 3 (Mean ± SD) [Range]	Cluster 4 (Mean ± SD) [Range]
Hairiness of Tuber	2.27 ± 0.43 [1.22-2.78]	1.97 ± 0.34 [1.22-2.66]	2.12 ± 0.69 [1.38-2.78]	2.07 ± 0.38 [1.22-2.78]
Internode (cm)	21.56 ± 0.94 [20.14-23.36]	20.42 ± 0.98 [18.02-22.42]	18.20 ± 0.56 [17.57-18.93]	21.23 ± 0.81 [19.50-22.78]
Plant Vigour	5.43 ± 0.53 [4.75-5.85]	3.80 ± 0.47 [3.25-4.91]	3.58 ± 0.08 [3.49-3.64]	4.74 ± 0.49 [4.20-5.85]
Stem Length (cm)	214.44 ± 23.55 [186.20-252.46]	110.38 ± 18.52 [82.17-139.84]	51.13 ± 16.26 [31.59-64.72]	160.64 ± 10.69 [145.34-176.90]
Tuber Shape	3.32 ± 0.05 [3.19-3.41]	3.29 ± 0.05 [3.19-3.41]	3.29 ± 0.03 [3.26-3.34]	3.31 ± 0.04 [3.25-3.41]
Tuber Surface Crack	1.31 ± 0.24 [0.73-1.67]	1.23 ± 0.24 [0.86-1.67]	0.85 ± 0.35 [0.59-1.46]	1.27 ± 0.26 [0.86-1.84]
Tuber Thorniness Intensity	3.16 ± 1.55 [1.43-4.87]	2.63 ± 1.38 [1.02-5.63]	1.86 ± 0.68 [1.43-3.00]	2.62 ± 1.13 [0.90-5.12]
Tuber Length (cm)	30.30 ± 8.61 [13.01-42.91]	25.74 ± 5.21 [16.89-34.78]	18.95 ± 4.41 [13.00-23.99]	28.97 ± 6.63 [18.24-37.79]
No of Tubers	1.57 ± 0.50 [1.22-3.06]	1.75 ± 0.92 [1.22-4.20]	1.60 ± 0.32 [1.28-1.97]	1.80 ± 0.72 [1.14-4.20]
Tuber Weight (kg)	0.45 ± 0.32 [0.08-1.06]	0.24 ± 0.24 [0.10-1.04]	0.12 ± 0.03 [0.10-0.16]	0.39 ± 0.45 [0.09-1.98]
Tuber Width (cm)	8.58 ± 0.43 [7.59-9.34]	8.27 ± 0.60 [7.60-10.21]	8.28 ± 0.57 [7.44-8.89]	8.50 ± 0.51 [7.82-10.36]

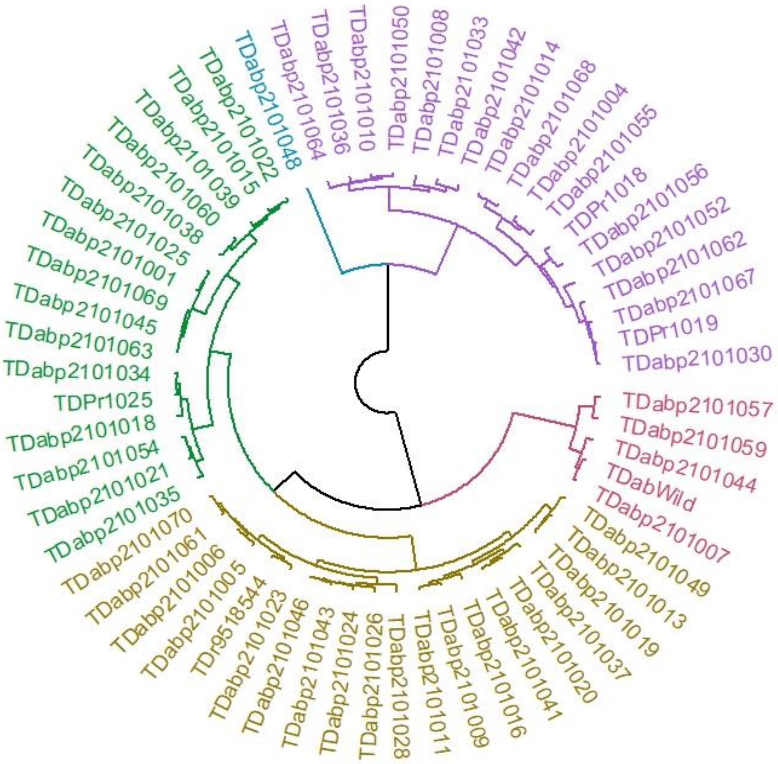
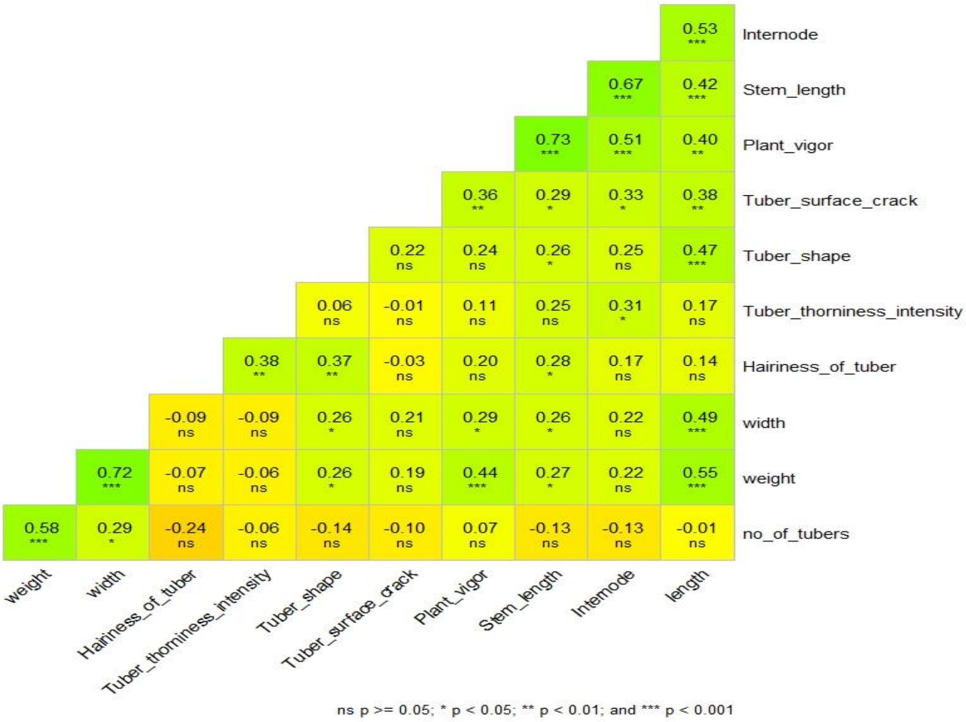


Figure 1: Phylogenetic tree showing the grouping patterns of hybrids of *Dioscorea* spp. Cluster 1- Green, Cluster 2- Yellow, Cluster 3- Red and Cluster 4- Purple.
Accession TDabp2101048 (blue color) appeared to distinguish itself from the other clusters but was closely related to cluster 4

Correlation of phenotypic traits and their relationships with hybrid accessions

Positive and highly significant correlations were observed between plant vigour and stem length (r = 0.73), tuber weight and tuber width (r = 0.72), and stem length and internode length (r = 0.67) (Figure 2), whereas tuber weight and the number of tubers (r = 0.58), tuber weight and tuber length (r = 0.55), internode length and tuber length (r = 0.53), and tuber width and tuber length (r = 0.49) were significantly associated at P < 0.01. On the other hand, tuber width was negatively correlated with tuber thorniness and hairiness (r = -0.09)



weight	width	Hairiness_of_tuber	Tuber_thorniness_intensity	Tuber_shape	Tuber_surface_crack	Plant_vigor	Stem_length	Internode	length	
									0.53 ***	Internode
								0.67 ***	0.42 ***	Stem_length
							0.73 ***	0.51 ***	0.40 **	Plant_vigor
						0.36 **	0.29 *	0.33 *	0.38 **	Tuber_surface_crack
					0.22 ns	0.24 ns	0.26 *	0.25 ns	0.47 ***	Tuber_shape
				0.06 ns	-0.01 ns	0.11 ns	0.25 ns	0.31 *	0.17 ns	Tuber_thorniness_intensity
			0.38 **	0.37 **	-0.03 ns	0.20 ns	0.28 *	0.17 ns	0.14 ns	Hairiness_of_tuber
		-0.09 ns	-0.09 ns	0.26 *	0.21 ns	0.29 *	0.26 *	0.22 ns	0.49 ***	width
	0.72 ***	-0.07 ns	-0.06 ns	0.26 *	0.19 ns	0.44 ***	0.27 *	0.22 ns	0.55 ***	weight
0.58 ***	0.29 *	-0.24 ns	-0.06 ns	-0.14 ns	-0.10 ns	0.07 ns	-0.13 ns	-0.13 ns	-0.01 ns	no_of_tubers

ns $p >= 0.05$; * $p < 0.05$; ** $p < 0.01$; and *** $p < 0.001$

Figure 2: Correlation of phenotypic traits in hybrids of *Dioscorea* spp

The Principal Component Analysis (PCA) biplot in Figure 3 are represented by the following characters: number of tubers, weight, width, internode length, tuber shape, tuber thorn intensity, and hairiness of the tuber. The PCA revealed that the first two principal components accounted for 52% of the variance in the phenotypic traits. Dimension (Dim) 1 accounted for 35.9% of the total variation while dimension 2 accounted for 16.1% of the total variation. The number of tubers, tuber weight, tuber width and tuber shape traits are strongly associated with Dim1, as shown by their longer vectors pointing towards the positive side of Dim1.

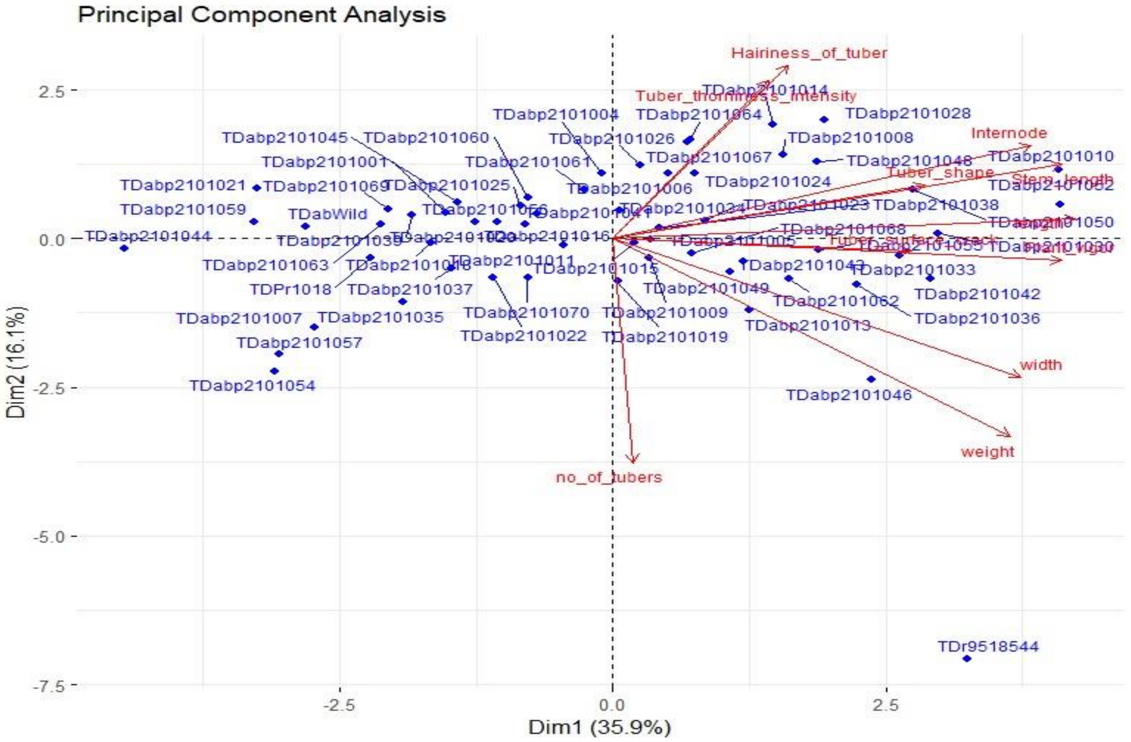


Figure 3: Principal Component Analysis (PCA) biplot of phenotypic traits in Wildyam. Hybrids

The tuber hairiness, tuber thickness, and intensity traits are more closely related to Dim2. The TDabp2101033, TDabp2101042, and TDabp2101046 accessions (lower right quadrant) were positively correlated with yield traits (tuber weight, tuber length, tuber width, and tuber number). The accessions in the upper right are more common in terms of growth traits, (plant vigour, internode and stem length). However, accessions TDabp2101044, TDabp2101021 and TDabp2101059 (left quadrants) are less strongly associated with the measured traits, while TDabp2101054 (far bottom-left) and TDr9518544 (bottom-right) are outliers.

Factor Analysis (FA) and Multi-Trait Genotype–Ideotype Distance Index (MGIDI) in Trait Selection

The Multi-trait Genotype Ideotype Distance Index (MGDI) identified 8 wild yam hybrids and *D. rotundata* (TDr9518544) as the best performing accessions across all the phenotypic traits assessed (Figure 4). Some growth-related traits, including Internode (-0.82), Plant Vigour (-0.79) and Stem Length (-0.85), strongly contributed to FA1 (Table 4). The accessions well defined with FA1 were TDabp2101010 and TDabp2101050 (Figure 5). FA2 had significant effects on yield-related traits, such as the number of tubers (0.83), tuber weight (0.88), and tuber width (0.70). TDabp2101013 and TDabp2101046 performed best among the wildyam hybrids (Figure 5) but were not as outstanding as *D. rotundata* (TDr9518544). Tuber thorniness intensity (0.76) and hairiness (0.69) were dominant in FA3 (Table 4), while, FA4 was predominantly influenced by tuber shape (-0.88) and tuber length (-0.57). TDabp2101010 and TDabp2101055 were associated with F3, whereas TDabp2101013, TDabp2101030, TDabp2101042 and TDabp2101046 were strongly associated with FA4 (Figure 5).

Table 4: Factor Analysis (FA), communality, and uniqueness of traits across four factors based on the Multi-Trait Genotype–Ideotype Index (MGDI)

TRAITS	FA1	FA2	FA3	FA4	Communality	Uniqueness
Hairiness_of_tuber	-0.09	-0.20	0.69	-0.47	0.74	0.26
Internode	-0.82	0.01	0.16	-0.13	0.71	0.29
Plant_vigour	-0.79	0.24	0.08	-0.08	0.69	0.31
Stem_length	-0.85	0.06	0.21	-0.11	0.79	0.21
Tuber_shape	-0.12	0.06	0.09	-0.88	0.80	0.20
Tuber_surface_crack	-0.57	-0.09	-0.45	-0.27	0.61	0.39
Tuber_thorniness_intensity	-0.27	-0.06	0.76	0.03	0.66	0.34
Tuber length	-0.50	0.33	-0.02	-0.57	0.69	0.31
no_of_tubers	0.15	0.83	0.04	0.30	0.80	0.20
Tuber weight	-0.26	0.88	-0.09	-0.24	0.91	0.09
Tuber width	-0.23	0.70	-0.21	-0.35	0.70	0.30

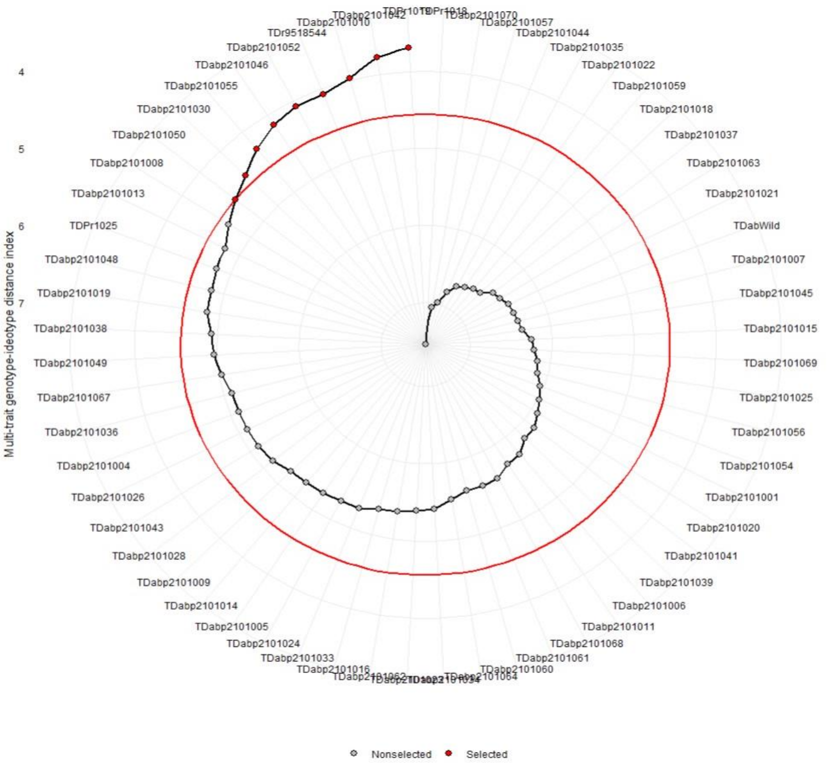


Figure 4: Rankings of wild yam hybrid accessions based on the Multi-Trait Genotype–Ideotype Index (MGIDI)
The selected accessions are represented by red dots, indicating their alignment with the desired ideotype. The red circle denotes the cut-off point determined by the selection pressure.

Figure 5: Strengths and weaknesses of selected accessions based on their contributions to the Multi-Trait Genotype–Ideotype Index (MGIDI)

The radar chart illustrates the strengths and weaknesses of selected accessions as proportions of each factor contributing to the computed MGIDI. A smaller proportion of a factor (closer to the outer edge) indicates that the traits within that factor are closer to the ideotype, representing the ideal trait combination. The black broken circle at the center represents the theoretical value where all factors contribute equally, serving as a baseline for comparison.

Discussion

The evaluation of 11 phenotypic traits (both quantitative and qualitative) variability and multi-trait selection in 60 accessions of hybrids of wild yams (*D. praehensilis* × *D. abyssinica*), highlighted the diversity and heritability of important phenotypic traits in yam crops (*Disocorea* spp.), providing key insights into genetic variability, trait interrelationships, and the potential for breeding superior hybrids.

The observed high genetic and phenotypic variability, heritability and genetic advances in important growth and yield traits highlight the potential for effective selection and genetic improvement in yam breeding programs. This finding is in agreement with that of Adewumi *et al*., (2023), who studied the variability of wild yam (*D. praehensilis*). Similarly, Olawuyi and Ajie (2023), emphasized the potential of additive genetic variance in driving effective selection for yield-related traits in tomato accessions. In addition, moderate genetic potential for traits such as tuber length and the number of tubers reflected a balance of genetic and environmental influences. These traits could serve as secondary selection criteria in breeding programs aimed at improving yield and growth performance in wild yam hybrids. Similar findings were reported in white Guinea yam (*D. rotundata*), where medium to high broad-sense heritability estimates were found for essential traits (Asfaw *et al*., 2020). In this study, the high F-value and the large variability proportion suggest that trait differences are primarily due to genetic effects rather than random variation. This variability indicates a strong potential for genetic improvement, although environmental factors may also significantly influence these traits.

Cluster analysis has proven effective in identifying distinct groupings of crop accessions based on phenotypic traits. This study identified distinct cluster groupings on the basis of phenotypic traits, with some clusters showing superior growth and yield performance. Studies on various crops, including yam (Norman *et al*., 2022; Adewumi *et al*., 2023), potato (Hossain *et al*. 2023), basil (Olawuyi, 2019), garlic (Tesfaye, 2022), and cassava (Bilate Daemo *et al*., 2023), have demonstrated the utility of this approach. Cluster 1 showed the best performance in stem length and tuber weight, making it the most promising group for further hybridisation. Cluster 2, exhibited intermediate performance with a high mean number of tubers, contributing to yield stability. This cluster relationship with the control *D. rotundata* (TDr9518544) supports Sugihara *et al*. (2020), that provided molecular evidence that white Guinea yam (*D. rotundata*) originated from hybrids from wild yam species (*D. praehensilis* × *D. abyssinica*). Accessions from this cluster can be considered for trait introgression into cultivated yams such as white Guinea yam (*D. rotundata*). Cluster 4 showed moderate performance and therefore offered opportunities for genetic gains and diversity, although it was genetically distant from Clusters 1 and 2. On the other hand, cluster 3, with the lowest number of accessions (5), performed the least in stem length and tuber weight and may therefore require targeted breeding interventions to improve traits. These studies demonstrated the value of diverse clustering methods in identifying promising genotypes for yam improvement programs, which is in agreement with the findings of Darkwa *et al*., 2020. Additionally, accession TDabp2101048 was genetically distinct but closely related to Cluster 4, indicating divergence. This suggests that it has unique traits that are worth exploring, making it valuable for breeding programs or conservation efforts. This methodology is consistent with approaches used in other crop studies such as Shaibu's (2021) whose study on maize hybrids utilised cluster and principal component analyses to assess genetic diversity, resulted in the identification of distinct groups with varying levels of Striga tolerance.

The strong positive correlations observed among key phenotypic traits, such as between plant vigour and stem length, and between tuber weight and tuber width, emphasize the interconnected nature of growth and yield traits in wild yams. These correlations suggest that selecting one trait may indirectly improve others. For example, selecting for a greater tuber weight is likely to enhance tuber width and yield potential. This finding is in agreement with Adejumobi et al., (2023), and Ouattara et al., (2024) on *Discorea* spp.

The use of the MGIDI allowed the identification of superior accessions based on their alignment with the ideotype. This finding makes it an effective tool for trait selection in crop breeding programs, in agreement with many recent studies in other crops, including sweet potato (Alam et al., 2024), wild yam (Adewunmi et al., 2023), guinea yam (Norman et al., 2022), wheat (Pour-Aboughadareh and Poczai, 2021) and cassava (Malik *et al*., 2020). The 8 selected hybrid accessions (TDabp2101010, TDabp2101013, TDabp2101030, TDabp2101042, TDabp2101046, TDabp2101050, TDabp2101052, TDabp2101055) and the check variety *D. rotundata* (TDr9518544) demonstrated strong performance across growth and yield traits. All the factors (FA1, FA2, FA3 and FA4) contributed well to all the phenotypic traits. Growth traits such as plant vigour, internode length and stem length were key contributors to FA1, while yield traits such as tuber weight, number of tubers and tuber width were key contributors to FA2, tuber thorniness intensity and tuber hairiness were major contributors to F3, and tuber shape and tuber length contributed to F4.

The radar chart visualization of MGIDI further highlights the strengths and weaknesses of the selected accessions. Among the hybrids, accessions TDabp2101010 and TDabp2101050 performed best in FA1; TDabp2101013 and TDabp2101046 exceled in FA2; TDabp2101010 and TDabp2101055 were very strong in FA3; and TDabp2101013, TDabp2101030, TDabp2101042 and TDabp2101046 were closer to the ideotype in FA4, making them the ideal candidates for further breeding efforts. This approach aligns with the findings of Singamsetti *et al*., (2023), that utilised MGIDI to assess tropical maize hybrids across various moisture regimes. Similarly, a study by Alam *et al*. (2024) conducted in Bangladesh utilised MGIDI to evaluate 71 sweet potato genotypes, identifying 11 top-performing genotypes based on yield and quality traits.

CONCLUSION

Our study explored the genetic potential of 60 hybrid accessions from wild yam species (*Dioscorea praehensilis X Dioscorea abyssinica*) for yam crop improvement. The findings from this study highlight the utility of integrating genetic variability analysis, cluster-based evaluations, and multi-trait selection indices in yam breeding programs. Significant genetic variability was observed in growth and yield traits assessed, with tuber weight showing the highest genotypic (104%) and phenotypic (127%) variance.

Heritability estimates suggested strong selection potential for stem length (74%), tuber weight (67%) and tuber hairiness (65%), while tuber shape (7%) and tuber width (9%) showed low genetic potential. The MGIDI analysis further identified 8 high-performing wild yam hybrid accessions (TDabp2101010, TDabp2101013, TDabp2101030, TDabp2101042, TDabp2101046, TDabp2101050, TDabp2101052, and TDabp2101055) with promising traits for introgression into cultivated yam species. In this study, the high F-value and the large variability proportion suggest that trait differences are primarily due to genetic effects rather than random variation. The identification of high-performing genotypes with desirable trait combinations offers a foundation for developing improved varieties that balance yield and growth traits. Future research should focus on integrating these hybrids to address specific challenges, such as disease resistance and climate resilience, in cultivated yams.

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