

Phenotypic variation of okra (*Abelmoschus esculentus* L.) genotypes cultivated in Burkina Faso based on qualitative traits

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1 ABSTRACT

The improvement of okra based on qualitative characters is important to enhance its value. This article summarizes the morphological variation of seven okra genotypes from five African countries. The trial was conducted in 2021 in Burkina Faso, following a Fisher block and twelve qualitative traits have been evaluated. To assess phenotypic, visual observations were used, Shannon diversity index and Factorial Correspondence Analysis. A variation of qualitative traits of the genotypes was observed except for the position of the fruit, which was completely erect. Shannon diversity index varied from 0.72 to 0.96. The results showed a high variation among genotypes for flower, fruit, stem and leaf colours, for fruit, leaf shape and for fruit and leaf pubescence. On the fruit, 5 colour modalities, 4 capsules modalities and 3 pubescence modalities were recorded. Factorial Correspondence Analysis revealed of correlations between genotypes and traits on $\frac{1}{2}$ plan. *UAE22* and *A2* are similar by fruit shape and genotype *PUSA* is identified by fruit colour and pubescence. The study found that genotypes *PI49*, *CII* are identified by fruit pubescence only. The introduction of new genotypes in Burkina Faso constitutes a basis for qualitative trait improvement of okra in this country.

2 INTRODUCTION

Tropical and subtropical regions of world are the centers of most domestication and diversity of okra (Kisher *et al.*, 2016). Among the domesticated species, *Abelmoschus esculentus* is one of the most important crops in the Sudano-Sahelian zone (Koechlin, 2006). Okra occupies a prominent place in urban and peri-urban areas due to the introduction of varieties that can perform better (Ndunguru *et al.*, 2004; Ouedraogo *et al.*, 2016). Okra is consumed as a fresh or dried vegetable. The fruits and leaves are sources of nutritional value, with Fe, Ca, Mg, mucilages, and vitamins (Oyelade *et al.*, 2003; Moyin-Jesu *et al.*, 2007). Different studies have revealed important sources of fibre, a dietary

component for lowering cholesterol (Kendall *et al.*, 2004). Okra typically differs from most other common vegetables in having high mucilage content (Jideani and Bello, 2009). Crop development through breeding is dependent on the genetic variability present in the germplasm how this variability is expressed in the genotypes (Kiran *et al.*, 2004; McFerson *et al.*, 1995). Phenotypic and molecular assessments have highlighted genetic variability in okra (Ouedraogo, 2016). Diversity derived from phenotypic and morphological traits generally vary across environments (Komolafe *et al.*, 2021). According to the okra typology based mainly on qualitative variables, groups of

varieties are found in local producers (Ouedraogo, 2016). Knowledge of morphological diversity among cultivated genotypes is very fundamental for a reasonable use of plant genetic resources (Aladele, 2009). Many research programs are oriented more towards the selection of performing genotypes based on yield criteria and cycle (Nesru *et al.*, 2021). Diversity in quality traits of okra genotypes is not as well studied as diversity in quantitative traits (Nesru *et al.*, 2021). Increasing yield only is not enough in crop improvement unless the quality of produce is considered (Binalfew and Yosef, 2016). Indeed, have to high adoption and maximum impact, qualitative traits with excellent quality are needed (Bationo/Kando *et al.*, 2007; Ouedraogo *et al.*, 2016). Traits such as shape, colour, and pubescence of leaves, fruits, flowers and seeds are the determining factors in consumer preference reported to be highly heritable (Nesru *et al.*, 2021). Varietal selection and breeding of the species are poorly developed in Burkina Faso, hence the absence of improved local okra varieties (Ouedraogo, 2016; Ouedraogo *et al.*, 2016). This indicates a genetic basis that is not very favourable to the development of desirable okra genotypes. In

3 MATERIAL AND METHODS

3.1 Plant material and experiment area:

A set of seven (07) genotypes of *Abelmoschus esculentus* originated from different ecological zones, Burkina Faso (UAE 22, Grcy1), Côte d'Ivoire (CI1), Ghana (A2), Kenya (PUSA) and Mali (PI49, Paysan) were used. The experiment was conducted in July 2021 in the experimental garden of the Joseph KI ZERBO University, located at 12°21'56" north and 1°32'01" west. The climate is of the north-Sudanian type, characterized by a rainy season, which extends from June to October and a dry season from November to May with precipitation fluctuates from year to year.

3.2 Experiment design and data collection: The field experiment was a completely randomized Fischer block design with three replications. The row length was 2 m

in addition to agronomic performance, plant breeding must take into account the emerging market needs, which are more based on qualitative traits. However, there is little qualitative diversity of okra grown around Ouagadougou (Sawadogo *et al.*, 2009). This corroborates the work of Aryo (1970) who found that the morphological diversity of *Abelmoschus esculentus* is low. This makes impossible to satisfy the demand on the qualitative level in urban and peri-urban areas. The introduction of okra genotypes from other countries can strengthen the genetic base of the crop and provide opportunities for varietal improvement of the species. While diversity based on quantitative traits is a good opportunity to improve the crop (Nesru *et al.*, 2021), diversity related to qualitative traits will enhance okra. With regard to the genetic improvement of okra, it is advisable to work on ideotypes chosen according to specific objectives (Koechlin, 1989). The present study is conducted with aim to contributing to the identification of genotypes of interest for national and international markets. The general objective is to know the qualitative characteristics of seven genotypes of okra in Burkina Faso.

with 0.8 m interrow distance and 0.4 m distance between hills within a row. Morphological variation assessment (12 traits) provided by okra descriptors (IPGRI, 1991). Thus the colour of the limb (CLI), stem colour (CTI), flower colour (CFL), colour fruit (COF), petiole colour (COP), limb shapes (FLI), fruit shape (FOF), fruit position (POF) were directly observed with the naked eye. Stem pubescence (PBTI), leaf pubescence (PBFEL), and fruit pubescence (PBFRL) were assessed. The variables related to the leaf and the stem were evaluated from the 8th leaf stage (Koechlin, 1989), those of the fruit from fruiting. The shape of the fruit was assessed from the length of the capsule, the size of the carpel and the top of the fruit.

3.3 Data analysis: The distribution of morphological traits and genotypes on the plan

$\frac{1}{2}$ was performed by Correspondence Factorial Analysis (AFC) using R software version 3.6.0. Phenotypic variation of the traits based on

Shannon-Weaver diversity index was calculated according to Jain *et al.* (1975) and Gashaw *et al.* (2016).

4 RESULTS

4.1 Characteristics of genotypes: The appearance of the plants and the cycle of each genotype are shown in Table 1. It was observed that genotypes UAE22, Grcy1, A2, CI1 and PUSA had unbranched plants. The Genotypes

were large (UAE22, A2, Paysan), medium (Grcy, PI49) and small (PUSA, CI1). As for the cycle of the genotypes, it varied from 44 days (PUSA) to 65 days (A2, PI49) after sowing.

Table 1: Main characteristics of genotypes

Genotype	Origin	Climate zone	Plant aspect	Cycle
UAE 22	Burkina Faso	Sudano-Sahelian	unbranched tall	52 DAS
Grcy1	Burkina Faso	Sahelian	unbranched medium	58 DAS
A2	Ghana	Sudanian	unbranched tall	65 DAS
CI1	Ivory Coast	Sudanian	branched small	57 DAS
Paysan	Mali	Sahelian	branched tall	46 DAS
PI49	Mali	Sudano-Sahelian	branched medium	65 DAS
PUSA	Kenya	Sudanian	unbranched small	44 DAS

Legend: DAS: Days after sowing

4.2 Phenotypic variation of traits: The results revealed a wide variation in the qualitative variables of the cultivated genotypes (Table 2). Shannon diversity indices ranging from 0.72 to 0.96 showed an inter-genotype diversity. The morphological markers used showed a diversity of modalities ranging from classes 1 to 5. Indeed, fruit colour, stem colour and fruit shape showed the high variability with 5 modalities. Flower

colour (CFL), leaf blade shape (FLI), and fruit pubescence (PBFR) presented 4 modalities while fruit colour (COF), petiole colour (COP), and leaf pubescence (PBFE) showed 3 modalities. The majority of the stems were green and green with red stripes at 28.57% each. The leaves of the genotypes were predominantly green (71.42%), sparsely pubescent (71.42%) and digitate (61.90%).

Table 2: Estimation of variation traits

Characters	class number	Modalities	total	F (%)	H (Shannon index)
Leaf blade colour (CLI)	3	Green	5	71.42	0.72478743
		Dark green	1	14.28	
		Green striped with red	1	14.28	
petiole colour (COP)	3	Purple	2	28.57	0.98214438
		Purple striped with green	3	42.85	
		Red striped with green	2	28.57	
flower colour (CFL)	4	Yellow	1	14.28	0.83214097
		light yellow	4	57.14	
		Dark yellow	1	14.28	
		golden yellow	1	14.28	
Fruit colour (COF)	5	Purple	1	14.28	0.9628558
		Green	2	28.57	
		Dark green	2	28.57	
		Light green	1	14.28	
		Green striped with purple	1	14.28	
Rod colour CTI	5	Purple	1	14.28	0.9628558
		Green	2	28.57	
		Green striped with red	2	28.57	
		Red Bordeaux	1	14.28	
		Red striped with green	1	14.28	
Limb shape (FLI)	3	lobed	2	28.57	0.83421768
		Shallow digitate	4	57.14	
		deep digitate	1	14.28	
Fruit shape (FOF)	5	stocky short	2	28.57	0.91315176
		Filiform fluted	1	14.28	
		conical fruit	1	14.28	
		short taper	1	14.28	
		Fluted elongated	1	14.28	
Leaf pubescence (PBFE)	3	Glabrous	1	14.28	0.72478743
		Pubescent	1	14.28	
		Little pubescent	5	71.42	
Fruit pubescence (PBFR)	4	Glabrous	1	14.28	0.96928037
		Pubescent	1	14.28	
		Little pubescent	3	42.86	
		Very pubescent	2	28.57	
Stem pubescence (PBTI)	1	Glabrous	7	100	0
Fruit position (POF)	1	erect	7	100	0

4.3 Phenotypic description of genotypes

4.3.1 Flower colouring: Four types of flower colours were identified among genotypes (Figure 1). The flowers were light yellow for the genotypes CI1, PUSA, UAE22, A2 (Figure 1a);

yellow for the genotype PI49 (Figure 1b), cream for the genotype Paysan (Figure c) and golden yellow for the genotype Grcy1 (Figure 1d).

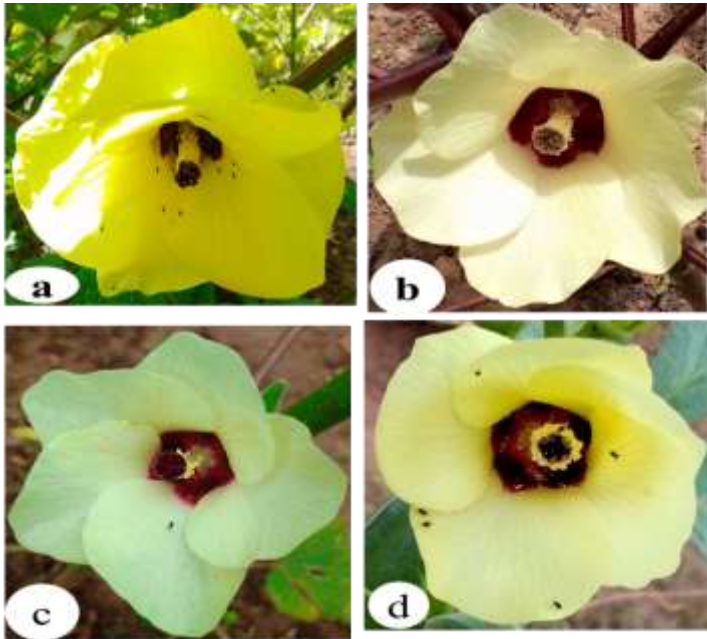


Figure 1: Flower colouring of okra genotypes: a: Golden yellow: Grcy1; b: cream: peasant; c: Yellow: PI49; d: Light Yellow: CI1, PUSA, UAE22, A2

4.3.2 Stem colouring: Figure 2 shows the five-rod colour modalities that were noted in the genotypes. Stems of uniform colours including green (*UAE22*, *PUSA*), red (*Grcy1*) and purple (*CI1*) have been recorded. However, stems with

heterogeneous colorations were also observed: green stems with purple stripes in genotypes A2 and Paysan and green-red stems in genotype PI49.



Green



Red



Purple



Green striped with purple

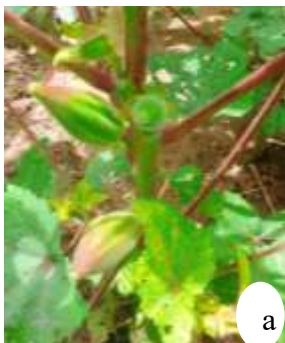


Green striped with red

Figure 2: Staining of genotype stems

4.3.3 Fruit colour and shape: Fruit colours were very diverse among the seven genotypes (Figure 3). Green coloured fruits were *UAE22* and *PI49* genotypes, light green coloured fruits in genotype *PUSA*. The *A2* and *CI1* genotypes showed dark green fruits, *Paysan* genotype has green fruits striped with purple and finally *Gry 1* genotype has purple fruits. According to the shape and apex of the fruit, four modalities have been identified. Elongated, thread-like fruits

with an acute apex were observed in *UAE22* (Figure 3d), *Gry 1* (Figure 3e) and *A2* (Figure 3g) genotypes. On the other hand, short, large fruits with an acute apex were noted in *Paysan* (Figure 3a) and *CI1* (Figure 3f) genotypes. Fruits of *PI49* (Figure 3b) were short, medium with a wide acute apex while those of *PUSA* (Figure 3c) were elongated, filiform with a narrow acute apex.



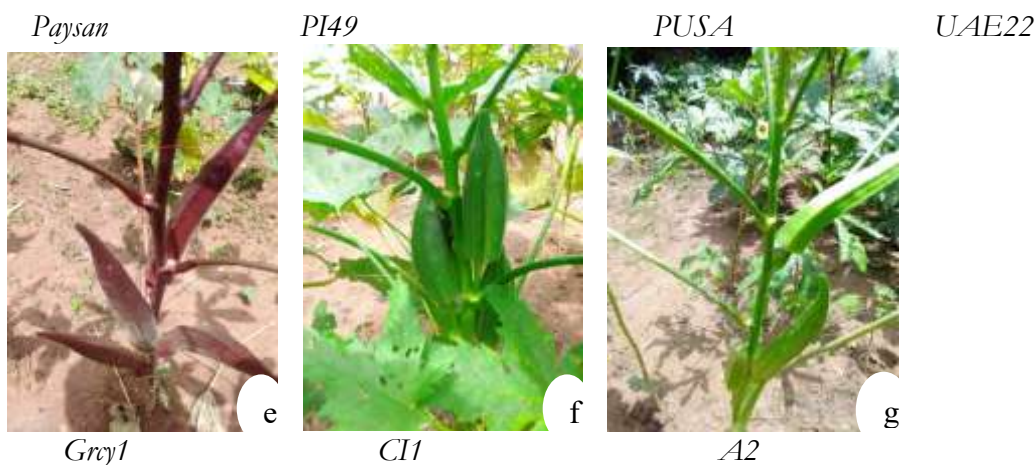


Figure 3: Fruit colour and shape

4.3.4 Leaf colour and shape: Observation of the leaves revealed two main blade shapes (lobed and digitate) with four variants: lobed, shallow digitate, medium digitate and deep digitate

(Figure 4a, b, c, d). Exception of genotypes Paysan and Grcy1, whose limbs are respectively green with red and dark green veins, all the genotypes have green limbs.

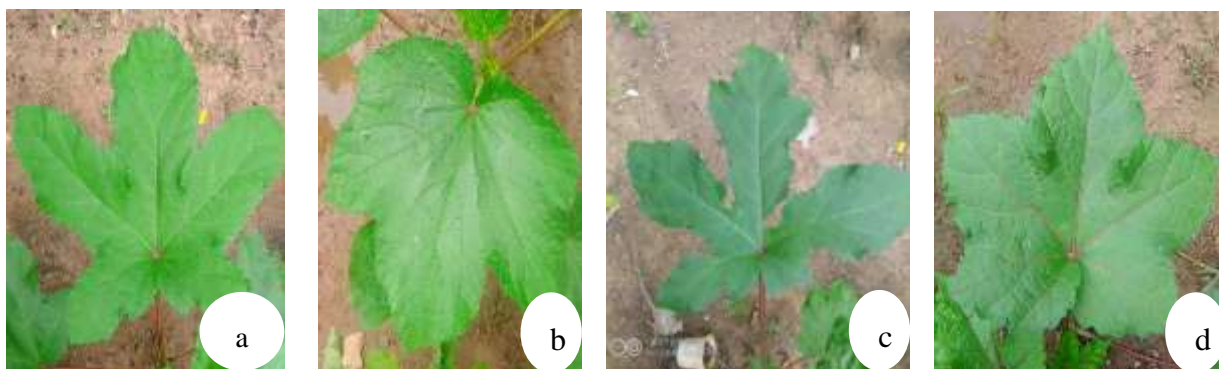


Figure 4: a: blade lobed, green (UAE22, A2); b: medium digitate blade, green (PI49, PUSA, CI1) C: shallow digitate blade, green with red veins (Paysan); d: deep digitate blade, dark green (Grcy1)

4.4 Distribution of genotypes according to discriminating traits: The factorial correspondence analysis shows a distribution of the variables on the $\frac{1}{2}$ plane (Figure 5). It shows the relationships that exist between variables, between genotypes and between variables and genotypes. Dimensions 1 and 2 account for respectively 56.70% and 26.54% of total variance. Dimension 1 indicates that genotypes *Grcy1* and *Paysan* was group around the variables

flower colour (CFL), petiole colour (COP), leaf colour (CFE). On the other hand, dimension 2 shows a grouping on the one hand genotypes UAE22 and A2 was similar by fruit shape (FOF) and on the other hand the group of genotype PUSA characterized by fruit colour (CFI), fruit shape (FOF), and fruit pubescence (PBFI). The genotypes PI49, CI1 are differentiated from the others genotypes by fruit pubescence (PBFR).

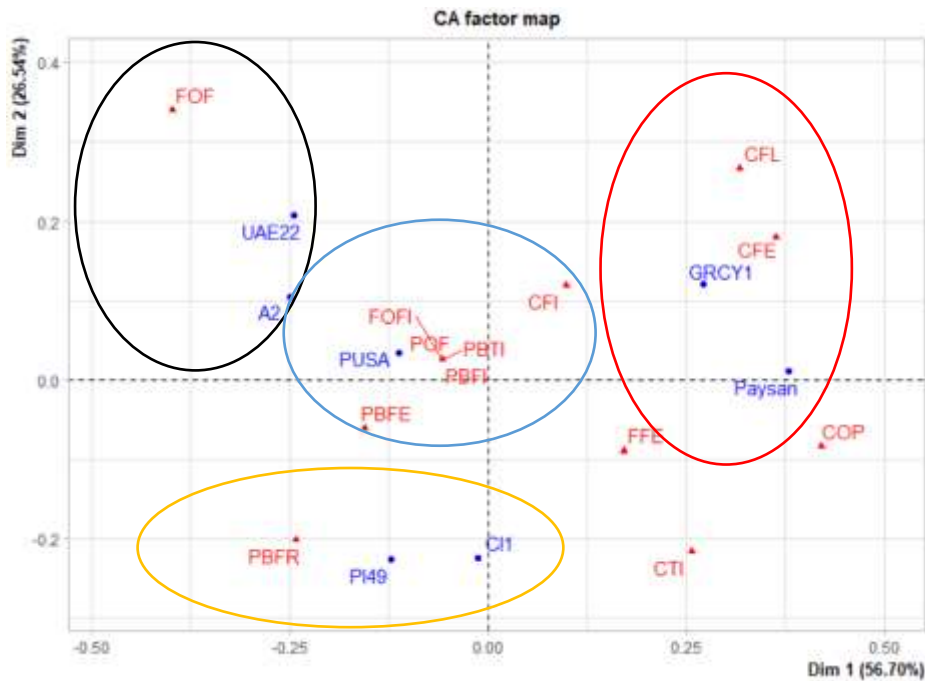


Figure 5: Factorial correspondence analysis of genotypes according to qualitative variables

5 DISCUSSION

Significant differentiation was found between the okra genotypes studied. Ouédraogo (2016) documented a similar situation in okra including colouring, pubescence and shape of the different organs. Overall, authors as Erickson and Couto (1963); Nath and Dutta (1970); and Kalia and Padda (1962) showed that variation in organ coloration and pubescence is linked to simple genetic determinism. However, it is interesting to note that phenotypic variation may result not only from the outbreeding reproduction system of okra but also from the important seed flow observed at the regional scale. Qualitative traits variation between okra genotypes reported in several studies (Nesru *et al.*, 2021). This study results constitute a potential for varietal selection in Burkina Faso where, according to Ouédraogo (2016), the lack of quality seeds is one of the main constraints of cultivation. There are several flower colorations within cultivated okra genotypes. In addition to the yellow, golden yellow and cream colorations that characterize okra flowers, our results highlight the existence of an intermediate light yellow coloration. This phenotype would result from crossbreeding due to the partial allogamy of okra. According to

Charrier (1983), only the colouring of the base of the petals would have a simple monogenic determinism, with a dominant red allele. This difference in flower coloration suggests a polymorphism in qualitative traits related to the fruits. Five colouring modalities noted in the stems and fruits among seven genotypes studied reflect significant qualitative diversity of okra. According fruit colour, five modalities were also stated by Binalfew and Yosef (2016). Indeed, the coloration of the organs can be justified by parent's origin, pleiotropy effect in colour characters of the stem and the fruit expression (Koechlin, 1989). Others authors as Hamon *et al.* (1997) explained the variation in stem colour as being due to expression of four genes, similar as a duplicated gene responsible for the red colouring, an inhibitor acting on these two genes and an anti-inhibitor on the inhibitor. Several authors have revealed that the pubescence of organs, the colorations of stems, fruits and petals are linked (Erickson and Couto, 1963; Nath and Dutta, 1970; Kalia and Padda, 1962). The phenotypic variability linked to the coloration would therefore be essentially of genetic origin. Based on fruits and leaves shape different types

of genotypes were found. Overall, the results obtained from leaves shape are in line with Charrier (1983) who identified five classes of forms. Sawadogo *et al.* (2009) reported that the shape of the fruit is one of the main criteria for assessing the quality of okra. According, Marose and Peter (1990) fruit shape is a digenic and dominant character, which explains its strong contribution in okra morphological variability expression. The high differentiation of okra genotypes is the organs pubescence. This study identified at leaf level one genotype pubescent, five genotypes slightly pubescent and one genotype glabrous. However, on fruits two genotypes very pubescent, one genotype pubescent, one genotype slightly pubescent and three genotypes glabrous were found. In similar study Nesru *et al.* (2021) obtained more genotypes with pubescent leaves and AdeOluwa and Kehinde (2011) revealed two types of fruit pubescence i.e. mostly glabrous and pubescent.

6 CONCLUSION

Wide variation qualitative traits revealed the potential usefulness of these genotypes for okra improvement program. This phenotypic variation would be linked to heritable polygenic characters that contribute to the expression of okra morphological variability. It is possible to

Concerning plant cycle, early maturing genotypes (*UAE22*, *Gry1*, *PUSA*, and *Paysan*) and late maturing genotypes (*A2*, *CI1* and *PI49*) were distinguished. Similar observations were reported by Nana (2010) who attributed okra genotypes with flowering cycle between 50-60 days after sowing as early. Some variation for shape, colour and pubescence of the fruit revealed a distinction among the genotypes and formed four distinct groups as presented by AFC (Fig.5). The differentiation among okra genotypes based on fruit shape and colour (Charrier, 1989). A distribution between genotypes showed fruit shape (*UAE22* and *A2*), fruit colour (*Gry1* and *Paysan*), fruit pubescence (*CI1* and *PI49*) and fruit colour and shape and cycle early (*PUSA*). In addition, environmental factors could justify the variations between these genotypes. Nesru *et al.* (2021) indicated the possibility of improving fruit quality traits through selection or crossing of genotypes.

develop new varieties and a diverse of varieties that respond to farmers' current and satisfying needs. To continue this work, a better knowledge on the heritability of traits, molecular biology and biochemical parameters of okra would be necessary.

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