Original Research Article

Impact of the Seasons on the Evolution of Tomato-infecting Geminivirus and Identification of Plant Reservoirs Harboring Geminivirus in Burkina Faso

ABSTRACT

Geminiviruses are known as responsible for huge damage to vegetable crops in many tropical, subtropical, and temperate regions. In Burkina Faso, tomato was reported as the most infected vegetable crop with the involvement of several geminivirus species despite its socioeconomic importance. This suggests and underlines the pressing need for additional information on virus population evolution (diversity, prevalence, and host plant reservoirs). Thus, to address this problem, surveys and sample collection were carried out in three localities in Burkina Faso (Goué, Léguéma, and Toussiana). Tomato leaves and those of cultivated and non-cultivated plants around the tomato fields were collected. The total DNA extracted from these samples was subjected to diagnosis based on the polymerase chain reaction (PCR) protocol with or without amplicon sequencing. Results showed that depending on the season and locality, the prevalence of the disease varied from 0 to 53.33% and that of the virus species varied from 0 to 76.67%. The highest prevalence was observed in the dry season. In addition, PepYVMLV was the virus that was widely detected in all three localities in the rainy (18.89%) and dry (52.22%) seasons. The DNA-B molecule associated with this virus was associated with other begomoviruses (ToLCMLV). In addition, out of 200 samples collected in the vicinity of the tomato fields, only 63 were positive based on PCR diagnosis. Amplicon sequencing yielded 63 partial sequences of virus from ten plant species, including six non-cultivated species. Based on phylogenetic analysis, the 63 partial sequences belonged to three phylogenetic groups (the ToLCV group, the PepYVMLV group, and the CLCuGV group). This study allowed a better understanding of the evolution of tomato leaf curl/yellow disease in Burkina Faso and the diversity of plant species serving as reservoirs for involved viruses. This constitutes an important step in the search for adequate control methods.

Keywords: Geminiviridae, vegetable crops, B-DNA, PCR, Burkina Faso

1. INTRODUCTION

Solanum lycopersicum (tomato) is an important food crop in the world. In 2022, 186 million tons of tomatoes were produced worldwide [1]. For the same year, in Africa, the total production of this vegetable was estimated at 23 million tons with 13 tons per hectare, while in Burkina Faso, total production was around 291 thousand tons with 16 tons per hectare [1]. In addition, tomato crops contribute to food security by providing vitamins and minerals. At the socio-economic level, tomatoes generate income for rural and peri-urban communities [2]. It also contributes to the dietary balance of the population through its high intake of

nutrients such as carbohydrates, vitamins B3, B5, and B9, anti-oxidants, and minerals [3]. However, despite its potential, this crop is confronted with numerous abiotic and biotic constraints, such as viral diseases that are most devastating, with the resurgence of leaf deformation diseases in recent decades. These diseases are caused by viruses that belonged to the *Geminiviridae* family, which consists of 15 genera, of which the genera *Begomovirus* and *Mastrevirus* are the most widely described [4,5]. These viruses are transmitted to plants by the whitefly *Bemisia tabaci* and were responsible for leaf curling, leaf yellowing, and stunted growth symptoms, with yield losses of up to 100% when infection occurs early [6]. In Burkina Faso, tomato is reported to be a crop highly impacted by these diseases with six and one species belonged to the *Begomovirus* and *Mastrevirus* genera, respectively [7]. Furthermore, among these viruses, the pepper yellow vein Mali virus (PepYVMLV) was recognized as the most widespread virus in Burkina Faso [7]. Although previous studies have identified some causes and viruses responsible for these diseases, a number of questions remain unanswered. Several studies have reported that geminiviruses are hosted by plants belonged to the families including Amaranthaceae, Asteraceae, Lamiaceae, Malvaceae, and Solanaceae, etc. [7]. Among these plants are the reservoirs, which allow the maintenance of virus populations during inter-culture periods. As soon as a new culture is established, the virus population shifts from reservoir plants to cultivated plants via *B. tabaci*. This study was therefore initiated to catalog geminiviruses infecting vegetables and identify weeds serving as potential reservoirs in the field.

2. MATERIAL AND METHODS

2.1 Survey and samples collection

Surveys were carried out in the locality of Goué, located in the sub-humid Sudan-Sahel area (annual rainfall between 600 and 900 mm), and the localities of Léguéma and Toussiana located in the humid Sudan area (annual rainfall between 900 and 1100 mm) (Fig. 1). Tomato samples were collected regardless of symptomatology (blind random sampling) as described elsewhere [7]. Sample collections were conducted during the rainy season (July to September 2020) and during the dry season (October 2020 to March 2021). Fifteen leaf samples of tomato plants were collected per field and two fields per locality were prospected. A total of 180 samples, with 90 per season, were used to access the tomato disease prevalence, while 200 samples were collected from non-cultivated (*Sida acuta, Physalis ixocarpa)* and cultivated (*Capcicum annuum, Amaranthus hybridus*) plant species around tomato fields to establish the host range of the detected viruses. All collected samples were first placed in envelopes and then oven-dried in the laboratory at 50°C for 48 hours [7] before molecular analysis described below.

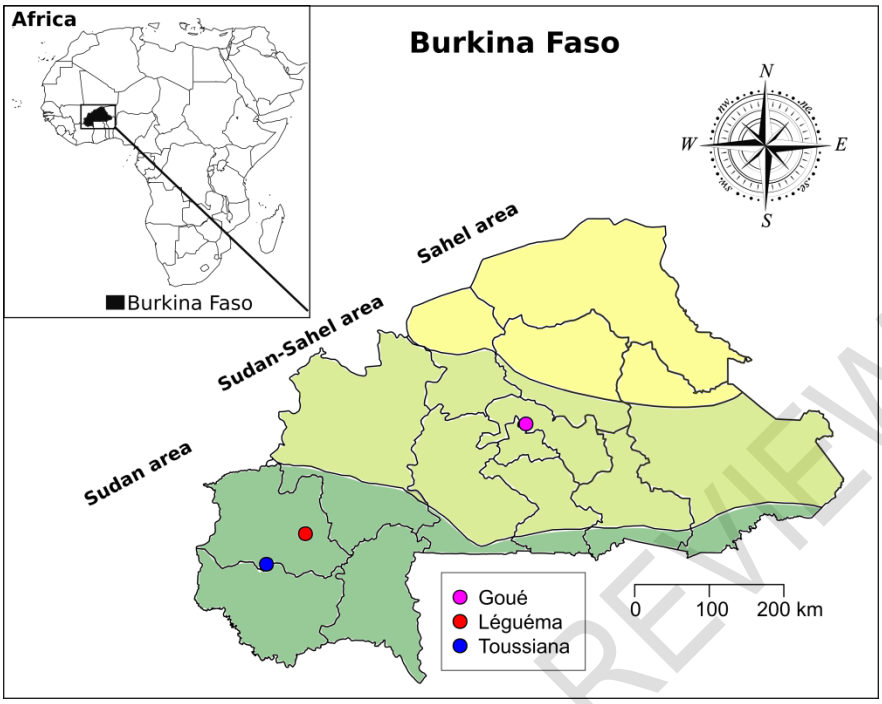

Fig. 1: Map of Burkina Faso showing the three agroclimatic zones and the localities from which leaf samples of plants were collected

2.2 Molecular analysis of collected samples

Total DNA was extracted from 20 mg of leaves of all collected samples using the adapted cetyl trimethylammonium bromide method [8], as described elsewhere [2,9]. The resulting DNA was stored at -20°C before use. Six sets of primer pairs (Table 1) were used for the specific detection of DNA-A-like components of geminiviruses in tomato samples and plant samples collected around tomato fields [7]. PCR was carried out in 25 µL volumes containing 5 µL of 5× buffer, 2.5 µL of deoxynucleotide triphosphates (2 mM), 1.5 µL of $MgCl_2$ (25 mM), 1 µL of forward and reverse primers (10 mM), and 1 U of GoTaq Flexi DNA polymerase (Promega) as described by Ouattara et al. [2]. After an initial denaturation of 5 minutes at 94°C, 30 cycles consisting of 30 seconds at 94°C, 30 seconds at 50-62°C (according to primers used), and 1 minute at 72°C were conducted, followed by a final elongation step for 5 minutes at 72°C. Amplicons were checked by electrophoresis on 1% agarose gels [2].

Table 1: Primers used to amplify begomoviruses

Primers name	Primers sequences (5'– 3')	Length (bp)	Hybridation temperature (°C)	Targeted component
PepYVMLV-A-F PepYVMLV-A-R	GCTCTTGAGTGCGTAATTC ATGCAGATTCCGCTGAAG	559	55	PepYVMLV DNA-A
PepYVMLV-B-F PepYVMLV-B-R	GAGATCCAGACAGGTACTG GTCGACCTTCACTACTTCTC	1290	57	PepYVMLV DNA-B

ToLCBFV-F ToLCBFV-R	GTCTCTATATACTTCCTCC GTTCTCAAGCATCTGAAGC	1156	60	ToLCBFV DNA-A like
ToLCGHV-F ToLCGHV-R	CACTCTTGGTCACGATCTG CACTTGATAACGGTCTCTG	595	62	ToLCGHVD NA-A like
ToLCMLV-F ToLCMLV-R	TGTCATGTTCTACTTGGTC GAACCACGACATGATATCAG	652	62	ToLCMLV DNA-A like
CpCDV-F CpCDV-R	TGTCGTCACACCAACAAG AGTCACTGAACGTGCCTCT	671	60	CpCDV DNA-A

2.3 Sequencing of PCR products and bioinformatics analysis

Amplicons of positive samples out of the 200 cultivated and non-cultivated plant samples collected around tomato fields were submitted for the sequencing process (Macrogen, Europe). Partial sequences from the sequencing were assembled using Geneious software. Then the alignment of the consensus sequences obtained with reference sequences loaded from the databases (GenBank, EMBL and DDBJ) was done using the Mega 11 software. A phylogenetic tree was created from the alignment obtained using FastTree 2 [10] and visualized using FigTree v1.4.4 (available at http://tree.bio.ed.ac.uk/software/figtree/).

2.4 Statistical analysis of the data

All statistical analyses were performed using the R v.4.6.2 (R Core Team, 2023) statistical software. The prevalence of disease (PD) was calculated according to the formula 1.

$$PD = \frac{NDP}{TNP} \times 100 \text{ (Formula 1)}$$

with NDP the number of diseased plants and TNP the total number of plants

The prevalence of the different geminiviruses detected (PV) in the collected samples were calculated according to the formula 2.

$$PV = \frac{NPS}{TNS} \times 100 \text{ (Formula 2)}$$

with NPS the number of positive samples and TNS the number of tested samples. Differences in prevalence were examined using the Chi-square test.

3. RESULTS AND DISCUSSION

3.1 Results

3.1.1 Prevalence of tomato leaf deformation and/or yellowing disease in fields

Based on data collected in the rainy season, the prevalence of tomato leaf deformation and/or yellowing disease varied from 0 to 30% in the three localities, while in the dry season it ranged from 46.67 to 53.33%. The highest prevalence values were observed in the locality of Goué in both the rainy and dry seasons. The lowest values of prevalence in the dry and rainy seasons were observed in Léguéma and Toussiana, respectively. In general, the

highest prevalence values of the disease were observed more in the dry season than in the rainy season, which confers a highly significant difference (p<0.001) between the two seasons (Fig. 2).

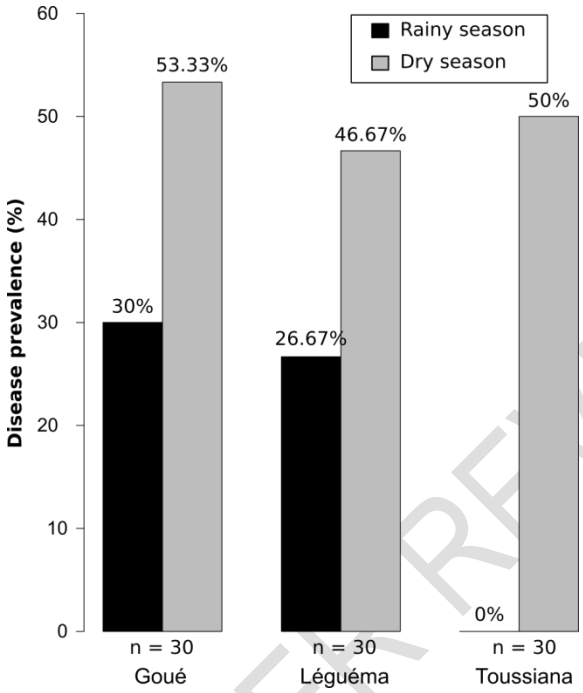

Fig. 2: Disease prevalence in the wet and dry seasons. *The height of each bar corresponds to the prevalence of disease (%) calculated by the ratio of the number of symptomatic plants to the total number of observed plants (n) from that location*.

3.1.2 Prevalence of viral species

A complex of five viruses comprising PepYVMLV, ToLCMLV, ToLCBFV, ToLCGHV, and CpCDV was detected on the basis of PCR diagnosis. Depending on the locality and the season, the viral prevalence varied from 0 to 76.67%. Taken together, the dry season recorded the highest viral prevalence values regardless of locality with significant differences (p<0.001). PepYVMLV was the virus that was widely detected in both dry and rainy seasons' samples, with a maximum prevalence of 30% in the rainy season and 66.67% in the dry season (Fig. 3).

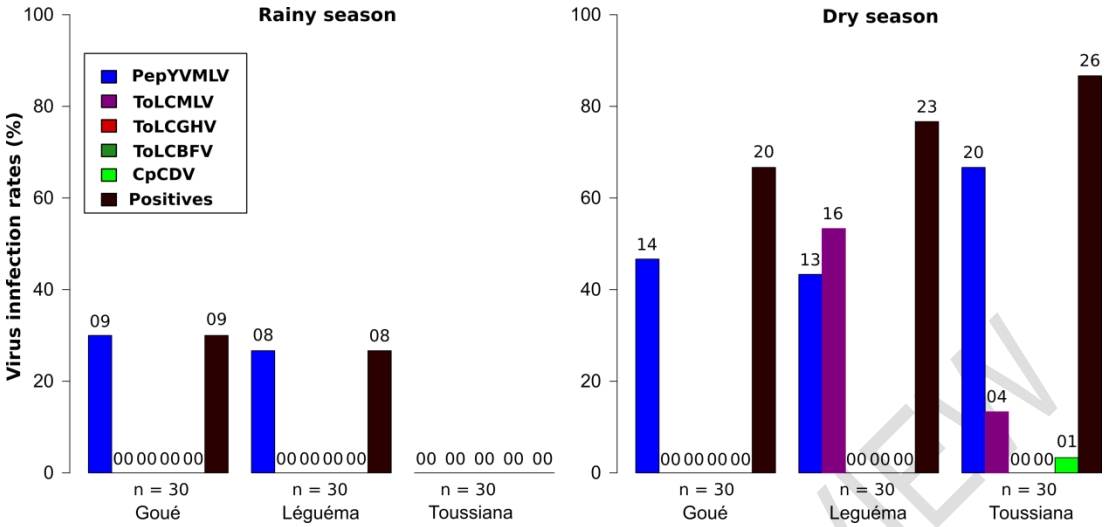

Fig. 3: Prevalence of virus species in the rainy and dry seasons. *Total numbers of infected and tested plants are indicated at the top and bottom of each bar*.

3.1.3 Detection of the B-DNA molecule in association with begomoviruses

PCR diagnosis using specific primers for the detection of the DNA-B molecule resulted in positive cases in all three localities, with frequencies varying from 0 to 60% when detected in association with a geminivirus, more precisely PepYVMLV, and from 0 to 20% when detected alone. In the rainy season, DNA-B was only detected in the locality of Goué in association with a geminivirus DNA-A-like molecule with a prevalence of 6.67%. In contrast, this molecule was detected in single infection or in association with geminivirus DNA-A in all localities in the dry season, with prevalence ranging from 13.33% to 60% (Table 1).

Table 2: Frequency of detection of DNA-B in association with a begomovirus in the samples collected

Localities	Seasons	Detection frequency (%)[infected plants/tested plants]		
		Single infection with DNA A	Single infection with DNA B	DNA A and B Association
Goué	Rainy	23,33 [7/30]	0 [0/30]	6,67 [2/30]
	Dry	20 [6/30]	20 [6/30]	26,67 [8/30]
Leguema	Rainy	26,67 [8/30]	0 [0/30]	0 [0/30]
	Dry	10 [3/30]	13,33 [4/30]	33,33 [10/30]
Toussiana	Rainy	0 [0/30]	0 [0/30]	0 [0/30]
	Dry	6,67 [2/30]	13,33 [4/30]	60 [18/30]

3.1.4 Establishing the host range of viruses

PCR diagnostics based on universal primers and sequencing were carried out to assess the diversity of viruses that can be hosted by different crops and uncultivated plants. A total of

63 partial sequences corresponding to the capsid protein of geminivirus were obtained. The similarity search throughout nucleotide sequence databases showed that these sequences were related to viruses of the genus *Begomovirus*. Phylogenetic analysis showed that these 63 sequences are divided into three groups supported by Bootstrap values above 70 (Fig. 4). The pepper yellow vein Mali virus (PepYVMLV) group contained 37 sequences that were detected in eight plant species (*Capsicum annum*, *Capsicum frutescens*, *Solanum lycopersicum*, *Amaranthus hybridus*, *Boerhavia erecta*, *Ageratum* sp., *Sida acuta*, and *Physalis ixocarpa*) followed by the ToLCV group containing nine sequences detected on three plant species (*Solanum lycopersicum*, *Amaranthus spinosus,* and *Melochia* sp.) and the cotton leaf curl Gezira virus (CLCuGV) group containing 17 sequences, detected in two plant species (*Sida acuta, Boerhavia erecta*) (Fig. 4, Appendix 1).

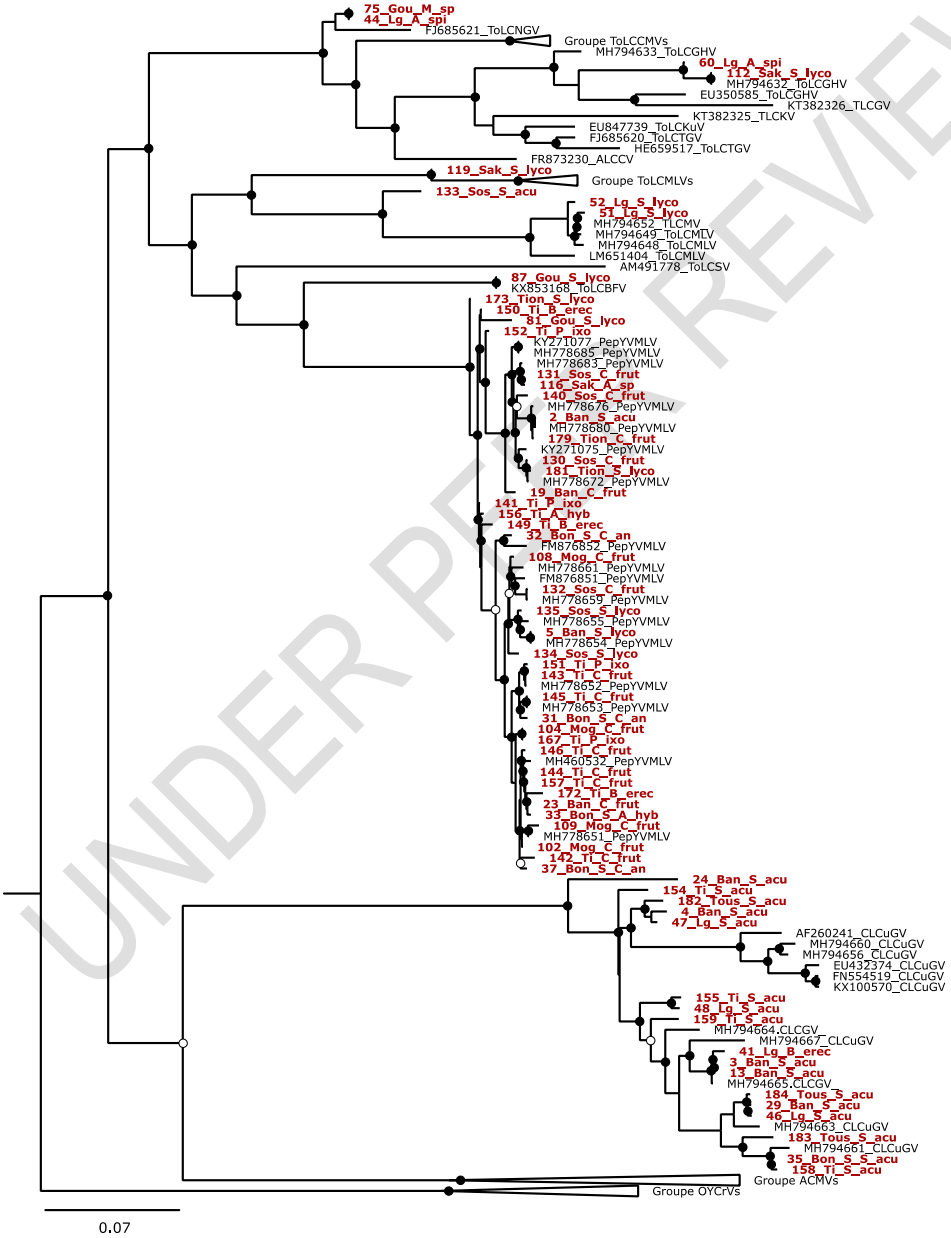

Fig. 4: Maximum-likelihood phylogenetic tree showing the diversity and relatedness of the different virus groups detected in the plant samples collected around the fields and a representative sample of African begomoviruses.
The tree was rooted using Okra yellow crinkle virus (OYCrVs) as an out group. Sequence names from our samples are highlighted in red. For better visibility, Bootstrap values between 50 and 70 are represented by white dots and those above 70 are represented by black dots. The horizontal scale indicates the genetic distance.

3.2 Discussion

The study showed that geminiviruses, particularly begomoviruses, were detected in most samples from plants showing leaf curling and/or yellowing and dwarfing. This highlights the involvement of begomoviruses in these leaf deformation diseases, as reported in several studies [7,11–14]. High prevalence values of diseases and viruses obtained in the dry season compared to the rainy season could be explained by the abundance and biotype of the vector, *B. tabaci,* and/or the presence of alternative host plants in the area. Thus, Gnankiné *et al.* [15] showed that the Q biotype of *B. tabaci* was dominant on tomato crops in Burkina Faso and that the abundance of the *B. tabaci* population is compatible with the high diversity and prevalence of begomovirus diseases on these crops. Another explanation for this result is the impact of climate parameters on the outbreak of the insect vector. Bao-li *et al*. [16] reported that the highest natural growth rate of B. tabaci was at a temperature of 29 °C, while N'zi *et al*. [17] demonstrated that 35.8% of the fluctuations of adult B. tabaci populations were related to the influence of climatic parameters on these insects. Furthermore, the pedoclimatic position in the Sudano-Sahelian zone of the locality of Goué could explain the high prevalence that was observed in this locality. This result corroborates that of Ouattara *et al.* [7], stipulating that the viral infection rate of tomato plants was higher in the Sudano-Sahelian area surveyed compared to the Sudanian area. *B tabaci* would then have a higher occurrence when temperatures increase.

Furthermore, the widely spread of PepYVMLV reported in this study and early studies [7,18] can be due to the fact that this virus is associated with a second DNA component (DNA-B) that is a strong activator of virulence [12]. Thus, it was recently demonstrated by Ouattara *et al*. [12] that this DNA-B molecule allows not only a better transmission of PepYVMLV by the vector but also a better accumulation of PepYVMLV DNA-A molecules in the plant tissues. The results on the frequency of detection of DNA-B also revealed that, independently of PepYVMLV, the DNA-B molecule is capable of associating with other begomoviruses, notably ToLCMLV, thus justifying the existing affinity between this molecule and the begomoviruses infecting this tomato. The degree of this affinity would depend on the percentage of similarity between the CRs (Common Region) of the begomovirus DNA-A and the DNA-B, which is 90% identical to that of PepYVMLV and less than 80% identical to that of the other begomoviruses [7]. A progressive and wide spread of DNA-B would represent a major threat to tomato cultivation in Burkina Faso, in Africa, and more widely in the world.

Assessment of the host range of the viruses revealed the presence of a wide range of geminivirus hosts. This confirms and completes the list of geminivirus host plants in Burkina Faso provided in the early works [7,13,19,20]. This result could be explained by the species-hopping and adaptation character of these viruses to plants. Indeed, most of the emerging diseases caused by begomoviruses are related to viruses naturally infecting native wild plants and which would have adapted to introduced cultivated plants [21]. In addition, the non-perennial nature of the majority of cultivated plants suggests the existence of alternative host plants or reservoirs that allow virus populations to maintain during the inter-culture period.

4. CONCLUSION

The study showed that there is a diversity of geminiviruses infecting crops and non-cultivated plants. Non-cultivated plants represent reservoir plants for these viruses. Furthermore, this study also showed that the prevalence of tomato leaf deformation and/or yellowing disease and viruses is more dominant in the dry season than in the rainy season. Moreover, it should be added that the locality of Goué recorded the highest prevalence for each season, certainly due to its pedoclimatic position (Sudan-Sahel zone). Molecular analysis showed that PepYVMLV was the virus with the highest prevalence. This study showed that the evolution of leaf deformation and/or yellowing diseases is seasonally related, and the wide alternative host range is preserved around the fields.

Disclaimer (Artificial intelligence)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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APPENDIX

Appendix 1: General information about partial sequences obtained and results of similarity search in NCBI data base.

ID	Sample	Crops	Locality	Host	Genus	Family	Virus	Accession number	Similarity (%)
2	2_Ban_S_acu	0	Banakeledara	*Sida acuta*	*Sida*	Malvaceae	CLCuGeV	MH778675	100
3	3_Ban_S_acu	0	Banakeledara	*Sida acuta*	*Sida*	Malvaceae	CLCuGeV	MH794665	99,85
4	4_Ban_S_acu	0	Banakeledara	*Sida acuta*	*Sida*	Malvaceae	CLCuGeV	MH794665	97,48
5	5_Ban_S_lyco	1	Banakeledara	*Solanum lycopersicum*	*Solanum*	Solanaceae	PepYVMLV	MH778654	100
13	13_Ban_S_acu	0	Banakeledara	*Sida acuta*	*Sida*	Malvaceae	CLCuGeV	MH794665	99,85
19	19_Ban_C_frut	1	Banakeledara	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778654	100
23	23_Ban_C_frut	1	Banakeledara	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778685	98,97
24	24_Ban_S_acu	0	Banakeledara	*Sida acuta*	*Sida*	Malvaceae	CLCuGeV	MH794665	94,11
29	29_Ban_S_acu	0	Banakeledara	*Sida acuta*	*Sida*	Malvaceae	CLCuGeV	MH794663	98,36
31	31_Bon_S_C_an	1	Bon_Srima	*Capsicum annuum*	*Capsicum*	Solanaceae	PepYVMLV	MH778652	99,33
32	32_Bon_S_C_an	1	Bon_Srima	*Capsicum annuum*	*Capsicum*	Solanaceae	PepYVMLV	MH778651	98,28
33	33_Bon_S_A_hyb	0	Bon_Srima	*Amaranthus hybridus*	*Amaranthus*	Amaranthaceae	PepYVMLV	MH778651	99,37
35	35_Bon_S_S_acu	0	Bon_Srima	*Sida acuta*	*Sida*	Malvaceae	CLCuGeV	MH794661	99,54
37	37_Bon_S_C_an	1	Bon_Srima	*Capsicum annuum*	*Capsicum*	Solanaceae	PepYVMLV	MH778651	99,71
41	41_Lég_B_erec	0	Léguéma	*Boerhavia erecta*	*Boerhavia*	Nyctaginaceae	CLCuGeV	MH794665	99,3
44	44_Lég_A_spi	0	Léguéma	*Amaranthus spinosus*	*Amaranthus*	Amaranthaceae	ToLCNGV	Fj685621	97,9
46	46_Lég_S_acu	0	Léguéma	*Sida acuta*	*Sida*	Malvaceae	CLCuGV	MH794663	98,34
47	47_Lég_S_acu	0	Léguéma	*Sida acuta*	*Sida*	Malvaceae	CLCuGV	MH794664	97,44

48	48_Lég_S_acu	0	Léguéma	*Sida acuta*	*Sida*	Malvaceae	CLCuGV	MH794665	97,81
51	51_Lég_S_lyco	1	Léguéma	*Solanum lycopersicum*	*Solanum*	Solanaceae	ToLCMLV	MH794652	99,68
52	52_Lég_S_lyco	1	Léguéma	*Solanum lycopersicum*	*Solanum*	Solanaceae	ToLCMLV	MH794652	99,53
60	60_Lég_A_spi	0	Léguéma	*Amaranthus spinosus*	*Amaranthus*	Amaranthaceae	ToLCGHV	MH794632	99,39
75	75_Goué_M_sp	0	Goué	*Melochia sp.*	*Melochia*	Malvaceae	ToLCNGV	Fj685621	98,22
81	81_Goué_S_lyco	1	Goué	*Solanum lycopersicum*	*Solanum*	Solanaceae	PepYVMLV	MH778664	98,23
87	87_Goué_S_lyco	1	Goué	*Solanum lycopersicum*	*Solanum*	Solanaceae	ToLCBFV (PepYVMLV)	KX853168	100 (90,08)
102	102_Mog_C_frut	1	Mogtédo	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778651	99,84
104	104_Mog_C_frut	1	Mogtédo	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778651	99,52
108	108_Mog_C_frut	1	Mogtédo	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778668	99,67
109	109_Mog_C_frut	1	Mogtédo	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778651	99,51
112	112_Sak_S_lyco	1	Sakabi	*Solanum lycopersicum*	*Solanum*	Solanaceae	ToLCGHV	MH794632	100
116	116_Sak_Ag_sp	0	Sakabi	*Ageratum sp*	*Ageratum*	Asteraceae	PepYVMLV	MH778683	99,66
119	119_Sak_S_lyco	1	Sakabi	*Solanum lycopersicum*	*Solanum*	Solanaceae	TYLCMLV	LM651403	96,17
130	130_Sos_C_frut	1	Sossogona	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778672	100
131	131_Sos_C_frut	1	Sossogona	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778683	99,84
132	132_Sos_C_frut	1	Sossogona	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778659	100
133	133_Sos_S_acu	0	Sossogona	*Sida acuta*	*Sida*	Malvaceae	ToLCMLV	MH794652	90,27
134	134_Sos_S_lyco	1	Sossogona	*Solanum lycopersicum*	*Solanum*	Solanaceae	PepYVMLV	MH778664	100

135	135_Sos_S_lyco	1	Sossogona	*Solanum lycopersicum*	*Solanum*	Solanaceae	PepYVMLV	MH778654	99,18
140	140_Sos_C_ frut	1	Sossogona	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778680	100
141	141_Tié_P_ixo	0	Tiébélé	*Physalis ixocarpa*	*Physalis*	Solanaceae	PepYVMLV	MH778652	99,56
142	142_Tié_C_frut	1	Tiébélé	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778651	99,08
143	143_Tié_C_frut	1	Tiébélé	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778652	100
144	144_Tié_C_frut	1	Tiébélé	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH460532	99,55
145	145_Tié_C_frut	1	Tiébélé	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778653	100
146	146_Tié_C_frut	1	Tiébélé	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778651	99,1
149	149_Tié_B_erec	0	Tiébélé	*Boerhavia erecta*	*Boerhavia*	Nyctaginaceae	PepYVMLV	MH778652	99,01
150	150_Tié_B_erec	0	Tiébélé	*Boerhavia erecta*	*Boerhavia*	Nyctaginaceae	PepYVMLV	MH778652	99,7
151	151_Tié_P_ixo	0	Tiébélé	*Physalis ixocarpa*	*Physalis*	Solanaceae	PepYVMLV	MH778652	99,85
152	152_Tié_P_ixo	0	Tiébélé	*Physalis ixocarpa*	*Physalis*	Solanaceae	PepYVMLV	MH778659	99,39
154	154_Tié_S_acu	0	Tiébélé	*Sida acuta*	*Sida*	Malvaceae	CLCuGV	MH794663	97,4
155	155_Tié_S_acu	0	Tiébélé	*Sida acuta*	*Sida*	Malvaceae	CLCuGV	MH794665	97,56
156	156_Tié_A_hyb	0	Tiébélé	*Amaranthus hybridus*	*Amaranthus*	Amaranthaceae	PepYVMLV	MH778652	99,7
157	157_Tié_C_frut	1	Tiébélé	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778651	99,55
158	158_Tié_S_acu	0	Tiébélé	*Sida acuta*	*Sida*	Malvaceae	CLCuGV	MH794661	99,25
159	159_Tié_S_acu	0	Tiébélé	*Sida acuta*	*Sida*	Malvaceae	CLCuGV	MH794662	99,09
167	167_Tié_P_ixo	0	Tiébélé	*Physalis ixocarpa*	*Physalis*	Solanaceae	PepYVMLV	MH778652	99,25

172	172_Tié_B_erec	0	Tiébélé	*Boerhavia erecta*	*Boerhavia*	Nyctaginaceae	PepYVMLV	MH778651	98,02
173	173_Tion_S_lyco	1	Tionkui	*Solanum lycopersicum*	*Solanum*	Solanaceae	PepYVMLV	MH778668	99,7
179	179_Tion_C_frut	1	Tionkui	*Capsicum frutescens*	*Capsicum*	Solanaceae	PepYVMLV	MH778678	100
181	181_Tion_S_lyco	1	Tionkui-	*Solanum lycopersicum*	*Solanum*	Solanaceae	PepYVMLV	MH778672	99,85
182	182_Tous_S_acu	0	Toussiana	*Sida acuta*	*Sida*	Malvaceae	CLCuGV	MH794663	97,43
183	183_Tous_S_acu	0	Toussiana	*Sida acuta*	*Sida*	Malvaceae	CLCuGV	MH794665	97,7
184	184_Tous_S_acu	0	Toussiana	*Sida acuta*	*Sida*	Malvaceae	CLCuGV	MH794663	98,47