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Multi-Trait Selection Index for Simultaneous Selection of Water Yam (*Dioscorea alata* L.) Genotypes

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Abstract: Water yam (*Dioscorea alata* L.) is the most widely cultivated yam species with good agronomic attributes. However, several biotic and abiotic constraints and its lower food quality such as poor pound ability limit its production and use. Therefore, the identification of superior genotypes with suitable characteristics is needed for water yam improvement. This study aims to assess a panel of half-sib (progenies with one parent in common) and full-sib (progenies with the same male and female parents) progenies as well as their parents for selection of desirable ideotypes based on their agronomic and quality characteristics. A total of 280 progenies from bi-parental populations as well as five parents were evaluated, and a significant variation was observed ($p < 0.01$) in their performances for the eight traits used in the study. A moderate to high broad-sense heritability ($30\% < H2–H2 \geq 60\%$) was observed for all traits except for tuber pound ability ($H2 < 30\%$). Positive correlations were displayed between the traits, while the hierarchical clustering grouped genotypes into three clusters indicating the potential for selection of diverse genotypes for multiple traits from the four families under study. Plant vigor and number of tubers per plant contributed ($p < 0.01$) positively to the yield per plant in the path coefficient analysis. Using the multi-trait genotype–ideotype distance index (MGIDI), a total of 39 most promising genotypes were identified. These promising genotypes could be further used as progenitors in *D. alata* improvement programs targeting good agronomic and quality traits targeted for farmers and end users.

Keywords: *Diosorea alata*; water yam; agronomic-quality traits; multi-trait selection; yam improvement

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1. Introduction

Yam (*Dioscorea* spp.) is an economically important staple food for over 300 million people in the tropics and subtropics [1]. West Africa, called the "Yam Belt" accounts for 96% of the world production and 98% of the total yam production area (8.2 million ha out of 8.7 million in 2021) [2]. Nigeria (50.3 million tons), Ghana (8.3 million tons), Côte d'Ivoire (7.9 million tons), Benin (3.2 million tons), and Togo (888 thousand tons) account for 92% of the total yam production [2]. In West African countries, yams are known as "king of crops" due to their nutritional benefits, which include protein, carbohydrates, and vitamin C [3], source of calories [3,4], and for their socio-cultural importance [5]. *D. alata* (L.), also known as water yam or greater yam, is one of the most important globally cultivated species of Dioscoreaceae family, which is believed to have originated in South-East Asia [6]. It was introduced to Africa in the 16th century and its ability to produce in low to average soil

fertility, ease of propagation through the development of bulbils and high multiplication ratio, early vigor for weed suppression, and decreased post-harvest losses make it superior to most farmed yam species [3,6]. However, there are several constraints to its production that limit the full potential of the crop as food, feed, industrial application, and source of income. The constraints include biotic and abiotic stress factors that contribute to low yields and poor market-quality tuber. Additionally, biotic factors such as yam anthracnose disease cause severe yield losses and restrict international movement and the exchange of germplasm [5].

Generally, yam is consumed in different forms, mainly boiled, fried, or baked. Tubers are often dried and milled into flour for various products. Boiled yam could also be pounded and eaten with sauce. Boiled yam, pounded yam, and amala are the forms of yam most consumed in West Africa, especially in Nigeria, Benin, and Côte d'Ivoire [7,8]. However, very few varieties of *D. alata* are used for major food products in West Africa, or further processed due to its perceived unimpressive food quality traits such as its less suitability for the preferred cohesive and elastic dough in fufu or pounded yam. Even though *D. alata* is eaten as boiled, it is less preferred to *D. rotundata* (white yam) [9–11]. There is a need to improve the quality characteristics of water yam such as high dry matter content, less oxidation, and better organoleptic qualities (tuber boiled and pounded quality) for consumer preference and acceptance. It is necessary to evaluate *D. alata* germplasm (breeding lines and landraces) to select the best performing genotypes targeting agronomic (plant vigor, number of tubers per plant, tuber yield, etc.) and quality traits.

Mapping population represents crossing between two or more genetically diverse parents. The progenies consisting of half-sibs and full-sibs in mapping populations are important in the selection of desirable ideotypes (a high-performing genotype for desirable traits) in plant breeding because they allow breeders to simultaneously evaluate the performance of multiple genotypes that share a common parent. It is well known that selection based on related individuals for both agronomic and quality traits increases broad-sense heritability and leads to higher predicted selection gains [12]. This is particularly useful when the goal is to select traits that are controlled by multiple genes, as this allows breeders to assess the performance of several genotypes under similar environmental conditions [13,14]. In quantitative genetics, the evaluation of progenies and their respective parents under a similar environment reduces the environmental component of the phenotypic variation, thus increasing the selection efficiency of polygenic traits [14]. Assessing half-sib and full-sib progenies helps in accelerating the breeding process by reducing the time and resources required to develop new cultivars with improved performance through the simultaneous selection of multiple traits [14]. However, it is difficult to effectively incorporate multiple trait data into the selection method without introducing multicollinearity. The Smith-Hazel (SH) index [15,16], a popular multi-trait selection index, is not recommended due to biased index coefficients and multicollinearity issues that erode real genetic gains [17–21]. Olivoto and Nardino [18] compared several multi-trait selection indices and proposed the novel multi-trait genotype–ideotype distance index (MGIDI) to select genotypes with desirable mean performances across multiple traits while overcoming the limitations of traditional linear indices. The use of multiple traits in the selection of superior yam genotypes has been reported for *D. rotundata* wherein FAI-BLUP (multi-trait index-based factor analysis and ideotype design) [22] and MGIDI method [23] were used, while the MGIDI method was used for *D. praehensilis* [24] species, but none for *D. alata* species. In this context, an attempt was made in this study to assess a panel of *D. alata* mapping population progenies as well as their parents for selection of desirable genotypes/ideotypes based on their agronomic and quality characteristics.

2. Materials and Methods

2.1. Plant Materials

This study included 280 half- and full-sib *D. alata* progenies and five parents (four females and one male) maintained by the Yam Breeding Unit at the International Institute

of Tropical Agriculture (IITA), Ibadan, Nigeria. The progenies represent four bi-parental mapping populations generated using the five parental lines. Each mapping population is represented as TDa1419, TDa1427, TDa1403, and TDa1402 (Table 1) with a variable number of progenies per family. This is related to the variable/viable number of seeds harvested from each mapping population followed by the poor germination rate [25]. Healthy tubers of each genotype were cut into mini-sets of 50 g, pre-treated with a fungicide (Mancozeb 80% WP) for 5 min, and dried under shade to prevent the rotting of cut surfaces of sets.

Table 1. Description of the planting material used in the experimentation.

Family Name	Parents		Number of Progenies Used
	Female	Male	
TDa1419	TDa99/00240	TDa0200012	138
TDa1427	TDa95/00328	TDa0200012	84
TDa1403	TDa0000005	TDa0200012	25
TDa1402	TDa0500015	TDa0200012	33
	Total		280

Note: A total of 280 progenies and five parents were used for making a total of 285 genotypes. TDa0200012 was a common male parent across the four populations.

2.2. Experimental Site and Design

The planting of the materials was carried out under field conditions at IITA, located in Ibadan, Nigeria (7°40′19.62″ N, 3°91′73.13″ E, 189 m above sea level). Ibadan represents a forest savannah transition zone and has a bimodal rainfall pattern with a total of 1305.55 mm and two distinct rainy and dry seasons. IITA experimental station represents a mean minimum and maximum air temperature of 22.7 °C and 30.4 °C, and a mean minimum and maximum relative humidity of 54.8% and 92.4%, respectively. The 285 genotypes were evaluated in two cropping seasons in 2021 and 2022. The mini-sets were planted using a 16 × 18 alpha-lattice design with three replications and three plants per plot. A spacing of 1 m × 1 m was used between ridges and plants on ridges. The trial plots were hand weeded to keep the plots weed free throughout the crop cycle.

2.3. Phenotypic Data Collection

Data were collected on eight traits (four agronomic and four quality traits) according to the standard operating protocol for the yam performance evaluation trial [26] and yam trait ontology (http://www.cropontology.org/ontology/CO_343/Yam; Accessed on 15 May 2021) (Table 2).

Table 2. List of the assessed traits.

Traits	Data Collection Period	Trait Type	Method
1. Plant Vigor (Pvig)	Three months after planting	Agronomic	Visual assessment of the strong and healthy growth of each plant per plot using a 1–3 scale where 1 = weak (75% of the plants or all the plants in a plot are small and have few leaves and thin vines), 2 = medium (intermediate or normal), and 3 = vigorous (75% of the plants or all the plants in a plot are robust with thick vines and leaves very well developed or with abundant foliage).
2. Number of tubers per plant (NTTP)	At harvest nine months after planting	Agronomic	By counting the total number of tubers harvested in a plot.
3. Tuber yield per plant (YPP)	At harvest nine months after planting	Agronomic	Using the weighting balance to record in kilograms the tuber's weight on a plant basis.

Table 2. *Cont.*

Traits	Data Collection Period	Trait Type	Method
4. Yam Anthracnose Disease severity (YAD)	Two–six months after planting	Agronomic	Severity score was assessed based on a visual assessment of the relative area of plant leaf surfaces affected by the fungus disease using a five-ordinal scale of 1–5 where 1 = no visible symptoms of anthracnose disease, 2 = few anthracnose spots or symptoms on 1 to ~25% of the plant, 3 = anthracnose symptoms covering ~26 to ~50% of the plant, 4 = symptoms on >51% of the plant, and 5 = severe necrosis and death of the plant.
5. Dry Matter Content (DMC)	Post-harvest	Quality	Chopping 100 g of fresh tuber flesh into shredded pieces, and then oven drying at 105 °C for 16 h, after which a constant weight was achieved.
6. Tuber Oxidation Browning (TBOxi)	Post-harvest	Quality	The intensity of tuber flesh oxidation (color change or browning of cut tuber flesh) assessed at different time intervals (0, 30, 60, and 180 min after cutting) using a Chroma meter (colorimeter) (CR-400, Konica Minolta, Japan).
7. Boiled Tuber Quality (BldT)	Post-harvest	Food quality	Scoring based on boiling quality at 30 min for fresh tubers (250–500 gm) of each genotype. Scoring based on components described in Table 3.
8. Pounded Tuber Quality (PndT)	Post-harvest	Food quality	Scoring based on poundability of the boiled yam. The components of pounded yam are described in Table 3.

Table 3. Sensory evaluation traits for boiled and pounded yam and scales of rating used by panelists in this study [27].

Traits	Rating Scale
Boiled yam	
Appearance	1 = Dislike extremely; 2 = Dislike; 3 = Neither like nor dislike; 4 = Like; 5 = Like extremely
Color	1 = Dislike extremely; 2 = Dislike; 3 = Neither like nor dislike; 4 = Like; 5 = Like extremely
Aroma	1 = Dislike extremely; 2 = Dislike; 3 = Neither like nor dislike; 4 = Like; 5 = Like extremely
Taste	1 = Dislike extremely; 2 = Dislike; 3 = Neither like nor dislike; 4 = Like; 5 = Like extremely
Texture	1 = Strong; 2 = Intermediate; 3 = Soft
Mealiness	1 = Soggy; 2 = Slightly mealy; 3 = Mealy
Pounded yam	
Appearance	1 = Dislike extremely; 2 = Dislike; 3 = Neither like nor dislike; 4 = Like; 5 = Like extremely
Aroma	1 = Dislike extremely; 2 = Dislike; 3 = Neither like nor dislike; 4 = Like; 5 = Like extremely
Color	1 = Dislike extremely; 2 = Dislike; 3 = Neither like nor dislike; 4 = Like; 5 = Like extremely
Mealiness	1 = Soggy (seedy); 2 = Slightly mealy; 3 = Mealy
Mouldability	1 = not mold well/sticky at hand; 2 = intermediate; 3 = easy to mold
Stretchability	1 = Not elastic/stretch at all; 2 = Intermediate; 3 = Stretch very well or very elastic
Taste	1 = Dislike extremely; 2 = Dislike; 3 = Neither like nor dislike; 4 = Like; 5 = Like extremely
Texture	1 = strong; 2 = intermediate; 3 = soft

The YAD severity score values were converted to percentages, and then used to estimate the area under disease progress curve (AUDPC) values as described by Forbes et al. [28]:

$$AUDPC = \sum_{i=1}^{N} \left(\frac{y_{i+yi+1}}{2} \right) (t_{i+1} - t_i) \quad (1)$$

where N is the number of observations, y_i is the disease severity at *i*th observation, and t_i is the time at *i*th observation.

The dry matter content was determined by chopping 100 g of fresh tuber flesh into shredded pieces, and then oven drying at 105 °C for 16 h, after which a constant weight was achieved. The percentage of the dry matter content was then estimated as follows:

$$\%\ dry\ matter\ content\ (DMC) = \frac{\text{Dry tuber flesh weight (g)}}{\text{Wet tuber flesh weight (g)}} \times 100 \quad (2)$$

The intensity of tuber flesh oxidation (color change or browning of cut tuber flesh) was assessed 180 min after cutting using a Chroma (colorimeter) meter (CR-400, Konica Minolta, Japan). The L^* (lightness), a^* (red/green coordinate), and b^* (yellow/blue coordinate) values were recorded. A reference of white and black porcelain tiles was used to calibrate the Chroma meter before each reading. The total delta color difference (ΔE*) among all three coordinates was determined following the formula [27]:

$$\Delta E^* = \left(L^* + a^* + b^*\right)^{1/2} \quad (3)$$

$$\text{Oxidative browning (TBOxi)} = F\Delta E^* - I\Delta E^* \quad (4)$$

where FΔE* is the final delta and IΔE* is the initial delta.

For boiled and pounded yam, healthy yam tubers were selected from each genotype, peeled and cut with a kitchen knife into roughly uniform-sized slices, and cooked in an electric yam cooking and pounding machine (QYP-6000, Qasa, Cheerfengly Industrial Co., Ltd., Taipei city, Taiwan) for 15–30 min or more (depending on the yam texture) with 380 mL of water. The cooked yam was divided into 2 parts whereas one part was used to assess the boiled properties. Thereafter, the remaining cooked yam was pounded within 3 min using the pounding machine. A total of ten panelists were used to evaluate the genotypes for the boiled and pounded characteristics. The panelists are IITA trained staff familiar with sensory evaluation techniques for several years. The sensory evaluation of both boiled and pounded yam was based on traits (Table 3) such as texture, mealiness, appearance, color, aroma, taste, stretchability, and mouldability [29].

2.4. Data Analysis

Statistical analyses were carried out using R software version 4.2.2 [30]. The MGIDI analysis was conducted based on each family, while the rest of the analysis was conducted by combining the four families. This allowed for overcoming the error effect due to the smaller number of progenies in some families while taking advantage of half-sib progenies in the selection process.

In the sensory evaluation, data for each trait were combined together and an index for boiled and pounded characteristics was generated using the MGIDI index [14,31]. The indices were then used for further analysis.

The analysis of variance (ANOVA) was performed and the best linear unbiased estimations were generated using Lme4 [30] as follows:

$$Y_{ijk} = \mu + G_h + S_i + (G_h * S_i) + R_{ij} + R(B_k) + \varepsilon_{jijk} \quad (5)$$

where Y_{ijk} is the value of the observed quantitative trait, μ is the population mean, G_h is the effect of the h_{th} genotypes, S_i is the effect of the i_{th} growing season, $(G_h * S_i)$ is the genotypes × season interaction associated with genotype h and season i, R_{ij} is the effect of the j_{th} replicate (superblock) in the season i_{th}, $R(B_k)$ is the effect of the k_{th} incomplete block within the j_{th} replicate, and ε_{hijk} is the experimental error.

The mean error ($\delta^2 e$), genotypic ($\delta^2 g$), and phenotypic ($\delta^2 p$) variances were calculated from the expected mean squares (EMSs) of ANOVA following Kresovich's [32] method where genotypes were considered as the random effect.

From the variance component analysis, the following genetic parameters were determined: genotypic variance, phenotypic variance, genotypic coefficients of variation, phenotypic coefficient of variation, and broad-sense heritability H^2, using the variability R package [33]:

$$H^2 = \left(\frac{\delta_g^2}{\delta_g^2 + \delta_{\frac{p}{n}}^2}\right) \times 100 \quad (6)$$

Phenotypic coefficient of variance:

$$(PCV) = \frac{\sqrt{\delta_p^2}}{Grand\ mean} \times 100 \quad (7)$$

Genotypic coefficient of variance:

$$(GCV) = \frac{\sqrt{\delta_g^2}}{Grand\ mean} \times 100 \quad (8)$$

where $\delta^2 g$ is the genotypic variance and $\delta^2 p$ is the phenotypic variance.

Broad-sense heritability (h^2) was categorized as 0–29% for low, 30–60% for intermediate, and greater than 60% for high according to Johnson et al. [34].

Pearson's correlation coefficient was generated among the estimated traits using the Corrplot R package v0.92 [30]. In order to identify the most discriminative traits with a high contribution to the observed genotypic variation, the principal component analysis (PCA) was performed using the FactoMineR package v2.6 [30]. Genotype grouping was carried out using the Gower dissimilarity matrix based on the Ward.D2 method [35]. The final hierarchical tree was built using the cluster package v2.1.4, and viewed using the dendextend package v1.16.0 [36] and the circlize package v0.4.15 [37] in R v4.2.2. The optimum number of clusters was identified using the NbClust package v3.0.1 [38].

To examine the relationships between variables, and determine the direct and indirect effect of agronomic and tuber quality traits on tuber yield and dry matter content for indirect selection, the path coefficient analysis was led using the lavaan package v0.6-14 [39] and the semPlot package v1.1.6 [40].

The MGIDI index [14] theory was based on four key steps: (i) rescaling the traits so that they all have a 0–100 range, (ii) factor analysis to account for the correlation structure and data dimensionality reduction, (iii) planning an ideotype based on known/desired trait values, and (iv) computing the distance between each genotype and the planned ideotype.

(i) Formula used to rescale traits:

$$rX_{ij} = \frac{\eta_{nj}}{\eta_{oj}} - \frac{\varphi_{nj}}{\varphi_{oj}} * (\Theta_{ij} - \eta_{nj}) + \eta_{nj} \quad (9)$$

where η_{nj} and φ_{nj} are the new maximum and minimum values for the trait j after rescaling, respectively, φ_{oj} and φ_{oj} are the original maximum and minimum values for the trait j, respectively, and h_{ij} is the original value for the jth trait of the ith genotype/treatment. The values for η_{nj} and φ_{nj} were chosen as follows. For the traits in which negative gains are desired, then $\eta_{nj} = 0$ and $\varphi_{nj} = 100$ should be used. For the traits in which positive gains are desired, then $\eta_{nj} = 100$ and $\varphi_{nj} = 0$ should be used [14,41]. In the rescaled two-way table (rX_{ij}), each column has a 0–100 range that considers the desired sense of selection (increase or decrease) and maintains the correlation structure of the original set of variables.

(ii) The factorial scores of each genotype were estimated using the rescaled values and by computing a factor analysis to group the correlated traits into factors as follows:

$$X = \mu + Lf + \varepsilon \quad (10)$$

where X is a $p\ x\ 1$ vector of rescaled observations, μ is a $p\ x\ 1$ vector of standardized means, L is a $p\ x\ f$ matrix of factorial loadings, f is a $p\ x\ 1$ vector of common factors, and ε is a $p\ x\ 1$ vector of residuals. Furthermore, the initial loadings were obtained by the traits having more than one eigenvalue that is acquired from the correlation matrix of *rXij*.

Then, final loadings were estimated using the varimax rotation criterion [14] as given by:

$$F = Z(A^T R^{-1})^T \quad (11)$$

where F is a $g \times f$ matrix with the factorial scores, Z is a $g \times p$ matrix with the standardized means (rescaled), A is a $p \times f$ matrix of canonical loadings, R is a $p \times p$ correlation matrix between the traits, and g, f, and p denote the number of test genotypes, factors retained (FA), and traits analyzed, respectively.

(iii) Ideotype planning

In designing the ideotype (ID), it was assumed that the selected genotype has the highest rescaled value (i.e., 100) across all the traits analyzed. Hence, the ID can be defined by $1 \times p$ vector ID such that ID = [100, 100, . . .,100]. In addition, the ID final scores were calculated according to the above formula (Equation (11)).

(iv) The MGIDI index

The MGIDI index was calculated based on the following formula using the mgidi() function included in the metan package. Additionally, the MGIDI index was calculated for ranking the genotypes based on the multi-trait, and not based on multicollinearity [42] as follows:

$$MGIDIi = \left[\sum_{j=1}^{f}(\gamma_{ij} - \gamma_j)^2\right]^{0.5} \quad (12)$$

where γ_{ij} is the score of the ith genotype in the *j*th factor (i = 1, 2, . . ., g; j = 1, 2, . . ., f) and γ_j is the *j*th score of the ideotype. The genotypes with the lowest *MGIDI* values, i.e., genotypes closer to the ID, exhibited the desired values for all the traits studied.

The proportion of the MGIDI index of the *i*th genotype explained by the *j*th factor (ω_{ij}) was used to show the strengths and weaknesses of genotypes and was computed as follows:

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=i}^{f}\sqrt{D_{ij}^2}} \quad (13)$$

where D_{ij} is the distance between the *i*th genotype and the ideotype for the *j*th factor. Low contributions of a factor specify that the traits within that factor are similar to the ideotype designed.

The radar chart was then generated using the radar chart function of the fmsb package [16]. This is a data visualization chart displaying multiple dimensions of multi-variate data represented on axes starting from the same point showing outliers and commonality clearly. The predicted genetic gain SG (%) was computed from the *MGIDI* index for each trait considering α% selection intensity as follows:

$$\text{SG (\%)} = \frac{(\bar{X}_s - \bar{X}_o)h^2}{\bar{X}_o} \quad (14)$$

where $\bar{X}_s$ is the mean of the selected genotypes, $\bar{X}_o$ is the mean of the original population, and h^2 is the heritability.

3. Results

3.1. Variability in Agronomic and Tuber Quality Traits

The analysis of variance (ANOVA) on combined data across all genotypes (285 genotypes) showed significant differences ($p < 0.001$) in mean squares for all the evaluated agronomic and quality traits (Table 4). The year's main effect was not significant ($p > 0.05$) for dry matter content (DMC), boiled tuber (BldT), and pounded yam tuber (PndT). However, the interaction among years and genotypes was significant ($p < 0.001$) for all traits except for plant vigor (Pvig). The response to YAD severity based on the AUDPC score varied from 133.75 to 362.92, with an average of 232.5, which implies that most of the genotypes were moderately resistant to the anthracnose disease. The average yield per plant (YPP) was 1.56 kg, ranging from 0.65 kg to 3.16 kg, while tuber oxidation varied from 2.15 to 29.76 with an average of 15.91, and dry matter content showed an average of 27.49%, ranging from 19% to 37.17%. The variation in oxidation and dry matter content detected the presence of genotypes with no oxidation and high dry matter content. The sensory evaluation showed an overall index mean of 2.99, ranging from 1.08 to 4.84 for boiled yam, while pounded yam displayed an average index of 4.38 ranging from 2.26 to 6.17 signifying that some genotypes displayed good boiled and pounded characteristics. The coefficients

of variation varied from 6.88% for dry matter content to 47.80% for the number of tubers per plant, indicating a high level of diversity among the genotypes.

Table 4. ANOVA representing the mean squares of variance across agronomic and quality traits of *D. alata* mapping populations for two years.

Source of Variation	Df	YAD	Pvig	NTPP	YPP	TOxB	DMC	BldT	PndT
Year	1	21,672.71 *	74.14 ***	25.44 **	5.72 *	1098.48 ***	1.86 NS	1.147 NS	0.88 NS
Genotypes	284	5950.54 ***	0.54 ***	2.29 ***	1.25 ***	158.84 ***	59.77 ***	2.97 ***	2.54 ***
Genotypes × Year	284	2416.67 ***	0.27 NS	1.46 ***	0.73 ***	69.08 ***	19.83 ***	2.06 ***	1.85 ***
Residual	1158	1386.8	0.243	0.747	0.469	13.83	3.582	0.34	1.07
Mean		232.5	1.87	1.81	1.56	15.91	27.49	2.99	4.38
Min		133.75	1	1	0.65	2.15	19	1.08	2.26
Max		362.92	3	8	3.16	29.76	37.17	4.84	6.17
CV (%)		16.01	26.34	47.80	44.06	23.47	6.88	19.48	23.63

*, **, *** Significant at $p < 0.05$, $p < 0.01$, and $p < 0.001$, respectively; NS: Non-significant. YAD: yam anthracnose disease; Pvig: plant vigor; NTPP: number of tubers per plant; YPP: yield per plant; TOxB: tuber oxidation browning; DMC: dry matter content; BldT: boiled tuber quality; PndT: pounded tuber quality. Note: genotypes represent 280 progenies and five parental lines.

3.2. Genetic Variability and Broad-Sense Heritability of Agronomic and Tuber Quality Traits

Genotypic and phenotypic variance components, genotypic and phenotypic coefficients of variation, and broad-sense heritability of agronomic and quality traits are presented in Table 5. Genotypic coefficients of variation (GCV) ranged from low (<10%) to high (>20%). The lowest GCV (7.78%) was observed for pounded yam quality, and the highest (24.21%) was observed for tuber flesh oxidative browning, while the phenotypic coefficient of variation (PCV) varied from 11.48% for tuber dry matter content and 34.10% for number of tubers per plant. Broad-sense heritability (H^2) ranged from 27% for pounded yam to 67% for dry matter content. A moderate H^2 (30% < H^2 > 60%) was observed for all the other traits.

Table 5. Genotypic coefficients, phenotypic coefficients, and broad-sense heritability of agronomic and quality traits of *D. alata* genotypes across two cropping seasons.

Combined	Genetic Parameters					
Traits	**δ^2p**	**δ^2g**	**δ^2e**	**PCV (%)**	**GCV (%)**	**H^2**
YAD	993.67	590.64	1387.88	13.55	10.45	0.59
Pvig	0.089	0.04	0.24	15.93	11.15	0.49
NTPP	0.38	0.14	0.73	34.10	20.57	0.36
YPP	0.21	0.08	0.46	29.28	18.80	0.41
TOxB	26.31	14.71	13.63	32.37	24.21	0.56
DMC	9.98	6.70	3.52	11.48	9.41	0.67
BldT	0.5	0.15	0.25	23.54	13.12	0.31
PndT	0.42	0.12	0.35	14.85	7.78	0.27

YAD: yam anthracnose disease; Pvig: plant vigor; NTPP: number of tubers per plant; YPP: yield per plant; TOxB: tuber oxidation browning; DMC: dry matter content; BldT: boiled tuber quality; PndT: pounded tuber quality.

3.3. Principal Component Analysis

The principal component analysis was based on a combined analysis of eight traits for 285 water yam genotypes. The first four principal components (PCs) accounted for 73.51% of the total phenotypic variation (Table 6; Figure 1A). The first PC explained 23.04% of the variation and was associated with tuber oxidation browning, dry matter content, and boiled tuber quality. The second PC accounted for 20.4% with plant vigor and yield per plant as major contributors, while 17.12% of the total variation was explained by the third PC with the number of tubers per plant and tuber pounded quality as major contributors. The fourth PC accounted for 12.95% of the variation explained majorly by the yam anthracnose disease. The variable contribution plot (Figure 1B) indicated that for combined PC1 and PC2 explaining 43% of variability, traits such as number of tubers per

plant, pounded tuber quality, and yam anthracnose disease have a low contribution to the variability. However, tuber yield per plant, plant vigor, and boiled tuber have a high contribution, while tuber oxidation and dry matter content have a moderate contribution The TOxB, BldT, and PndT variables are grouped around the PC1 axis, which represents the yam quality axis. PC2 could be considered as the quantity with plant vigor and yield as the main contributor variables.

Table 6. Principal component analysis and contributions of agronomic and tuber quality traits to the genetic variability.

Variables	PC1	PC2	PC3	PC4
Yam Anthracnose Disease	−0.202	−0.491	0.191	0.680
Plant vigor	−0.145	0.764	0.194	0.134
Number of tubers per plant	−0.268	0.246	0.610	0.441
Yield per plant	0.232	0.836	−0.077	0.141
Tuber oxidation browning	0.652	−0.127	−0.146	0.439
Dry matter content	−0.663	−0.119	0.461	−0.227
Boiled tuber quality	0.763	−0.093	0.427	−0.073
Pounded tuber quality	0.457	−0.091	0.708	−0.303
Eigenvalues	1.358	1.278	1.170	1.018
Variance (%)	23.04	20.4	17.12	12.95
Cumulative variance (%)	23.04	43.44	60.56	73.51

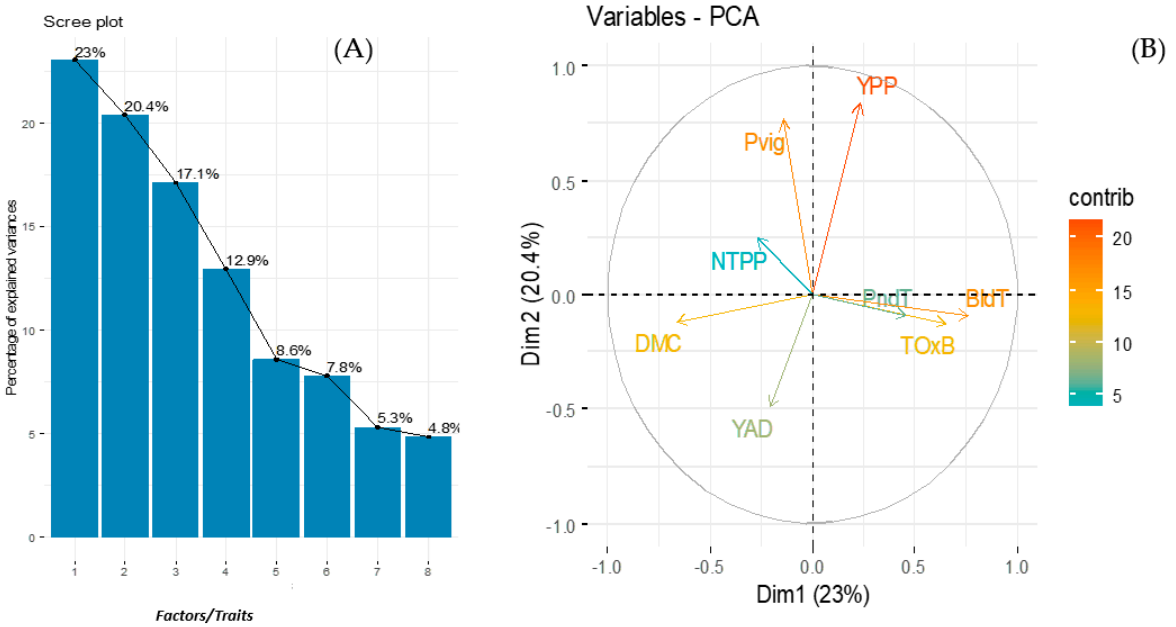


Figure 1. PCA scree plot representing the number of PCs obtained for eight variables (**A**) and a plot showing the total contribution (**B**) of variables accounting for the variability in PC1 and PC2. YAD: yam anthracnose disease; Pvig: plant vigor; NTPP: number of tubers per plant; YPP: yield per plant; TOxB: tuber oxidation browning; DMC: dry matter content; BldT: boiled tuber quality; PndT: pounded tuber quality.

3.4. Relationships among Agronomic and Tuber Quality Traits

Pearson's correlation coefficients are presented in Figure 2. A significant positive correlation indicates a parallel direction in trait performance in which any improvement in one trait results in an equal improvement in the correlated trait. A significant positive correlation was observed between tuber yield per plant with plant vigor ($r = 0.44$, $p < 0.001$) and number of tubers per plant ($r = 0.12$, $p < 0.05$). A significant negative correlation was

observed between dry matter content and tuber yield per plant (r = −027), tuber oxidation browning (r = −0.36) and boiled tuber quality (r = −0.26) at $p < 0.001$. YAD severity showed a significant negative correlation with tuber yield per plant (r = −0.29, $p < 0.001$) and plant vigor (r = −0.12, $p < 0.05$), while a positive correlation was observed between YAD and number of tubers per plant (r = 0.14, $p < 0.05$). A significant positive relationship was also observed between boiled tuber quality with tuber oxidation (r = 0.31) and pounded tuber quality (r = 0.50) at $p < 0.001$.

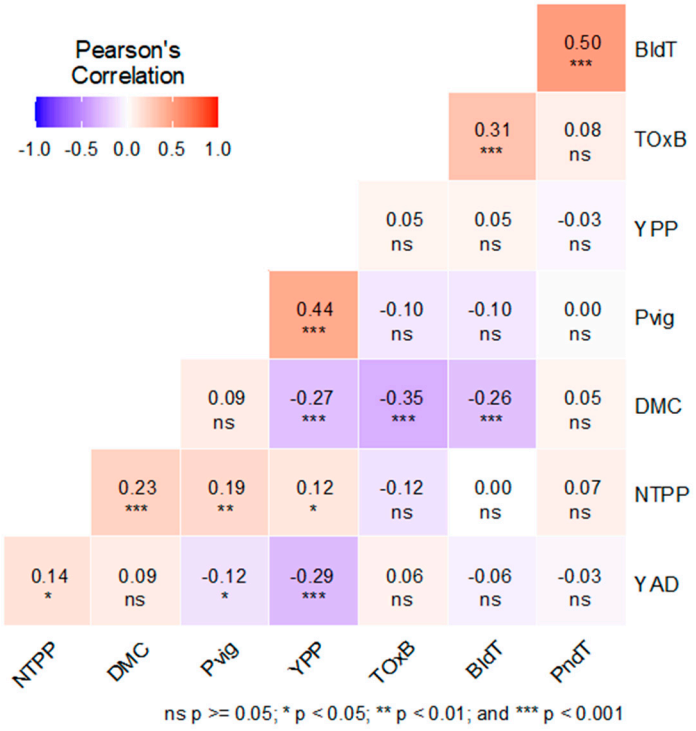


Figure 2. Correlation coefficients among agronomic and tuber quality traits. YAD: yam anthracnose disease; Pvig: plant vigor; NTPP: number of tubers per plant; YPP: yield per plant; TOxB: tuber oxidation browning; DMC: dry matter content; BldT: boiled tuber quality; PndT: pounded tuber quality.

3.5. Hierarchical Clustering Based on Grouping of Yam Genotypes

Hierarchical clustering based on four agronomic and four quality traits grouped 285 yam genotypes into three clusters (Figure 3; Supplementary Table S1). Cluster 1 (C1) comprised progenies of Family1 (27), Family2 (24), Family3 (13), Family4 (15), and the male parent. These genotypes are characterized by moderate resistance to YAD (score 3), high plant vigor (score 3), high number of tubers per plant (3–7), moderate tuber yield per plant (1.5 kg–1.99 kg/plant), moderate tuber flesh oxidation (5–9.99), and high dry matter content (DMC > 30).

Cluster 2 (C2) had the largest cluster membership, which comprised progenies of Family1 (72), Family2 (33), Family3 (6), Family4 (2), and the female parents of Families 2 and 3. These genotypes are characterized by high tuber yield per plant (yield > 2 kg), moderate resistance to YAD (score 3), high plant vigor (score 3), low dry matter content (DMC < 25), and moderate yam pounded quality (PndT < 5). Similarly, Cluster 3 (C3) comprised progenies of Family1 (39), Family2 (27), Family3 (6), Family4 (16), and the female parents of Families 1 and 4. These genotypes are characterized by low susceptibility to YAD (score = 2), moderate plant vigor (2), moderate number of tubers per plant (NTPP = 2), moderate tuber yield per plant (1.5 < 1.99), low tuber flesh oxidation (<5), high dry matter content (>kg), high yam tuber boiled quality (>2.5), and high yam pounded quality (3 < yield ≤ 5).

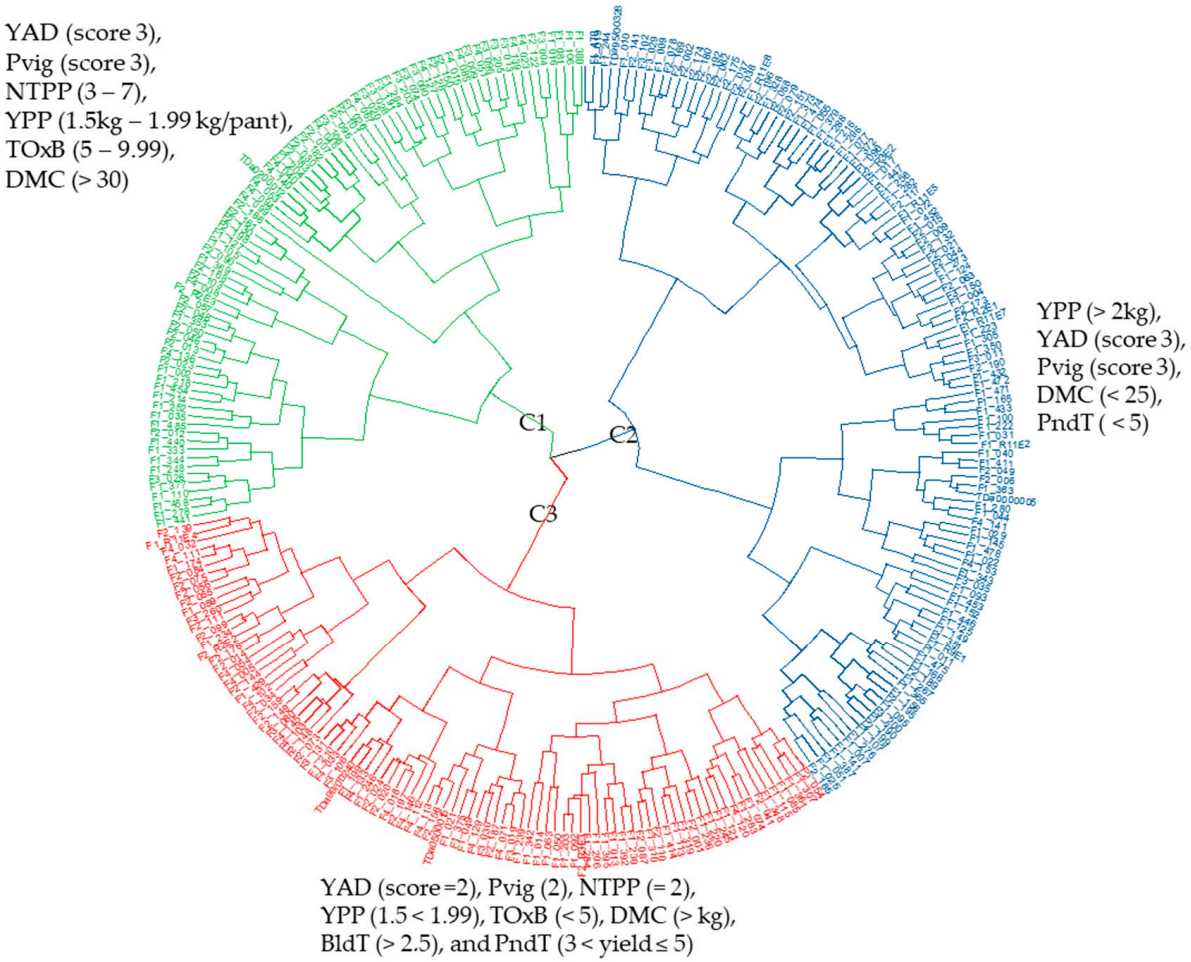


Figure 3. Hierarchical clustering that grouped 285 yam genotypes into three clusters using eight traits.

3.6. Path Analysis among Assessed Traits of Four Bi-parental Mapping Populations

The path analysis depicting the direct effect of all six traits on tuber yield and dry matter content for indirect selection is presented in Figure 4. The path analysis was carried out following the model where tuber yield and dry matter content were considered as response variables against correlated agronomic and tuber quality parameters (yam anthracnose disease severity, plant vigor, number of tubers per plant, tuber oxidation, boiled tuber quality, and pounded tuber quality). Yam anthracnose disease severity and plant vigor significantly predicted tuber yield (b = −0.004, SE = 0.001, $p < 0.001$; b = 0.62, SE = 0.08, $p < 0.001$; b = 0.89, SE = 0.28, respectively) such that a unit increase in anthracnose severity was associated with a 0.004 unit decrease in tuber yield, and a unit increase in plant vigor was associated with a 0.62 unit increase in tuber yield. Similarly, the number of tubers per plant, tuber oxidation browning, tuber boiled quality, and tuber pounded quality significantly predicted tuber dry matter content (b = 0.89, SE = 0.28, $p = 0.001$; b = −0.16, SE = 0.035, $p < 0.001$; b = −1.225, SE = 0.29, $p < 0.001$; b = 0.95, SE = 0.30, $p = 0.001$, respectively). A unit increase in tubers per plot and tuber pounded quality was associated with a 0.89 unit and a 0.95 unit increase in tuber dry matter content, respectively, while a unit increase in tuber oxidation browning and tuber boiled quality was associated with a 0.16 unit and a 1.225 unit decrease in tuber dry matter content, respectively.

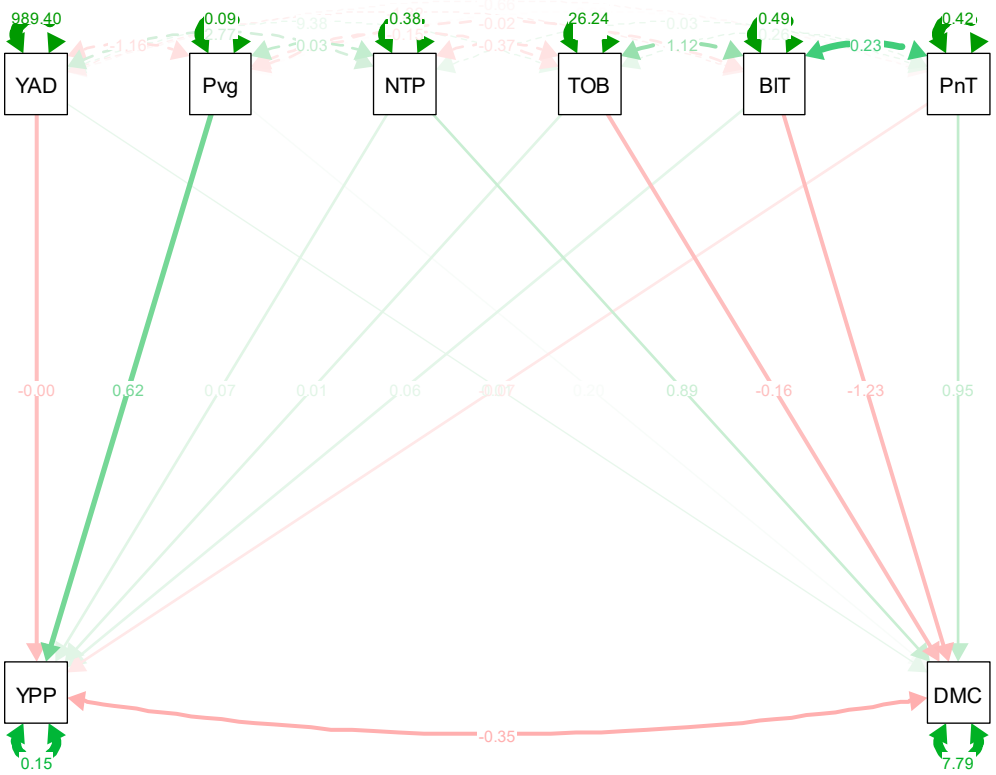


Figure 4. Path coefficient analysis among eight evaluated traits using tuber yield per plant and dry matter content as dependent variables. YAD: yam anthracnose disease; Pvig: plant vigor; NTPP: number of tubers per plant; YPP: yield per plant; TOxB: tuber oxidation browning; DMC: dry matter content; BldT: boiled tuber quality; PndT: pounded tuber quality.

3.7. Selection of Genotypes Based on the Multi-Trait Genotype–Ideotype Distance Index (MGIDI)

The best performing yam genotypes from each family were determined using the factor analysis, in which the traits were grouped into four factors (Supplementary Table S2).

Based on the MGIDI index, four traits showed the desired genetic gains such as plant vigor, number of tubers per plant, yield per plant, and dry matter content across all the families (Supplementary Table S2). The remaining four traits that showed an undesired gain in selection are yam anthracnose disease, tuber oxidation browning, boiled yam quality, and pounded yam quality across all the families. The dry matter content in F4 showed an undesired selection gain. The MGIDI index provided the total genetic gains of 56.3%, 85.55%, 43.43%, and 45.2% for F1, F2, F3, and F4, respectively for the four traits that showed the desired genetic gains, while the total genetic gains were −52.46%, −72.96%, −85.11%, and −45.16% for F1, F2, F3, and F4, respectively for the four traits that showed an undesired selection gain (Supplementary Table S2).

The MGIDI analysis identified twenty-one, nine, four, and five best performing genotypes in F1 (Figure 5a), F2 (Figure 5b), F3 (Figure 5c), and F4 (Figure 5d) families, respectively. The selected genotypes displayed the potential for simultaneous improvement of the studied traits in the water yam improvement program.

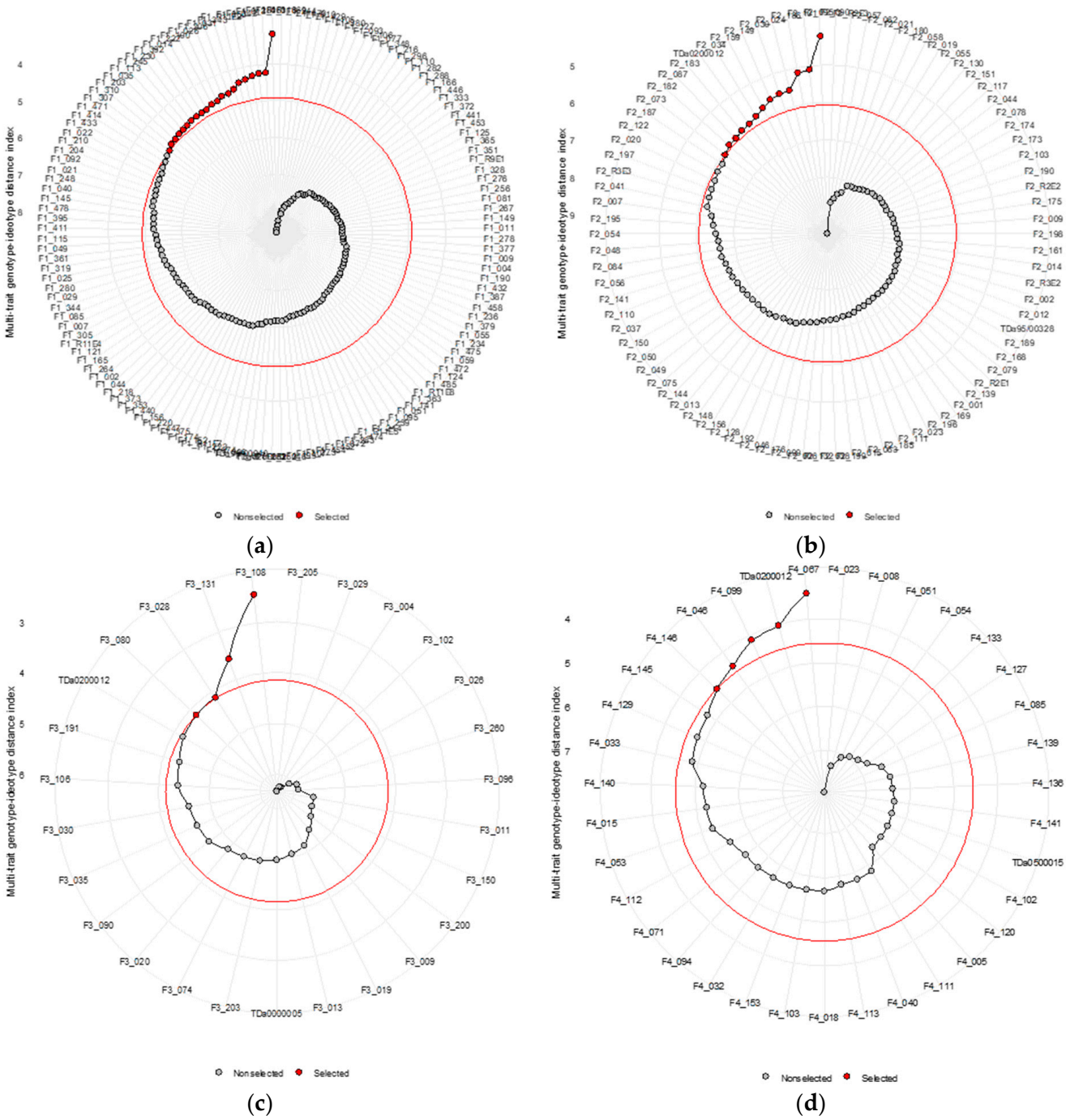
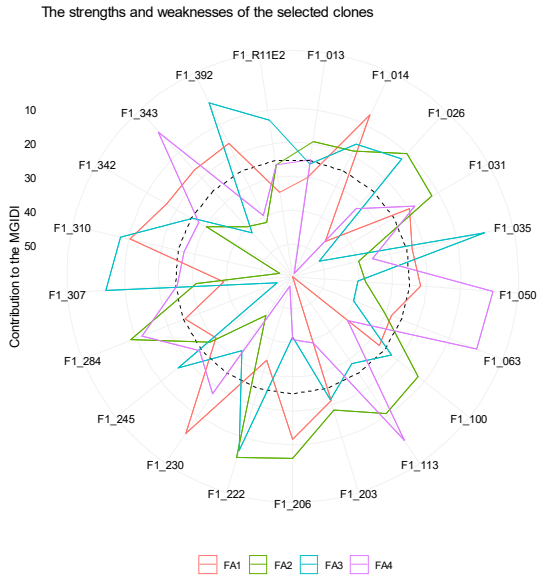


Figure 5. Ranking of selected genotypes based on the MGIDI analysis. The selected genotypes are shown as red dots, while the unselected genotypes are in black circles. The red circle represents the cut-off point according to the selection pressure. (**a**) Family1 (F1), (**b**) Family2 (F2), (**c**) Family3 (F3), and (**d**) Family4 (F4).

3.8. Strengths and Weaknesses of Selected Genotypes

Figure 6 illustrates the strengths and weaknesses of the selected genotypes from the four families. The MGIDI contribution for each genotype was ranked between the most contributing factor (FA) (close to the plot center) and least contributing factor (away from the plot center). The traits were grouped into four (Figure 6a), three (Figure 6b), two (Figure 6c), and three (Figure 6d) factors for F1, F2, F3, and F4 families, respectively. In F1, the genotypes (F1_014, F1_031, F1_050, F1_203, F1_206, F1_230, F1_310, F1_342,

F1_343, and F1_392) associated with FA1 displayed strengths based on plant vigor, number of tubers per plant, and dry matter content (Supplementary Table S3; Figure 6a), while genotypes (F1_013, F1_014, F1_026, F1_031, F1_100, F1_113, F1_203, F1_206, F1_222, and F1_284) related to FA2 showed strengths based on traits such as dry matter content, boiled tuber quality, and pounded tuber quality. Similarly, genotypes (F1_014, F1_026, F1_035, F1_100, F1_203, F1_222, F1_245, F1_307, F1_310, F1_392, and F1_R11E2) showed strengths linked to FA3 based on resistance to yam anthracnose disease and good yield per plant, while genotypes (F1_031, F1_050, F1_063, F1_113, F1_230, F1_245, F1_284, and F1_343) were associated with FA4 based on only tuber oxidation browning. In F2, the genotypes (F2_030, F2_034, F2_073, F2_087, F2_149, F2_159, F2_182, and F2_183) linked to FA1 showed strengths based on number of tubers per plant, tuber oxidation browning, boiled and pounded tuber quality (Supplementary Table S3; Figure 6b), while genotypes (F2_087, F2_101, F2_183, and F2_186) related to FA2 showed strengths based on traits such as resistance to anthracnose disease and good tuber yield per plant. Similarly, genotypes (F2_027, F2_030, F2_073, F2_095, F2_180, and TDa0200012) related to FA3 showed strengths for plant vigor and dry matter content. In family 3 (F3), the genotype F3_080 associated with FA1 showed strengths based on resistance to anthracnose disease, number of tubers per plant, tuber yield per plant, tuber oxidation browning, boiled and pounded tuber quality (Supplementary Table S3; Figure 6c), while genotypes (F3_108, F3_131, and F3_028) associated with FA2 showed strengths based on plant vigor, tuber yield per plant, and dry matter content. For family 4 (F4), the genotypes (F4_096 and F4_146) associated with FA1 displayed strengths based on resistance to anthracnose disease, plant vigor, and boiled tuber quality (Supplementary Table S3; Figure 6d), while the genotype F4_146 linked to FA2 showed strengths based on number of tubers per plant and tuber oxidation browning. Furthermore, the genotypes (F4_046, F4_067, and TDa020012) showed strengths for tuber yield per plant, dry matter content, and pounded tuber quality linked to FA3.



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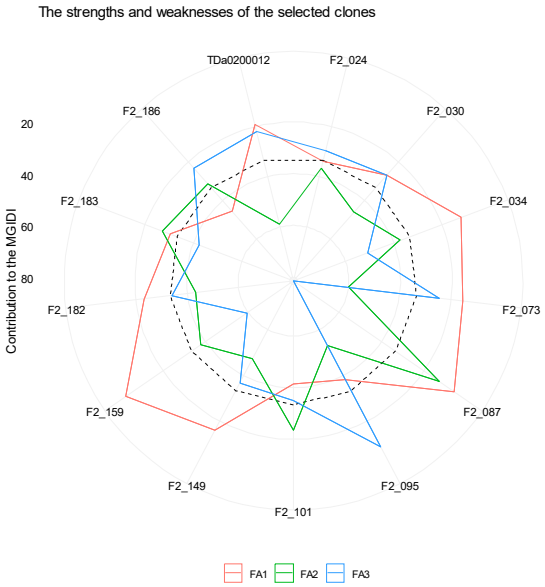

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Figure 6. *Cont.*

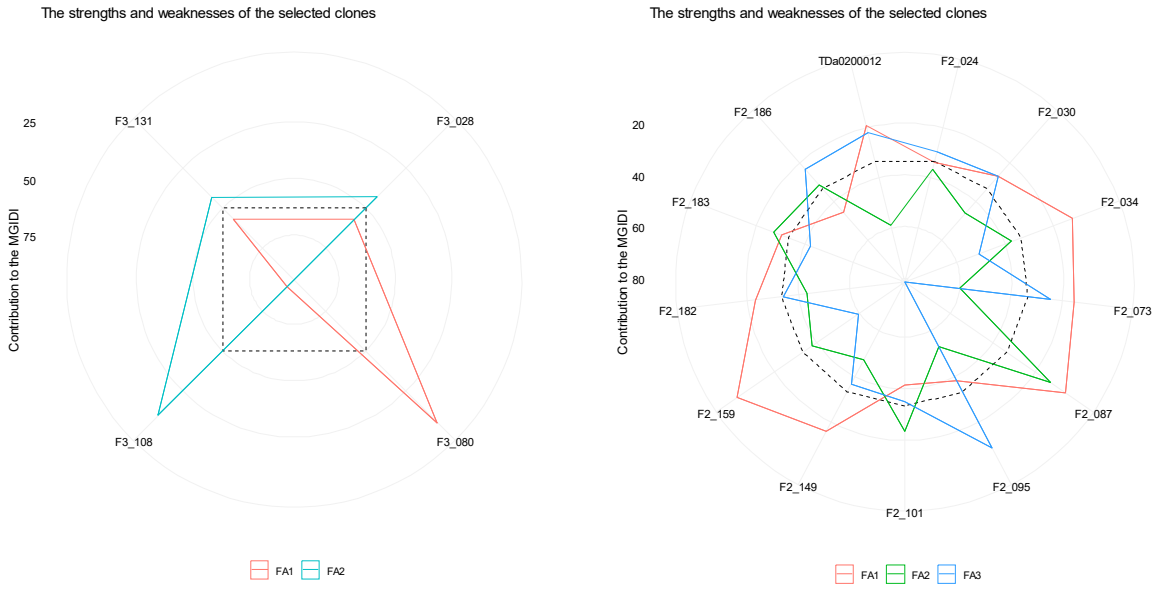

Figure 6. Radar chart with relative scale (0–100%) across eight variables displaying strengths and weaknesses of the selected genotypes in each family based on the MGIDI analysis. The black dashed line at the center displays the theoretical value if all the factors contributed equally. (**a**) F1, (**b**) F2, (**c**) F3, and (**d**) F4.

3.9. Best Selected Genotypes/Ideotypes through Combining the Selected Individuals from Four Families, Their Strengths, and Weaknesses

The 39 best performing genotypes identified from four families were combined to select the best ideotypes/genotypes using the MGIDI analysis. This resulted in the selection of six ideotypes with the potential for positive gains in water yam breeding program (Table 7; Figure 7). The average communality was 0.69 with three factors contributing to their selection. The traits such as yam anthracnose disease, yield per plant, boiled tuber quality, and pounded tuber quality constituted the first factor. The second factor was associated with the number of tubers per plant and tuber oxidation, while the third factor was related to plant vigor and dry matter content. The total genetic gain was 16.56% and 33.59% for traits that showed undesired (decrease) and desired (increase) selection gains, respectively.

Table 7. Factorial loadings, communalities, uniqueness, and predicted genetic gains based on the multi-trait genotype–ideotype distance index for 39 best performing genotypes (bold values represent traits with high contribution to each factor).

VAR	FA1	FA2	FA3	Communality	Uniquenesses	Genetic Gain (%)	Sense	Goal
YAD	−0.81	−0.29	−0.21	0.78	0.22	11.29	decrease	0
Pvig	0.08	0.22	−0.81	0.71	0.29	9.75	increase	100
NTPP	0.03	0.91	0.11	0.85	0.15	19.9	increase	100
YPP	−0.52	−0.08	−0.45	0.48	0.52	−7.62	increase	0
TOxB	0.34	−0.53	0.44	0.58	0.42	30.13	decrease	0
DMC	0.2	0.26	0.7	0.6	0.4	1.81	increase	100
BldT	0.71	−0.5	0.14	0.77	0.23	−5.11	decrease	100
PndT	0.8	−0.26	−0.12	0.72	0.28	−19.74	decrease	100
		Average communality		0.69				
		Total decrease			16.56			
		Total increase			33.59			

YAD: yam anthracnose disease; Pvig: plant vigor; NTPP: number of tubers per plant; YPP: yield per plant; TOxB: tuber oxidation browning; DMC: dry matter content; BldT: boiled tuber quality; PndT: pounded tuber quality.

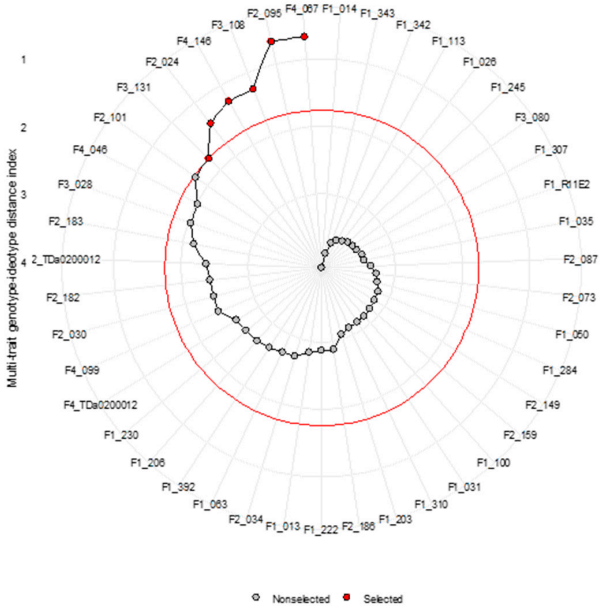

Figure 7. Ranking of selected genotypes using the MGIDI analysis. The selected genotypes are shown as red dots, while the unselected genotypes are in black circles. The red circle represents the cut-off point based on the selection pressure.

The genotypes (F2_024, F2_095, F3_108, and F3_131) related to FA1 showed strengths based on plant vigor, tuber yield per plant, and tuber oxidation browning, whereas the genotypes (F4_067 and F2_095) associated with FA2 displayed strengths based on number of tubers per plant, dry matter content, and boiled tuber quality. The genotypes (F4_146, F3_131, and F3_108) linked to FA3 showed strengths based on resistance to anthracnose disease and good pounded tuber quality (Table 8; Figure 8).

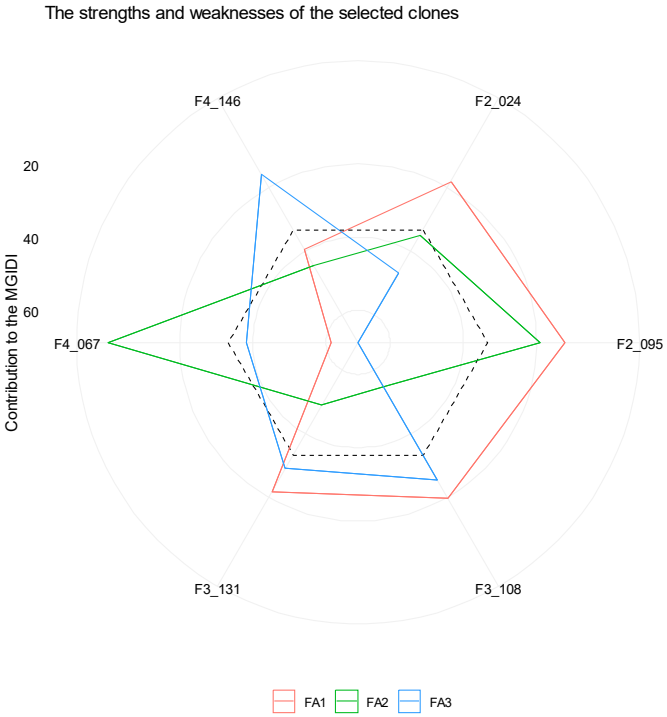

Figure 8. Radar chart with relative scale (0–100%) across eight variables displaying strengths and weaknesses of the six best selected genotypes. The black dashed line at the center displays the theoretical value if all the factors contributed equally.

Table 8. Factorial loadings, communalities, and uniqueness based on the multi-trait genotype–ideotype distance index for the six best genotypes selected (bold values represent traits with high contribution to each component).

VAR	FA1	FA2	FA3	Communality	Uniquenesses
YAD	0.52508	0.476091	**−0.65446**	0.930687	0.069313
Pvig	**−0.94958**	0.152789	−0.03541	0.926292	0.073708
NTPP	0.064233	**−0.9762**	−0.02321	0.957636	0.042364
YPP	**−0.90556**	−0.32666	−0.04856	0.929107	0.070893
TOxB	**−0.77529**	0.300607	0.307627	0.786067	0.213933
DMC	−0.1216	**−0.88398**	0.248702	0.858064	0.141936
BldT	0.407909	**−0.57433**	0.249473	0.558478	0.441522
PndT	−0.04828	0.108744	**−0.91704**	0.855124	0.144876

YAD: yam anthracnose disease; Pvig: plant vigor; NTPP: number of tubers per plant; YPP: yield per plant; TOxB: tuber oxidation browning; DMC: dry matter content; BldT: boiled tuber quality; PndT: pounded tuber quality.

4. Discussion

The present study aimed to evaluate the performance of 280 progenies representing four bi-parental mapping populations as well as five parental lines based on eight phenotypic traits. It is common for plant breeders to strive for developing or selecting the best performing new genotype or an ideotype that can show genetic progress by integrating multiple desirable characteristics. Various selection indices and multi-trait methods are commonly employed for the purpose of clustering traits and the selection of superior genotypes [43]. Two methods are commonly used in plant breeding programs: the creation of genetic variability by crossing diverse parents, followed by the selection of suitable individuals among the segregating progenies [44,45]. In this study, different multi-variate analyses were used to first group the genotypes based on eight traits, and then the best performing genotypes were selected. The analysis of variance showed significant variations among the genotypes across all eight traits indicating a high level of diversity among the genotypes. A similar genetic differentiation among yam genotypes showing high coefficients of variation (CVs > 20) for agronomic and quality traits was reported by Cao et al. [45], Adejumobi et al. [46], and Adewumi et al. [24].

The lower GCV observed in this study for traits such as dry matter content and pounded tuber quality was also reported in studies by Norman et al. [47], Evans et al. [48], and Asfwa et al. [49], which implies that these traits can only be improved using selection methods that are not under environmental influence such as marker assisted selection. The higher phenotypic variance observed for YAD in this study may be due to genetic factors such as observed higher heritability (0.59) than non-genetic factors suggesting that the selection progress for YAD could be achieved faster compared to other traits. Norman et al. [50] also reported a similar finding for YAD.

Understanding the correlation between specific traits is important for a breeding program [51]. A challenging aspect in yam improvement is the slow growth cycle of the genotypes. Indirect selection of correlated traits poses great benefits in choosing yam genotypes. In this study, Pearson's correlation analysis was used to assess the correlation between agronomic and quality traits with tuber yield. The results delineated the possibility of indirect selection of traits that showed a positive correlation, such as yield and its related traits (plant vigor and number of tubers per plant) with tuber quality traits. A positive correlation between yield and yield related traits has also been reported by other researchers in yam (Agre et al. [23], Adewumi et al. [24], Adejumobi et al. [46], Asfaw et al. [49], Agre et al. [35], and Padhan et al. [52]). Similarly, a positive correlation was observed between dry matter content and the number of tubers per plant in all the families except for F4. Dry matter content is a very important trait for consumer acceptability of yams [27]. Lebot et al. [53] and Martin [54] stated that *D. alata* varieties are characterized by high dry matter, starch, and amylose contents for consumer acceptability. However, *D. alata* genotypes are generally characterized as low dry matter compared to white yam (*D. rotundata*) genotypes resulting in its less preference by farmers and end users [9]. Improving the

quality traits of *D. alata* is an ongoing challenge to yam breeders and researchers [36]. In this study, hierarchical clustering based on eight phenotypic traits grouped several water yam genotypes with higher yield potential, lower tuber flesh oxidation, higher dry matter content, good boiled and pounded tuber qualities, as well as high resistance to anthracnose disease severity. The cluster analysis revealed rich information for breeders, especially in the selection of parents from each cluster aimed at improving particular trait (s).

It is well known that the identification of best performing genotypes based on multiple traits is challenging. Therefore, the MGIDI index is a unique selection technique for screening genotypes using multiple traits, as it is free from multicollinearity issues [15], and uses distance between genotypes for selection of the best genotype/ideotype [55]. This is a powerful tool in identifying genotypes with better mean performance and desired genetic gain, as well as in estimating the strengths and weaknesses of selected genotypes [56].

In this study, we followed a two-pronged approach in which the multiple trait-based selection of genotypes was first carried out from each family by ranking the genotypes based on eight traits. This resulted in the selection of a total of 39 genotypes including the male parent TDa0200012. Later, the MGIDI analysis was carried out on the selected 39 genotypes that ranked the six best performing genotypes (F4_067, F2_095, F3_108, F4_146, F2_024, and F3_131) based on these eight traits. The MGIDI model-based analysis was also used in other crops such as Bush yam [24], maize hybrids [56], Norway Spruce [57], wheat [58], white Guinea yam [22], and eggplant [59].

The graphic representation of strengths and weaknesses of the selected genotypes obtained from the MGIDI index is an important tool that demonstrates the proportion contribution of each factor towards the selection of best performing genotypes. The availability of such information on the strengths and weaknesses of genotypes helps breeders in selecting putative parents in their breeding programs.

5. Conclusions

In this study, a total of 280 progenies and their parents were assessed on eight phenotypic (four agronomic and four quality) traits. The study delineated the variation in the performance of these genotypes across all the traits. A moderate heritability was observed for most of the evaluated parameters. The correlation and path analysis revealed the possibility to indirectly select the correlated traits. The progenies and parental lines were grouped in three clusters with distinct characteristics. The MGIDI index has proven to be a powerful tool in the selection and identification of high-performing *D. alata* genotypes/ideotypes. These promising genotypes could be explored as progenitors in *D. alata* improvement programs targeting good agronomic and quality traits for farmers and end users. Further experiments such as multi-environment evaluation are necessary to confirm the stability of these selected genotypes. Additionally, we recommend genotyping of all four mapping populations, specifically TDa1419 and TDa1427, for dissecting traits of interest in the water yam crop improvement program.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/agronomy14010128/s1. Table S1: Description of clusters for eight quantitative traits of *D. alata* genotypes, Table S2: Factorial loadings, communalities, uniqueness, and predicted genetic gains based on the multi-trait genotype–ideotype distance index for each family, Table S3: Factorial loadings, communalities, and uniqueness of genotypes selected per family based on the multi-trait genotype–ideotype distance index (MGIDI).

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Data Availability Statement: All data supporting the findings in this study are available within this article and supplementary files. The metadata used in MGIDI analyses are available on request to the corresponding authors.

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Conflicts of Interest: The authors declare no conflicts of interest.

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