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Multi-Trait Selection Index for Superior Agronomic and Tuber Quality Traits in Bush Yam (*Dioscorea praehensilis* Benth.)

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Abstract: *Dioscorea praehensilis* Benth. is a semi-wild yam species and a valuable source of resistance trait genes. To access the agronomic and tuber quality performance, eleven quantitative phenotypic traits were used to discriminate and identify promising accessions among 162 accessions of *D. praehensilis* collected in Ghana. Significant and high genetic variability ($p < 0.001$) for all eleven quantitative traits was found among the evaluated accessions. Moderate broad-sense heritability (H^2) (30–60%) was observed for all the evaluated quantitative traits except the response to YMV and tuber hardness. The accessions were clustered into three groups; each cluster displayed genotypes with good potentiality for the different traits evaluated. Path coefficient analysis revealed positive contributions ($p < 0.01$) of the number of tubers per plant, tuber length, tuber width, stem internode length, number of internodes, and tuber flesh hardness to the total tuber weight per plant. Through the multi-trait genotype–ideotype distance index (MGIDI), 24 accessions were identified from the 162 evaluated accessions as top-ranking and could be used as progenitors for trait introgression. The results of this study provide insight for future yam breeding and improvement programs in West Africa.

Keywords: *D. praehensilis*; quantitative traits; MGIDI index; trait profiling; multi-trait selection

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1. Introduction

Yam (*Dioscorea* species) is a popular tropical and subtropical food crop. It is widely grown in West Africa, contributing significantly to food security and poverty reduction [1,2]. West Africa accounts for more than 95% of global yam production, with Nigeria, Ghana, Côte d'Ivoire, and Benin as the leading producers [3].

D. praehensilis is an edible semi-cultivated wild yam species used chiefly to ease food insecurity among local farmers in forest zones of West African nations such as Nigeria, Ghana, Benin, and Togo during lean seasons [4,5]. *D. praehensilis* has a high yield potential, pest and disease tolerance, in-soil storage ability, and the capacity to blossom and fruit profusely, making it ideal for hybridization in breeding programs [5].

Despite these significances, the economic values of *D. praehensilis* have not been fully realized due to the oxidative browning and hardening of tuber flesh a few days after harvesting, resulting in poor utilization and under-exploitation of its potential [5]. The germplasm collection and the estimation of morphological divergence in *D. praehensilis*, compared to widely cultivated and utilized yam species such as *D. rotundata* and *D. alata*, are partial and not comprehensive, especially in Ghana. These factors have resulted in rapid genetic erosion and the risk of extinction of this valuable yam species [5]. The information

on tuber culinary quality traits, yield performance in a natural environment, and disease resistance of *D. praehensilis* is highly deficient and not fully documented. Identifying accessions with high-yielding attributes, tolerance to yam mosaic virus (YMV), and good post-harvest tuber qualities that farmers and consumers prefer will contribute to unlocking the genetic potential of bush yam.

Several studies have been carried out on yam using morphological descriptors [6–9]. Many authors [10–13] have reported the effectiveness of morphological markers in assessing genetic diversity in *D. alata*. In Guinea yams (*D. rotundata* and *D. cayenensis*), morphological traits have been successfully employed in evaluating genetic variability [14,15]. The application of morphological descriptors has also been used in *D. bulbifera* [16]. In addition, the genetic diversity among 140 accessions of *D. trifida* was successfully determined in the municipality of Caapiranga, in the central Amazon region of Brazil, using 64 morphological descriptors [17]. The genetic diversity in *D. praehensilis* germplasm in Ghana has been less explored, and there is also uncertainty about the applicability of morphological traits to evaluate the genetic diversity in the crop. Hence, a comprehensive analysis of the phenotypic diversity of *D. praehensilis* germplasm indigenous to Ghana may be critical for identifying and developing cultivars with economically valuable traits and for the conservation and sustainable utilization of the species.

In any crop improvement initiative, breeders often keep in mind a combination of attributes that, when combined into a genotype, would result in excellent performance; this genotype is referred to as an ideotype [18]. The goal of ideotype design is to improve crop performance by selecting genotypes based on many attributes at the same time [19]. The Smith–Hazel (SH) index is a linear selection index frequently used by breeders for multi-trait selection [20,21]. However, in the case of the SH index, the presence of multicollinearity and the difficulties in assigning economic weightage to the qualities under evaluation can have an impact on genetic gain [19]. To address these shortcomings, a multivariate selection index, the multi-trait genotype–ideotype distance index (MGIDI), has been created [19]. This index accounts for multi-collinearity and favorably selects all variables under consideration, resulting in significant genetic gain [19]. The application of MGIDI as a multi-trait selection index has been reported for white Guinea yam (*D. rotundata*) [22], but limited information is available on *D. praehensilis*.

The objectives of the present study were: (i) to quantify the agronomic and tuber quality trait performance of *D. praehensilis* accessions in Ghana, and (ii) to identify *D. praehensilis* accessions with higher agronomic and yield-related traits for future genetic improvement initiatives.

2. Materials and Methods

2.1. Experimental Site

The study was conducted at the Teaching and Research Farm of the School of Agriculture, the University of Cape Coast, Ghana (5°07′7.6″ N, 1°17′18.9″ W; 15 m above sea level). This farm is located in the Central region with semi-deciduous forests and coastal savannah ecozones. The trial was conducted under field conditions during the 2020 and 2021 growing seasons. The annual rainfalls for the experiment period were 1246.2 mm for 2020 and 1170.2 mm for 2021; the average maximum and minimum temperatures for 2020 were 27.9 and 26.9 °C, while those for 2021 were 28.6 and 25 °C, respectively. The average relative humidity for 2020 was 75.7%, and it was 81.2% for 2021. The soil on this experimental site is sandy loam with a pH of 6.72, 1.31% organic carbon, 754.6 µg/g of available phosphorus, and potassium content estimated at 0.081 cmol/kg.

2.2. Plant Materials and Experimental Design

A total of 162 *D. praehensilis* accessions were used, of which 71 were collected from the Central region, 25 from the Eastern region, and 66 from the Western North region of Ghana (Figure S1 and Table S1). These accessions were collected from farmers during the 2019 harvest season. The details, including the accession codes and regions of the

collection, are presented in Table S1. The experiment was laid out in a 15-by-11 simple lattice design with two replicates. Each plot size consisted of 3 m long ridges containing three plants at 1 m intra- and inter-row spacing. The field layout was generated using Agricolae package [23]. The recommended cultural practices, such as ridging, weeding, staking, etc., were implemented during the growing seasons.

2.3. Data Collection

Data were collected for 11 quantitative traits (Table S2) according to the standard operating protocol for yam performance evaluation trials [24] and the yam trait ontology available at YamBase (www.yambase.org, accessed on 7 January 2023). The area under the disease progression curve (AUDPC) for YMV severity, dry matter content, tuber flesh oxidation intensity, and tuber flesh hardness were evaluated as described below.

The AUDPC, a valuable quantitative summary of disease intensity or severity for YMV over time, was estimated using the trapezoidal method [25]. This method discretizes the time variable and calculates the average disease intensity or severity between each pair of adjacent time points:

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

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

The dry matter content was determined by chopping 100 g of fresh tuber flesh into small pieces and then oven-drying it at 105 °C for 24 h until a constant weight was achieved. The percentage of 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 60 min after cutting using a Chroma (colorimeter) meter (CR-400, Konica Minolta, Japan). The lightness (L*), red/green coordinate (a*), and yellow/blue coordinate (b*) values were recorded. A reference of white and black porcelain tiles was used to calibrate the Chroma meter before each reading. The delta (color difference) (ΔE*) among all three coordinates was calculated using the following formula:

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

Oxidative browning

$$(TBOxi) = F\Delta E^* - I\Delta E^* \quad (4)$$

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

Tuber flesh hardness was assessed with a 6.00 mm probe digital penetrometer. Tuber samples of 1 cm thickness and ~5 cm diameter were prepared from each genotype/accession, and the probe was pressed into the tuber. The force necessary for its penetration into the tuber was considered an indicator of the hardness of the tuber. Three measurements were taken per accession, the average was calculated, and the data were expressed in Newtons.

2.4. Data Analysis

Lme4 [23], an R package, was used to perform the analysis of variance (ANOVA) using a mixed linear model (MLM) fitted across cropping seasons, as shown below.

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

where Y_{ijk} is the value of the observed quantitative trait; μ is the population mean; G_h is the effect of the hth accession; S_i is the effect of the ith growing season; $(G_h * S_i)$ is the

accessions and season interaction associated with accession h and season i; R_{ij} is the effect of the jth replicate (superblock) in the season ith; B_k is the effect of the kth incomplete block within the jth replicate; and ε_{hijk} is the experimental error.

Accessions were considered fixed effects, while growing seasons, replicates, and blocks were considered random effects. The means between growing seasons were compared using the least significant difference (LSD) test at a p-value threshold of 0.05. Variations in the quantitative traits among *D. praehensilis* accessions were assessed using descriptive statistics such as means, standard deviations, minimum and maximum values, and coefficients of variation. Pearson's correlation coefficients (phenotypic and genotypic) among the quantitative traits were estimated using the Corrplot R package [26]. FactoMineR [27] and Factoextra [28] in R were used to evaluate the contributions of the quantitative traits using principal component analysis (PCA). Path coefficient analysis was conducted using lavaan and semPlot in the R package [23], considering the tuber weight per plant and dry matter content as response variables. A path diagram was constructed to depict the direct effect of key agronomic and tuber quality traits on the tuber yield and dry matter content to determine which traits can be adopted for indirect selection. A cluster dendrogram for estimating the genetic relationship among the 162 *D. prehensilis* was visualized using the dendextend [29] and circlize [30] packages. The variance components for each quantitative trait were estimated from the expected mean square (EMS) in the analysis of variance. The broad-sense heritability and genotypic and phenotypic coefficients of variation were calculated based on the estimated variance components as follows:

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

Phenotypic coefficient of variance

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

Genotypic coefficient of variance

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

where $\delta^2{}_g$ is the genotypic variance and $\delta^2{}_p$ is the phenotypic variance. Shabanimofrad et al. [31] categorized the estimated values of PCV and GCV as low for 0–10%, intermediate for 10–20%, and high for greater than or equal to 20%. Broad-sense heritability (h^2) was categorized as low for 0–29%, intermediate for 30–60%, and high for greater than 60%.

The multi-trait genotype–ideotype distance index (MGIDI) index theory is based on four key steps: (i) rescaling the traits so that they all have a 0–100 range, (ii) using 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. The following formula was used to rescale traits:

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

where η_{nj} and φ_{nj} are the new maximum and minimum values for trait j after rescaling, respectively; φ_{oj} and φ_{oj} are the original maximum and minimum values for trait j, respectively, and hij 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, η_{nj} = 0 and φ_{nj} = 100 should be used. For the traits in which positive gains are desired, η_{nj} = 100 and φ_{nj} = 0 [32,33]. 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.

The factor analysis and ideotype design index (MGIDI) were calculated for ranking the genotypes based on multiple traits free from multi-collinearity [34]. The radar chart was generated using the radar chart function of the fmsb package [35]. The predicted genetic gain *SG* (%), was computed using the MGIDI index for each trait considering the α% selection intensity, as follows:

$$\text{SG (\%)} = \frac{\left(\bar{X}_s - \bar{X}_o\right)h^2}{\bar{X}_o} \quad (10)$$

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. Quantitative Traits Variation

The interactions among seasons and accessions were significant ($p < 0.05$) for only the tuber flesh hardness. Significant differences ($p < 0.001$) among the accessions were observed across all evaluated quantitative traits. The season main effect was significant ($p < 0.05$) for the tuber length and tuber flesh hardness. The overall mean, range, and coefficients of variation of the evaluated traits are presented in Table 1. The responses to YMV severity based on the AUDPC score varied from 135.00 to 320.00, with an average of 149.44. The average dry matter content was 34.01%, ranging from 17.84 to 50.49%. The tuber flesh oxidation varied from −46.71 to 7.77, with an average of −13.34. The tuber flesh hardness ranged from 48.43 to 55.26 N, averaging 50.86 N. The coefficients of variation varied from 2.39% for the tuber flesh hardness to 76.70% for the tuber flesh oxidation.

Table 1. Mean squares, mean performance, and variance components and broad-sense heritability of quantitative traits of *D. praehensilis* accessions across two seasons.

Source	Df	TWPL	NTP	TBL	TBW	SDMP	NIFB	SINL	YMV	DMC	TBOXI	TBHard
Gen	161	4.07 ***	2.36 ***	340.90 ***	265.53 ***	2.70 ***	4.73 ***	33.81 ***	3815.80 ***	44.43 ***	267.87 ***	5.17 ***
Season	1	4.13 ^{ns}	0.13 ^{ns}	4694.20 *	5.85 ^{ns}	5.10 ^{ns}	0.40 ^{ns}	56.65 ^{ns}	5.50 ^{ns}	34.45 ^{ns}	534.22 ^{ns}	2.59 *
Gen*Season	161	0.42 ^{ns}	0.57 ^{ns}	46.20 ^{ns}	0.37 ^{ns}	0.43 ^{ns}	0.24 ^{ns}	1.63 ^{ns}	0.10 ^{ns}	3.59 ^{ns}	21.20 ^{ns}	0.15 ***
Residual	321	0.75	0.77	7.67	3.82	0.81	1.07	3.08	0.59	2.49	6.44	0.26
Mean		1.75	1.85	39.04	29.08	3.42	2.93	15.50	149.44	34.01	−13.34	50.86
Min		0.11	1.00	12.00	11.00	1.37	1.50	7.70	135.00	17.84	−46.71	48.43
Max		10.00	9.00	97.00	63.00	7.50	12.00	41.50	320.00	50.49	7.77	55.26
CV (%)		70.23	55.66	30.28	29.82	33.84	50.19	24.51	20.74	12.12	76.70	2.39
GCV (%)		52.79	35.99	21.44	27.67	19.93	32.81	16.48	20.72	9.01	56.48	2.30
H^2		0.57	0.42	0.50	0.87	0.35	0.46	0.45	0.99	0.57	0.55	0.92
PCV (%)		70.23	55.74	30.32	29.74	33.24	48.19	24.52	20.79	11.97	76.32	2.40

TWPL: tuber weight per plant; NTP: number of tubers per plant; TBL: tuber length; TBW: tuber width; SDMP: stem diameter per plant; NIFB: number of internodes before first branching; SINL: stem internode length; YMV: yam mosaic virus; DMC: dry matter content; TBOXI: tuber flesh oxidation; TBHard: tuber flesh hardness; Gen: genotype; Min: minimum; Max: maximum; CV: coefficient of variation; GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation; H^2: broad-sense heritability.

3.2. Genotypic Coefficients, Phenotypic Coefficients, and Broad-Sense Heritability

High genotypic coefficients of variation (GCV) (≥20%) were observed for most of the evaluated traits. The stem diameter and stem internode length had moderate GCV (10–20%), while the dry matter contents and tuber flesh hardness had low GCV (0–10%) (Table 1). High phenotypic coefficients of variation (PCV) (≥20%) were recorded in all the evaluated quantitative traits except in the dry matter content and flesh tuber hardness, where low PCV (0–10%) were observed (Table 1). Moderate broad-sense heritability (H^2) (30–60%) was observed for all the evaluated quantitative traits, whereas the response to YMV and the tuber flesh hardness had high H^2 (>60%) (Table 1).

3.3. Principal Component Analysis of Evaluated Quantitative

The first three principal components (PCs) accounted for ~55% of the total variation (Table 2; Figure 1 (left)). PC1 explained ~23% of the total variation, with traits such as the number of tubers per plant, tuber length, and tuber width having larger contributions to the explained variation by the PC. PC2 contributed 16.55% of the total variation, with traits such as the stem diameter, shoot internode, and dry matter content having larger contributions to the explained variation by this PC. Approximately 15% of the total variation was detected in PC3, with the number of internodes to the first branch, tuber oxidation, and tuber hardness having larger contributions to the explained variation by this PC (Table 2). The influence of the traits on the principal components and the levels of correlation among them are presented in Figure 1 (right). The PCA biplot indicates higher and positive correlations between the tuber weight per plant and the number of tubers per plant and between the dry matter content and the tuber flesh oxidation, but negative correlations between the tuber flesh hardness and the dry matter content and between the response to YMV severity and the dry matter content.

3.4. Phenotypic and Genotypic Correlation Coefficients of Quantitative Traits

The results of the phenotypic and genotypic relationships among the quantitative traits are presented in Figure 2. Significant correlation coefficients (genotypic and phenotypic) were observed between the tuber weight per plant and the number of tubers per plant, tuber length, tuber width, stem diameter, and stem internode length ($p < 0.001$). The dry matter content was positively correlated with the tuber flesh oxidation ($p < 0.05$), the number of tuber per plant ($p < 0.01$), tuber length ($p < 0.001$), and the number of internodes to the first branching ($p < 0.01$), but significantly and negatively correlated with the tuber flesh hardness ($p < 0.001$), the response to YMV severity ($p < 0.01$), and stem diameter and stem internode length ($p < 0.001$). Tuber flesh oxidation was significantly and negatively correlated with the tuber flesh hardness ($p < 0.001$), the response to YMV severity ($p < 0.01$), and tuber length ($p < 0.001$). Tuber flesh hardness revealed significant and positive correlations with the response to YMV severity ($p < 0.001$) and tuber length ($p < 0.01$) (Figure 2).

Table 2. Principal components and correlations among quantitative traits of *D. praehensilis* accessions (Bold values represent traits with high contribution to each component).

Variables	PC1	PC2	PC3
Tuber weight per plant	**0.866**	−0.059	−0.037
Number of tuber per plant	**0.735**	0.183	−0.025
Tuber length	**0.852**	−0.064	−0.008
Tuber width	**0.676**	−0.04	−0.063
Stem diameter per plant	−0.02	**−0.641**	−0.538
Number of internode to first branch	−0.099	−0.187	**−0.619**
Shoot internode	0.05	**−0.606**	−0.482
Yam mosaic virus disease	−0.072	0.454	−0.182
Dry matter content	0.162	**0.597**	−0.277
Tuber oxidation	0.081	−0.438	**0.582**
Tuber hardiness	−0.066	0.458	**−0.547**
Eigenvalues	2.530	1.820	1.660
Variance (%)	22.990	16.550	15.080
Cumulative. variance (%)	22.990	39.540	54.620

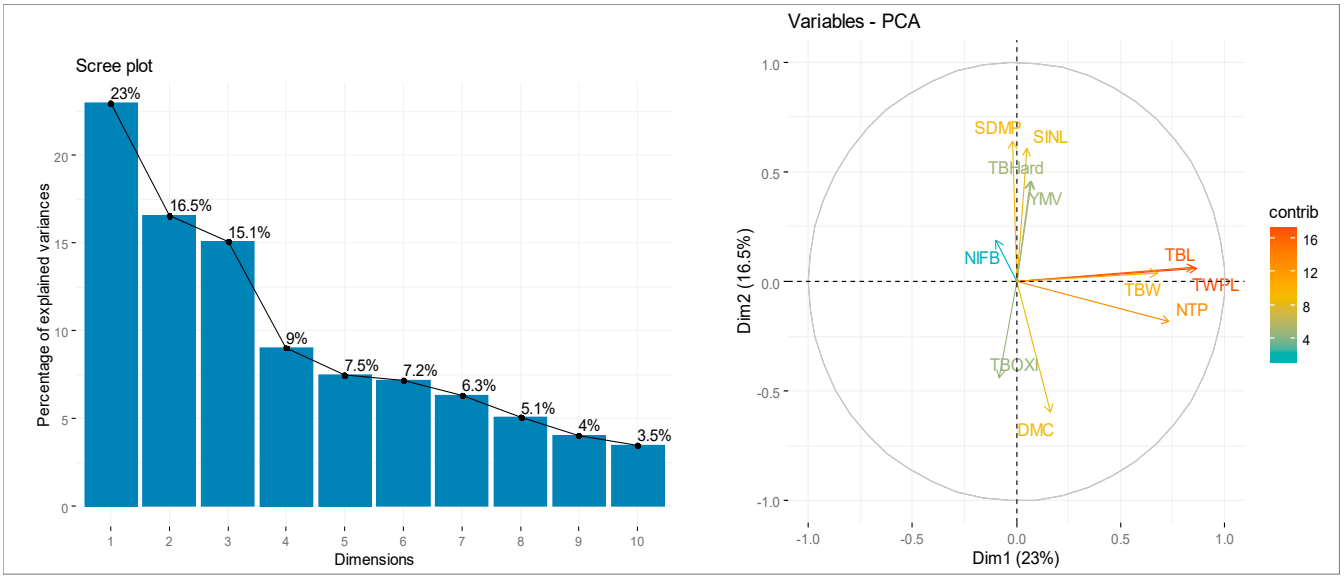

Figure 1. PCA scree plot (**left**) and plot showing the total contribution of variables accounting for the variability in PC1 and PC2 (**right**). TWPL: tuber weight per plant; NTP: number of tubers per plant; TBL: tuber length; TBW: tuber width; SDMP: stem diameter per plant; NIFB: number of internodes before first branching; SINL: stem internode length; YMV: yam mosaic virus; DMC: dry matter content; TBOXI: tuber flesh oxidation; TBHard: tuber flesh hardness.

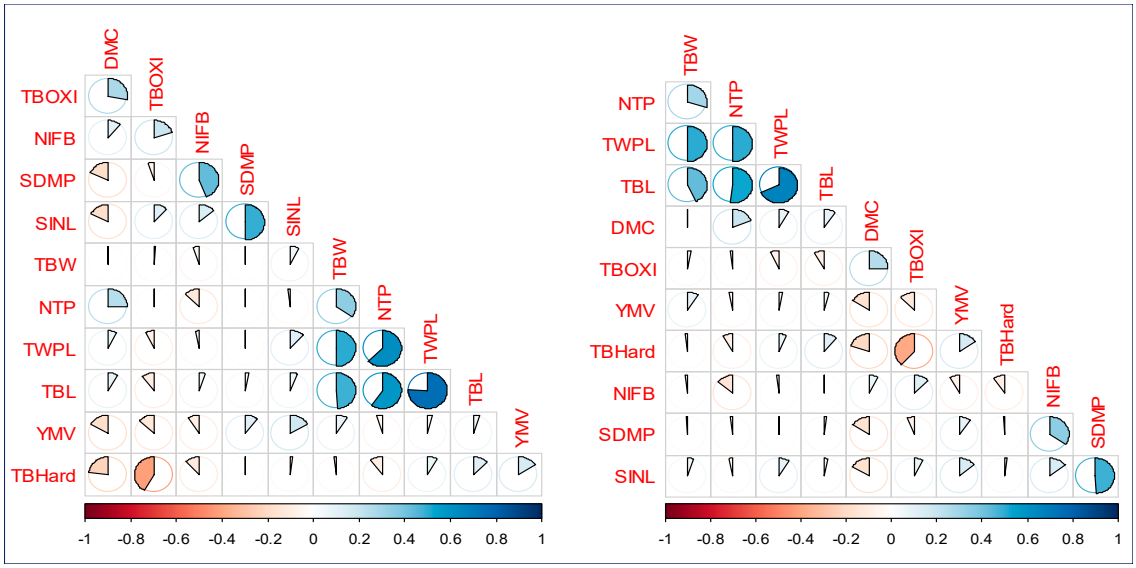

Figure 2. Genotypic (**left**) and phenotypic (**right**) correlation coefficients among 11 quantitative traits. TWPL: tuber weight per plant; NTP: number of tubers per plant; TBL: tuber length; TBW: tuber width; SDMP: stem diameter per plant; NIFB: number of internodes before first branching; SINL: stem internode length; YMV: yam mosaic virus; DMC: dry matter content; TBOXI: tuber flesh oxidation; TBHard: tuber flesh hardness.

3.5. Path Coefficient Analysis

Direct path coefficient analysis revealed that the tuber weight per plant gained significant positive contributions from the number of tubers per plant (r = 0.26; $p \leq 0.05$), tuber length (r = 0.05; $p \leq 0.05$), and tuber width (r = 0.03; $p \leq 0.05$), while the dry matter content gained significant positive contributions from the number of tubers per plant (r = 0.80; $p \leq 0.05$) and tuber flesh oxidation (r = 0.08; $p \leq 0.05$) (Figure 3).

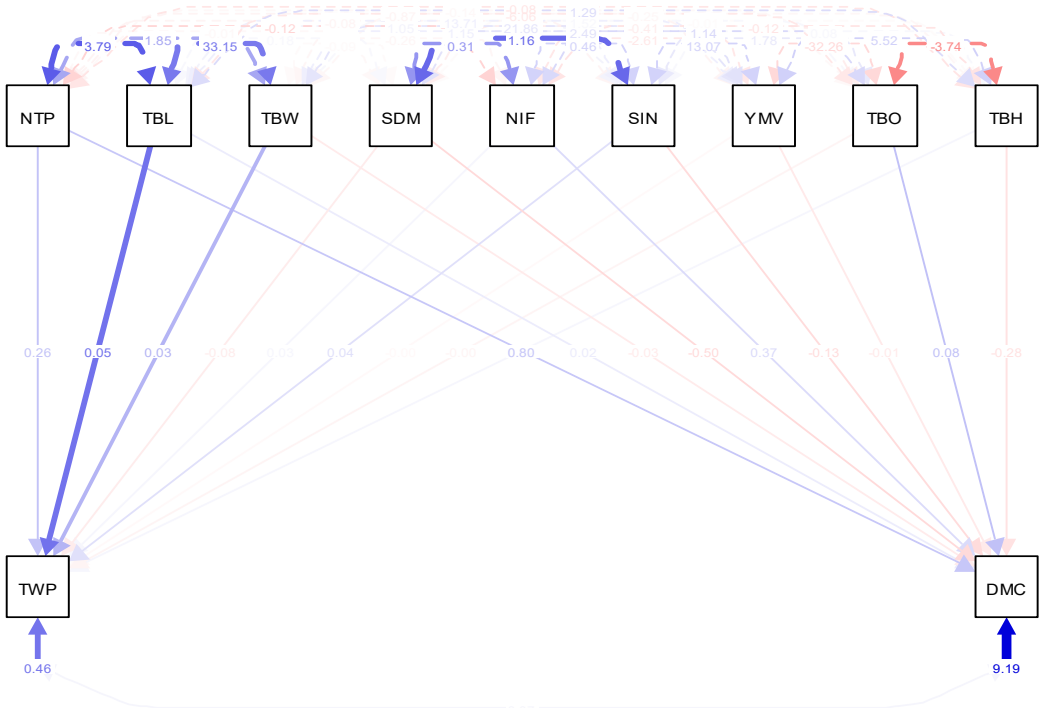

Figure 3. Path coefficient analysis among evaluated 11 quantitative traits using tuber weight per plant and dry matter contents as dependent variables. TWPL: tuber weight per plant; NTP: number of tubers per plant; TBL: tuber length; TBW: tuber width; SDMP: stem diameter per plant; NIFB: number of internodes before first branching; SINL: stem internode length; YMV: yam mosaic virus; DMC: dry matter content; TBOXI: tuber flesh oxidation; TBHard: tuber flesh hardness.

3.6. Hierarchical Clustering

Hierarchical clustering based on the Gower dissimilarity matrix grouped the 162 *D. praehensilis* accessions into three clusters, accounting for 51, 69, and 42 accessions for clusters 1, 2, and 3, respectively (Figure 4). Cluster 1 was characterized by accessions with increased tolerance and resistance to the YMV severity, high dry matter content, and moderately low tuber flesh oxidation and hardness but low tuber weight per plant and a low number of tubers per plant (Table 3). Cluster 2 consisted of accessions that were characterized by a significantly high yield (tuber weight per plant, long, and many tubers), resistance to YMV severity, high dry matter content, moderately low tuber flesh oxidation, and low tuber flesh hardness (Table 3). The accessions in Cluster 3 were associated with high tuber yield component attributes (tuber weight per plant, tuber length, and width) and low tuber flesh oxidation.

3.7. Factor Analysis and Selection-Based Multi-Trait Genotype–Ideotype Distance Index (MGIDI)

The MGIDI index identified three factors based on the eleven quantitative traits. Factor analysis 1 was associated with the tuber weight per plant, the number of tubers per plant, and tuber length and width. Factor analysis 2 was correlated with the dry matter content, tuber flesh oxidation, and tuber flesh hardness, while Factor analysis 3 was associated with the stem diameter per plant, number of internodes, and stem internode length (Table 4). The average communality and uniqueness accounted for 55% and 46% of all the genetic variability in the dataset, respectively (Table 4).

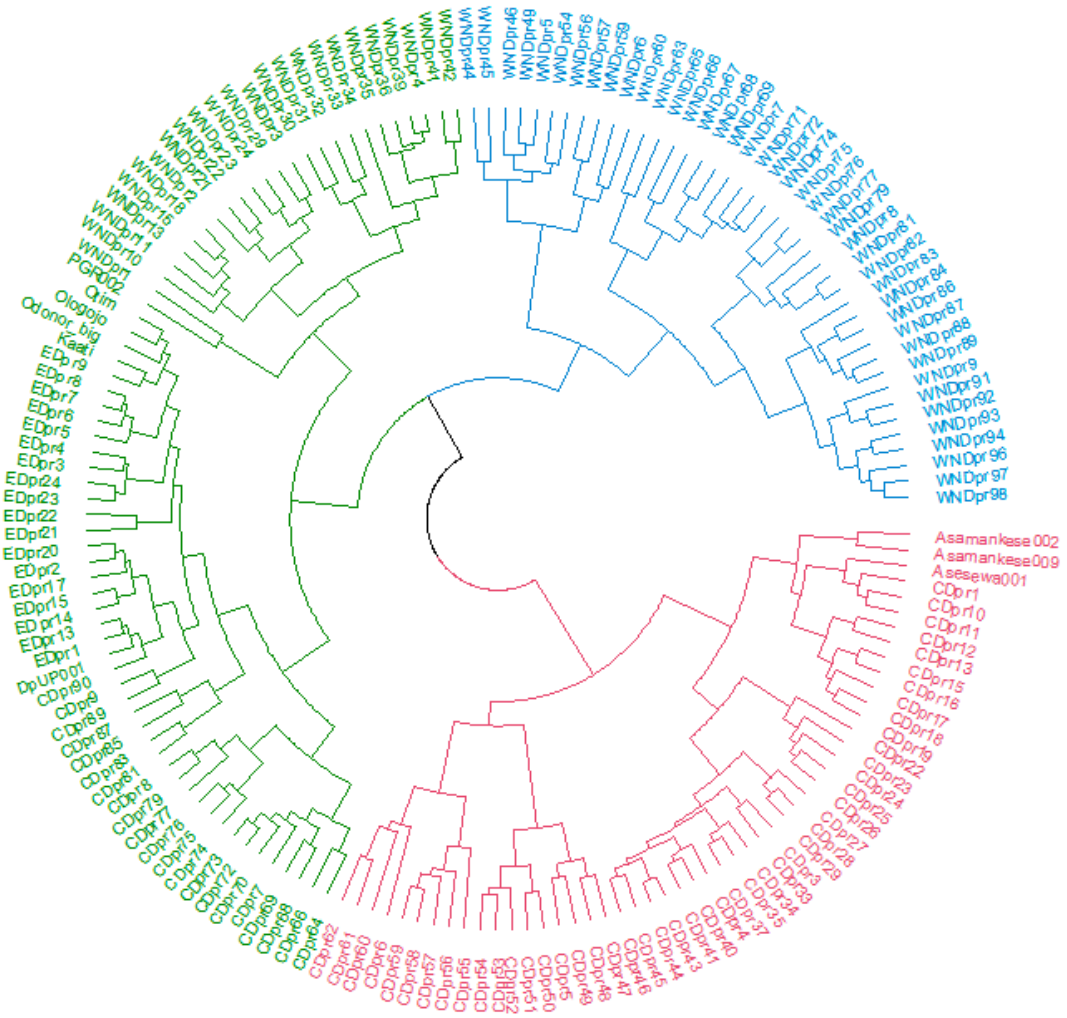

Figure 4. Clustering showing the grouping patterns of *D. praehensilis* accessions using 11 quantitative traits based on the Gower dissimilarity matrix. Cluster 1—Red, Cluster 2—Green, and Cluster 3—Blue.

Table 3. Description of clusters for 11 quantitative traits of *D. praehensilis* accessions.

Variables	Cluster 1—Red (51)		Cluster 2—Green (69)		Cluster 3—Blue (42)	
	Mean ± SD	Range	Mean ± SD	Range	Mean ± SD	Range
TWPL	0.96 ± 0.55 ^{b}	0.23–2.52	**2.04 ± 0.99** ^{a}	1.00–6.18	**2.23 ± 0.91** ^{a}	1.04–6.20
NTP	1.28 ± 0.38 ^{c}	1.00–2.75	**2.24 ± 0.78** ^{a}	1.00–5.00	1.89 ± 0.69 ^{b}	1.00–3.25
TBL	30.52 ± 7.65 ^{b}	12.50–42.00	**42.09 ± 7.66** ^{a}	28.00–73.50	**44.36 ± 6.33** ^{a}	34.50–60.50
TBW	23.06 ± 7.59 ^{b}	11.56–49.69	**32.08 ± 7.23** ^{a}	19.69–53.38	**31.46 ± 6.37** ^{a}	20.56–51.13
SDMP	3.48 ± 0.87 ^{a}	2.01–6.02	3.33 ± 0.79 ^{a}	1.37–5.20	3.48 ± 0.82 ^{a}	2.19–5.29
NIFB	**3.28 ± 1.48** ^{a}	1.50–7.25	2.75 ± 0.83 ^{b}	1.50–6.00	2.80 ± 0.77 ^{b}	1.50–5.50
SINL	**16.22 ± 3.55** ^{a}	11.24–27.97	15.03 ± 2.05 ^{b}	10.77–20.04	15.45 ±3.15 ^{ab}	10.30–22.70
YMV	**146.52 ± 24.77** ^{b}	137.00–272.00	**141.57 ± 15.92** ^{b}	137.00–227.00	165.93 ± 47.01 ^{a}	137.00–317.00
DMC	33.71 ± 4.13 ^{ab}	22.44–44.69	**34.76 ± 3.21** ^{a}	27.54–44.75	33.16 ± 2.05 ^{b}	28.61–38.67
TBOXI	−10.17 ± 7.86 ^{a}	−32.88–3.59	−11.63 ± 7.08 ^{a}	−32.40–0.82	**−20.01 ± 6.89** ^{b}	(−35.69)–(−4.33)
TBHard	50.64 ± 1.03 ^{b}	48.49–52.87	**50.18 ± 0.65** ^{c}	48.57–52.26	52.22 ± 0.89 ^{a}	50.41–53.57

TWPL: tuber weight per plant; NTP: number of tubers per plant; TBL: tuber length; TBW: tuber width; SDMP: stem diameter per plant; NIFB: number of internodes before first branching; SINL: stem internode length; YMV: yam mosaic virus; DMC: dry matter content; TBOXI: tuber flesh oxidation; TBHard: tuber flesh hardness.

Table 4. Factorial loadings, communalities, uniqueness, and predicted genetic gains (PSG) based on the multi-trait genotype–ideotype distance index (Bold values represent traits with high contribution to each component).

Variables	FA1	FA2	FA3	Communality	Uniqueness	Goal	PSG (%)	Sense
TWPL	**0.87**	−0.05	−0.04	0.76	0.25	100	0.65	increase
NTP	**0.74**	0.13	0.12	0.57	0.43	100	0.18	increase
TBL	**0.85**	−0.08	−0.02	0.73	0.27	100	3.42	increase
TBW	**0.68**	−0.02	−0.05	0.46	0.54	100	5.56	increase
SDMP	0.00	−0.13	**−0.83**	0.70	0.30	100	0.29	increase
NIFB	−0.07	0.27	**−0.59**	0.43	0.57	100	0.34	increase
SINL	0.07	−0.15	**−0.76**	0.60	0.40	100	1.30	increase
YMV	−0.06	0.47	0.16	0.25	0.76	0	1.92	decrease
DMC	0.18	**0.63**	0.19	0.50	0.54	100	0.30	increase
TBOXI	0.05	**−0.72**	0.16	0.54	0.46	100	1.97	decrease
TBHard	−0.04	**0.71**	−0.12	0.51	0.49	100	−0.20	decrease
Average				0.55	0.46			

TWPL: tuber weight per plant; NTP: number of tubers per plant; TBL: tuber length; TBW: tuber width; SDMP: stem diameter per plant; NIFB: number of internodes before first branching; SINL: stem internode length; YMV: yam mosaic virus; DMC: dry matter content; TBOXI: tuber flesh oxidation; TBHard: tuber flesh hardness.

Of the 11 traits evaluated, nine had desired genetic gains using the MGIDI index (Table 4). The traits with undesired selection gain using the MGIDI index were the response to YMV severity (1.92%) and tuber flesh oxidation. The MGIDI index provided a total genetic gain of 12.04% for the assessed multi-traits for which increases are desired and 3.69% for those for which decreases are desired (Table 4).

3.8. Selection of Genotypes

Of the 162 *D. praehensilis* accessions evaluated, the MGIDI identified 24 accessions as high-performing accessions for multiple traits (Figure 5, Table S3). These accessions show the greatest potential for the simultaneous improvement of the measured traits in a yam breeding program.

Accessions associated with FA1 (WNDpr13, WNDpr18, WNDpr4, WNDpr46, WNDpr84, WNDpr88, Asamankese002, CDpr1, CDpr28, CDpr29, CDpr4, CDpr68, and CDpr72) showed strength for traits such as the dry matter content, yam mosaic virus severity, tuber flesh hardness, and stem internode length (Figure 6; Table 5). Accessions related to FA2 (WNDpr63, WNDpr76, Asamankese009, CDpr24, and CDpr8) had strength for the tuber weight per plant, the number of tubers per plant, tuber length, and the number of internodes to the first branching (Figure 6; Table 5), while accessions associated with FA3 (WNDpr71, CDpr46, CDpr48, CDpr57, EDpr23, and PGR002) revealed strength for traits such as the tuber width, tuber flesh oxidation, and stem diameter.

Table 5. Factorial loadings, communalities, and uniqueness of twenty-four selected genotypes based on the multi-trait genotype–ideotype index (MGDI). (Bold values represent traits with high contribution to each component).

VAR	FA1	FA2	FA3	Communality	Uniqueness
TWPL	−0.09	**0.72**	0.05	0.53	0.47
NTP	−0.31	**0.79**	0	0.73	0.27
TBL	−0.07	**0.78**	−0.12	0.62	0.38
TBW	0.08	−0.11	0.7	0.51	0.49
SDMP	0.47	−0.26	**−0.68**	0.75	0.25
NIFB	−0.3	−0.6	**−0.58**	0.78	0.22
SINL	**0.67**	−0.2	0.04	0.49	0.51
DMC	**−0.85**	0.19	−0.21	0.8	0.2

Table 5. *Cont.*

VAR	FA1	FA2	FA3	Communality	Uniqueness
TBOXI	0.35	0.48	**−0.54**	0.64	0.36
TBHard	**−0.74**	−0.09	0.17	0.59	0.41
YMV	**−0.56**	0.01	0.37	0.45	0.55

TWPL: tuber weight per plant; NTP: number of tubers per plant; TBL: tuber length; TBW: tuber width; SDMP: stem diameter per plant; NIFB: number of internodes before first branching; SINL: stem internode length; YMV: yam mosaic virus; DMC: dry matter content; TBOXI: tuber flesh oxidation; TBHard: tuber flesh hardness.

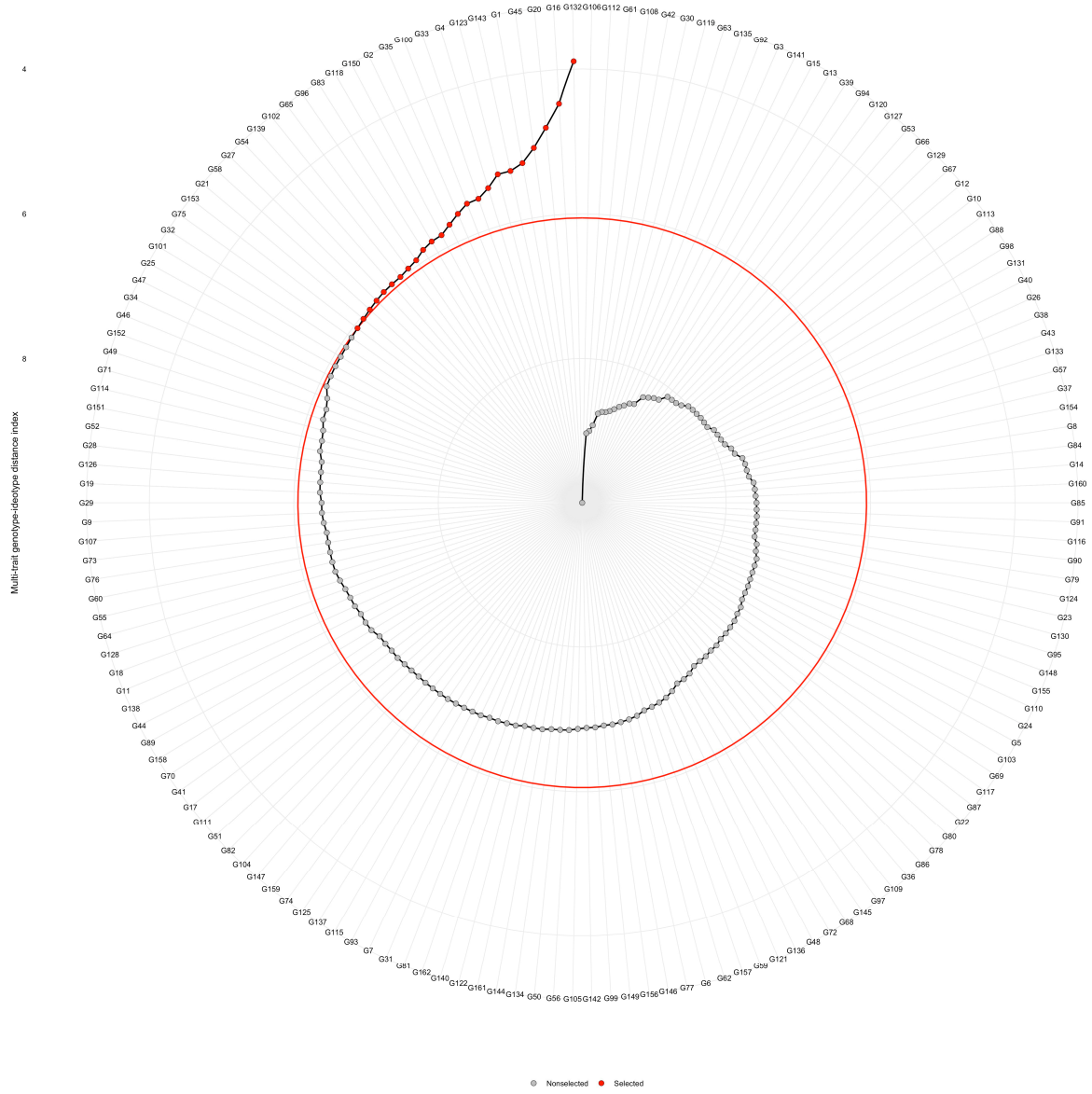

Figure 5. *D. praehensilis* accession rankings showing selected accessions using the multi-trait genotype–ideotype index (MGIDI). The selected accessions are shown as red dots, while the unselected accessions are shown as black dots. The red circle represents the cut point according to the selection pressure.

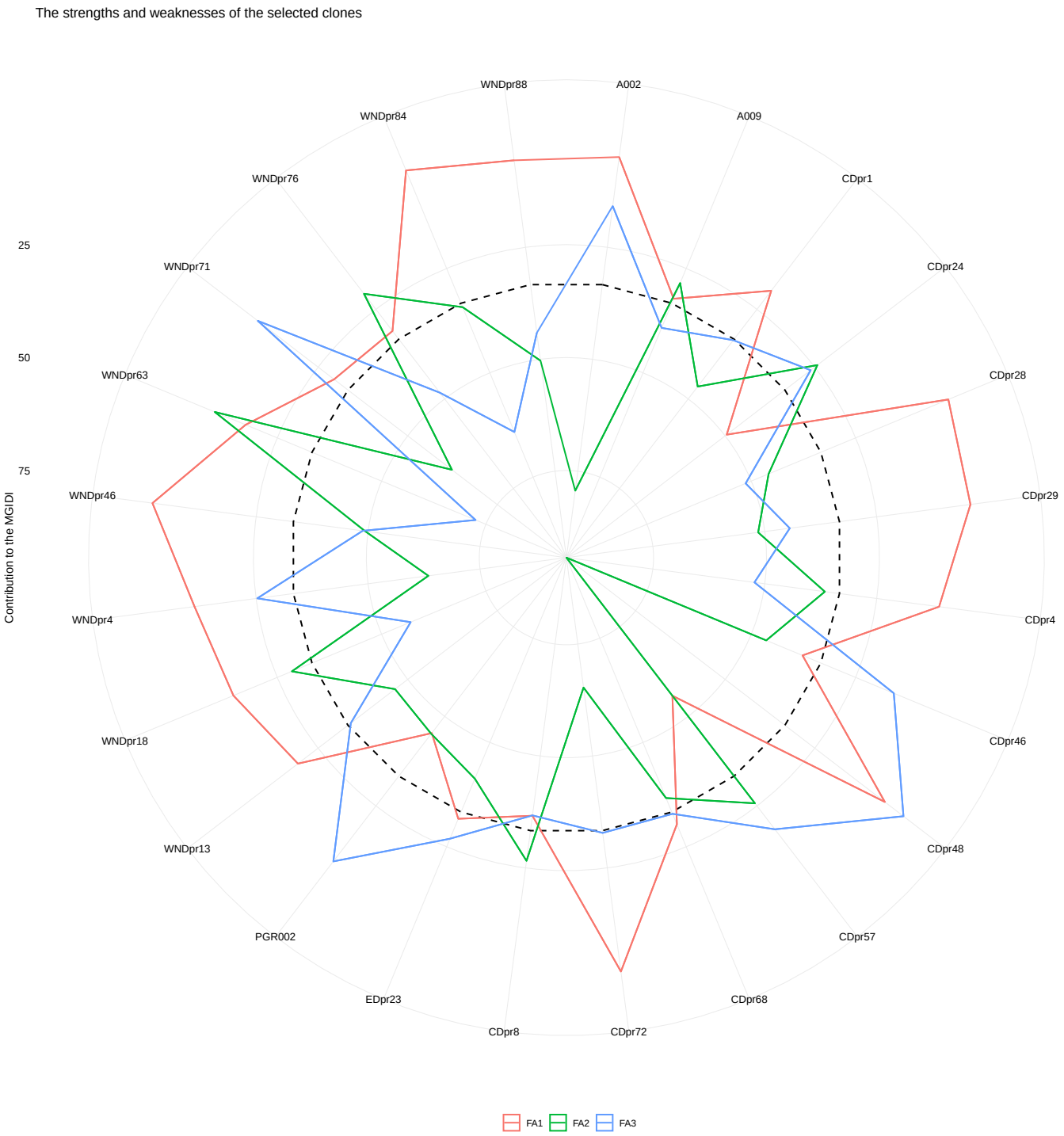

Figure 6. The strengths and weaknesses of the selected genotypes are shown as the proportion of each factor on the computed multi-trait genotype–ideotype index (MGIDI). The smaller the proportion explained by a factor (closer to the external edge), the closer the traits within that factor are to the ideotype. The black broken circle at the center shows the theoretical value if all the factors contributed equally. A002: Asamankese002; A009: Asamankese009.

4. Discussion

In this study, we employed 11 quantitative traits to assess the variations among 162 accessions of bush yam collected from three different regions of Ghana. The results show significant variations among the accessions of *D. praehensilis* in all the evaluated traits, indicating a high level of diversity among the *D. praehensilis* accessions studied. The high

coefficients of variation (CV > 20) that were observed in some of the quantitative traits, especially the yield component traits, indicate huge and readily available genetic differentiation in *D. praehensilis*. Kouam et al. [16] reported high coefficients of variation for tuber yield components in a study conducted on *D. bulbifera* accessions. Similar observations of high genetic variability using quantitative traits have been reported in other yam species such as *D. alata* [20], *D. rotundata* [24], and *D. dumetorum* [36,37]. These high variations in quantitative traits are an indication that these traits could be used as the basis for the selection of accessions with high genetic merit. The knowledge of existing variability and the degrees of association among quantitative traits are paramount for selecting superior accessions for breeding programs.

The degree of genetic variability and heritability determines the response to selection in any crop improvement initiative [38]. The high GCV (>20%) and moderate broad-sense heritability (30–60%) observed for all the yield-related traits suggest high selection pressure, which could be enforced on these traits for future breeding activities. The GCV coupled with heritability estimates offers the best information about the extent of progress that can be expected from selection [39]. In contrast, the low GCVs recorded for the dry matter content and YMV severity response imply that these traits can only be improved using selection methods that are not under the influence of environmental factors. Norman et al. [40] and Asfaw et al. [41] have reported high GCVs and PCVs for tuber yield-related traits and low GCVs and PCVs for the dry matter content in studies conducted on advanced and early-generation breeding populations of *D. rotundata*, respectively. Padhan et al. [42] also reported high GCVs and PCVs for tuber yield in a study conducted on India's wild and cultivated yam species. High H^2 observed in the YMV severity response is an indication that this trait could be improved through natural selection for superior accessions. The results from this study corroborate the findings by Agre et al. [43], who reported high H^2 in the YMV severity response in their study conducted on elite populations of *D. rotundata*.

The correlation analysis in this study revealed that improvement in yield and superior tuber quality traits is possible through the selection of attributing traits, such as an increased size of tubers and resistance and tolerance to YMV. The positive relationships observed among yield-related traits in this study imply that indirect selection could be adopted for significantly correlated traits. Positive correlations observed among yield-related traits have been reported by Asfaw et al. [41] and Padhan et al. [42]. The significant positive correlation observed in this study between the dry matter and the number of tubers per plant agrees with the findings of Satie et al. [44] in a study on eight white yam landraces.

The cluster analysis showed that Cluster 2 was the most promising group for superior tuber yield attributes, high resistance to YMV severity, high dry matter content, and low tuber flesh hardness. Cluster 1 had some promising accessions for resistance to YMV severity and Cluster 3 had accessions with potential for high tuber yield attributes and low tuber flesh oxidation. Hybridization within each cluster may result in less genetic gain due to the close relatedness of the accessions within each cluster [45]. Similarly, hybridization between accessions belonging to different clusters will result in the generation of different breeding materials.

Breeders frequently attempt to blend numerous desirable features into a new genotype in order to create high performance. It is frequently difficult to choose a genotype from the ideotype when assessing many attributes. The MGIDI was used to rank the *D. praehensilis* accessions based on the data from the multiple traits that were measured. The MGIDI index selected accessions (Asamankese 002, Asamankese 009, CDpr1, CDpr24, CDpr28, CDpr29, CDpr4, CDpr46, CDpr48, CDpr57, CDpr68, CDpr72, CDpr8, EDpr23, PGR002, WNDpr13, WNDpr18, WNDpr4, WNDpr46, WNDpr63, WNDpr71, WNDpr76, WNDpr84, and WNDpr88) as promising *D. praehensilis* accessions for a yam improvement program. The MGIDI model has also been used to assess ideal yield and yield-related variables in white Guinea yam genotypes [22], wheat genotypes [46], and eggplant genotypes [47]. Multiple trait selection using the MGIDI was found to be beneficial in identifying high-performing bush yam accessions and estimating the expected genetic gains of the selected

accessions for the qualities studied. This supports the notion that the MGIDI is a potentially useful strategy for simultaneously improving many attributes using projected genetic influences [35].

The MGIDI index's strengths and weaknesses determined that the proportion of each factor is a useful tool for identifying the strengths and weaknesses of the evaluated accessions. WNDpr13, WNDpr18, WNDpr4, WNDpr46, WNDpr84, WNDpr88, Asamankese002, CDpr1, CDpr28, CDpr29, CDpr4, CDpr68, and CDpr72 were selected for low tuber flesh hardness and resistance to YMV; WNDpr63, WNDpr76, Asamankese009, CDpr24, and CDpr8 were selected for the tuber weight per plant, the number of tubers, and tuber length; and WNDpr71, CDpr46, CDpr48, CDpr57, EDpr23, and PGR002 were selected for tuber flesh oxidation and tuber width. The knowledge of contributions by these accessions helps in the selection of prospective putative progenitors for future breeding in *D. praehensilis*. The initiation of a hybridization program among the promising accessions of *D. praehensilis* could help develop varieties that meet the preference criteria of farmers and consumers for better post-harvest tuber quality traits, such as low tuber flesh oxidation, low tuber flesh hardness, and high yield.

5. Conclusions

This study explored the potential of 11 morphological traits to reveal the degree of genetic diversity among 162 accessions of *D. praehensilis*. The results show that improving bush yam for yield-related traits and post-harvest tuber quality can be achieved by exploring the genetic diversity among quantitative traits. The MGIDI index identified some promising *D. praehensilis* accessions that could be explored as progenitors for a bush yam improvement initiative targeting good agronomic and tuber quality traits for end users. Further assessment of these bush yam accessions with high throughput molecular markers is necessary to confirm the results of this study.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/agronomy13030682/s1, Figure S1. Map showing the locations of collection of *D. praehensilis* accessions; Table S1. List of samples with their sources; Table S2. Description of quantitative traits evaluated; Table S3. Factorial loadings, multi-trait genotype–ideotype indexes, and selection status of the 162 *D. praehensilis*.

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