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OCCURRENCE OF TOMATO LEAF CURL VIRUS ON CASSAVA (Manihot esculenta Crantz) IN TOGO

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ABSTRACT

Background and Objective: Climate change forces insect vectors to adapt to plants that were not their natural hosts, and this contributes to the emergence of begomoviruses. Cassava mosaic disease (CMD) caused by cassava whitefly-transmitted Begomoviruses is the main constraint on the progress of cassava production in Africa. The present study aims to examine the potential Begomoviruses infecting cassava other than those responsible for CMD.

Material and Methods: Foliar samples are collected from cassava, nine associated crops, and weeds in cassava fields across the five economic regions of Togo in 2015. PCR is performed with the degenerate primers AV494/AC1048 to amplify the coat protein gene of begomoviruses, followed by a direct sequencing.

Results: The presence of begomoviruses other than the traditional well-known ones on cassava is detected in cassava samples. Analyses of partial sequences of coat protein of ten amplicons reveal the presence of five begomovirus groups: *African cassava mosaic virus* (ACMV), *East African cassava mosaic virus* (EACMV), *Tomato leaf curl Kumasi virus* (ToLCKuV) on cassava; ToLCKuV and *Tomato leaf curl Nigeria virus* (ToLCNV) on tomato, and *Ageratum leaf curl Cameroon virus* (ALCCMV) on pepper.

Conclusion: Tomato begomoviruses ToLCKuV are then identified on cassava, and ALCCMV on pepper. This study will help understand the epidemiology related to whitefly transmissible geminiviruses. This is the first report of ToLCKuV on cassava and ALCCMV on pepper in Togo.

Keywords: Begomovirus, cassava, climate, PCR, ToLCKuV

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INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is an important root crop in many regions of the tropical area, mostly in sub-Saharan Africa. It plays a vital role in food security. Unfortunately, pests and diseases, especially cassava mosaic disease (CMD) caused either by isolated or a combination of the whitefly-transmitted cassava mosaic geminiviruses (Legg and Fauquet, 2004; Dutt *et al*., 2005) are among diseases that are basically responsible for low yields. Cassava mosaic geminiviruses (CMGs) are included in the genus *Begomovirus* of the family *Geminiviridae*. Begomoviruses can contain two genomic components of 2.7- 2.8 Kb size namely DNA-A and DNA-B then called bipartite, or a single genomic component equivalent to DNA-A component of bipartite and called monopartite (Briddon *et al*., 2008). Seven CMGs species have been reported from Africa: *African cassava mosaic virus* (ACMV), *East African cassava mosaic virus* (EACMV), *East African cassava mosaic Cameroon virus* (EACMCV), *East African cassava mosaic Kenya virus* (EACMKV), *East African cassava mosaic Malawi virus* (EACMMV), *East African cassava mosaic Zanzibar virus* (EACMZV) and *South African cassava mosaic virus* (SACMV), and two from the Indian subcontinent: *Indian cassava mosaic virus* (ICMV) and *Sri Lankan cassava mosaic virus* (SLCMV) (Fauquet *et al*., 2008). Cassava is cultivated either in monoculture and intercropped. In Togo it is usually intercropped with maize, tomato, okra, pepper, cowpea, yam, taro. Among crops that are cultivated in association with cassava, some are sensitive to begomovirus. Tomato leaf curl virus (ToLCV) is particularly a major constraint in reducing tomato yield and responsible for tomato leaf curl virus disease. This disease is found in several Middle Eastern, African, Asian and Mediterranean countries (Abhary *et al*., 2007). ToLCV is also a Geminivirus group transmitted by *Bemisia tabaci* (Genn.) in a circulative and persistent manner. In the event of severe attacks, yield losses can reach up to 100% (Boykin *et al*., 2007). Begomoviruses are widespread, regarding their incidence and geographical distribution. They have emerged as a potential threat because of many factors including frequent recombination, mixed infections, and wide host range. The use of various pesticides/chemicals against the insects fails to get *Bemisia tabaci* under control and leads to the begomovirus diseases management (Naveen *et al*., 2017). Cassava mosaic disease in Togo is to such extent that there is no cassava cultivar which is not sensitive to the disease (Adjata *et al*., 2009; 2010). The objective of this study is to characterize cassava mosaic begomoviruses and possibly other begomoviruses (i.e. begomovirus infecting associated crops with cassava in fields) infecting cassava in order to show that begomoviruses (known and unknown) have emerged with the climate change and infected new hosts in cassava-based intercropping systems.

MATERIAL AND METHODS

Foliar sampling and DNA isolation

Foliar samples from crops showing mosaic symptoms are collected in cassava field where cassava is associated with such other crops as yam (*Dioscorea* sp), taro (*Colocasia esculenta*),

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tomato (*Solanum lycopersicum*), okra (*Abelmoschus esculentus*), jute (*Corchorus Olitorius*), pepper (*Capsicum sp*), cowpea (*Vigna Unguiculata*), peanut (*Arachis hypogaea*), soybean. (*Glycine max*). Samples are georeferenced and collected in all the economic regions of Togo in 2015. Weeds samples from *Blactuca taraxacifolia*, *Emilia coccinea*, *Erigeron floribundus*, *Euphorbia heterophylla*, *Mitracarpus villosus*, *Physalis angulate* and *Synedrella nodiflora* are also collected in cassava fields. The method of mini preparation of Dellaporta *et al*., (1983) is used to extract viral DNA from foliar samples.

Amplification of viral components

The extracted DNA is used as a template for Polymerase Chain Reaction (PCR) using the thermocycle "Mastercycle gradients Eppendorf (Hamburg, Germany)". The PCR is performed using begomovirus coat protein specific primers, AC1048/AV494 (Table 1) in a 25µl reaction mixture containing: template DNA 2 µl, dNTPs 0.5 µl (200 µM), primers 1.25 µl (each), Taq polymerase 0.16 µl (0.8 U), reaction buffer 2.5 µl (1X), MgCl2 2.5 µl (2.5 mM), BSA 0.5 µl (0.4µg/µl), and sterile water 14.34 µl.

Table 1: Primers sequences

Primer	***Sequence (5'……3')***	***Sens***	***Size (bp)***	***Amplified region***	***Reference***
AC 1048	GGRTTDGARGCATGHG TACATG	Forward	550 to 570	CP	Wyatt and Brown, 1996
AV 494	GCCYATRTAYAGRAAG CCMAG	Reverse			

D=A,G,T ; H=A,C,T ; K=G,T ; M=A,C ; N=A,C,G,T ; R=A,G ; W=A,T ; Y=C,T

The PCR thermal profile is as follows: a 94°C denaturation step for 2 min followed by 35 cycles of denaturing at 94°C for 1 min, annealing at 55°C for 2 min and extension at 72°C for 1 min and then a final extension step at 72 °C for 10 min (Wyatt and Brown, 1996). A fraction of the amplified product (3 µl) is visualized by agarose gel electrophoresis in 10 % agarose gels.

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DNA sequencing and phylogenetic analysis

Indexes are added to positive amplified PCR products (rest of volume). Then PCR indexed products are reduced to the same DNA concentration and purified with magnetics balls using DynaMagTM-2 Magnetic Particle Concentrator and Invitrogen. Purified products are used for sequencing. The sequencing is done in both direction using Miseq V2 Reagent Kit (Illumina Inc., San Diego, CA, USA) according to manufacturer's instructions in Molecular Biology Laboratory at the University of "Picardie Jules Verne (UPJV), France".

BLASTn program (http://blast.ncbi.nlm.nih.gov/Blast.cgi) is used for the similar analysis with GenBank sequences. Multiple alignments are achieved in ClustalX 2.1 program (Larkin *et al*., 2007). Neighborjoining method and one thousand bootstrap iterations are used in the DARWin6 program to construct the phylogenetic tree. Pairwise nucleotide identities are calculated with SDT 1.2 program (Muhire *et al*., 2014).

RESULTS

Incidence of Begomovirus

Two hundred and fifty-one foliar samples are collected in one hundred and forty-two cassava fields. Cassava samples are collected both in monocultures and intercropped fields and weeds (*Blactuca taraxacifolia, Emilia coccinea, Erigeron floribundus, Euphorbia heterophylla, Mitracarpus villosus, Physalis angulata, Synedrella nodiflora*,) are collected in the same way. But yam, taro, tomato, pepper, okra, cowpea, peanut, soybean and Corchorus olitorius are collected only in fields where cassava is intercropped (Table 2).

To diagnose begomovirus infection, samples are submitted to PCR analysis using the degenerated primers AC1048/AV494 and positive PCR products with expected size are obtained (Fig 1-3). Begomovirus infection is detected in five crops and in one weed. The rates of disease plants are as follows: cassava (18,08 %), tomato (13,63 %), *Corchorus olitorius* (9,09 %), pepper (26,31), soybean (50 %) and weed, *Euphorbia heterophylla* (5 %). Begomovirus infection is not detected in yam, taro, okra, cowpea, and peanut (Table 3).

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Table 2: Samples collected from the five economic regions of Togo in 2015

Crops	Region					Total
	Maritime	*Plateau*	*Central*	*Kara*	*Savanna*	
Cassava	23	39	17	11	4	94
Yam	2	7	4	4	1	18
Taro	2	13	0	1	0	16
Tomato	7	10	2	2	1	22
Okra	3	15	1	0	1	20
Jute	2	8	1	0	0	11
Pepper	7	9	1	0	2	19
Peanut	6	3	0	0	0	9
Cowpea	7	10	3	0	0	20
Soybean	2	0	0	0	0	2
Weeds	5	12	3	0	0	20

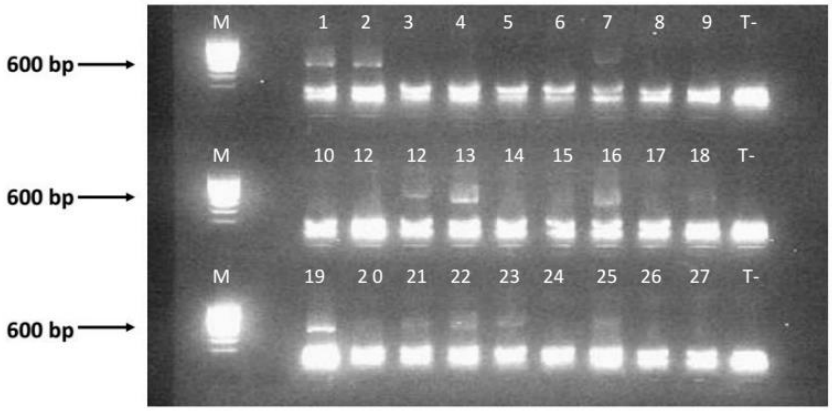

Fig 1: Begomovirus detection by PCR on DNA extraction obtained from cassava disease plant from Togo using degenerate primers specific to the coat protein

(AC1048 and AV494). M = marker, T- = negative control (water), 1-27 = cassava isolates. Samples 1, 2, 7, 12, 13, 16 and 19 react positively to the presence of begomoviruses

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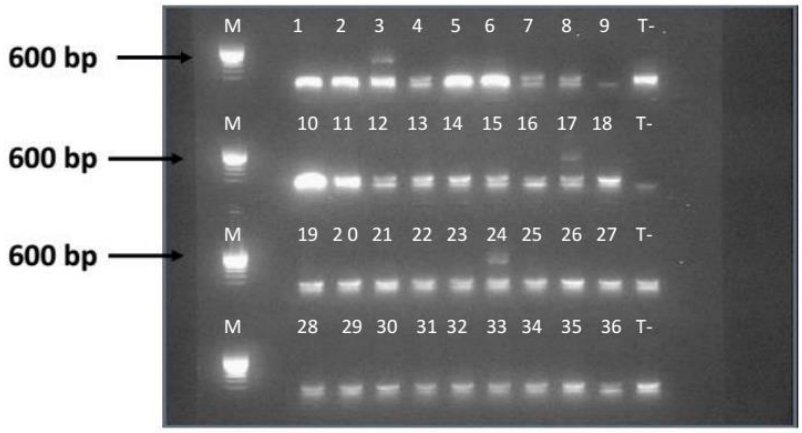

Fig 2: Begomovirus detection by PCR on DNA extraction obtained from tomato disease plant from Togo using degenerate primers specific to the coat protein

(AC1048 and AV494). M = marker, T- = negative control (water). Samples 3 and 24 from tomato react positively to the presence of begomoviruses

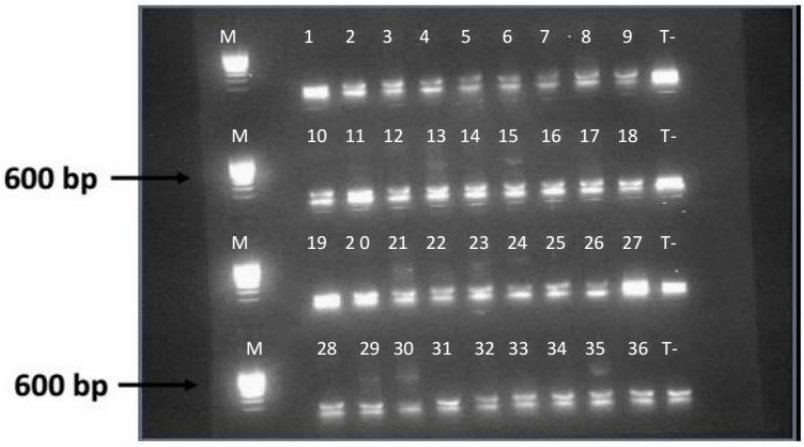

Fig 3: Begomovirus detection by PCR on DNA extraction obtained from pepper disease plant from Togo using degenerate primers specific to the coat protein

(AC1048 and AV494). M = marker, T- = negative control (water). Samples 13, 29 and 30 from pepper react positively to the presence of begomoviruses.

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Table 3: Percentages of diseased plants according to crops and regions

Crops	Region					Total %
	Maritime	*Plateau*	*Central*	*Kara*	*Savanna*	
	Percentages of diseased plants %					
Cassava	**4.35**	**20.51**	**17.65**	**36.36**	**25**	**18.08**
Yam	0	0	0	0	0	0
Taro	0	0	-	0	-	0
Tomato	**14.28**	**10**	**50**	0	0	**13.63**
Okra	0	0	0	-	0	0
Jute	**0**	**12.5**	**0**	**-**	**0**	**9.09**
Pepper	**28.57**	**22.22**	**0**	-	**50**	**26.31**
Peanut	0	0	-	-	-	0
Cowpea	0	0	0	-	-	0
Soybean	**100**	-	**0**	-	-	**50**
Weeds	**0**	**8.33**	**0**	-	-	**5**

Sequence analysis

Ten amplicons are submitted to sequencing and eleven partial sequences of begomovirus coat protein gene are obtained. BLASTn (NCBI) analysis confirms that they are begomoviruses (Table 4). Levels of similar identity are up to 90 % and four groups of begomoviruses are identified: *African cassava mosaic virus*, *East African cassava mosaic virus*, Tomato leaf curl virus and *Ageratum leaf curl virus*. Isolates G18aA, G42aA and G64aA share high similar identity (95-96 %) with *African cassava mosaic virus* (X17095.1). Isolates G7aB, G76aB and G76cB share high identity (93-97 %) with *East African cassava mosaic Cameroon virus* (KJ887944.1). Isolates G56a, G65a and G126a are closely related to *Tomato leaf curl Kumasi virus* (FM210062.1) with 94-98 %. Isolates G44a and G128a are closely related to *Ageratum leaf curl Cameroon virus* (FR873230.1) with 96 % and 95 % respectively and to *Tomato leaf curl Nigeria virus* (JF685621.1) with 96 % and 97 % respectively. The pairwise nucleotide sequence identities scores between isolates found in this study and begomoviruses from GenBank database (Table 5) is presented as shown in Fig 4.

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Table 4: Blastn analysis results with partial sequences of CP obtained in this study with related begomoviruses

Sample extracted				Blastn analysis (NCBI)	
N°	Isolate	Crop	Location/*Region*	Accession	Acronym
1	G7aB	Cassava	YEBONA KOPE/*Plateaux* E 000°33, N 07°35	AY211468.1 (92%) KJ887944.1(93%)	EACMV EACMV
2	G18aA	Cassava	WOGBA/*Maritime* E 001°30, N 06°16	X17095.1 (96%) HE979761.1 (96%)	ACMV ACMV
3	G42aA	Cassava	DEFALE/*Kara* E 001°05, N 09°53	X17095.1 (95%) KR476372.1 (95%)	ACMV ACMV
4	G44a	Pepper	KAMBERE/*Savanes* E 001°30, N 06°16	FR873230.1 (96%) FJ685621.1 (95%)	ALCCMV ToLCNGV
5	G56a	Tomato	AYOME/*Plateaux* E 000°57, N 07°29	FR873230.1 (94%) FM210062.1 (94%)	ALCCMV ToLCKuV
6	G64aA	Cassava	ADJOGBE KOPE/*Plateaux* E 000°41, N 07°29	X17095.1 (97%) HE979761.1 (96%)	ACMV ACMV
7	G65a	Tomato	BOWOU KOPE/*Centrale* E 000°50, N 08°12	FM210063.1 (97%) FM210062.1 (98%)	ToLCKuV ToLCKuV
8	G76aB	Cassava	HOUDJE/*Plateaux* E 000°55, N 07°33	KJ887944.1 (94%) JN165089.1 (93%)	EACMV EACMV
	G76cB	Cassava		KJ887945.1 (97%) JF909192.1 (95%)	EACMV EACMV
9	G126a	Cassava	KPELE TSIKO/*Maritime* E 000°43, N 07°07	FM210063.1 (96%) FM210062.1 (97%)	TLCV TLCV
10	G128a	Tomato	Zio/Maritime E 001°11, N 06°27	FJ685621.1 (97%) FR873230.1 (95%)	ToLCNV ALCCMV

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Table 5: GenBank sequences used in this study

Accession	***Name***
AF112354.1	*East African cassava mosaic Cameroon virus*
AY211468.1	*East African cassava mosaic virus,* isolate BB
AY211465.1	*African cassava mosaic virus,* isolate CM/H7
AY211887.1	*East African cassava mosaic virus,* isolate KO
EU155147.1	*African cassava mosaic virus isolate EAC05-50S*
EU685318.1	*African cassava mosaic virus isolate ACMV*-[NG:Mg:03]
EU685323.1	*East African cassava mosaic Cameroon virus,* isolate EACMCV-CM[NG:So:03]
FJ685620.1	*Tomato leaf curl Togo virus*
FJ685621.1	*Tomato leaf curl Nigeria virus*
FM210062.1	*Tomato leaf curl Kumasi virus,* isolate LIONGO1
FM210063.1	*Tomato leaf curl Kumasi virus,* isolate AMJ11
FM210085.1	*Tomato leaf curl Kumasi virus,* isolate TOS21
FM210086.1	*Tomato leaf curl Kumasi virus,* isolate TOS42
FR717144.1	*Ageratum leaf curl Cameroon virus,* isolate pBal
FR873228.1	*Ageratum leaf curl Cameroon virus,* isolate AGFG24
FR873230.1	*Ageratum leaf curl Cameroon virus,* isolate AGFG23
HE616781.1	*African cassava mosaic Burkina Faso virus,* isolate BF:Oua:BF128C:08
HE659517.1	*Tomato leaf curl Togo virus - Fontem,* isolate TFB2
HE979761.1	*African cassava mosaic virus* , isolate ACMV-[UG:Nam:CMD-MI24:12]
HE979766.1	*African cassava mosaic virus,* isolate ACMV-[UG:Nam:CMD-MI31:12]
HG530110.1	*African cassava mosaic virus,* isolate KE:mtw:CMD-MI64:12
JF909084.1	*East African cassava mosaic virus-Kenya* isolate Comoros
JF909277.1	*East African cassava mosaic Cameroon virus,* isolate Comoros
JN165089.1	*East African cassava mosaic Cameroon virus-Ghana,* isolate EACMCV
KJ887944.1	*East African cassava mosaic Cameroon virus,* isolate MG:MG178B2:09
KJ887945.1	*East African cassava mosaic Cameroon virus,* isolate MG:MG179A1:09
KJ888051.1	*East African cassava mosaic Kenya virus,* isolate MG:MG583A1:11
KJ888092.1	*East African cassava mosaic Cameroon virus,* isolate MG:MG704B1:11
KR476372.1	*African cassava mosaic virus,* isolate TG:Con2:14
X17095.1	*African cassava mosaic virus*-[Nigeria]

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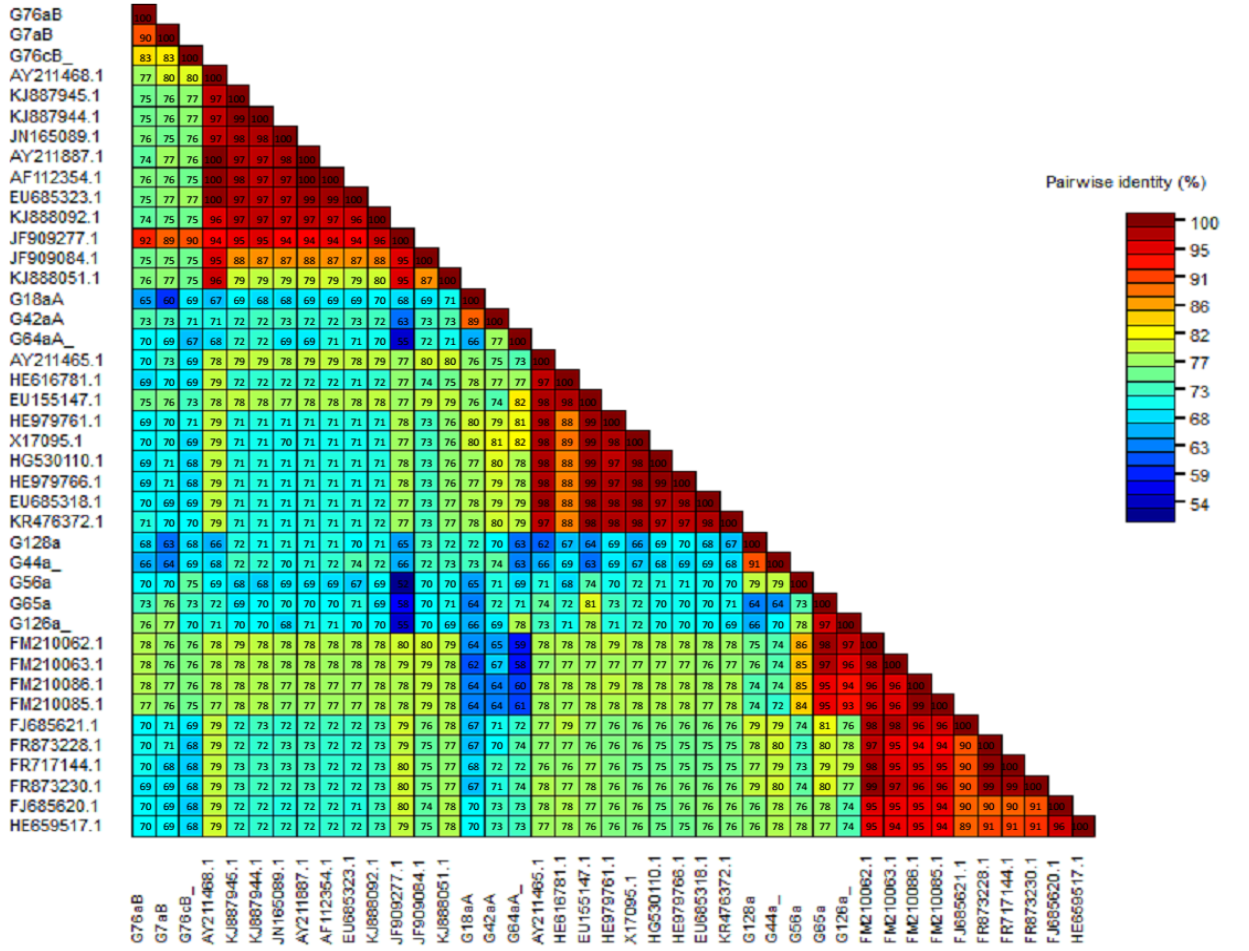

Fig 4: SDT 1.2 Pairwise nucleotide identities scores between isolates found in this study and selected begomoviruses from GenBank

Phylogenetic tree is generated with isolates sequences and the most closely related begomovirus (Fig 5). Isolates G126a, G65a, and G64aA form a distinct clade (Group 1) with FM210062.1 (*Tomato leaf curl Kumasi virus*). Isolate G56a is placed in a distinct clade (Group 4) but can be clustered with isolates from Groups 2 and 3 (Fig 5).

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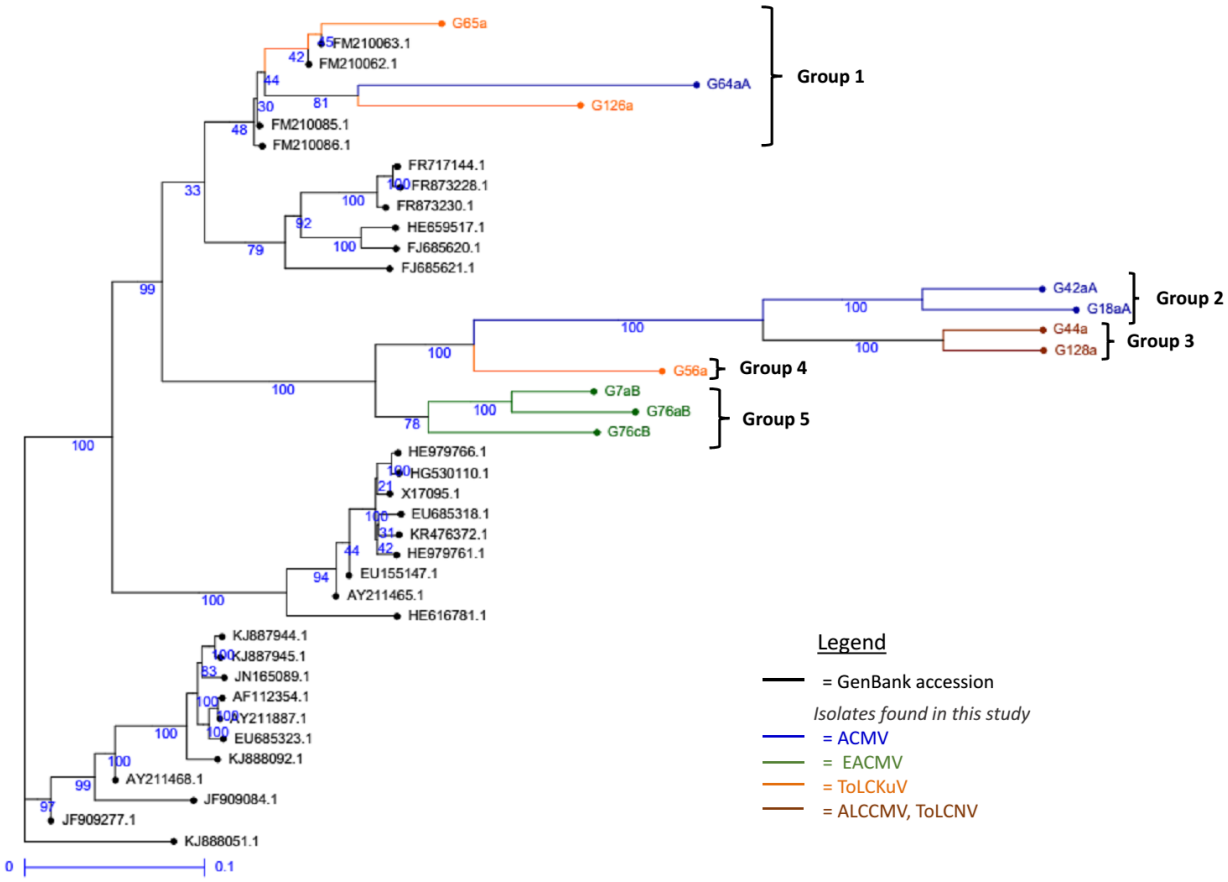

Fig 5: Phylogenetic tree (1000 bootstrap replications) obtained from comparison of the CP sequences of Isolates found in this study and selected begomoviruses from GenBank

DISCUSSION

To look at the potential begomovirus infecting cassava other than these responsible for cassava mosaic disease (CMD), foliar samples are collected in cassava fields. Cassava fields in monoculture and intercropping are visited. Foliar samples from cassava, nine associated crops and weeds are collected. PCR is performed with the degenerate primers AV494 and AC1048, which direct the amplification of the core or middle region of the coat protein gene, to amplify the expected size of 550 to 570 bp and positive PCR products are sequenced.

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PCR results reveal the presence of begomoviruses in five crops and show a variation in the percentages of the infected plants according to types of crops and production zones. Positive PCR products of cassava, tomato, and pepper are sequenced and five groups of begomoviruses infecting these crops are found. Isolates G65a and G56a from tomato and isolate G126a from cassava reveal the highest level of nucleotide sequence identity of 98 %, 86 % and 97% respectively with FM210062.1 (*Tomato leaf curl Kumasi virus*) (Fig 4). This founding suggests that isolates G65a and G126a are variants of *Tomato leaf curl Kumasi virus* (ToLCKuV) while isolate G56a would be a new strain of Tomato leaf curl virus (ToLCV) according to the pairwise identities of 91 % and 94 % proposed as the demarcation threshold for begomoviruses belonging to different species and strains, respectively (Brown *et al*., 2015).

Likewise, according to the nucleotide identity scores and the cutoff of begomovirus thresholds, firstly, isolates G18aA, G42aA and G64aA belong to three different ACMV strains; secondly, isolates G7aB, G76aB and G76cB belong to two different strains of EACMV. Isolates G7aB and G76aB are the same strain while G76cB is a different species. Fig 4). Isolate G44a from pepper reveal the highest level of nucleotide sequence identity (80 %) with *Ageratum leaf curl Cameroon virus* (FR873230.1). It would be a new strain of *Ageratum leaf curl virus*, because the nucleotide sequence identity is inferior to the cutoff of species (91 %) percent (Brown *et al*., 2015). Isolate G128a from tomato shares the highest level of nucleotide sequence identity (79 %) with *Tomato leaf curl Nigeria virus* (JF685621.1) and with *Ageratum leaf curl Cameroon virus* (FR873230.1), but since it shared the highest level of similar identity with JF685621.1, isolate G128a would be a new strain of JF685621.1.

A previous study reveals that three-essential species of cassava mosaic geminiviruses (CMGs): *African cassava mosaic virus* (ACMV), *East African cassava mosaic virus* (EACMV) and *South African cassava mosaic virus* (SACMV) occurred in Africa (Berrie *et al*., 2001) and several begomoviruses have been reported in vegetable crops such as Tomato leaf curl virus (ToLCV) on tomato, *Pepper golden mosaic virus* (PepGMV) on pepper (Leke *et al*., 2015; Brown *et al*., 2005), *Corchorus yellow vein virus* on jute (Ha *et al*., 2006), *Soybean mild mottle virus* (SbMMV) on soybean (Alabi *et al*., 2010). Results are in agreement with those of Adjata *et al*., (2010; 2009) who characterized cassava begomoviruses in Togo. Results confirm the presence of cassava mosaic begomoviruses in Togo except that *Indian cassava mosaic virus* (ICMV) is not found in this study.

Tomato leaf curl Kumasi virus (ToLCKuV) is found on tomato in Togo by Kon, and Gilbertson (2012), but in this study, it is found not only in tomato, but also in cassava. This is the first time ToLCKuV is identified on cassava, *Tomato leaf curl Nigeria virus* (ToLCNGV) on tomato and *Ageratum leaf curl Cameroon virus* (ALCCMV) on pepper in Togo. *Ageratum leaf curl Cameroon virus* (ALCCMV) is a new begomovirus infecting *Ageratum conyzoides* in Cameroon (Leke *et al*., 2012). A beta satellite found in tomato from Togo is closely related to Ageratum leaf curl Cameroon betasatellite (Kon and Gilbertson, 2012). A recent research indicates that

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Ageratum enation virus, a new weed begomovirus is capable of infecting crops (Tahir *et al*., 2015).

The occurrence of *Tomato leaf curl Kumasi virus* on cassava and *Ageratum leaf curl Cameroon virus* on pepper suggests that the vector, *Bemisia tabaci* feeds firstly on a ToLCKuV host plant (tomato) and later on, cassava. In another case, the vector feeds first on an ALCCMV host plant (*A. conyzoides*), and then on pepper. In a cassava-based intercropping system the production cycle of crops overlaps and *Bemisia tabaci* could easily feed on plant from one crop to another. *Ageratum conyzoides* is an annually occurring global weed and it has been present in prospected fields. Cassava, tomato, and pepper are sensitives to begomoviruses and *A. conyzoides* has been described as a natural host of begomoviruses. A Recent study in Cameroon shows that this weed is infected by a complex of begomovirus, alpha satellite, and betasatellite (Leke *et al*., 2015). In addition, *Bemisia tabaci*, vector of begomovirus is a species complex of about 41 biotypes with different ability to transmit viruses (De Barro *et al*., 2011; Brown, 2000). It is supposed that begomoviruses do not replicate within their insect vectors (Harrison, 1985). However, data showing an accumulation of TYLCV DNA in *B. tabaci* raised on a TYLCV non-host plant, after first feeding on a TYLCV-infected plant, suggest a multiplication of TYLCV in its vector (Mehta *et al*., 1994; Sinisterra *et al*., 2005). *B. tabaci* can transmit different strains of TYLCV at once or separately (Ohnishi *et al*., 2011). The success of begomoviruses as emerging pathogens has been attributed partly to their genomic plasticity, which allows them to adapt to new environments and hosts, and leading to the increased prevalence of their highly polyphagous whitefly vector (Navas-Castillo *et al*., 2011). And results suggest the occurrence of a polyphagous biotype of *Bemisia tabaci* on cassava.

The position of each isolate on the phylogenetic tree confirms their distribution in the different groups of discovered begomovirus and suggests a possible recombination action. The presence of isolate G64aA in group 1 indicates that it would come from a possible recombination of *Tomato leaf curl Kumasi virus* and *African cassava mosaic virus*. The conflicting status between the pairwise sequence comparisons and phylogenetic results may be due to a possible recombination (Brown *et al*., 2015). Genetic exchanges through recombination enable a rapid evolution of plant viruses and the role of recombination in the emergence, establishment, and evolution of the new and better adapted begomovirus is well established (Lima *et al*., 2013; Rocha *et al*., 2013).

This study identifies and characterizes ToLCKuV known as the major tomato constraint on cassava. This finding has important implications for a better understanding of the disease epidemics, related to whitefly transmissible begomoviruses. Indeed, this finding challenges the assumptions established about Bemisia tabaci biotypes behavior on cassava. Previous studies show that Bemisia tabaci biotypes can infest cassava plants. Burban *et al*. (1992) reported the presence, in West Africa, of one biotype which is almost monophagous, feeding only on cassava, wild eggplant and another that has a broad range of hosts including sweet potato, okra and

tomato. Later Abdullahi *et al*., (1998) works lead to the same conclusion; these authors find that the cowpea population of *Bemisia tabaci*, together with other populations collected from sweet potato and tomato give another isoenzyme pattern different from those isolated from cassava. Thus, the cassava biotype of *Bemisia tabaci* is known to colonize cassava (*Manihot esculenta* Crantz) whereas the sweet potato biotype colonizes various plant and weed species but not cassava (Abdullahi *et al*., 1998). But Tompson, (2003) showed that both biotypes can successfully feed, survive and reproduce on a new host plant species, *Nicotiana debneyi* Domin. And Carabalia *et al.*, 2005 showed that biotype B of *Bemisia tabaci* can gradually get adapted to cassava. Findings of this study suggest that *Bemisia tabaci* biotypes would have acquired new abilities or perhaps a new polyphagous biotype has occurred. Further researches will bring more information about biotypes occurring in cassava-based intercropping systems.

CONCLUSION

The rapid evolutionary potential of begomoviruses combined with the polyphagous feeding behavior of their whitefly vector (*Bemisia tabaci*) can lead to the emergence of damaging viral strains. New begomoviruses are found in cassava, tomato, and pepper in Togo: *Tomato leaf curl Kumasi virus* (ToLCKuV) on cassava, *Ageratum leaf curl Cameroon virus* on the pepper. The occurrence of ToLCKuV on cassava can explain the quick rate at which the cassava mosaic disease is spreading and the collapse of cassava clones. Further experimentation will be necessary to better understand the dynamics of the new begomoviruses and their relationship with the begomoviruses infecting crops and weeds in Togo.

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