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Original Research Article

Agromorphological Characterization and Evaluation of the Susceptibility of 19 Cassava Clones (*Manihot esculenta* crantz) to Cassava Mosaic Disease and Cassava Bacteriosis in Togo

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Abstract: Cassava (*Manihot esculenta* Crantz) is an important tuber crop grown in many countries around the world that contributes to people's food security and is a source of income for producers. But it is clear that cassava cultivation encounters enormous constraints, among which cassava mosaic disease (CMD) and cassava bacteriosis are the most important. Thus, knowledge and exploitation of the diversity of cassava is of particular importance for maintaining and improving its productivity. It is in this perspective that the present study is carried out, the objective of which is to identify the morphological characteristics of 19 cassava clones, and to evaluate the susceptibility of the clones to cassava mosaic disease (CMD) and cassava bacteriosis at the Lomé Agronomic Experimentation Station. The results of this study revealed significant phenotypic variability within the clones. The evaluation of the phytosanitary state of the clones showed that the mean attack severity varied from 1.07 to 2.70 for CMD and from 1.81 to 2.11 for bacteriosis. Fresh tuber yields varied from 12.86 t/ha to 75.71 t/ha. Seven clones (GB20, GA24, D24, N22, Cm, C04, C02) obtained a higher yield than the control clone C01 (40 t/ha). The GB20 clone (75.71 t/ha) was the most productive, 89.26% more than the control clone.

Keywords: Bacteriosis, CMD, cassava, yield, Togo, variability.

INTRODUCTION

Cassava (Manihot esculenta Crantz) introduced from Latin America to Africa by the Portuguese towards the end of the 16th century (Maroya., 1997), constitutes the staple food of more than 800 million people in the world (Uarrota and al., 2016). Since its introduction in Africa, cassava cultivation has spread to sub-Saharan Africa mainly in the humid tropics. Cassava has become one of the dominant products in the starchy diet of populations. According to the FAO (2010), cassava ranks fourth in the world for plant food production behind maize, rice and wheat. Global production of fresh cassava tubers in 2019 was around 303.57 million tonnes (Mt) with Africa as the largest producer (70% of global production). In the same year, Togo produced 1.12 Mt of cassava with a yield of 3.95 t/ha (FAOSTAT, 2019). Cassava is a key crop in terms of food security and poverty reduction. The demand for cassava products continues to increase. However, this plant is subject to the pressure of several abiotic and biotic constraints among which, cassava mosaic disease (CMD) and cassava bacteriosis are the most damaging (Abessolo-Meye, 2013). To fight effectively against these diseases, several research works have been undertaken in Africa (Ambang *et al*., 2007). Knowledge and exploitation of the diversity of cassava varieties found in growing areas is of particular importance for maintaining and improving cassava productivity in developing countries (Ratnadass *et al.*, 2012; Adjebeng- Danquah *et al*., 2016). There are many procedures for quantifying and analyzing genetic diversity; among these procedures, morphological descriptors are the most used. The analysis of morphological descriptors makes it possible to reveal diversity as it is perceived and selected by local farmers, the main actors in the management of

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varietal diversity (Sawadogo *et al*., 2010). It is in this perspective that the present study is inscribed, the objective of which is to identify the morphological characteristics of 19 cassava clones in selection at the Agronomic Experimentation Station of Lomé (SEAL) and to evaluate the sensitivity of these clones against cassava mosaic disease (CMD) and cassava bacteriosis.

1. MATERIALS AND METHODS

Experimental site

The study took place at the Agronomic Experimentation Station of Lomé of the Higher School of Agronomy of the University of Lomé located in the south of Togo in the Maritime region on the coastal strip between 6°22 'latitude North and 11°13' East longitude and at an altitude of 50 m (Ayi, 2008). It is a ferralitic soil commonly called "Bar lands", formed from the continental deposit, covers part of the arable land in Ghana, Togo, Benin and Nigeria (Kadanga and Sogbédji, 2017). The average temperature of the site is 27°C. The amount of precipitation varies between 800 and 1100 mm per year.

Plant material studied

The plant material consists of 19 cassava clonent (Manihot esculenta Crantz) from the collection of the Laboratory of Plant Virology and Biotechnology (LVBV) of the University of Lomé.

Experimental device

The experimental device used is a complete randomized block with the 1m x 1m cropping pattern for a density of 10,000 plants per hectare. The clones were distributed over a useful area of 190 m2 at the rate of 10 plants per clone. The cassava cuttings were planted on January 29, 2021. The observations began on February 3, 2021 and ended on October 11, 2021. These observations focused on the one hand, on the evaluation of the incidence and the severity of cassava mosaic disease (CMD) and cassava bacteriosis on the clones for a period of 06 months, and on the other hand on the determination of the phenotypic classes of the clones at the 3rd, 6th and 9th month after burial. The clones were also evaluated with respect to their production in fresh tubers.

Determination of phenotypic classes

Twenty-two of the descriptors proposed by Fukuda *et al*. (2010) for the agro-morphological characterization of cassava were used. These descriptors took into account characters concerning leaves, stems and tuberous roots (Table 1).

Table-1: Descriptors used

N°	Traits and stages of evaluation	Phenotypic classes
1	Color of apical leaves (3 Map)	Light green, Dark green, Purple green
2	Pubescence of apical leaves (3 Map)	Absent, Present
3	Leaf retention (6 Map)	Very poor retention, Average, Average retention, very good retention
4	Petiole color (6 Map)	Yellow green, Green, Red green, Light green, Purple red, Red yellow.
5	Number of leaf lobes (6 Map)	Seven lobes, Nine lobes
6	Leaf vein color (6 Map)	Green, Reddish green
7	Petiole Orientation (6 Map)	Downward, Horizontal, Irregular
8	Flowering (6 Map)	Absent, Present
9	Pollen (9 Map)	Absent, Present
10	Stem cortex color (9 Map)	Light green, Dark green
11	Stem skin color (9 Map)	Cream, Light brown, Dark brown, Orange
12	External rod color (9 Map)	Grey, Gold, Brown, Yellowish green, Silver green
13	Color of apical branches (9 Map)	Green, Purple green, Red yellow
14	Fruit (9 Map)	Absent, Present
15	Plant shape (9 Map)	Compact, Umbrella, Cylindrical
16	Peduncle (9 Map)	Sessile, Pedunculate, Mixed
17	Root pulp color (9 Map)	Cream, Yellow
18	Root cortex color (9 Map)	Cream, Yellow, Pink
19	External Root Color (9 Map)	Cream, Yellow, Light Brown, Dark Brown
20	Stem skin color (9 Map)	Light brown, dark brown, Cream
21	Stem Growth Mode (9 Map)	Straight, Zig Zag
22	Stem branching mode (9 Map)	Erect, Dichotomous, Trichotomous

Map = Months after planting

Assessment of the incidence rate of cassava mosaic disease and cassava bacteriosis

The cassava mosaic disease incidence rate and that of cassava bacteriosis were determined from the formula: **PPI = (NPI x 100) / NPT**, PPI = Percentage of Infected Plants (of the clone considered), NPI = Number of Infected Plants (of the clone considered), NPT = Total Number of Plants observed (of the clone considered)

Assessing the severity of symptoms of cassava mosaic disease and cassava bacterial blight. The severity of the cassava mosaic disease symptoms and that of the cassava bacteriosis symptoms were evaluated

on the clones using the IITA (1990) rating scale and the Boher and Agbobli rating scale respectively (1992). From the severity scores, the intensity of the infection or the severity of attack "I" of each of these diseases within each clone was calculated as a function of time according to the formula of Tchoumakov and Zaharova (1990): **I = ∑ab / N**; I = attack severity; ∑ab = sum of the multiplications of the number of diseased plants (a) by the corresponding degree of infection (b) and N = total number of plants observed.

Determination of fresh tubé yields

The fresh cassava tubers were harvested on October 11, 2021, i.e. 9 months after the cuttings were planted. The tubers of each plant were weighed for the 19 clones. The yield (Yield) of fresh cassava tubers was determined using the formula: Yield (t/ha) = PMP x NP, PMP = Average production per plant; NP = Number of plants per hectare.

DATA ANALYSIS

The data collected was recorded and analyzed using the Excel 2016 spreadsheet. Duncan's test was used to discriminate the means at the threshold of α = 5% using R software version 4.1.1.

2. RESULTS

2.1 Analysis of qualitative characteristics

A very high phenotypic variability was observed in the 19 clones for all the qualitative traits studied. The frequencies of the different identified phenotypic classes are shown in Table.2.

Table-2: Variability of the qualitative characters of the 19 cassava clonent

N° Traits and stages of evaluation	Phenotypic classes (%) Sheets
Sheets	
1 Apical Leaf Color (3 Wap)	Purple Green (52.63), Dark Green (26.32), Green (15.79), Purple (5.26)
2 Pubescence of apical leaves (3 Wap)	Present (21.05), Absent (78.95)
3 Leaf Retention (6 Wap)	Good (42.11), Very Good (26.32), Poor (26.32), Fair (5.26)
4 Petiole color (6 Wap)	Green (31.58), Greenish purple (26.32), Greenish red (15.79), Purple (15.79), Red yello (10.53)
5 Number of leaf lobes (6 Wap)	Seven lobes (73.68), Nine lobes (26.32)
6 Leaf vein color (6 Wap)	Greenish red (52.63), Green (47.37)
7 Petiole orientation (6 Wap)	Up (47.37), Horizontal (21.05), Irregular (15.79),
Flowers	Down (15.79)
8 Flowering (6 Wap)	Absent (15.79), Present (84.21)
9 Fruit (9 Wap)	Absent (15.79), Present (84.21)
10 Pollen (9 Wap)	Absent (15.79), Present (84.21)
Rods	
11 Stem cortex color (9 Wap)	Light green (52.63), Dark green (47.37)
12 Stem skin color (9 Wap)	Orange (31.58), Light Brown (26.32), Da Brown (26.32), Cream (15.79)
13 Stem branching mode (9 Wap)	Erect (52.63), Dichotomous (36.84), Trichoto mous (10.53)
14 Stem Growth Mode (9 Wap)	Straight (78.95), Zig Zag (21.05)
15 Stem skin color (9 Wap)	Orange (31.58), Cream (26.32) Dark Brown (26.32), Light Brown (15.79)
16 Outer Shaft Color (9 Wap)	Silver Green (73.68), Gold (10.53), Light rown (10.53), Yellowish Green (5.26)
17 Color of apical branches (9 Wap)	Green (52.63), Purple green (47.37)
18 Plant shape (9 Wap)	Cylindrical (52.63), Umbrella (36.84), Co pact (10.53)
Roots	
19 Peduncle (9 Wap)	Sessile (36.84), Pedunculate (31.58), Mixed (31.58)
20 Root pulp color (9 Wap)	Cream (78.95), Yellow (10.53), White (10.53)
21 Root cortex color (9 Wap)	Cream (57.89), Pink (42.11)
22 External Root Color (9 Wap)	Light Brown (78.95), Dark Brown (10.53), Yellow (5.26), Cream (5.26)

Map = Month after planting

2.2 Susceptibility of clones to cassava mosaic disease

The results of the incidence and severity of cassava mosaic disease (CMD) are presented in Tables 3 and 4 respectively.

Table-3: Incidence of cassava mosaic disease (CMD) on clones.

Clones	Wap4	Wap6	Wap8	SAP10	Wap12	Wap14	Wap16	Wap18	Wap20	Wap22	Wap24
C01	0	11.11	0	11.11	11.11	0	0	0	0	11.11	100
C02	77.78	88.89	100	100	100	100	100	100	100	100	100
C03	33.33	44.44	0	0	0	0	0	0	0	100	100
C04	100	100	100	100	100	100	100	100	100	100	100
C05	55.56	88.89	77.78	77.78	77.78	66.67	66.67	87.5	87. 05	100	100
Cm	0	22.22	11.11	33.33	33.33	37.5	25	33.33	33,33	16.67	16.67
D01	0	0	0	0	0	0	0	0	0	100	100
D16	66.67	100	100	100	100	100	100	100	100	100	100
D24	75	87.5	75	75	50	75	75	75	87.5	100	100

GA06	11.11	0	0	0	0	0	0	0	0	100	100
GA22	11.11	0	0	0	0	0	0	0	0	100	100
GA24	22.22	0	0	0	0	0	0	0	0	100	100
GB12	11.11	11.11	0	0	0	0	0	0	0	100	100
GB20	100	100	100	100	100	100	100	100	100	100	100
M	33.33	11.11	11.11	0	11.11	11.11	0	0	0	0	0
N14	0	0	0	0	0	0	0	0	0	100	100
N21	11.11	0	0	0	0	0	0	0	0	100	100
N22	33.33	22.22	11.11	0	11.11	0	0	0	0	0	100
Y0	11.11	22.22	0	0	0	0	0	0	0	100	100

Wap = Week after planting

Table-4: Average severity of cassava mosaic disease (CMD) attack on clones

Clones	Wap4	Wap6	Wap8	Wap10	Wap12	Wap14	Wap16	Wap18	Wap20	Wap22	Wap24	Av
C01	1.00	1.11	1.00	1.11	1.11	1.00	1.25	1.33	1.33	1.17	1.17	1.24
C02	1.89	2.00	2.00	2.00	2.11	2.00	1.00	1.00	1.00	1.00	2.00	1.17
C03	1.33	1.44	1.00	1.00	1.00	1.00	1.00	1.00	1.00	2.00	2.00	1.21
C04	2.44	2.22	2.44	2.44	2.00	2.00	2.00	2.00	2.00	2.11	4.00	2.33
C05	1.56	1.89	1.78	1.78	1.78	1.67	1.00	1.00	1.00	1.11	2.00	1.13
Cm	1.00	1.22	1.11	1.33	1.33	1.38	1.63	1.63	2.00	2.38	4.00	1.98
D01	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.20	3.20	1.28
D16	1.89	2.50	2.25	2.00	2.00	2.00	1.67	1.88	1.88	2.88	4.00	2.07
D24	1.63	1.88	1.88	1.75	1.38	1.63	1.00	1.00	1.00	2.33	3.00	1.31
GA06	1.11	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	3.00	2.00	1.27
GA22	1.11	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	3.00	4.00	1.53
GA24	1.22	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	2.00	4.00	1.43
GB12	1.11	1.11	1.00	1.00	1.00	1.00	1.89	2.33	2.00	4.00	4.00	2.38
GB20	2.44	2.67	2.89	2.56	2.00	2.00	1.00	1.00	1.00	1.00	1.00	1.07
M	1.33	1.11	1.11	1.00	1.11	1.11	1.00	1.00	1.00	2.00	2.00	1.19
N14	1.00	1.00	1.00	1.00	1.00	1.00	2.00	2.11	3.00	4.00	4.00	2.70
N21	1.11	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	2.00	2.00	1.20
N22	1.44	1.22	1.11	1.00	1.11	1.00	2.00	2.00	2.00	2.75	2.88	2.21
YO	1.11	1.22	1.00	1.00	1.00	1.00	1.00	1.00	1.00	2.00	2.11	1.20

WAP = Week after planting Av = Average

2.3. Susceptibility of clones to bacteriosis

The results of the bacteriosis evaluation showed that during the first 03 months after planting (4th to 14th Sap) clonent C01, GA06, GB12, N21 and YO recorded an incidence rate of less than 50% (Table 5). During the following months (14th to 24th Wap) all clones recorded an incidence rate of 100%.

Table-5: Incidence rate of bacteriosis

Clones	Wap4	Wap6	Wap8	Wap10	Wap12	Wap14	Wap16	Wap18	Wap20	Wap22	Wap24
C01	11.11	33.33	22.22	55.55	66.67	100	100	100	100	100	100
C02	11.11	77.78	88.89	88.89	88.89	100	100	100	100	100	100
C03	55.56	88.89	10.	88.89	77.78	100	100	100	100	100	100
C04	11.11	44.44	88.89	88.89	100	100	100	100	100	100	100
C05	44.44	66.67	88.89	88.89	66.67	100	100	100	100	100	100
Cm	55.56	77.78	88.89	88.89	100	100	100	100	100	100	100
D01	44.44	88.89	100	100	100	100	100	100	100	100	100
D16	22.22	75	100	100	100	100	100	100	100	100	100
D24	0	75	75	87.5	100	100	100	100	100	100	100
GA06	22.22	44.44	66.67	66.67	77.78	100	100	100	100	100	100
GA22	77.78	88.89	100	100	100	100	100	100	100	100	100
GA24	77.78	77.78	100	100	100	100	100	100	100	100	100
GB12	0	88.89	100	88.89	100	100	100	100	100	100	100
GB20	22.22	44.44	88.89	33.33	66.67	100	100	100	100	100	100
M	88.89	88.89	100	88.89	88.89	88.89	100	100	100	100	100
N14	77.78	77.78	88.89	77.78	88.89	100	100	100	100	100	100
N21	33,33	44.44	55.56	77.78	88.89	100	100	100	100	100	100
N22	0	33.33	88.89	66.67	100	100	100	100	100	100	100
Y0	33.33	77.78	100	77.78	100	100	100	100	100	100	100

Wap = Week after planting

The mean bacteriosis attack severity varied from 1.81 (clone C01) to 2.11 (clone YO) during the trial period (Table 6). A total of 47.36% of the clones had an attack severity in round 2 ($I \leq 2$) and 52.64% an attack severity greater than 2 ($2 < I < 3$). The attack of the different clones by bacteriosis was felt the most in the 3rd and 6th months after planting (14th Wap and 24th Wap).

Table-6: Severity of bacteriosis disease

Clones	SAP4	SAP6	SAP8	SAP10	SAP12	SAP14	SAP16	SAP18	SAP20	SAP22	SAP24	Av
C01	1.11	1.33	1.22	1.56	1.67	2.00	2.00	2.00	2.00	2.00	3.00	1.81
C02	1.11	1.78	1.89	1.89	1.89	2.00	2.00	2.00	2.00	2.00	2.67	1.93
C03	1.56	1.89	2.22	1.89	1.78	2.00	2.00	2.00	2.00	2.00	2.67	2.00
C04	1.11	1.56	2.00	1.89	2.00	2.00	2.00	2.00	2.00	2.00	3.00	1.96
C05	1.44	1.67	1.89	1.89	1.67	2.00	2.11	2.22	2.00	2.00	2.75	1.97
Cm	1.56	1.78	1.89	1.89	2.00	2.63	2.38	2.75	2.00	2.17	2.00	2.09
D01	1.44	1.89	2.00	2.00	2.00	2.00	2.00	2.00	2.00	2.00	2.89	2.02
D16	1.22	1.75	2.13	2.13	2.00	2.13	2.00	2.00	2.00	2.13	3.00	2.04
D24	1.13	1.75	1.88	1.88	2.00	1.88	2.00	2.00	2.00	2.25	2.75	1.95
GA06	1.22	1.44	1.67	1.67	1.78	2.00	2.00	2.00	2.00	2.00	2.89	1.88
GA22	1.78	1.89	2.00	2.00	2.00	2.00	2.00	2.00	2.00	2.11	2.78	2.05
GA24	1.78	1.89	2.11	2.00	1.89	2.00	2.00	2.00	2.00	2.00	3.00	2.06
GB12	1.00	1.89	2.00	1.89	2.00	2.00	2.00	2.00	2.00	2.00	2.89	1.97
GB20	1.22	1.56	1.89	1.33	1.67	2.00	2.00	2.00	2.00	3.00	3.00	1.97
M	2.00	1.89	2.00	1.89	1.89	1.89	2.00	2.00	2.00	2.00	2.00	1.96
N14	1.78	1.78	1.89	1.78	1.89	2.00	2.00	2.00	2.00	2.00	2.67	1.98
N21	1.33	1.44	1.56	1.78	1.89	2.00	2.00	2.00	2.00	2.11	3.00	1.92
N22	1.00	1.33	1.89	1.67	2.00	2.11	2.44	2.44	2.44	2.00	3.00	2.03
Y0	1.44	1.78	2.00	1.78	2.00	2.22	2.33	2.33	2.33	2.00	3.00	2.11

Wap = Week after planting Av = Average

2.4. Production and yield of fresh tubers

The statistical analyzes carried out at the 5% threshold showed a significant difference between the clones and made it possible to group them into 6 groups (Table 7).

Table-7: Production and yield of fresh tubers

Clones	Production per plant (kg)	Yield (t/ha)
Cm	4.586	45.86^{bcd}
N22	5.043	50.43^{bc}
YO	1.857	18.57^{cd}
C04	4.386	43.86^{bcd}
C01	4.000	40.00^{bcd}
GA24	6.114	61.14^{ab}
C05	2.686	26.86^{cd}
D24	5.086	50.86^{bc}
GA06	1683	16.83^{cd}
N14	2.086	20.86^{cd}
C03	2.786	27.86^{bcd}
C02	4.100	41.00^{bcd}
M	3.614	36.14^{bcd}
D01	1.986	19.86^{cd}
N21	3.971	39.71^{bcd}
GB20	7.571	75.71^{a}
GB12	3.929	39.29^{bcd}
D16	1.286	12.86^{d}
GA22	2.957	29.57^{bcd}

The values assigned the same letter index are statistically identical at the 5% threshold

3. DISCUSSION

3.1. Analysis of qualitative characteristics

The analysis of the results showed that the purple green (52.63%) and dark green (26.32%) colors were the most dominant in the leaves; almost 80% of the clones had apical leaves without pubescence.

At the level of the stems, the colors green and greenish purple were dominant respectively in 31.58% and 26.32% of the clones; 43.37% of the clones had upward facing petioles and 78.95% of the clones had leaves whose central lobe was lanceolate in shape. These results are similar to those of Mezette *et al*. (2013), who recorded more than 50% of clones with apical purple-green leaves in Brazil.

In Chad, Nadjam *et al*. (2016) also recorded a high percentage (93%) of hairless accessions for the trait "Pubescence". The phenotypic classes, good and very good retention, were also observed by Gmakouba *et al*. (2018).

Two to four phenotypic classes have been recorded based on stem traits; 73.68% of clones had silver-green stems; about 80% of clones have straight stems. Moreover, the number of clones with cream-colored stem epidermis is equal to the number of clones with dark brown epidermis (26.32%). The majority of the clones, (31.58%), had an orange color for the "Stem epidermis color" trait. These results also corroborate those of Mezette *et al*. (2013). With regard to the character "Mode of branching of the stems", more than half of the clones have erect plants which is directly related to the results of Nadjam *et al*. (2016). These authors concluded from their study that the erect mode of branching is predominant in Chad.

At the root level, more than half of the clones (57.89%) had a cream-colored cortex, while 42.11% had a pink-colored cortex. The analysis of the results showed that 78.95% of the clones presented the light brown color for the character "external color of the tubers". These results are similar to the results obtained in Brazil by Mezette *et al*. (2013) who showed that more than 60% of cassava clones had a light brown color for the "external tuber color" trait. N'Zue *et al*. (2014) also obtained different results for the "root cortex color" trait with 57% of clones with pink root cortex and 91% of clones with white pulp for the "pulp color" trait.

Apart from the leaves, stems and roots, a phenotypic variability was observed at the level of the flowers where the results showed that 84.21% of the clones were devoid of both flowers, fruits and pollen seeds. On the other hand, fruits and flowers containing pollen grains were observed in the 15.79% of the remaining clones. These results are similar to the results of N'Zué *et al*. (2014) who obtained 80% of accessions without flowers.

3.2. Susceptibility of clones to cassava mosaic disease (CMD)

Analysis of the results of the incidence and severity of cassava mosaic disease (CMD) showed that the disease evolved differently from one clone to another over time. Apart from the Cm and M clones from the 14th to the 24th week after planting (Wap), all the other clones recorded an incidence rate of 100%. The mean CMD attack severity oscillated between rating scores 1 and 3 (Table 4). During the trial period, only clones C02, C03, C04, D24, GB20 recorded the maximum severity score (4) and this at the 6th month after planting (24th SAP). Less than half of the clones (26.32%) had an average attack severity (I) greater than 2, while 73.68% had an average attack severity between 1 and 2 ($1 < I < 2$). These results show that the clones studied are sensitive to CMD with different degrees of sensitivity. Mupenda and Walangululu (2016) in Mudaka in the Democratic Republic of Congo also obtained a CMD incidence rate of more than 50%. The appearance of CDM symptoms from the first weeks of observation in certain clones could be explained by the presence of the virus strains responsible for the cassava mosaic disease in the cuttings before they were planted thus confirming the results of Ambang *et al*. (2007). The rapid evolution of the CDM in certain clones would be due to the fact that the resistant clones at the beginning of the observation saw their resistance broken.

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3.3. Susceptibility of clones to bacteriosis

These results are in agreement with those of Wonni *et al*. (2014) and Yameogo (2018) who reported and described the bacteriosis pathogen in Burkina Faso. Leaf incidences reaching 100% were also recorded in the Cascades and Hauts Bassins regions by these authors. In Côte d'Ivoire, Affery *et al*. (2018) obtained an incidence of more than 70% on several cassava varieties.

Boher and Agbobli (1992) had already reported cassava bacteriosis in Togo in the 1990s with an average attack severity of less than 3. Banito *et al*. (2007) showed during the study on the remediation of major cassava diseases that 90% of cassava accessions assessed in Togo showed symptoms of cassava bacteriosis and that the varieties of cassava grown in Togo are in the majority susceptible to this disease and cassava mosaic disease. Djinadou *et al*. (2018) showed that cassava mosaic disease and bacteriosis are stresses to which cassava experiences a certain vulnerability.

3.4. Production and yield of fresh tubers

The yields of fresh tubers of the 19 clones varied from 12.86 t/ha (clone D16) to 75.71 t/ha (clone GB20). These results are similar to those of Ambang *et al*. (2007) who recorded average yields of 15.6 t/ha, 32.1 t/ha, 34.5 t/ha respectively for the varieties IITA 8034, IITA 8061 and the wild species *Manihot glaziovii.*

Analysis of the results revealed that despite the fact that the clones were susceptible to cassava mosaic disease and bacteriosis, the majority of the clones recorded a yield close to and higher than the yield of the control clone C01(40 t/ha). Wembonyama *et al*. (2020) in DR Congo, showed that despite the susceptibility of cassava varieties to African cassava mosaic, the root yield varied from 34.2 to 44.7t/ha with an average of 39.8t/ha. Thus, in view of the results, the 19 clones evaluated would all be tolerant to cassava mosaic disease (CMD) and cassava bacteriosis

CONCLUSION

At the end of this study, a significant phenotypic variability was observed within the clones evaluated. The evaluation of the phytosanitary status of these clones showed that they are susceptible to cassava mosaic disease (CMD) and cassava bacteriosis but with different degrees of susceptibility with attack severity. Less than 3 for both diseases. The yield of fresh cassava tubers was not proportional to disease intensity and varied from 12.8 t/ha to 75.71 t/ha. The GB 20 clone was the most productive followed by the GA24, D24, N22 clones. This study thus highlighted the presence of strong heterogeneity between the clones studied and a tolerance to CMD and bacteriosis. These results could be exploited in selection and varietal improvement programs. Other studies based on molecular techniques (PCR, SSR) will be necessary in order to identify the strains of pathogenic agents responsible for the symptoms observed and to better characterize the clones.

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