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RESEARCH ARTICLE

PHENOTYPIC DIVERSITY OF SWEET POTATO (*IPOMOEA BATATAS*[L.]LAM.) GERMPLASMUSING QUANTITATIVE TRAITS: A PRE- BREEDING STUDY IN TOGO

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Abstract

Objective: Sweet potato is a root and tuber crop which contribute to food security in Togo. However, little scientific data exists on the genetic variability of cultivars grown in Togo, although this information is a prerequisite for development of new varieties. The objective of this study was to explore the phenotypic diversity within Togo's sweet potato cultivars.

Materials and Methods: The germplasm is composed of sixty five (65) cultivars from Togo and sixteen (16) exotic varieties introduced from Burkina Faso breeding unit. The experiment was laid out in a 9 x 9 lattice square design with three replicates. In total, sixteen (16) quantitative traits were evaluated using the sweet potato ontology as described by CIP.

Results: Descriptive statistics, ANOVA and PCA revealed high variability for traits such as root yield, dry matter content, aboveground biomass, stem length, internode length and stem diameter. Cluster analysis performed on the basis of the Euclidean distance between cultivars using Ward method as aggregation criterion has revealed four phenotypic clusters. Clusters I and II are composed of varieties with low root yield (12.95 and 15.87 $t.ha^{-1}$) and high dry matter content (29.68 and 26.86%). Clusters III and IV are made of varieties exhibiting high aboveground biomass (37.74 and 50.75 $t.ha^{-1}$), high fresh root yield (16.06 and 20.18 $t.ha^{-1}$) and low dry matter content (24.62 and 23.84%). The variability observed in this gene bank constitutes a basis for genetic improvement programmes of sweet potato in Togo.

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Introduction:-

Sweet potato [*Ipomoea batatas* (L.) Lam] is a perennial herbaceous crop of the convolvulaceae family. The stems are creeping and only the tips are erect (David et al., 2018). The flowers are white to purple and can be fertile, particularly in tropical climates.Sweet potato is cultivated in tropical and subtropical regions for its roots rich in starch and vitamins (B and C), but also for its leaves, which are rich in protein and mineral salts (Kouassi et al., 2023). Orange-fleshed varieties also contain carotene (provitamin A). Roots are used in a wide range of culinary preparations (boiled, fried, cakes, etc.) (Gobena et al., 2022). Certain industrial processes enable them to be preserved in different forms: tinned whole roots, sliced; dehydrated flakes; ready-to-use frozen roots, peeled whole or sliced. The food industry also use sweet potato roots as a source of starch or, in flour form, as a substitute for cereal flours. The roots are also used in animal feeding. The leaves are eaten as a condiment or in the form of legumes, or as fodder for livestock (Somé et al., 2014).

Sweet potato is by far the second most important root and tuber crop after cassava, with world production of about 86.41 million tonnes in 2022. Worldwide, its consumption is around 70 kg/capita/year (FAOSTAT, 2022). In Togo, sweet potato is the fourth most important root and tuber crop, after cassava, yam and taro. With a water requirement of 500 - 600 mm, well distributed over the length of the cycle, all areas of the country are suitable for cultivation. Sweet potato is grown over a total area of 2738 hectares, with annual production estimated at 9919 tonnes. In some regions, the area planted annually and the consumption levels are higher. In Maritime and Plateaux regions, for example, 108 and 95 kg of sweet potato is consumed per capita per year respectively, in Central region nearly 61 kg, and in Kara and Savannah regions 60 and 35 kg respectively (FAOSTAT, 2022).

In most case, sweet potato is considered to be more resilient to climat change than cereals or legumes (Tibiri et al., 2019), and should therefore see its production areas increase. Compared with other crops, sweet potato grow in a variety of soil and climate conditions (Adjatin et al., 2018). Given its relatively easy production methods and high nutritional value, increasing its production and use in sub-Saharan Africa can help to reduce poverty in rural areas and guarantee food security in a sustainable manner (Christinck et al., 2016). However, this potential, which is still largely unexploited, is threatened by the emergence and spread of new diseases and pests, encouraged by the vegetative propagation method of sweetpotato and the lack of reliable formal seed system. There is a need for research to support the development of this sector in order to help increase sweet potato productivity. Selection of high-yielding and high-nutrition varieties that are resilient to climate change is therefore a priority of breeding programmes and projects of many National Agricultural Research System.

In Togo, very little research has focused on knowledge of the local or farmers' varieties of sweetpotato grown and the possibilities of using them in a breeding programme (Glato et al., 2017). The study ofGlato et al in 2017 highlighted the genetic variability within a collection of accessions from West Africa (Togo and Senegal) as a function of the climatic gradient. However, this study did not explore the genetic structure of the local gene bank with a view of identifying traits and heterotic groups of agronomic interest that could be exploited in a national breeding programme. Further more, this collection has not been maintained for use in subsequent genetic improvement studies. As a result, there is very little scientific data on the phenotypic diversity of local sweetpotato cultivars in Togo, even though this information is a prerequisite for implementation of an effectivebreeding and plant genetic resources programmes. The documentation and identification of high yielding varieties preferred by farmers and processors will help to define the best breeding and germplasm conservation strategies in Togo.

Phenotyping is a process of scoring all observable traits that could help identify varieties in a collection and define the possibilities for their uses(Doussoh et al., 2018). It can take various forms depending on the objectives assigned, using morphological markers (qualitative descriptors), agronomic markers (quantitative descriptors) and molecular markers (RFLP, microsatellites, AFLP and RAPD techniques, SNP, etc) (Sembiring et al., 2022). Unlike traditional markers (morphological, agronomic and biochemical), molecular markers are not influenced by environmental fluctuations and are independent of the organ analysed and the plant’s stage of development. In Brazil (Da Silva et al., 2014; Veasey et al., 2007), East Africa (Grüneberg et al., 2004; P. Rukundo et al., 2015; Yada et al., 2010), West and Central Africa (Djinet et al., 2015; Kotchofa et al., 2019), morphological and agronomic markers have already been successfully used to assess the genetic diversity of sweetpotato varieties collections. Thus, the main objective of this study was to contribute to a sustainable increase of sweetpotato productivity in Togo. Specifically, the aim was to explore the phenotypic variability in a panel of sweetpotato cultivars using quantitative traits.

Materials and Methods:-

Plant material

The plant material consists of a set of sixty-five (65) cultivars obtained from a germplasm collection carried out in 2018 (Table 1) and sixteen (16) improved varieties introduced from the gene bank of Burkina Faso (Table 2).

The identification of the collections area was based on the importance of sweet potato in local farming system and visiting a maximum number of fields has been adopted as collection strategy. In each region, the collection sites were determined with the aid of the agricultural extension agents. A meeting was organized with the extension service to define the best itinerary that would facilitate the capture of the diversity of sweet potato cultivars grown in the area. In each village, sweet potato germplasm (veins) were obtained from farmers, mostly in the fields that are nearly 10 km apart. Geographical coordinates were collected using a GPS instrument. In addition, a data form was used to collect data such as name of the locality, agroecological zone, local name of the cultivar, ethnic group and farmer's name.

Table 1:- List, origin and colour of the flesh of the roots of sweet potato cultivars collected in Togo.

Code	Cultivar name	Flesh colour	Village	Prefecture	Agro-ecological zone
TG01	YIBOEVI 1	YELLOW	KPOGUEDE	VO	COASTAL ZONE
TG10	CHAIR ORANGE 2	ORANGE	ADJODOGOU	VO	COASTAL ZONE
TG11	DJETE KAHE 4	WHITE	ADAKAKPE	HAHO	WET SAVANE
TG12	DJETE GBAZE DJIN 1	WHITE	KPELE	HAHO	WET SAVANE
TG13	DJETE JAUNE 1	WHITE	KPELE	HAHO	WET SAVANE
TG14	DJETE JAUNE 5	YELLOW	KPELE	HAHO	WET SAVANE
TG15	DJETE JAUNE 2	ORANGE	NYIGBE	ZIO	COASTAL ZONE
TG16	KAWLI 1	WHITE	NYIGBE	ZIO	COASTAL ZONE
TG17	KADAYI GBAZE DJIN	YELLOW	NYATIVE	ZIO	FOREST ZONE
TG18	KADAYI	YELLOW	NYATIVE	ZIO	FOREST ZONE
TG19	DJETE JAUNE4	YELLOW	NYATIVE	ZIO	FOREST ZONE
TG02	ANAGO DJETE 1	YELLOW	KPOGUEDE	VO	COASTAL ZONE
TG20	KPEDEVI DJETE 2	YELLOW	AGBODJOPKOE	ZIO	COASTAL ZONE
TG21	DJETE GBAZE DJIN 2	YELLOW	KPEVEGO	ZIO	COASTAL ZONE
TG22	DJETE KAHE 5	WHITE	KPADAPE	KLOTO	FOREST ZONE
TG23	DJETE JAUNE 3	YELLOW	AKATA	KPELE	FOREST ZONE
TG24	DJETE HE SUGAR	WHITE	AGOUGADZEPE	AGOU	FOREST ZONE
TG25	DJETE HE 1	WHITE	AGOUGADZEPE	AGOU	FOREST ZONE
TG26	DJETE GBAZE HE 1	YELLOW	YOKELE	KLOTO	FOREST ZONE
TG27	ANAGO DJETE 2	YELLOW	BADJA	AVE	COASTAL ZONE
TG28	DJETE HE 2	WHITE	KOSSIGAN	AGOE NYIVE	COASTAL ZONE
TG29	DJETE HE 4	WHITE	KOSSIGAN	AGOE NYIVE	COASTAL ZONE
TG03	DJETE KAHE 1	YELLOW	KPOGUEDE	VO	COASTAL ZONE
TG30	DJETE HE 3	WHITE	GUERIN KOUKA	DANKPEN	DRY SAVANNA
TG31	DENKELE PIENE	WHITE	TANTOATRE	TONE	DRY SAVANNA
TG32	DENKELE MONE 1	WHITE	TANTOATRE	TONE	DRY SAVANNA
TG33	DENKELE MONE 2	WHITE	TANDJOUARE	TANDJOUARE	DRY SAVANNA

TG34	DENKELE MONE 3	WHITE	NAKI-EST	NAKI-EST	DRY SAVANNA
TG35	ANAGO DJETE 3	YELLOW	ASSAHOUN	AVE	COASTAL ZONE
TG36	DJETE GBAZE DJIN 4	WHITE	ZEGLE	ZIO	COASTAL ZONE
TG37	CHAIR ORANGE 3	ORANGE	ZEGLE	ZIO	COASTAL ZONE
TG38	DJETE GBAZE HE 2	WHITE	DAVIE	ZIO	COASTAL ZONE
TG39	DJETE GBAZE DJIN 3	WHITE	DAVIE	ZIO	COASTAL ZONE
TG04	CHAIR ORANGE 1	ORANGE	ZOTI ATSANVE	VO	COASTAL ZONE
TG40	ANAGO DJETE 4	YELLOW	ZEGLE	ZIO	COASTAL ZONE
TG41	ANAGO DJETE 5	YELLOW	ADJENGRE	SOUTOUBOUA	WET SAVANNA
TG42	DJETE GBAZE DJIN 5	WHITE	ATCHANGBADE	KOZAH	DRY SAVANNA
TG43	CARROTE 3	ORANGE	ZEGLE	ZIO	COASTAL ZONE
TG44	ANAGO DJETE 6	YELLOW	DJAMDE	KOZAH	DRY SAVANNA
TG45	ANAGO DJETE 7	YELLOW	KPELE-TSIKO	KPELE	FOREST ZONE
TG46	DJETE GBAZE DJIN 6	YELLOW	DANYI APEYEME	DANYI	FOREST ZONE
TG47	DJETE GBAZE DJIN 7	YELLOW	DAVIE	ZIO	COASTAL ZONE
TG48	KAWLI 2	WHITE	DAVIE	ZIO	COASTAL ZONE
TG05	CARROTE 1	ORANGE	ZOTI ATSANVE	VO	COASTAL ZONE
TG06	KPEDEVI DJETE 1	WHITE	ZOTI ATSANVE	VO	COASTAL ZONE
TG65	CARROTE 4	ORANGE	BADJA	AVE	COASTAL ZONE
TG66	WOULDJO	WHITE	GUERIN KOUKA	DANKPEN	DRY SAVANNA
TG67	DJETE HE 5	WHITE	AGOUGADZEPE	AGOU	FOREST ZONE
TG68	DJETE GBAZE ROSE 1	WHITE	GLEI	OGOU	WET SAVANNA
TG69	CARROTE 5	ORANGE	KOSSIGAN	AGOE NYIVE	COASTAL ZONE
TG07	DJETE KAHE 2	YELLOW	ZOTI ATSANVE	VO	COASTAL ZONE
TG70	DJETE GBAZE HE 3	YELLOW	TCHEBEBE	SOUTOUBOUA	WET SAVANNA
TG71	DJETE GBAZE DJIN 8	YELLOW	KPADAPE	KLOTO	FOREST ZONE
TG72	YIBOEVI 2	YELLOW	KPELE-TSIKO	KPELE	FOREST ZONE
TG73	KAWLI 3	WHITE	TCHALO	TCHAOUDJO	WET SAVANNA
TG74	DJETE GBAZE DJIN 9	YELLOW	TCHALO	TCHAOUDJO	WET SAVANNA
TG75	DJETE HE 6	WHITE	TCHEBEBE	SOUTOUBOUA	WET SAVANNA
TG76	DJETE KAHE 6	YELLOW	ADJENGRE	SOUTOUBOUA	WET SAVANNA
TG77	YELLOW DJET 4	YELLOW	GLEI	OGOU	WET SAVANNA
TG78	DJETE GBAZE DJIN 10	BLANCHE	AMAOUDE	TCHAOUDJO	WET SAVANNA
TG79	DJETE GBAZE ROSE 1	BLANCHE	GLEI	OGOU	WET SAVANNA
TG08	DJETE KAHE 3	YELLOW	ATSANSSI	VO	COASTAL ZONE
TG80	CARROTE 6	ORANGE	AGOVE	BAS-MONO	COASTAL ZONE
TG81	KAWLI 4	WHITE	ASSAHOUN	AVE	COASTAL ZONE
TG09	CARROTE 2	ORANGE	AGOVE	BAS-MONO	COASTAL ZONE

Table 2:- Name, origin and colour of root flesh of sixteen (16) sweet potato varieties introduced from Burkina Faso.

Code	Variety name	Flesh Colour	Village	Country	Maintainer
BF49	SAFARE	WHITE	KOMBISSIRI	BURKINA FASO	INERA
BF50	BF 82 TAINUNG 8	YELLOW	KAMBOINSIN	BURKINA FASO	INERA
BF51	NAKALBO	YELLOW	KOMBISSIRI	BURKINA FASO	INERA
BF52	TIEBELE 2	ORANGE	TIEBELE	BURKINA FASO	INERA
BF53	KB OR 3	ORANGE	KAMBOINSIN	BURKINA FASO	INERA
BF54	KB OR 1	ORANGE	KAMBOINSIN	BURKINA FASO	INERA
BF55	DJAKANI	WHITE	SAMOROUGOUAN	BURKINA FASO	INERA
BF56	BF 51	ORANGE	KOMBISSIRI	BURKINA FASO	INERA
MZ57	BELLA	ORANGE	-	MOZAMBIQUE	CIP
MZ58	IRENE	ORANGE	-	MOZAMBIQUE	CIP
NG59	MOTHER DELIGHT	ORANGE	-	NIGERIA	CIP
OG60	NASPOT 9	ORANGE	-	UGANDA	CIP
OG61	NASPOT 13	ORANGE	-	UGANDA	CIP
OG62	NEW KAWOGO	WHITE	-	UGANDA	CIP
US63	KB OR-4	ORANGE	-	USA	CIP
US64	PURPLE TUSKEGEE	PURPRE	-	USA	CIP

Site description

The trial was conducted during the rainy season from May to September at Davié Research Station (6° 23' 5" N; 1°12' 18" E and 76 m above sea level).The site has a sub-equatorial guinean climate, with two rainy seasons and two dry seasons. The long rainy season is observed from mid-March to the end of July and the short rainy season from September to mid-November (Ayisah et al., 2015). During the experiment, annual rainfall varied between 1000 and 1400 mm, while temperature ranged between 24 °C and 34 °C and relative humidity between 70% and 90%. The soil is ferralitic, slightly acidic, deep and draining. It has a sandy-loam texture and low nitrogen and phosphorus (Detchinli et al., 2017).

Experimental design, field layout and crop management

The experimental design adopted was a '9 x 9 lattice square' with three replicates (Figure 1). Each replicate was subdivided into 9 sub-blocks of 9 plots each. The replicates were separated by a distance of 1.5 m and the sub-blocks by 1 m. The plot measured 30 m² and consisted of six ridges 5 m long and 60 cm high. The ridges were spaced 1 m apart and 16 cuttings were planted on each ridge at 0.3 m intervals. Data were collected from the plants of the four central rows within each plot.

Prior to thetrial establishment, the site was first ploughed deeply using a tractor. Ridges were then made in accordance with the sweet potato cropping pattern. On each ridge, eight weeks old cuttings, 20 cm long and with at least 4 nodes were planted. In each of the replications, the varieties were randomly assigned to each plot using CROPSTAT software. In total, ninety-six (96) cuttings per variety were planted in each plot at a spacing of 0.3 m on the row and 1 m between rows. After planting, each plot was labelled with the variety code, plot number, replication number and planting date. The field was kept weed free at an interval of one weeding every three weeks. Harvesting was carried out 5 months after planting, when the varieties reached physiological maturity, and data were collected using the protocol described by the International Potato Centre.

Data collection

A total of sixteen (16) quantitative traits from the CIP/AVRDC/IBPGR sweetpotato descriptor proposed by Huamàn (1991) were evaluated from the vegetative phase to harvest (Table 3). These traits were evaluated on four central rows of each of the plots. Data collected on the stem and leaves were measured at 3 MAP, while those relating to roots were collected at 5 MAP. Flowering and the production cycle were also observed throughout the experiment.

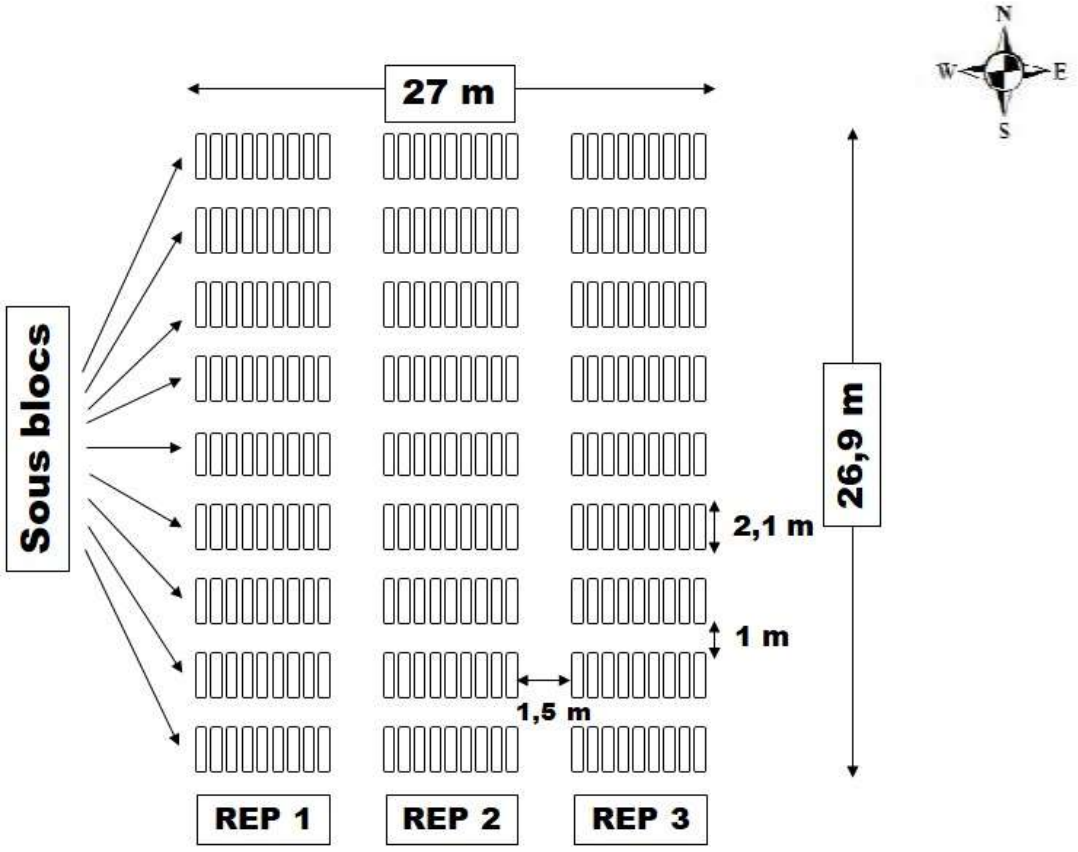

Figure 1:- Diagram of the experimental design.

Table 3:- Quantitative traits measured and method of evaluation during the experiment.

N°Characters	Code	Evaluation method	
Stem (3 MAP)	1	Length of main stem	LgTiP	Measure length of main stem from base to tip (cm)
	2	Length of internodes	LgEN	Average expression of the length measured on 4 internodes taken from the median section of the stem (cm)
	3	Diameter of internodes	DmEN	Average diameter measured on 4 internodes taken from the median section of the stem (cm)
Leaf 4 (3 MAP)		Length of mature leaf blades	LgLIMB	Mean expression of the length of the leaf blades of 4 leaves located in the middle part of the stem (cm)
	5	Length of petioles	LgPET	Average length of petioles of 4 leaves in the middle part of the main stem (cm)
Root6 (5 MAP)		Length of root stalk	LPeRT	Measurement of the length of the peduncles joining the roots to the main stem (cm)
	7	Thickness of root cortex	ECoRT	Measurement of the length of the thickness of 4 roots per plant (cm)
	8	Average length of roots	LgRT	Measurement of the average length of 4 roots per plant in the plot (cm)
	9	Average diameter of roots	DmRT	Measurement of the average diameter of 4 roots per plant in the plot (cm)
	10	Diameter/length ratio of roots	DmRT/LgRT	Ratio of average diameter to average length of roots

	11	Number of marketable roots per plant	NbRT	Average of 10 plants
	12	Average weight of roots per plant	PMRT	Measurement of the weight of all roots per plant (Kg)
	13	Fresh root yield	RdTF	Weight of fresh roots in a plot extrapolated in tons per hectare ($t.ha^{-1}$)
	14	Dry matter content	TMS	Percentage between the weight of dry roots and the weight of fresh roots
Biomass (5 MAP)	15	Aboveground biomass	BMA	Measurement of the weight of fresh aboveground biomass per plot and extrapolated in tonnes per hectare ($t.ha^{-1}$)
	16	Harvest index	IR	Ratio of root yield to total biomass

Data analyses

Data collected was entered and treated using Excel version 2016. They were then subjected to a descriptive analysis, an analysis of variance (ANOVA) and multivariate analyses (PCA, AHC and AFD) in order to highlight the traits and groups of interest within the collection (Agre et al., 2023). A correlation test was carried out between the variables in order to study the relationships that might exist between them. PCA was performed to determine the contribution of quantitative traits to the total variability of the collection. The Kaiser criterion ("absolute" criterion) was used to determine the number of axes to be taken into account when interpreting the PCA results. According to this criterion, axes with eigenvalues greater than 1 were retained (Gobena et al., 2022). Cluster analysis was carried out on the basis of the coordinates of the varieties on the relevant PCA axes, using Ward's method (Ward, 1963) as the aggregation criterion. The optimal number of clusterswas determined by comparing the intra-cluster and inter-cluster variance of the groups resulting from the AHC. These groups were then used as categorical variables to perform a discriminant factor analysis (DFA). The purpose of the DFA was to characterise the AHC groups and to test the validity of the classification. Mahalanobis distances were then used to study the relationships between the groups derived from the AHC. Analyses were performed using Statistix version 10 and XLSTAT version 2016.

Results:-

Agronomic performances of varieties

The agronomic performances of the varieties are shown in Table 4. Mean stem length (LgTiP) was 252.08 ± 72.98 cm and ranged from 96.67 to 513.33 cm. Internode length (LgEN) ranged from 2.67 to 11.67 cm, with an average value of 6 ± 1.51 cm. With an average value of 20.51 ± 4.60 cm, petiole length (LgPET) varied from 11 cm to 33.72 cm. The fresh root yield (RdTF) varied from 2.7 $t.ha^{-1}$ to 57 $t.ha^{-1}$ with an average of 17.47 ± 10.22 $t.ha^{-1}$. The average root weight (TRW) varied between 0.06 kg and 1.87 kg; the dry matter content (DMC) between 16.94% and 76.21% and the above-ground biomass (ABM) between 3.6 and 154.25 $t.ha^{-1}$ (Table 4).

With the exception of the traits internode diameter (DmEN), leaf blade length (LgLIMB), dry matter content (TMS) and cortex thickness (ECoRT), the other traits showed a high coefficient of variation (CV>20%). In addition, ANOVA revealed significant differences between varieties for all the traits assessed (Table 4).

Table 4:- Agronomic performances of a collection of sweet potato from Togo.

Variables	Minimum	Maximum	Mean ± standard deviation	CV(%)	F
LgTiP (cm)	96,67	513,33	252,08 ±72,98	28,95	11,04**
LgEN (cm)	2,67	11,67	6,00 ± 1,51	25,18	10,17**
DmEN (cm)	0,42	0,95	0,63 ± 0,12	19,04	17,09**
LgLIMB (cm)	8,50	20,67	12,47 ± 1,71	13,74	12,46**
LgPET (cm)	11,00	33,72	20,51 ± 4,60	22,44	6,17**
PMRT (kg)	0,06	1,87	0,28 ± 0,19	70,27	1,81*
RdTF ($t.ha^{-1}$)	2,70	57,00	17,47 ± 10,22	58,52	2,44**
IR	0,05	0,81	0,36 ± 0,16	45,85	2,30**
TMS (%)	16,94	76,21	25,42 ± 5,06	19,90	22,97**
NbRT	1,00	5,00	2,26 ± 0,90	39,67	2,13**

BMA (t.ha $^{-1}$)	3,60	154,25	36,12 ± 24,63	68,21	2,89**
LgRT (cm)	10,50	42,00	22,09 ± 5,40	24,45	4,32**
DmRT (cm)	2,10	16,30	6,37 ± 1,90	29,85	5,50**
DmRT/LgRT	0,09	0,80	0,31 ± 0,13	42,97	6,70**
LPeRT (cm)	1,20	31,50	7,74 ± 4,98	64,35	3,61**
ECoRT (mm)	2,00	5,00	3,77 ± 0,69	18,40	1,73*

LgTiP: Length of main stem; LgEN: Length of internodes; DmEN: Diameter of internodes; LgLIMB: Length of mature blades; LgPET: Length of petioles; PMRT: Average weight of roots (RT); RdTF: Fresh RT yield; IR: Harvest index; TMS: Dry matter content; NbRT: Number of RT per plant; BMA : Aboveground biomass; LgRT: Length of RT; DmRT: Diameter of root; DmRT/LgRT: Ratio of diameter to length of root; LPeRT: Length of peduncle of root; ECoRT: Thickness of cortex of root; SD: Standard deviation; CV: Coefficient of variation; F: Fisher's value; *: Significant difference at 5%, **: Significant difference at 1%.

Phenotypic correlations between traits

Significant correlations were observed between foliage characteristics (Table 5). Internode diameter (DmEN) was positively correlated with petiole length (LgPET) (r = 0.81) and blade length (LgLIMB) (r = 0.45), while main stem length (LgTiP) was correlated with internode length (LgEN) (r = 0.81); and petiole length (LgPET) was correlated with blade length (LgLIMB) (r = 0.58). Aboveground biomass (BMA) was correlated with internode diameter (DmEN) (r = 0.45), petiole length (LgPET) (r = 0.45) and leaf blade length (LgLIMB) (r = 0.25). (Table 5).

Significant correlations were also observed between agronomic traits. Fresh root yield (RdTF) was positively correlated with average root weight (PMRT) (r = 0.73), root diameter (DmRT) (r = 0.58), harvest index (IR) (r = 0.35) and number of roots (NbRT) per plant (r = 0.31). Root yield (RdTF) was also correlated with aboveground biomass (BMA) (r = 0.44), internode diameter (DmEN) (r = 0.39) and petiole length (LgPET) (r = 0.34) (Table 5).

Dry matter content (TMS) is negatively correlated with above-ground biomass (BMA) (r = -0.29), root yield (RdTF) (r = -0.25), root weight (PMRT) (r = 0.24), internode diameter (DmEN) (r = -0.26) and petiole length (LgPET) (r = -0.23).

Table 5:- Correlation between quantitative traits measured in a collection of sweet potato from Togo.

Variables	LgTiP	LgEN	DmEN	LgLIMB	LgPET	PMRT	RdTF	IR	TMS	NbRT	BMA	LgRT	DmRT
LgTiP	**1**												
LgEN	**0,81****	**1**											
DmEN	**-0,34***	**-0,36****	**1**										
LgLIMB	**-0,25***	**-0,31***	**0,45****	**1**									
LgPET	**-0,23***	-0,17	**0,81****	**0,58****	**1**								
PMRT	-0,11	-0,1	**0,46****	0,08	**0,34***	**1**							
RdTF	-0,17	-0,19	**0,39****	**0,26***	**0,34***	**0,73****	**1**						
IR	-0,12	-0,12	-0,17	-0,03	-0,17	**0,29***	**0,35****	**1**					
TMS	0,13	-0,07	**-0,26***	0,08	**-0,23***	**-0,24***	**-0,25***	0,09	**1**				
NbRT	-0,07	-0,14	-0,12	0,2	-0,11	**-0,29***	**0,31***	0,05	0,06	**1**			
BMA	-0,22	-0,17	**0,45****	**0,25***	**0,45****	**0,37****	**0,44****	**-0,48****	**-0,29***	0,04	**1**		
LgRT	-0,03	0,04	0,18	0,18	**0,3***	0,12	0,16	0,14	-0,13	0,06	-0,03	**1**	
DmRT	-0,2	-0,15	0,22	0,03	0,06	**0,6****	**0,58****	**0,48****	-0,12	0,01	-0,04	**-0,24***	**1**
DmRT/LgRT	-0,13	-0,14	0,03	-0,14	-0,17	**0,33***	**0,27***	**0,27***	-0,02	-0,05	-0,04	**-0,72****	**0,8****
LPeRT	0,1	0,14	**0,34***	-0,11	**0,29***	**0,25***	-0,04	-0,2	-0,14	**-0,32***	0,07	0,1	0,04
ECoRT	-0,06	-0,07	**0,3***	-0,03	**0,23***	**0,25***	0,19	-0,12	-0,1	-0,03	0,17	0,15	0,06

LgTiP: Length of main stem; LgEN: Length of internodes; DmEN: Diameter of internodes; LgLIMB: Length of mature blades; LgPET: Length of petioles; PMRT: Average weight of roots (RT); RdTF: Yield in fresh root; IR: Harvest index; TMS: Dry matter content; NbRT: Number of root per plant; BMA: Aboveground biomass; LgRT: Length of root; DmRT: Diameter of root; DmRT/LgRT: Ratio of diameter to length of root; LPeRT: Length of peduncle of root; ECoRT: Thickness of cortex of root; *: Significant correlation at the 5% level, **: Significant correlation at the 1% level.

Traits of interest identified in the germplasm

The first seven (7) axes, each with an eigenvalue greater than or equal to one and explaining 85.13% of the germplasm variability, were selected (Table 6). Axis 1, with 24.73% of the germplasm variability, combines the traits internode diameter (DmEN), petiole length (LgPET), average root weight (PMRT), fresh root yield (RdTF) and aboveground biomass (BMA). This is defined as the productivity axis. Axis 2, with 17.23% of the germplasm

variability, is positively correlated with harvest index (RI), root diameter (DmRT), and root diameter to length ratio (DmRT/LgRT). This axis is therefore defined as the tuberisation axis. Axis 3, with 12.69% inertia, combines the traits length of main stem (LgTiP), length of internodes (LgEN), number of roots and length of root stalk (LPeRT). It can therefore be defined as the axis of the plant's vegetative development (Table 6).

Table 6:- Eigenvalues and contributions of quantitative variables to the composition of the first seven PCA axes.

	PC 1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**
Eigenvalue	3,96	2,76	2,03	1,59	1,29	1,07	0,92
Variability (%)	24,73	17,23	12,69	9,96	8,07	6,69	5,75
Cumulative	24,73	41,97	54,65	64,62	72,68	79,38	85,13
LgTiP	-0,25	-0,05	**0,40**	0,21	0,31	0,35	0,13
LgEN	-0,23	-0,06	**0,46**	0,23	0,31	0,22	-0,06
DmEN	**0,41**	-0,18	0,04	-0,11	-0,13	0,15	0,02
LgLIMB	0,24	-0,17	-0,33	0,05	0,04	**0,53**	-0,04
LgPET	**0,37**	-0,28	0,03	0,01	-0,07	0,29	-0,05
PMRT	**0,37**	0,17	0,28	0,17	-0,02	0,00	0,00
RdtF	**0,38**	0,18	-0,01	0,29	0,34	-0,03	0,04
IR	0,04	**0,38**	-0,11	0,48	-0,27	0,01	-0,09
TMS	-0,18	0,06	-0,21	-0,01	-0,20	0,50	**0,54**
NbRT	-0,01	0,04	**-0,40**	0,17	0,51	-0,06	0,20
BMA	**0,29**	-0,20	0,03	-0,27	0,43	-0,09	-0,07
LgRT	0,08	-0,32	-0,04	**0,58**	-0,17	-0,17	-0,06
DmRT	0,26	**0,46**	0,11	0,05	-0,01	0,10	0,02
DmRT/LgRT	0,12	**0,51**	0,10	-0,30	0,05	0,11	0,04
LPeRT	0,11	-0,15	**0,42**	-0,09	-0,29	0,07	0,05
ECoRT	0,17	-0,11	0,15	0,03	-0,03	-0,36	**0,79**

LgTiP: Length of main stem; LgEN: Length of internodes; DmEN: Diameter of internodes; LgLIMB: Length of mature blades; LgPET: Length of petioles; PMRT: Average weight of tuberous roots (RT); RdTF: Fresh RT yield; IR : Harvest index; TMS: Dry matter content; NbRT: Number of RT per plant; BMA: Above-ground biomass; LgRT: Length of RT; DmRT: Diameter of RT; DmRT/LgRT: Ratio of diameter to length of RT; LPeRT: Length of RT peduncle; ECoRT: Thickness of RT cortex.

Identification and characterisation of heterotic groups

Cluster analysis has revealed four distinct groups (Figure 2). These groups are made up of 16, 11, 20 and 33 varieties respectively (Table 7). Discriminant factor analysis (DFA) was used to characterise the 4 groups resulting from the cluster analysis on the basis of the quantitative traits studied (Figure 3). Group I (GI) varieties are characterised by long stems (350.14 cm), long internodes (7.41 cm), short petioles (18.62 cm), average biomass yield (28.35 t/ha), low fresh root yield (12.94 t/ha) and high dry matter content (29.68%). Group II (GII) varieties are characterised by poorly developed vegetative apparatus (short stems (163.03 cm), short internodes (4.45 cm), medium-length petioles (19.47 cm)), low biomass yield (22.68 t/ha), low root yield (15.87 t/ha) and high dry matter content (26.86%). Group III (GIII) is made up of varieties with average vegetative apparatus (stem length = 280.87 cm, internode length = 6.54 cm, internode diameter = 0.6, petiole length = 19.93 cm), biomass yield = 37.74 t/ha, average tuberous root yield = 16.06 t/ha and average dry matter content = 24.62%). Group IV (GIV) is made up of varieties with a highly developed vegetative apparatus (stem length = 216.76 cm, internode length = 5.52 cm, internode diameter = 0.67 cm, petiole length = 22.12 cm), a very high biomass yield (50.75 t/ha), an average root yield (20.18 t/ha) and an average dry matter content (23.84%). Significant differences were revealed between the groups by considering the Mahalanobis distances (Table 8). Groups I and II are the most genetically distant (d = 68.86) and groups III and IV are genetically closer (d = 9.49). Analysis of variance (ANOVA) also revealed significant differences between groups for the traits stem length (LgTiP), internode length (LgEN), internode diameter (DmEN), petiole length (LgPET), tuberous root yield (RdTF), dry matter content (TMS) and biomass yield (BMA) (Table 9).

Table 7:- Composition of four heterogeneous groups resulting from the AHC on the basis of quantitative characteristics measured in a collection of sweet potatoes from Togo.

Group	**Group I**	**Group II**	**Group III**	**Group IV**
Number of variety	16	11	20	33

Variety					
	BF49	BF55	BF50	BF52	TG40
	BF51	MZ57	TG12	BF53	TG41
	BF54	MZ58	TG13	BF56	TG45
	NG59	OG60	TG16	OG62	TG46
	TG28	TG11	TG22	OG61	TG71
	TG30	TG25	TG29	TG24	TG72
	TG31	TG01	TG33	TG34	TG74
	TG32	TG20	TG36	TG42	TG76
	TG48	TG07	TG38	TG66	TG08
	TG06	TG65	TG39	TG67	TG10
	TG68	TG69	TG79	TG75	TG37
	TG73		TG14	TG78	TG04
	TG17		TG18	TG02	TG43
	TG47		TG19	TG21	TG05
	TG77		TG23	TG27	TG80
	TG15		TG26	TG03	US64
			TG44	TG35	
			TG70		
			TG09		
			US63		

Table 8:- Mahalanobis distance between the 4 groups resulting from the AHC on the basis of quantitative characteristics measured in a collection of sweet potatoes from Togo.

	Group I	**Group II**	**Group III**	**Group IV**
Group I	0			
Group II	**68,86****	0		
Group III	**11,26****	**28,88****	0	
Group IV	**37,95****	**11,56****	**9,**49**	0

**: significant difference at the 5% and 1% thresholds respectively.

Table 9:- Average performance of 4 groups based on quantitative traits measured in a sweet potato collection of Togo.

Variables	**GI**	**GII**	**GIII**	**GIV**	**F**
LgTiP (cm)	**350,14^{a}**	**163,03^{d}**	**280,87^{b}**	216,76^{c}	128,66**
LgEN (cm)	**7,41^{a}**	**4,45^{d}**	**6,54^{b}**	5,52^{c}	22,72**
DmEN (cm)	**0,56^{b}**	0,64^{ab}	**0,6^{b}**	**0,67^{a}**	5,1*
LgLIMB (cm)	12,12^{a}	12,9^{a}	12,31^{a}	12,6^{a}	0,65^{ns}
LgPET (cm)	18,63^{b}	19,47^{b}	19,93^{b}	**22,12^{a}**	3,69*
PMRT (kg)	0,22^{b}	0,25^{ab}	0,25^{ab}	0,31^{a}	2,42^{ns}
RdTF (t/ha)	**12,95^{b}**	**15,87^{ab}**	16,06^{ab}	**20,18^{a}**	3,53*
IR	0,33^{a}	0,42^{a}	0,32^{a}	0,34^{a}	1,87^{ns}
TMS (%)	**29,68^{a}**	26.86ab	**24,62b**	23,84b	3,49*
NbRT	2,12^{a}	2,29^{a}	2,38^{a}	2,32^{a}	0,44^{ns}
BMA (t/ha)	28,35^{b}	**22,68^{b}**	**37,74^{b}**	**50,75^{a}**	7,33**
LgRT (cm)	20,55^{b}	20,6^{ab}	22,06^{ab}	23,35^{a}	2,03^{ns}
DmRT (cm)	5,76^{b}	7,10^{a}	6,06^{ab}	6,6^{ab}	2,01^{ns}

DmRT/LgRT	0,30[a]	0,37[a]	0,29[a]	0,31[a]	1,24[ns]
LPeRT (cm)	7,69[a]	7,46[a]	8,96[a]	7,21[a]	0,82[ns]
ECoRT (mm)	3,53[a]	3,50[a]	3,88[a]	3,91[a]	1,84[ns]

LgTiP: Length of main stem; LgEN: Length of internodes; DmEN: Diameter of internodes; LgLIMB: Length of mature leaf blades; LgPET: Length of petioles; PMRT: Average weight of roots; RdTF: Fresh root yield; IR: Harvest index; TMS: Dry matter content; NbRT: Number of root per plant; BMA: Aboveground biomass; LgRT: Length of RT; DmRT: Diameter of root; DmRT/LgRT: Ratio of diameter to length of root; LPeRT: Length of peduncle of root; ECoRT: Thickness of cortex of root; F: Fisher's value; *: significant difference at 5%, **: significant difference at 1%, ns: not significant.

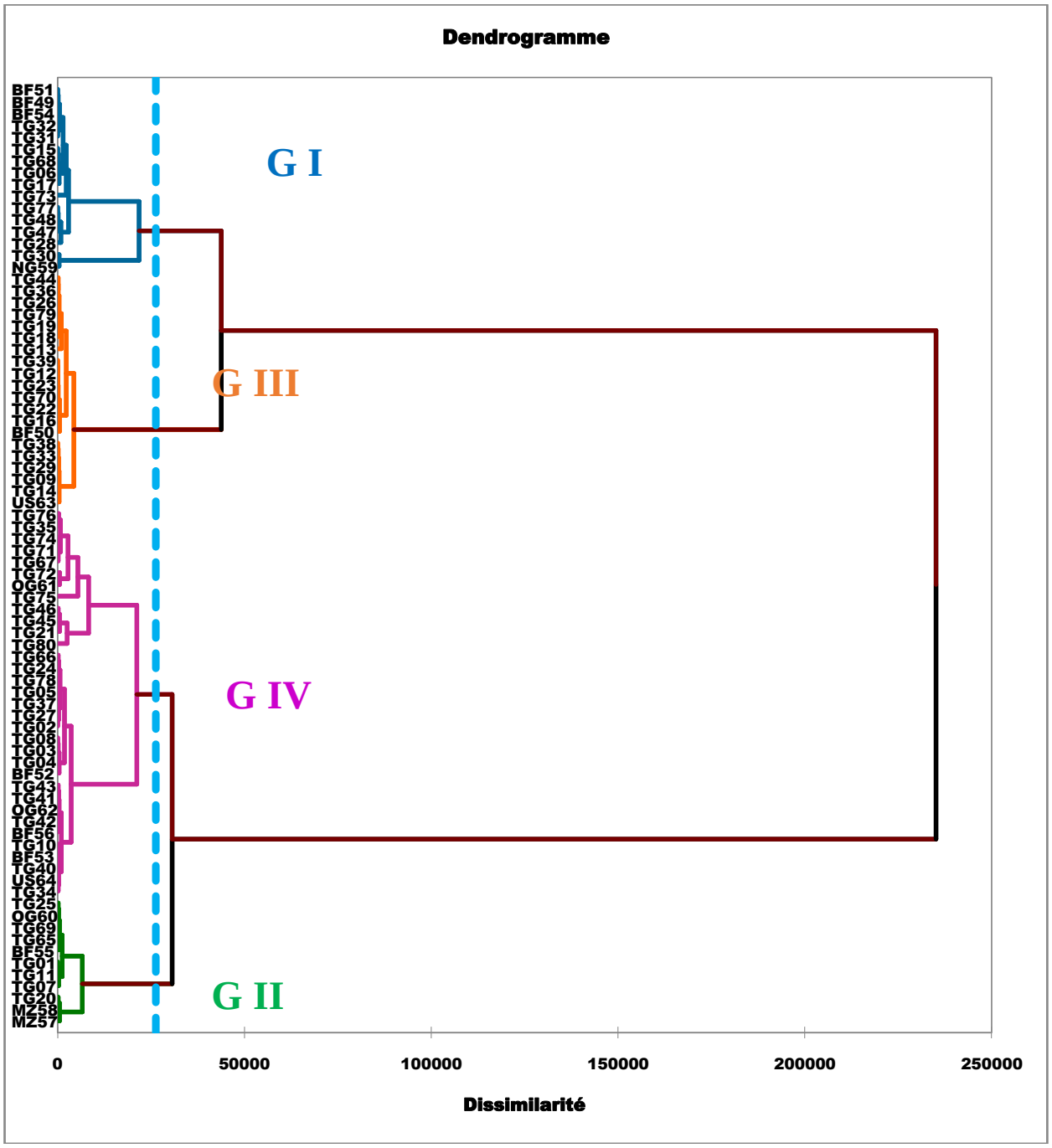

Figure 2:- Dendrogram from the HAC of the Togo sweet potato collection based on quantitative traits.

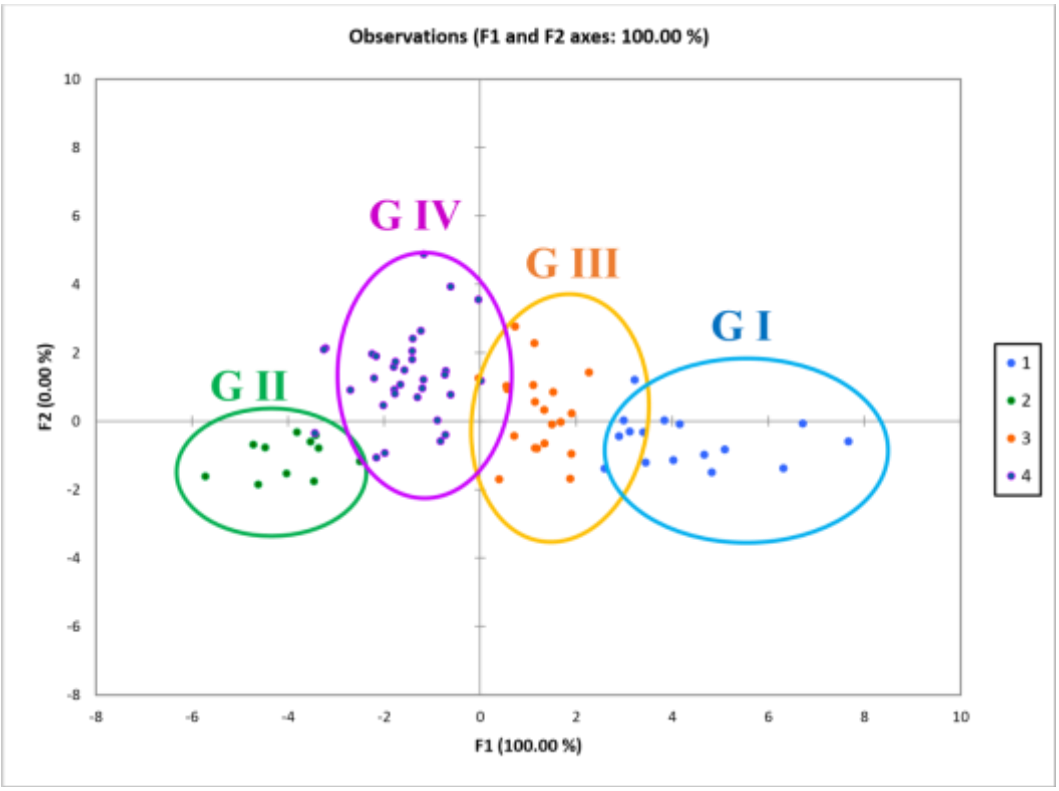

Figure 3:- Projection of four groups from the AHC on the basis of quantitative characteristics of a collection of sweet potatoes from Togo in the plane formed by the first two axes of the SFM..

Discussion

Agronomic performances of varieties

Descriptive analysis of the traits measured revealed significant differences between the varieties. As a result, most of the traits had a high coefficient of variation. The differences observed and the high coefficients of variation indicate the existence of considerable variability within the germplasm studied. The analysis of variance of the traits also revealed significant genotype effects, highlighting a high level of phenotypic variability for the different traits. These results corroborate those found by Gobena et al (2022) in Ethiopia and byKouassi et al (2023) in Côte d'Ivoire. This phenotypic variability is thought to be the result of farmers' seed management practices, in particular the exchange of cultivars between farmers, which is the source of significant diversity between cultivated plant populations (Karuri et al., 2010; Veasey et al., 2007).

Correlation between quantitative traits

Positive and significant correlations were observed between traits related to aboveground organs (root diameter, petiole length and aboveground biomass) and those related to below-ground organs (root yield, average root weight, number of roots per plant and harvest index). These significant correlations suggest a high degree of proportionality between the vegetative organs of the sweet potato. According to Koechlin (1989) and Ouédraogo (2016), these traits have an identical genetic and environmental link, meaning that they are governed by the same group of genes. The positive correlations found between these traits indicate that genotypes with strong vegetative development are the most productive. Tarpaga (2001) also found that long-cycle cultivars are the most productive. According to ITRA (2008), strong vegetative development favours root production, with an increase in small roots. Strong correlations between vegetative traits were also observed in the work of Lebot (2019). Strong correlations were observed between root yield and internode diameter and between root yield and petiole length. This result indicates that genotypes with large internodes and long petioles have good root yields. So, for high root production, selection should focus on genotypes with large internodes and long petioles. Dry matter content was negatively correlated

with aboveground biomass, root yield, average root weight, internode diameter and petiole length. These correlations indicate that cultivars with developed vegetative apparatus have low dry matter content and high productivity. The negative correlations found between dry matter content and yield components were also reported by Nanema (2005).

Identification and characterisation of heterotic groups

The collection was structured into four phenotypic groups whose distinguishing characters are: stem length, internode length, internode diameter, petiole length, above-ground biomass, root yield, harvest index and dry matter content. These results corroborate those of Shumbusha et al. (2017) who mentioned the parameters relating to foliage, root yield and dry matter content as being relevant in structuring the phenotypic variability of a collection of sweetpotato cultivars from Rwanda.

Analysis of the composition of the four phenotypic groups reveals that each group is made up of local or exotic varieties from different agro-ecological zones. With reference to the collection survey, farmers acquire their seed by donation, exchange or purchase. This method of obtaining seed could be a factor in the dispersal of varieties from one village to another or from one agro-ecological zone to another (Doussoh et al., 2016; Rukundo, 2015). Theclusters identified are different in terms of the genetic distance. However, these clusters can be grouped together with a view to sweetpotato breeding in Togo. Groups I and II are made up of genotypes with high dry matter content, while groups III and IV are made up of genotypes with high root and aboveground biomass productivity. In the short term, it is suggested that multi location trials be conducted over at least three consecutive years with the aim of selecting stable, high performance genotypes for dissemination to growers in order to boost sweet potato productivity at national level. In the long term, a programme to create new varieties for industrial and nutritional use could exploit this variability in the choice of parent genotypes.

Conclusion

Knowledge of the phenotypic variability of a germplasm is a prerequisite for a breeding programme The specific objective of this study was to assess the phenotypic diversity of agermplasm bank cultivars grown across the country. The study revealed a great deal of variability within Togo's sweetpotato germplasm. The phenotypic diversity observed is mainly organised around the following traits: root yield, dry matter content, aboveground biomass, stem length, internode length and petiole diameter. In all, four distinct phenotypic groups of agronomic interest were identified. These phenotypic groups offer opportunities for breeding or creating new varieties in Togo. However, evaluation of the agronomic and phytosanitary potential (resistance or tolerance of cultivars to virus and weevils) of the varieties over at least three consecutive years in the various agroecologies of production in Togo is essential in order to understand their phenotypic stability. Genotyping of this gene bank is also necessary to complete this study. This should provide a better picture of the germplasm genetic diversity and enable the establishment of a national *core* collection for breeding purpose in Togo. However, the introduction of new varieties from national sweetpotato research programmes and systems should broaden the genetic base of this gene bank for use in a breeding programme.

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