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Phenotypic evaluation of six cassava families (*Manihot esculenta* Crantz) from seed in Burkina Faso

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Abstract

Phenotypic markers are important in plant genetic characterisation studies. They are used in the present study to assess the phenotypic structuring of cassava genotypes obtained by biparental crossing. The plant material studied consists of 56 cassava genotypes from the third generation of vegetative reproduction following germination of seeds from six families resulting from crosses. To evaluate these genotypes, an Alpha lattice experimental design was used with three replicates and three blocks per replicate. Blocks I and II each contained 19 genotypes and block III 18 genotypes. Data was collected on 10 qualitative traits on leaves, stems and roots. All the variables evaluated presented several modalities. The frequencies showed that: the green-purple color (41%) was dominant for the apical leaf color characteristic. Stems color were predominantly light brown (30%). Green color (57%) was most common in the petioles. Genotypes showed more dichotomous ports (44%). In addition, the relative Shannon-Weaver diversity index (H') was very high for all characters within genotypes (H'=0.90) and families (H'=0.66). The most polymorphic traits between genotypes were flowering ability (H'=1), stem color (H'=0.99), tuberous root texture (H'=0.97), apical leaf color (H'=0.96) and branching type (H'=0.93). The same index showed high intra-family diversity, family VI (H'= 0.83), family II (H'= 0.76), family IV (H'=0.69), family I (H'= 0.61), family III (H'= 0.53) and family V (H'= 0.52) showing high internal variability. ACH was used to structure the genetics into three phenotypic groups. This observed diversity can be used for cassava breeding in Burkina Faso.

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Introduction

Manioc (*Manihot esculenta* Crantz 1766) is a perennial shrub 1 to 5 m high (Allem, 2002; Alves, 2002). It belongs to the class Dicotyledones, family Euphorbiaceae, genus *Manihot* and species *Manihot esculenta* Crantz (Isendahl, 2011; Soro, 2022). It has a diploid chromosome number of 2n=36 and a highly heterozygous genome (Alves, 2002). It is one of the most important tuberous root crops, highly valued for its starch content in tropical countries (N'Zué *et al.*, 2014). Cassava is grown all over the world, particularly in West Africa (Agré *et al.*, 2015). Cassava can be grown in areas with rainfall ranging from 500 mm to 8000 mm (François, 1989). Depending on the variety, production can be spread over a long period of the year, making the tuberous roots available when needed (François, 1989).

In recent years in Burkina Faso, climate variability has made farming very difficult. Crop diversification is very important to ensure food self-sufficiency. Tuber and root crops such as cassava can therefore be used to help achieve sustainable food security. In Burkina Faso, cassava production was estimated at around 17,081.25 tonnes in 2022 (FAOSTAT, 2024). As in all African countries, almost all cassava production in Burkina Faso is used for human and animal consumption (Amani *et al.*, 2007). The tuberous roots are eaten raw or in the form of local dishes: boiled roots, grilled roots, placali, con'godê, attiéké and gari (Guira *et al.,* 2017). In view of its food and nutritional potential, the quantities of cassava produced remain below national market demand, which in 2017 was estimated at around 124,917 tonnes of fresh tubers (Soro *et al.,* 2022). In Burkina Faso, the major constraints to large-scale production are linked to several factors, namely: the long production cycle of six to 9 or even 12 months, the unsuitable quality of the soils used for its cultivation, which results in low root yields, the lack of suitable varieties, and the very narrow genetic base of cassava (Gmakouba *et al.*, 2018). In order to meet consumer needs, production must be increased, and this requires efficient production technology based on the use of improved cassava varieties.

Exchanges of genetic material between producers mean that they end up with duplicates of the same cultivar (Soro *et al.,* 2022). The reproduction of cassava, which is generally done by cuttings, leads to the spread of its bio-aggressors, which become more and more numerous and infest new fields. Studies carried out by Tiendrébéogo *et al.* (2009, 2012) reported the presence of Cassava Mosaic Diseases (CMD) in certain areas of Burkina Faso. Cassava is often grown under rainfed and irrigated systems in Burkina Faso. This is due to the earliness of the rains in relation to the length of the vegetative cycle and the poverty of the arable land, which means that average yields in farming areas are low, less than or equal to 15t/ha (FAOSTAT, 2024). In response to this situation, a great deal of research has been carried out by INERA through the introduction and evaluation of six (06) improved varieties, catalogued and popularised, TMS 4(2) 1425; TMS 91/02312; TMS 92/0067; TMS 92/0325; TMS 92/0427; TMS 94/0270) with potential yield (40/ha) (Gmakouba, 2018; Soro, 2022; MASA, 2014). But of these, only TMS 94/0270, commonly known as V5, is the most widely produced for its very good attiéké quality. To meet this challenge, new cassava varieties need to be developed, with a view to broadening the genetic base so as to obtain varieties that are tolerant to FGD, rich in beta-carotene, and with yields of up to 40 tonnes per hectare. It is therefore essential to assess the agro-morphological diversity of this cassava collection (*Manihot esculenta* Crantz) in order to better exploit the potential of these genotypes. This study was therefore carried out with the overall aim of determining the structure of the 56 genotypes obtained by biparental crossing. Specifically, the aim was (i) to determine the variability of genotypes through phenotypic traits and (ii) to identify the traits that best discriminate between genotypes and families.

Materials and methods

Experimental site

The trial was planted on 8 August 2022 and harvested on 10 January 2024 on experimental plots at the Environmental, Agricultural Research and Training

Centre of Kamboinsé (CREAF/K). The center is located at longitude 001° 32.583'W, latitude 12°27.326' N and altitude 298 m (GARMIN GPSMAP 64S). According to Guinko (1984), the center has a North Sudanian climate, with two alternating seasons: a rainy season from June to October and a dry season from November to May. The site receives an average of 800 mm of rainfall per year. According to meteorological data from the Kamboinsé station in 2022 and 2023, the wet crop years of 2022-2023 and 2023-2024 recorded 1091.7 mm of rain in 57 days and 689 mm of rain in 48 days respectively. Over the same period, during the trial, average monthly temperatures ranged from 22.6°C (January 2022) to 36.2°C (June 2023). The extermes temperatures recorded ranged from 12.8°C in January 2022 to 46.8°C in May 2023. Fig. 1 below shows the rainfall and temperature variations recorded during the trial.

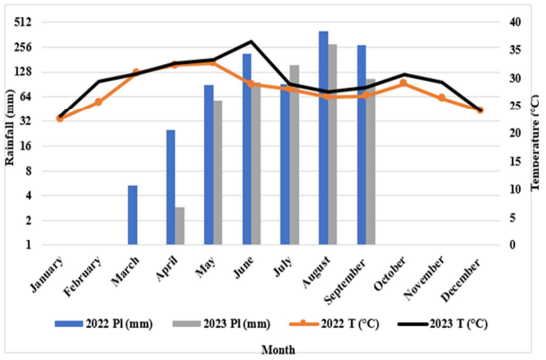

Fig. 1. Umbrothermal histogram for the Kamboinsé station in 2022 and 2023

Plant material

The plant material consists of 56 cassava genotypes. These genotypes come from six cassava families obtained by seed germination. The seeds are obtained by biparental crossing. These clonal hybrids are descended from high-performance parents with a high carotenoid content and a high dry matter content of between 25 and 29%. The parents were crossed in Nigeria by the cassava team at International Institute of Tropical Agriculture (IITA), and in Burkina Faso by poly cross where the female is known and the male parent is not. It was possible to obtain seeds in Nigeria thanks to good collaboration between IITA and INERA in Kamboinsé. These seeds were germinated at CREAF in Kamboinsé for this study. Genotypes are considered to belong to the same family if they are derived from the same biparental cross. The cuttings used in the trial were taken from the third generation of plants obtained after seeds germination. Table 1 below lists the genotypes studied and their families.

Table 1. Distribution of genotypes by family

Families	Females	Males	Hybrids/Genotypes
FAM I	TMS 30572	Poly cross	TMS 30572 (268)
FAM I			TMS 30572 (270)
FAM I			TMS 30572 (271)
FAM I			TMS 30572 (275)
FAM I			TMS 30572 (276)
FAM I			TMS 30572 (290)
FAM I			TMS 30572 (291)
FAM I			TMS 30572 (292)
FAM I			TMS 30572 (297)
FAM I			TMS 30572 (298)
FAM I			TMS 30572 (302)
FAM I			TMS 30572 (303)
FAM I			TMS 30572 (304)
FAM I			TMS 30572 (305)
FAM II	IBA070337	IKN130010	(IBA070337XIKN130010)-1
FAM II			(IBA070337XIKN130010)-11
FAM II			(IBA070337XIKN130010)-12
FAM II			(IBA070337XIKN130010)-14
FAM II			(IBA070337XIKN130010)-15
FAM II			(IBA070337XIKN130010)-16
FAM II			(IBA070337XIKN130010)-18
FAM II			(IBA070337XIKN130010)-2
FAM II			(IBA070337XIKN130010)-5
FAM II			(IBA070337XIKN130010)-9
FAM III	IBA070593	IBA011797	(IBA070593XIBA011797)-3
FAM III			(IBA070593XIBA011797)-4
FAM III			(IBA070593XIBA011797)-5
FAM III			(IBA070593XIBA011797)-7
FAM IV	IBA070593	IKN120210	(IBA070593XIKN120210)-1
FAM IV			(IBA070593XIKN120210)-14
FAM IV			(IBA070593XIKN120210)-2
FAM IV			(IBA070593XIKN120210)-3
FAM IV			(IBA070593XIKN120210)-4
FAM IV			(IBA070593XIKN120210)-8
FAM IV			(IBA070593XIKN120210)-9
FAM V	IBA070593	IIKN130010	(IBA070593XIKN130010)-1
FAM V			(IBA070593XIKN130010)-4
FAM V			(IBA070593XIKN130010)-5
FAM V			(IBA070593XIKN130010)-6
FAM V			(IBA070593XIKN130010)-9
FAM VI	TOGO 1	Poly cross	TOGO 1 (277)
FAM VI			TOGO 1 (278)
FAM VI			TOGO 1 (279)
FAM VI			TOGO 1 (279)
FAM VI			TOGO 1 (281)
FAM VI			TOGO 1 (282)
FAM VI			TOGO 1 (283)
FAM VI			TOGO 1 (284)
FAM VI			TOGO 1 (285)

FAM VI	TOGO 1 (286)
FAM VI	TOGO 1 (289)
FAM VI	TOGO 1 (290)
FAM VI	TOGO 1 (292)
FAM VI	TOGO 1 (293)
FAM VI	TOGO 1 (294)
FAM VI	TOGO 1 (296)
TOTAL	56

Experimental design

The experimental design used was an 'Alpha lattice' with three replicates. Each replication contains of 3 blocks. Blocks one and two contained 19 genotypes and block three contained 18 genotypes. The distance between blocks was 1.5 m and between replicates 2 m. The spacing between rows and between points where cuttings were planted was 1 × 1m. The line measured 4 m, with 5 planting points and was made up of the same genotype. The planting cuttings were 15 to 20 cm long and had at least three nodes. They were planted obliquely so that 1/3 of them were buried in the ground folow polar direction of the stem. To optimise competition between cassava plants and weeds, four (04) weedings were carried out during the vegetative phase of the plants. Water was added once every fortnight during dry periods during the trial from November 2022 to June 2023 and then from November 2023 to December 2023 in order to keep the plants alive and vigorous.

Data collection

The morphological descriptors used are those proposed by Fukuda *et al.* (2010). These descriptors have already been used by N'Zué *et al.* (2014); Agré *et al.* (2015) and Gmakouba *et al.* (2018) in agromorphological diversity studies of cassava grown in Côte d'Ivoire, Benin and Burkina Faso respectively. Ten (10) qualitatives traits taking into account leaves, stem, flowers and tuberous root were observed during the present study. The various observations were made on all the plants of the genotypes in each block. They were recorded at successive periods: at three, six and nine months after planting and then at harvesting of the tuberous roots. Table 2 below shows the said characters and the various scores relating to them observed during data collection.

Table 2. List of qualitative characteristics

Organs	Periods after planting (months)	Characters	Abbreviations	Phenotypic classes/scores
Leaves	3	Color of apical leaves	CAL	(3) Light green; (5) Dark-green; (7) Purplish-green; (9) Purple
	6	Shape of central leaflet	SCL	(1) Ovoid; (2) Elliptic-lanceolate; (3) Obovate-lanceolate; (4) Oblong-lanceolate; (5) Lanceolate; (6) Linear; (7) Pandurate; ...
	6	Petiole color	PEC	(1) Yellowish-green; (2) Green; (3) Reddish-green; (5) Greenish-red; (7) Red; (9) Purple.
Flowers	6	Flowering aptitude	FLAP	(0) Absent; (1) Present
Stems	9	Stem Color	SC	(3) Orange; (4) Yellow; (5) Golden; (6) Light-brown; (7) Silver; (8) Gray; (9) Dark-brown.
	9	Branching habit	BRH	(1) Erect; (2) Dichotomous; (3) Trichotomous.
	9	Color of end branches	CEB	(3) Green; (5) Green-purple; (7) Purple.
Roots	At harvest	Color of root pulp (parenchyma)	CRP	(1) White; (2) Cream; (3) Yellow
	At harvest	Root shape	ROS	(1) Conical; (2) Conical-cylindrical; (3) Cylindrical; (4) Irregular.
	At harvest	Texture of root epidermis	TRE	(3) Smooth; (5) Intermediate; (7) Rough

Data analysis

The data collected during the trial was entered into the Excel 2019 spreadsheet in the form of a « genotype × phenotype character » matrix. Data processing and frequency calculations were carried out using the same spreadsheet. Phenotypic character frequency distributions were calculated for all genotypes and within each family. The Shannon-Weaver diversity index noted (H) (Shannon and Weaver, 1949), as described by Jain *et al.* (1975) was calculated with the aim of determining the phenotypic diversity of cassava genotypes and revealing the

degree of polymorphism of the 10 qualitative traits analysed in order to detect the distribution of extra and intra family diversity. This formula was used to calculate the index.

$$H = -\sum_{i=1}^{n} piln(pi)$$

With:

H = Shannon-Weaver diversity index;

Pi = Frequency of each phenotypic class i of a given trait;

n = Number of phenotypic classes for each trait;

The Shannon-Weaver diversity index (H) was then converted into a relative phenotypic diversity index (H') by dividing it by its maximum value Hmax (ln (n)) to obtain values between 0 and 1.

$$H' = -\sum_{i=1}^{n} \frac{piln(pi)}{\ln(n)}$$

The relative or equitability diversity index of (H') reaches its minimum value, which is zero (0) for monomorphic characteristics. The value of the index increases with the degree of polymorphism of the characteristics. It reaches its maximum value of one (1) when all phenotypic classes have equal frequencies (Belhadj *et al.*, 2015; Gashaw *et al.*, 2016; Ka *et al.*, 2020; Sawadogo *et al.*, 2022).

Results

Phenotypic characteristics of cassava genotypes and families

Comparative analysis of the results for qualitative characteristics showed a diversity of colors and shapes between genotypes and within each family.

Leaf characteristics

The results of the morphological observations on the leaves showed variability for all the qualitative characteristics studied. As regards the coloration of the apical leaves, four modalities were observed: light-green (20%), dark-green (20%), green-purple (40%) and purple (20%). As for the families, they showed varying frequencies in the color of the young leaves. The families II and III had more genotypes with green apical leaves (60%) and (75%) respectively. The families I and V had a majority of genotypes with green-purple apical leaves (41%) and purple apical leaves (60%) respectively. The Figs 2 and 3 below show the distribution of frequencies of the different modalities linked to the coloration of the apical leaves of the families.

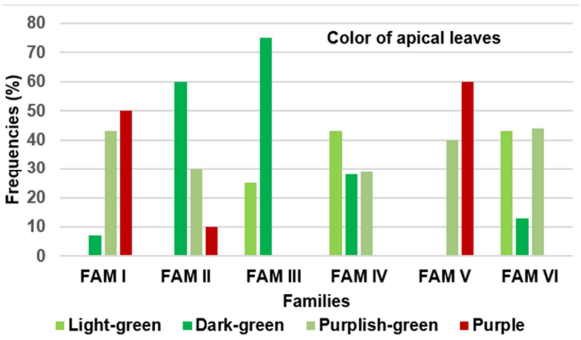

Fig. 2. frequencies distribution linked to the coloration of the apical leaves of genotypes within each

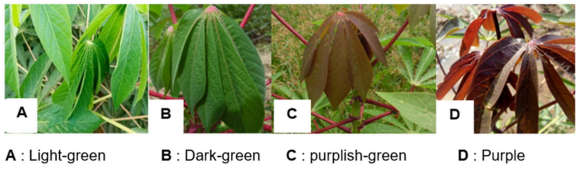

Fig. 3. Different colors of apical leaves

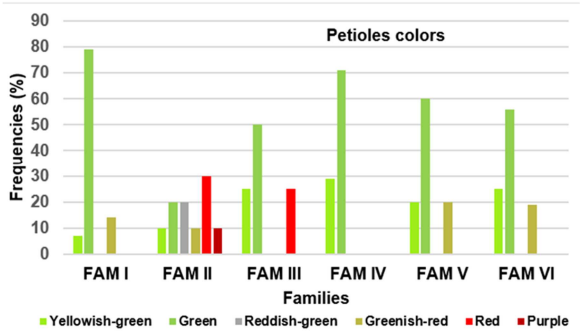

Fig. 4. Frequency distribution of leaf petiole color for each family

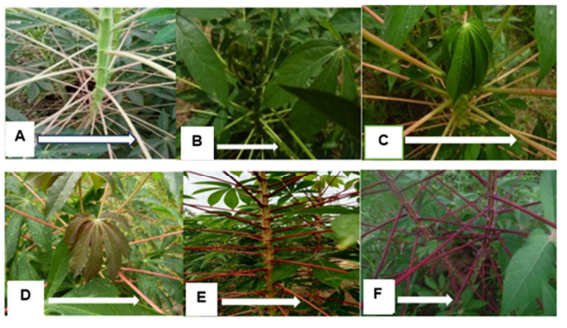

Fig. 5. Different colors of petioles

Regarding the petiole color, the frequency distribution showed varying degrees of color that differed markedly from one family to another. Family II contains genotypes with a wide variety of petiole colors, six modalities observed: yellowish-green (10%), green (20%), reddish-green (20%), greenish-red (10%), red (30%) and purple (10%). However, only two modalities of petiole color were found in family IV, yellowish-green (29%) and green (71%). The green color of petiole was dominant in family I (79%), family III (50%), family IV (71%), family V (60%) and family VI (56%). Figs 4 and 5 below show the different petiole color and the frequency distribution of leaf petiole color in each family.

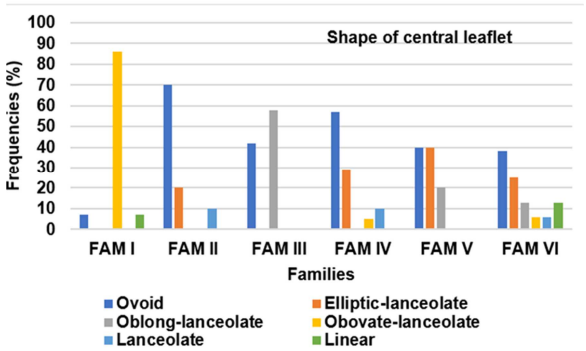

Fig. 6. Frequency distribution for central leaflet shape

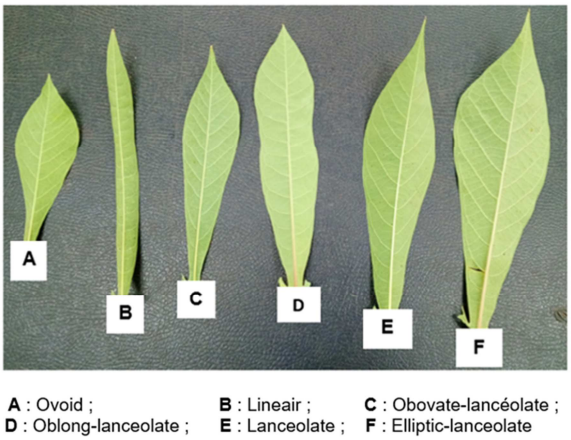

Fig. 7. Various shapes of the central leaflet

Shape of the central leaflet

Figs 6 and 7 show that the six families studied are made up of genotypes with various central leaflet shapes. The ovoid form (40%) and the oboval-lanceolate form (2%) are found respectively in the majority and minority of families. Figs 6 and 7 show that the six families studied are made up of genotypes of various central leaflet shape. The ovoid form (40%) is the most common in all families. On the other hand, oboval-lanceolate form (2%) is very rarely found in families. Family VI contains the genotypes with the most diverse leaflet shapes: ovoid (38%), Elliptic-lanceolate (25%), oboval-lanceolate (13%), oboval lanceolate (6%), lanceolate (6%) and linear (13%). On the other hand, the majority of genotypes in family I have the eliptical lanceolate shape (86%).

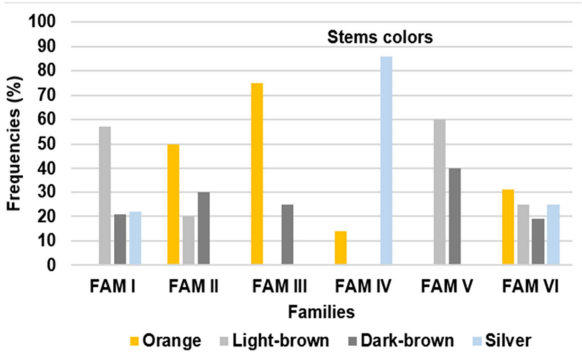

Fig. 8. Frequency distribution for family stem color

Stem characteristics

Stem color

Analysis of the stem coloration of the genotypes revealed four modalities. The families showed varying frequencies of cassava stem color. Families II (50%), III (75%) and VI (31%) contained more genotypes with orange stems. Family IV has a high proportion of silver colored stems (86%). Families I (57%) and V (60%) are dominated by genotypes with light brown stems. Fig. 8 below shows the distribution of frequencies for the different modalities linked to stem color in the families.

Types of branching

For the types of stem branching, the calculation of data frequencies showed three forms of branching in all families. Erect stems dominate in families I (64%) and III (38%). Dichotomous branching is the dominant modality in families II (40%), III (50%), V (80%) and VI (58%). Trichotomous type branching is weakly encountered in all families. However, the trichotomous form is found in family II (29%) and

family V (7%). Figs 9 and 10 below illustrate the various types of branching present in the families.

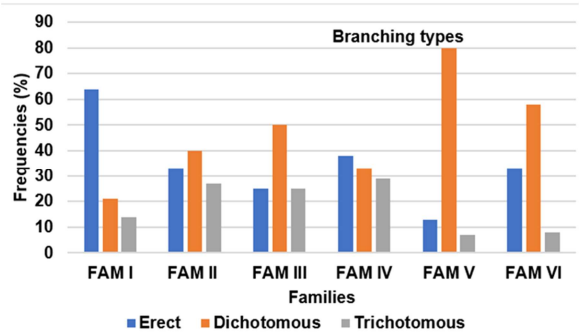

Fig. 9. Frequency distribution of branching types within families

Fig. 10. Types of branching linked to the stems of different families

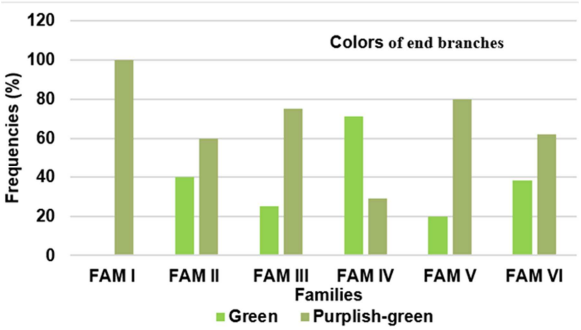

Fig. 11. Frequency distribution of branch color at the top for each family

Color of end branching

As for the color of the terminal branches (twigs at the top) studied, two modalities were observed: green (30%) and green-purple (70%). Both modalities were observed in almost all families, with the exception of family I, where all genotypes had green-purple twigs at the top. The green-purple color (68%) of the shoots was more common in all families except family III (29%). Figs 11 and 12 illustrate the frequency distribution of shoot color at the top of genotypes within the different families. Types of branches present in the families. Frequencies of the different modalities linked to stem color in the families.

Fig. 12. Different colors of twigs at the top
A: Green color, B: Purplish-green color

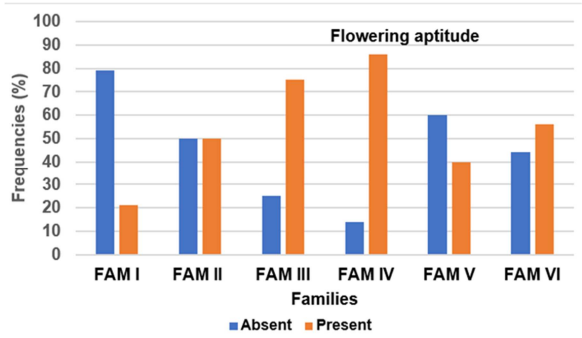

Fig. 13. Distribution of flowering aptitude frequencies for each family

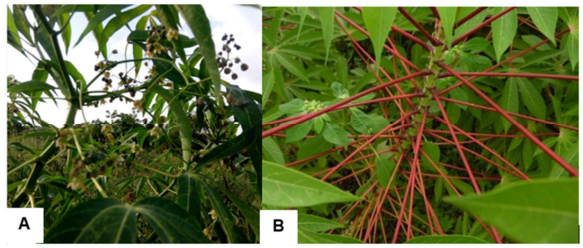

Fig. 14. Illustration of the presence and absence of flowers in cassava genotypes
A: flowering plant, B: non-flowering plant

Flowering ability

The results of the analysis recorded in Fig. 13 below show two modalities (presence, or absence) for the genotype flowering ability trait. The two modalities for this trait were observed in all families. Indeed, families III, IV and VII contain more genotypes that bore flowers (75%), (86%) and (56%) respectively during their vegetative cycle. However, families I (79%) and V (60%) are made up of genotypes the majority of which did not bear flowers during their vegetative cycle during the trial. As for family II, there

were as many flowering genotypes (50%) as non-flowering genotypes (50%). Figs 13 and 14 show the frequency distribution of genotypes in families according to their ability to flower. They also show the differences in stem color between families.

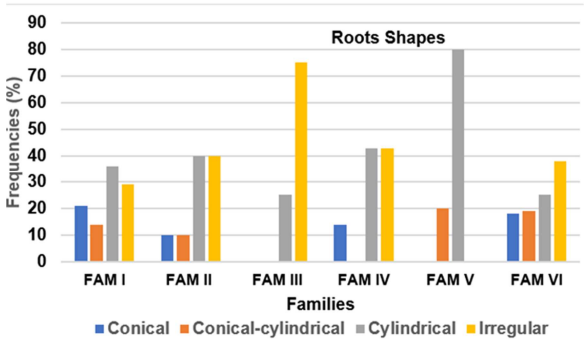

Fig. 15. Distribution of frequencies related the shape of roots for each family

A: Conical; **B:** Conical-cylindrical; **C:** Cylindrical; **D:** Irregular

Fig. 16. Different shapes of tuberous roots

Tuberous root characteristics

Roots shapes

The results of the assessment of tuberous root shape (Fig. 16) showed four modalities within families. Families I, II and VI are made up of genotypes with all four modalities (conical, conical-cylindrical, cylindrical and irregular) of tuberous root shape observed in the present study. The conical-cylindrical form (13%) is rarely found and the cylindrical form (38%) is strongly observed in all families. Family V is dominated by genotypes with cylindrical tuberous roots (80%). Family III is dominated by genotypes with irregular root shapes (78%). Cylindrical roots (38%) followed by irregular roots (36%) are the most common in all families, as shown in Fig. 15 below.

Root texture

The texture of the tuberous root discriminated between genotypes within families. Rough texture is the most common (45%), followed by smooth (30%) and intermediate (25%). Families I, IV and VI contain genotypes with all three root modalities (smooth, intermediate and rough). Families II and III are made up of genotypes with predominantly rough root texture. The genotypes in family V have more intermediate texture (80%) than smooth (20%) (Fig. 17).

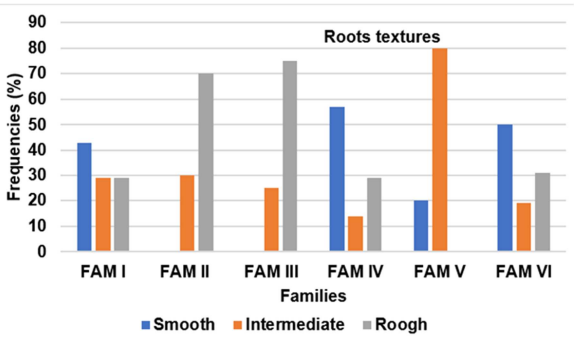

Fig. 17. Distribution of frequencies related the root texture for each family

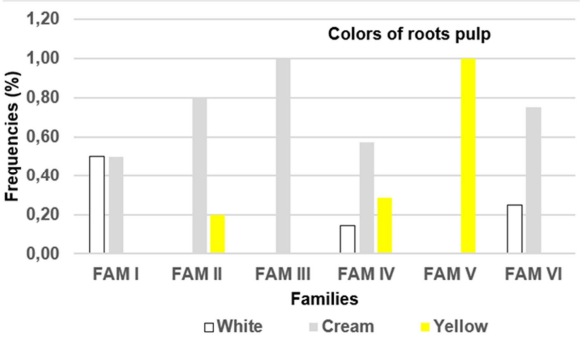

Fig. 18. Distribution of tuberous root pulp frequencies in families

A : White B : Cream C : Yellow

Fig. 19. The different colors of the root pulp

Fig. 18 below shows the frequency distribution of tuberous root pulp color for each family. The creamy color (63%) of tuberous root pulp is frequent in all families except family V. Families III and V are made up respectively of genotypes with a creamy (100%) and yellow (100%) pulp color only. Family IV

contains all 3 types of root pulp color: white (14%), creamy (57%) and yellow (29%) (Fig. 19).

Analysis of diversity indices for traits observed on genotypes

The relative Shannon-Weaver diversity index (H) calculated for the different characters linked to the leaves, stems, flowers and tuberous roots of all the genotypes and families revealed significant diversity between genotypes and also between families (Table 3). For all the traits studied, the relative Shannon-Weaver diversity index ranged from H'=0.71 (petiole color) to H'=1 (flowering ability) for the genotypes. The average relative index for genotypes was around 0.90. For families, the relative Shannon-Weaver index varied from 0.41 (pulp color) to 0.85 (flowering ability), with an average of 0.66 between families for all the characteristics studied.

Table 3. Variation in the relative Shannon-Weaver diversity index for the characteristics studied in the genotypes of the families

Characters	Modalities	Genotypes	H'						H'ave
			FAM I	FAM II	FAM III	FAM IV	FAM V	FAM VI	
CAL	4	0.96	0.65	0.65	0.41	0.78	0.49	0.71	0.62
SCL	6	0.8	0.28	0.45	0.38	0.58	0.59	0.88	0.55
PEC	6	0.71	0.37	0.95	0.58	0.33	0.53	0.55	0.53
CSE	4	0.99	0.71	0.74	0.41	0.3	0.49	0.99	0.61
BRH	3	0.93	0.81	0.99	0.95	0.99	0.57	0.81	0.85
CEB	2	0.89	0	0.97	0.81	0.86	0.72	0.95	0.72
FLAP	2	1	0.75	1	0.81	0.59	0.97	0.99	0.85
ROS	4	0.92	0.96	0.86	0.41	0.72	0.36	0.97	0.71
TRE	3	0.97	0.98	0.56	0.51	0.87	0.46	0.93	0.72
CRP	3	0.84	0.63	0.46	0	0.87	0	0.51	0.41
H'ave		0.9	0.61	0.76	0.53	0.69	0.52	0.83	0.66

CAL: color of apicales leaves, SCL: Shape of central leaflet, PEC: Petiole color, CSE: Color of stem, BRH: Branching habit, CEB: Color of end branches. FLAP: Flowering Aptitude, ROS: Root shape, TRE: Texture of root epidermis, CRP Color of root pulp, H': Shannon-Weaver relative diversity index; H'ave: Shannon-Weaver relative average diversity index.

Table 4. Variation in the relative index of leaf-related trait diversity

Characters	Modalities	H'						H'ave
		FAM I	FAM II	FAM III	FAM IV	FAM V	FAM VI	
CAL	4	0.65	0.65	0.41	0.78	0.49	0.71	0.62
PEC	6	0.37	0.95	0.58	0.33	0.53	0.55	0.55
SCL	6	0.28	0.45	0.38	0.58	0.59	0.88	0.53
H'ave		0.43	0.68	0.46	0.56	0.54	0.71	0.56

CAL: color of apicale leaves, PEC: Petiole color, SCL : Shape of central leaflet, H' : Shannon-Weaver relative diversity index, H'ave : Shannon-Weaver relative average diversity index.

Relatifs index of diversity of the various characters (H')

Relatifs index of diversity linked to the leaf

The relative Shannon-Weaver diversity index was calculated for all leaf related characters in the six (06) families. The four modalities observed for apical leaf color, the relative diversity index varied from 0.41 (family III) to 0.71 (family VI), with an average of 0.62 within the families. Concerning the color of the petiole, with six modalities encountered, the relative diversity index varied from 0.33 (family IV) to 0.95 (family II) with an average of 0.55. As for the shape of the central lobe, the six modalities also observed gave a low relative Shannon-Weaver diversity index (0.28) obtained by family I and a higher one (0.88) obtained by family VI with an average for all families of 0.53. The relative Shannon-Weaver diversity index for all leaf-related characters was more polymorphic for family VI, with an index of 0.71, and family I was less polymorphic, with an average index of 0.43. The

average relative index for all families was 0.56. Table 4 shows the diversity of the relative index of leaf-related characters for each family.

Relative Shannon Weaver diversity index (H') for stem and flower characteristics in families

The analysis of the relative Shannon-Weaver index presented in Table 5 below shows that in the families studied the index values linked to stem color varied from 0.30 (family IV) to 0.99 (family VI) with an average of 0.61 for all families. The relative index of low diversity (0.57) is held by family V and the highest (0.99) by families II and IV, with an average of 0.85 for the branching type character. The relative diversity index was zero for family I and 0.97 for family II, with an average of 0.72 for the character linked to the color of the branches at the top. This trait presented two modalities in all the genotypes that make up the families. The two modalities reflect the ability of the genotypes within the families to flower or not during their vegetative cycle. For this characteristic, the relative index showed an average diversity of the order of 0.59 obtained by family IV and the highest 0.99 obtained by family VI. The average relative Shannon-Weaver diversity index showed variability within families for stem and flower related characters, with the lowest diversity (0.57) observed in family I and the highest in family VI (0.94), with an average diversity of these characters of 0.76.

Table 5. Variation in the relative index of diversity of stem and flower characteristics

Characters	Modalities	H'						H'ave
		FAM I	FAM II	FAM III	FAM IV	FAM V	FAM VI	
CS	4	0.71	0.74	0.41	0.30	0.49	0.99	0.61
BRH	3	0.81	0.99	0.95	0.99	0.57	0.81	0.85
CEB	2	0	0.97	0.81	0.86	0.72	0.95	0.72
FAP	2	0.75	1	0.81	0.59	0.97	0.99	0.85
H'ave		0.57	0.93	0.75	0.69	0.69	0.94	0.76

CS: Color of stem, BRH: Branching habit, CEB: Color of end branches, FAP: Flowering Aptitude, H': Shannon-Weaver relative diversity index, H'ave: Shannon-Weaver relative average diversity index.

Table 6. Variation in the relative index of root-related trait diversity

Characters	Modalities	H'						H'ave
		FAM I	FAM II	FAM III	FAM IV	FAM V	FAM VI	
RS	4	0.96	0.86	0.41	0.72	0.36	0.97	0.71
TRE	3	0.98	0.56	0.51	0.87	0.46	0.93	0.72
CRP	3	0.63	0.46	0	0.87	0	0.51	0.41
H'ave		0.86	0.63	0.31	0.82	0.27	0.8	0.62

RS: Root shape, TRE: Texture of root epidermis, CRP: Color of root pulp, H': Shannon-Weaver relative diversity index; H'ave: Shannon-Weaver relative average diversity index.

Shannon weaver relative diversity index (H') of root-related traits in families

The diversity index was determined for all families studied (Table 6). From this analysis, family II showed the lowest diversity (H' = 0.41) and family VI (H' = 0.97) showed the highest diversity, for the tuberous root shape character with an average H'=0.71 for all families. For the tuberous root texture trait, the relative diversity index varied from H'=0.46 (family V) to H'=0.98 (family I), with an average H'=0.72 for all families. As for the color of the pulp of tuberous roots, families III and V showed a zero diversity index. On the other hand, for this same characteristic, family IV obtained the highest index H'= 0.87. The average relative diversity index for the families was H'= 0.41. Analysis of the average relative index of diversity for characteristics linked to tuberous root pulp color for all families ranged from 0.31 (family III) to 0.86 (family I), with an average H'= 0.62.

Barycentric distance between families

The Euclidean distance between families using Ward's aggregation method was used to determine

how close the families were. Families II and III are closer together. Families III and V are also close. On the other hand, families I and V are the furthest apart.

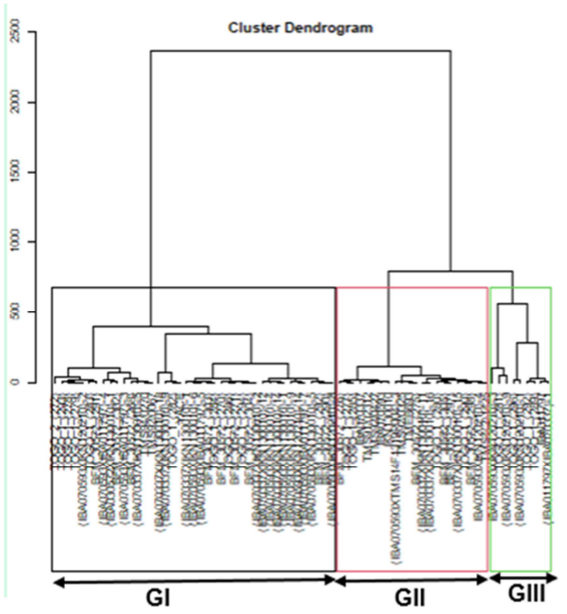

Fig. 20. Dendrogram from the CAH of the genotypes studied

Structuring the genotypes

Ascending classification Hierarchical (ACH) was carried out on the basis of Euclidean distances between genotypes, resulting in this dendrogram (Fig. 20) showing three (3) classes. These genotypes were distributed among the groups independently of the six family groups to which they genetically belong. The first group (GI) comprises 19 genotypes from family I (13 genotypes), family II (1 genotype), family V (3 genotypes) and family VI (2 genotypes). The second group (GII) is made up of 22 genotypes from family I (1 genotype), family II (4 genotypes), family III (2 genotypes), family IV (5 genotypes), family V (1 genotype) and family VI (9 genotypes). The third group (GIII) is made up of 15 genotypes from family II (5 genotypes), family III (2 genotypes), family IV (2 genotypes), family III (1 genotype) and family VI (5 genotypes).

Group characterisation

Discriminant factor analysis (DFA) was used to characterise the three morphological groups obtained from the ACH (Fig. 21). The first group (GI) is characterised by genotypes with purple apical leaves and greenish-red petioles. Adult leaves have lanceolate oblong central leaflet. The stems of the genotypes are upright and light brown in color; they do not flower.

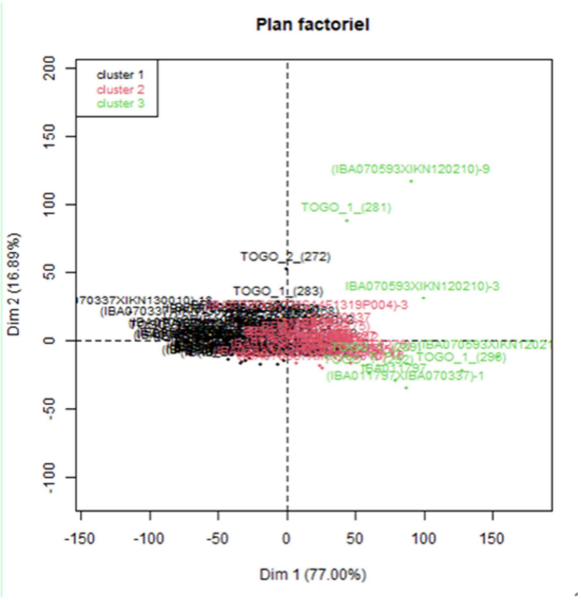

Fig. 21. Projections of families in the ½ plane of DFA

The terminal branches (twigs at the tops) are green-purple in color. The tuberous roots of the genotypes are conical-cylindrical and smooth-textured. Group (GII) is made up of non-flowering genotypes with dichotomous branching. The apical leaves are light-green with green petioles. The central leaflet of the leaves is ovoid in shape. The tuberous roots are smooth in texture and irregular in shape. The stems are silvery in color with green twigs at the top. The third group (III) is characterised by genotypes that have flowered at least once during their vegetative cycle. The immature leaves (apicals leaves) are dark-green color, and the adult leaves have elliptical-lanceolate and linear forme. The petioles of the genotypes are red and reddish-green or yellowish-green. The stems are orange. The texture of the tuberous roots is rough, with yellow pulp.

Discriminating traits

The results of the DFA enabled the three groups to be distinguished on the basis of phenotypic traits. These traits were polymorphic within genotypes. They are:

color of apical leaves (CAL) ; color of petioles (PEC) ; shape of central leaflet (FLOC); color of stems (CS); color of end branching (CEB) and aptitude at flowering (FLAP) and, to a lesser extent, the roots shape (RS) and the color of the pulp (CRP).

Discussion

The various phenotypic observations showed the presence of several modalities for all the qualitative traits. This translates into significant variability within the cassava genotypes evaluated in this study. Great phenotypic diversity was observed between families and within families for the apical leaf color trait, as shown by the high values of the relative Shannon-Weaver index between genotypes (H= 0.92) and between families (H'= 0.66). This result is similar to that of Gmakouba *et al.*, 2018, on a study of the analysis of the agromorphological diversity of a collection of cassava (*Manihot esculenta* Crantz) from Burkina Faso which had shown that a significant polymorphism is observed from the qualitative characters of cassava.

Cassava has wide range of phenotypic descriptors that allow genotypes or cultivars to be easily distinguished from one another. According to Mathura *et al.* (1989) and Robooni *et al.* (2014), the phenotypic variance of cassava is higher than the genotypic variance for traits of agronomic importance such as tuberous root weight. It should also be pointed out that certain characteristics showed very high variability, namely: flowering ability (H=0.85) and branching type (H = 0.85) in many families. In fact, these two characteristics are positively correlated, with two (02) or three (03) or even four (04) branches developing simultaneously at each flowering, giving a di, tri or tetrachotomous appearance, Raffaillac *et al.,* 2000.

In addition, genotypes newly produced from seeds have a strong aptitude for flowering, as shown by the high value of the relative Shannon-Weaver index (H'=0.85). High heat could also induce flowering in flowering genotypes. The flowering period can be influenced by temperature, of drought sequence and photoperiod in flowering genotypes (Matthews *et al.*, 1994). Unlike old cultivars with several generations of propagation, newly developed cultivars can show several successive flowerings in a single year of cultivation (Bakayoko *et al.*, 2013). Between these two extremes, there are intermediate forms which do not flower regularly. This close correlation between flowering and stem branching was mentioned by Médard in 1973, who reported that unbranched cassava cultivars do not flower. The color of the pulp of the tuberous roots was monomorphic for all the genotypes in the V family, and they were distinguished by the yellow color of the tuberous roots. This yellow coloration of the pulp of tuberous roots would presage a good content of carotenoids (β-carotene) in the roots, testifying to a good richness in provitamin A essential for the proper functioning of the human organism. In an agro-morphological characterisation of cassava cultivars in Chad, Djirabaye *et al.* (2016) showed that the yellow colour of the pulp is an indicator of a high carotenoid and amino acid content. This same trait was polymorphic in family IV, with the presence of three modalities (white, creamy and yellow). This study also revealed that for all the traits studied, families II and VI showed greater intra-family diversity in terms of the average relative index of diversity raised respectively (H'= 0.76) and (H'= 0.83). These two families represent an important pool of genotypes for the creation of new high-performance varieties.

Conclusion

The results of this study, based exclusively on phenotypic traits, showed that the cassava families studied are highly diverse, as evidenced by the presence of several highly polymorphic phenotypic modalities. The ACH results enabled the genotypes to be grouped into 3 phenotypic groups according to the most discriminating traits, namely: apical leaf color, stem color and tuberous root shape; for the families and, by extension, the genotypes. For the six families studied, families VI and II are very diverse for all the characters studied. On the other hand, families I, III, IV and V are less diverse and are referred to as homogeneous families. This study made it possible to determine polymorphic traits inter and intra-family

diversity, laying the foundations for cassava varietal selection, which should be consolidated by molecular characterisation of the said genotypes. In short, these results can be used in cassava genetic improvement programmes in Burkina Faso.

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References

Agré A, Dansi A, Rabbi I, Battachargee R, Dansi M, Melaku G. 2015. Agromorphological characterization of elite cassava (*Manihot esculenta* Crantz) cultivars collected in Benin. International Journal of Current Research in Biosciences and Plant Biology **2**(2), 1–14. https://cgspace.cgiar.org/bitstream/handle/10568/58355/A.P.%20Agre,%20et%20al.pdf.

Alam MK. 2021. A comprehensive review of sweet potato (*Ipomoea batatas* [L.] Lam): Revisiting the associated health benefits. Trends in Food Science and Technology **115**, 512–529. https://doi.org/10.1016/j.tifs.2021.07.001.

Allem AC. 2002. The origin and taxonomy of cassava. In: Hillocks RJ, Thresh JM, Bellotti AC, eds. Cassava: Biology, Production and Utilization. CABI Publishing, New York, 1–16. https://doi.org/10.1079/9780851995243.0001.

Alves AAC, Hillocks RJ, Thresh JM, Bellotti AC. 2002. Cassava botany and physiology. In: Cassava: Biology, Production and Utilization. CABI Publishing, London, 67–89. https://doi.org/10.1079/9780851995243.0067.

Bakayoko S, Soro D, N'dri B, Kouadio KK, Tschannen A, Nindjin C, Dao D, Girardin O. 2013. Étude de l'architecture végétale de 14 variétés améliorées de manioc (*Manihot esculenta* Crantz) dans le centre de la Côte d'Ivoire. Journal of Applied Biosciences **61**, 4471–4477. https://doi.org/10.4314/jab.v61i0.85595.

Belhadj H, Medini M, Bouhaouel I, Amara H. 2015. Analyse de la diversité phénotypique de quelques accessions autochtones de blé dur (*Triticum turgidum* ssp. *durum* Desf.) du sud tunisien. 11.

Djirabaye N, Papa SS, Naïtormbaïdé M, Mbaïguinam JM, Guisse A. 2016. Agro-morphological characterization of cassava (*Manihot esculenta* Crantz) cultivars from Chad. Agricultural Sciences **7**, 77049. https://doi.org/10.4236/as.2016.77049.

Elias M, McKey D, Panaud O, Anstett MC, Robert T. 2001. Gestion traditionnelle de la diversité morphologique et génétique du veuf par les Makushi Amérindiens (Guyana, Amérique du Sud): Perspectives pour la conservation à la ferme des ressources génétiques des cultures. Euphytica **120**, 143–157. https://doi.org/10.1023/A:1017501017031.

FAOSTAT. 2024. Food and Agriculture Organization of the United Nations Statistics Division. https://www.fao.org/faostat/en/#home.

Fukuda WMG, Guevara CL, Kawuki R, Ferguson ME. 2010. Selected morphological and agronomic descriptors for the characterization of cassava. International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria, 19.

Gashaw ET, Mekbib F, Ayana A. 2016. Genetic diversity among sugarcane genotypes based on qualitative traits. Advances in Agriculture **2016**, Article ID 8909506, 8p. https://doi.org/10.1155/2016/8909506.

Gmakouba T, Some K, Traore ER, KpemouA KE, Zongo JD. 2018. Analyse de la diversité agromorphologique d'une collection de manioc (*Manihot esculenta* Crantz) du Burkina Faso. International Journal of Biological and Chemical Sciences **12**(1), 402–421. http://www.ifgdg.org.

Guinko S. 1984. Végétation de la Haute Volta. Thèse de doctorat, Université Bordeaux III, 2 tomes, 556 p.

Guira F. 2016. Potentialités technologiques des racines de manioc à travers la production de l'attiéké: aspects nutritionnels, biochimiques, microbiologiques et moléculaires. Thèse de doctorat unique, Université Ouaga I Professeur Joseph KI-ZERBO, 173 p.

Isendahl C. 2011. The domestication and early spread of manioc (*Manihot esculenta* Crantz): A brief synthesis. Latin American Antiquity **22**(4), 452–468.

Jain SK, Qualset CO, Bhatt GM, Wu KK. 1975. Geographical patterns of phenotypic diversity in a world collection of durum wheat. Crop Science **15**, 700–704. https://doi.org/10.2135/cropsci1975.0011183X001500050026x.

Ka SL, Gueye M, Kanfany G, Diatta C, Mbaye MS, Noba K. 2020. Dynamique de levée des adventices du sorgho [*Sorghum bicolor* (L.) Moench] en zone soudanienne humide du Sénégal. International Review of Marine Science, Agronomy and Veterinary **8**, 286–2930. http://www.ifgdg.org.

Mathura R, Dhander DG, Varma SP. 1989. Variability studies of cassava varieties on growth and yield under Tripura conditions. Journal of Root Crops **12**, 25–28.

McKey D, Emperaireh L, Elias M, Pinton F, Robert T, Desmouliere S, Rival L. 2001. Gestions locales et dynamiques régionales de la diversité variétale du manioc en Amazonie, 26 p.

Médard R. 1973. Morphogénèse du manioc, *Manihot esculenta* Crantz, (Euphorbiacées-Crotonoidées): Étude descriptive. Adansonia **13**, 483–494.

Ministère de l'Agriculture et de la Sécurité Alimentaire (MASA). 2014. Catalogue National des Espèces et Variétés Agricoles du Burkina Faso.

N'zué B, Okana M, Kouakou A, Dibi K, Zouhouri G, Essis B. 2014. Morphological characterization of cassava (*Manihot esculenta* Crantz) accessions collected in the centre-west, south-west, and west of Côte d'Ivoire. Greener Journal of Agricultural Sciences **4**(6), 220–231. https://doi.org/10.15580/GJAS.2014.6.050614224.

Nartey F. 1978. Cassava cyanogenesis, ultrastructure, and seed germination. In: Denis R, Walter F, eds. Cassava. Copenhagen: Muksgaard, 234 p.

Raffaillac J-P, Second G. 2000. L'amélioration des plantes tropicales : le manioc.

Robooni T, Paul S, Rob M, Robert K. 2014. Combining ability analysis of storage root yield and related traits in cassava at the seedling evaluation stage of breeding. Journal of Crop Improvement **28**(4), 530–546. http://www.tandfonline.com/loi/wcim20.

Sawadogo N, Naoura G, Ouoba A, Yaméogo N, Tiendrebeogo J, Ouedraogo MH. 2022. Phenotypical characteristics and genetic diversity of three types of sorghum [*Sorghum bicolor* (L.) Moench] cultivated in Burkina Faso based on qualitative traits. Moroccan Journal of Agricultural Sciences **3**(2), 109–116. https://techagro.org/index.php/MJAS/article/view/941.

Sawadogo N. 2015. Diversité génétique des sorghos à grains sucrés [*Sorghum bicolor* (L.) Moench] du Burkina Faso. Thèse unique de doctorat, Université de Ouagadougou, 135 p.

Shannon CE, Weaver W. 1949. The mathematical theory of communication. University of Illinois Press, Urbana.

Soro M. 2022. Épidémiologie de la mosaïque du manioc (*Manihot esculenta* Crantz), diversité génétique et évaluation des accessions et variétés de manioc au Burkina Faso. Thèse unique de doctorat, Université Félix HOUPHOUËT BOIGNY, 184 p.

Tiendrébéogo F, Lefeuvre P, Hoareau M, Harimalala MA, De Bruyn A, Villemot J, Traoré VS, Konaté G, Traoré AS, Barro N, Reynaud B, Traoré O, Lett JM. 2012. Evolution of African cassava mosaic virus by recombination between bipartite and monopartite begomoviruses. Virology Journal **9**(67).

Tiendrébéogo F, Lefeuvre P, Hoareau M, Traoré VSE, Barro N, Reynaud B, Traoré AS, Konaté G, Traoré O, Lett JM. 2009. Occurrence of East African cassava mosaic virus - Uganda (EACMV-UG) in Burkina Faso. Plant Pathology **58**, 783.