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RESEARCH ARTICLE
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Occurrence of Viruses Infecting Yams on Potential Alternative Hosts in Côte d'Ivoire

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ABSTRACT

Yam is a crucial crop for food security and income in Côte d'Ivoire. However, its cultivation is threatened by various viral infections that lead to significant yield losses. The spread of these viruses is facilitated by weeds and crops associated with yam, which serve as reservoirs. This study aimed to identify the reservoirs of yam viruses, the prevalence of viruses, and the most widespread plant families hosting yam viruses. In 2019, surveys were conducted in yam fields in six agro-ecological zones (AEZ) of Côte d'Ivoire. A total of 131 symptomatic and asymptomatic leaves from potential yam virus reservoirs were collected and conserved. These samples were screened for *Badnavirus*es using Immuno-capture PCR (IC-PCR). *Potyvirus yamtesselati* (yam mosaic virus, YMV), *Potyvirus yamplacidum* (yam mild mosaic virus, YMMV) and *Cucumovirus CMV* (cucumber mosaic virus, CMV) were detected using DAS-ELISA and RT-PCR. Eighteen plant families were recorded, the most common of which were Solanaceae, Fabaceae and Poaceae. Additionally, 75.57% of the samples were food crops, while 24.43 % were weeds. Viruses were detected in plants collected in all the six AEZ, and the incidence for at least one virus was 46.56%. CMV (23.66%) is the most widespread in all the zones, followed by *Badnavirus*es (11.45%) and YMV in only 5.34% of the samples. One case of mixed infection between CMV and *Badnavirus*es was noticed at the rates of 6.11%. However, no samples were found to be infected by YMMV. Phylogenetic analysis confirmed that *Badnavirus*es detected in the alternate hosts are yam *Badnavirus*es. Farmers should be made aware of the threat that could represent these alternative hosts in yam crops, and of the impact of cultural techniques on the occurrence and treatment of viruses.

Keywords: Yam viruses, Potyvirus, Cucumovirus and *Badnavirus*, DAS-ELISA, IC-PCR, Alternate host.

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INTRODUCTION

Yam is a vital source of calories for millions of people in Africa, South America, Asia and the Pacific. It also holds great cultural and economic importance (Obidiegwu et al., 2020; Danquah et al., 2022, Kouakou et al., 2023). In terms of production, this crop ranks as the fourth most significant root and tuber, following the potato, sweet potato and cassava (Luo et al., 2022). West Africa accounts for over 92% of global yam production. Côte d'Ivoire is the third largest producer after Ghana and Nigeria, the leading producer with an estimated output of around 7.6 million tonnes in 2022 (FAOSTAT, 2023).

Yam is typically planted at the start of the rainy season in April. The tubers can be used in a variety of dishes, either boiled or fried, and served with staple foods such as rice, beans, plantain, sweetpotato, meat, or soups (Obidiegwu et al., 2020). As well as being used fresh, yam can be peeled, chopped, and dried to reduce its moisture content and can then be processed into flour or flakes (Kouakou et al., 2023). In different contexts, the significance of yam extends beyond nutrition to encompass religious, social, and cultural practices (Kouakou et al., 2023). Furthermore, recent studies have

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emphasized the various pharmacological and biological advantages of yam roots. These include their antioxidant properties, cholesterol-lowering effects, anti-inflammatory potential, and protection against ethanol-induced ulcers (Kim et al., 2019; Wang et al., 2025).

Yield losses caused by pests, diseases, and weed competition (Unamma & Akobundu, 2006, Tariq et al., 2024, Whedie et al., 2025) pose a significant challenge to yam cultivation. Viruses represent the most serious threat to yam production, as they are difficult to control and easily transmitted through planting material. Various virus species belonging to the families *Alphaflexiviridae* (genus *Potexvirus*), *Betaflexiviridae*, *Bromoviridae* (genus *Cucumovirus*), *Caulimoviridae* (genera *Badnavirus* and *Dioscovirus*), *Closteroviridae* (genus *Ampelovirus*), *Potyviridae* (genera *Macluravirus* and *Potyvirus*), and *Secoviridae* (genus *Sadwavirus*) have been reported to infect yams in cultivation regions worldwide (Luo et al., 2022; Gogile et al., 2024). Dioscorea bacilliform virus (DBV, genus *Badnavirus*), yam mosaic virus (YMV, genus *Potyvirus*), and yam mild mosaic virus (YMMV, genus *Potyvirus*) represent the three most common viruses infecting yams (Luo et al., 2022). The presence of weeds during in the first four months of yam growth can also decrease yields by up to 43% (Ekanayake & Asiedu, 2003). These wild plants can act as potential reservoirs for viruses capable of spreading to cultivated crops, which may result in epidemics or the emergence of new viral strains (Ma et al., 2020; Hasiów-Jaroszewska et al., 2021). They therefore constitute an essential ecological component in the transmission of viruses to cultivated plants. The presence of certain organisms can modify ecosystem functions, as they may act as pests and potential reservoirs for both known and unknown viral species (Asala et al., 2014; Rybicki, 2015). Moreover, a virus may persist in dormant propagative material or weeds, and subsequently infect seedlings that emerge after germination in the following growing season (Odedara et al., 2008; Asala et al., 2014; Amoakon et al., 2023). Viruses infecting wild plants are known to be highly diverse and frequently asymptomatic in their hosts (Hasiów-Jaroszewska et al., 2021, Maclot et al., 2023) and this represent a greater threat. Very few studies have been carried out on the plant reservoirs (Yoboué et al., 2025), especially of yam viruses alternates hosts. Amusa et al. (2005) identified viruses in Nigerian weeds that are not associated with yam crops. Most research on yam in Côte d'Ivoire has focused on propagation, breeding and cropping systems, growth, yield, detecting viruses in fields, and resistance (Kouakou et al., 2019; Bakayoko et al., 2021; Kouakou et al., 2023). No studies to date have been conducted on the reservoirs of yam viruses in Côte d'Ivoire. Understanding virus diversity in the potential alternate's hosts is therefore essential for gaining better insight into virus epidemiology in yam.

This study aims to assess the prevalence of viral infections in potential reservoir plants found in and around yam fields, in order to address this existing knowledge gap. The objective is to identify these potential reservoirs and to understand their interactions with the known viral species *Badnavirus*es, *Potyvirus yamtesselati* (Yam mosaic virus, YMV), *Potyvirus yamplacidum* (yam mild mosaic virus, YMMV) and *Cucumovirus CMV* (cucumber mosaic virus, CMV), detected in the samples.

MATERIALS & METHODS

Survey Site and Sampling

Field surveys were conducted between July and September 2019 across six agro-ecological zones (AEZs) (Fig. 1). A total of 81 fields were visited. In each zone, yam fields were evaluated, with a minimum distance of 10 km between fields. The number of fields sampled per agro-ecological zone depended on the density and sanitary status of yam fields (AEZ I: 33 fields; AEZ II: 12; AEZ III: 10; AEZ IV: 6; AEZ V: 4; AEZ VI: 16).

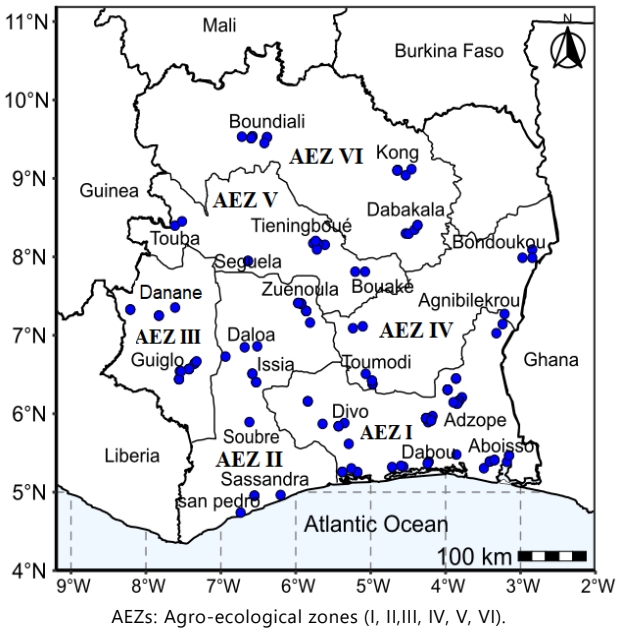

Fig. 1: Locations visited during surveys;

In each field, all crops other than yam were carefully examined for data collection. Symptomatic and asymptomatic weeds or other cultivated plants, whether showing or lacking yam virus-like symptoms such as chlorosis, mosaic, mottling, stunting, bleaching, or yellowing, were assessed within and around yam fields and collected for analysis.

Information on the coordinates, size of the farm, surrounding crops and some cultural practices of each field were also recorded. Leaf samples were collected, labelled, wrapped, and stored in envelopes before being transported to the Virology Laboratory of WAVE (Central and West African Virus Epidemiology) for serological and molecular analysis.

Serological Assay for YMV, YMMV and CMV Detection

Approximately 10 mg of the dried leaf sample was used for each analysis. Each sample was duplicated for the serological analysis, with the antibodies used in this study being diluted to 1:1000. Serological assays were performed

to detect YMV, YMMV, and CMV in the collected weeds and other plant samples using the double antibody sandwich enzyme-linked immunosorbent assay (DAS-ELISA) as outlined by the supplier, Leibniz-Institut DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Braunschweig, Germany. Antigen-antibody responses were identified, and the optical density (OD) of each well was quantified after one hour using an ELISA plate reader (Uniequip, Martinseed, Germany) at a wavelength of 405 nm (Clark & Adams, 1977). ELISA readings that were at least double those of the negative control were classified as positive.

YMV, YMMV and CMV Detection by RT-PCR

Only serologically positive samples were tested for the presence of these RNA viruses using PCR. RNA extraction was performed using a CTAB/LiCl protocol described by White et al. (2008). The detection of RNA viruses (yam mosaic virus (YMV), yam mild mosaic virus (YMMV), and cucumber mosaic virus (CMV) was performed in two steps. First, cDNA was synthesized from total RNA by reverse transcription (RT) using oligo (dT) primers and Random primers, dNTPs, M-MuLV reverse transcriptase, and RNase inhibitor under the following conditions: 65°C for 5min, 42°C for 1h, and 65°C for 20min. The resulting cDNA served as a template for PCR amplification using virus-specific primers (Table 1) in a 25µL reaction. PCR conditions included initial denaturation at 95°C for 5min, 35 cycles of 95°C for 30s, 55°C for 30s, and 72°C for 1 min, followed by a final extension at 72°C for 10 min. PCR products (10µL) were analyzed by electrophoresis on a 1% agarose gel at 90V for 1.5h then stained with ethidium bromide, and visualized under UV light.

Detection of *Badnavirus*es by Immuno-capture PCR (IC-PCR)

Immunocapture was performed using an adaptation of the coating and trapping technique developed by Clark & Adams (1977). Twenty-five (25µl) of a reaction mixture containing 1 x Taq reaction buffer, 0.20mM of each dNTP, 0.2µM of each *Badnavirus*es-specific forward and reverse primer (Table 1) and 0.625U of GoTaq DNA polymerase (Promega) were added to each tube. PCR was performed to detect *Badnavirus*es in a thermal cycler (nexus gradiant), using the following program: initial denaturation at 94°C for 4min; 40cycles of 94°C for 30s, 50°C for 30s, and 72°C for 30s; and a final extension at 72°C for 5min. PCR products (10µL) were analyzed by electrophoresis, then stained with ethidium bromide, and visualized under UV light.

Sequencing and Phylogenetic Analysis

Some positive PCR products from the viruses were sequenced by GENEWIZ® in Germany using the Sanger method. Sequences obtained were trimmed using Geneious Prime v. 2025.2.1. Then sequences for each isolate were used for sequence similarity searches in the GenBank databases using the BLAST program (https://blast.ncbi.nlm.nih.gov/Blast.cgi) to check for the identity of viruses. Sequences generated in this study and representative isolates from the GenBank and our sequences were used for multiple alignments using the ClustalW component of Mega12. The maximum-likelihood (ML) method with a model of TN93+G with a bootstrap of 1000 was adopted for the *Badnavirus*es. The phylogenetic tree was visualized using Mega12.

Statistical Analysis

To calculate infection percentages, data were organized and preliminary calculations were performed using Excel. Statistical analyses, including Chi-square (χ^2) tests, were conducted in R software v. 3.6.1 to assess the significance of differences in infection percentage among agro-ecological zones or host families.

RESULTS

Description of Symptoms Observed and Plant Families Concerned

A total of 131 symptomatic and asymptomatic samples were collected from six agro-ecological zones (AEZ) gathered in 34 localities. During the surveys, typical symptoms of yam viral diseases like mosaic, deformations, chlorosis, bleaching, and vein banding were observed on the leaves (Fig. 2). Most of the species collected were food crops (75.57%) and weeds (24.43%), and among the food crops, vegetables like tomato and pepper were more abundant. According to the plant life cycle, we recorded 79.39% of annual plants; then 14.50% were perennial, and 6.11% were annual/perennial. Eighteen families of plants were recorded, and Solanaceae (38.19%), Fabaceae (19.09%), and Poaceae (14.50%) were the most predominant among them (Fig. 3).

Alternate Hosts of Yam Viruses Detected

After serological and molecular analysis (PCR and RT-PCR), important viruses as *Badnavirus*es, yam mosaic virus (YMV), and cucumber mosaic virus (CMV) were detected (Table 2; Table 3). Also, the molecular detection of three viruses was confirmed by PCR, and the amplified products

Table 1: Primer pairs used for the detection of yam mosaic virus (YMV), yam mild mosaic virus (YMMV), cucumber mosaic virus (CMV) and *Badnavirus*es

Virus	Sequences	Size (pb)	Targeted region	References
YMV-F	5'-ATC CGG GAT GTG GAC AAT GA-3'	586	CP/3'UTR	Mumford & Seal, 1997
YMV-R	5'-TGGTCCTCCGCCACATCAAA-3'			
YMMV-F	5'-GGC ACA CAT GCA AAT GAA RGC-3'	249	CP/3'UTR	Mumford & Seal, 1997
YMMV-R	5'-CAC CAG TAG AGT GAA CAT AG-3'			
CMV-F	5'-GCC GTA AGC TGG ATG GAC AA-3'	500	CP	Wylie et al., 1993
CMV-R	5'-TAT GAT AAG AAG CTT GTT TCG CG-3'			
Badna FP	5'-ATG CCI TTY GGI ITI AAR AAY GCI CC-3'	579	RT-RNase H	Seal & Muller, 2007
Badna RP	5'-CCA YTT RCA IAC ISC ICC CCA ICC-3'			

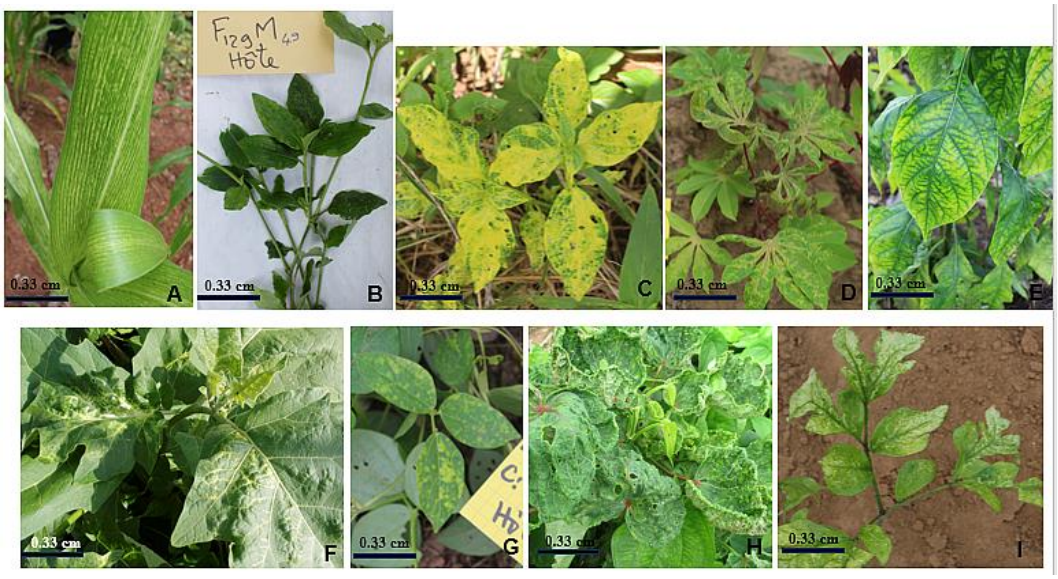

Fig. 2: Potential alternatives hosts with viral symptoms commonly observed in visited fields; (A) *Zea maize,* (B) *Commelina benghalensis L.,* (C) *Asystasia gangetica,* (D) *Manihot esculenta,* (E) *Solanum annuum,* (F) *Solanum macrocarpum,* (G) *Phaseolus Lunatus L.,* (H) *Abelmoschus esculentus,* (I) *Anchomanes differmi.*

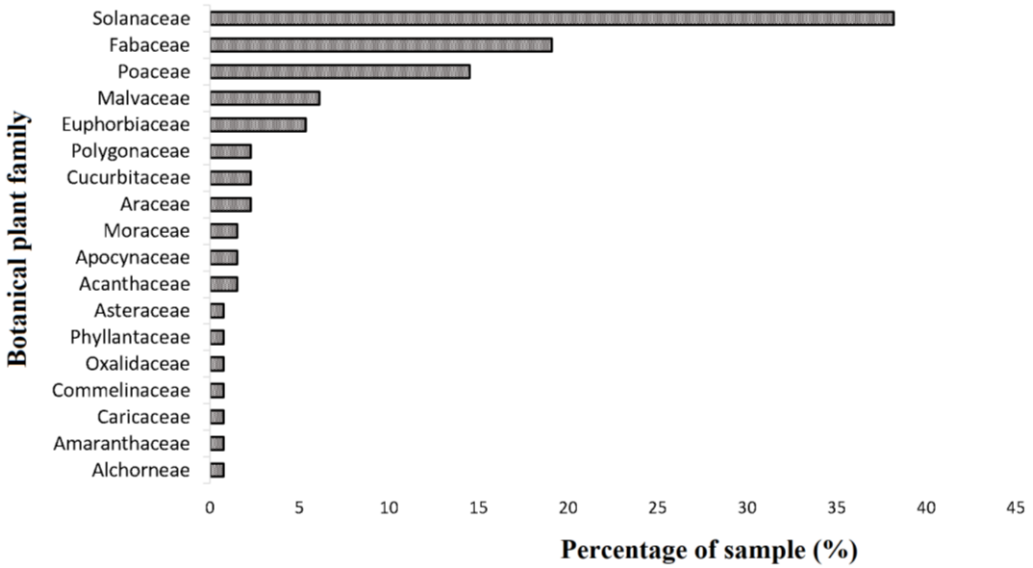

Fig. 3: Different families of potential alternative hosts reported. Data analysis by chi-squared ($\chi 2$). P<0.001. The results are expressed as percentage of sample (n=131).

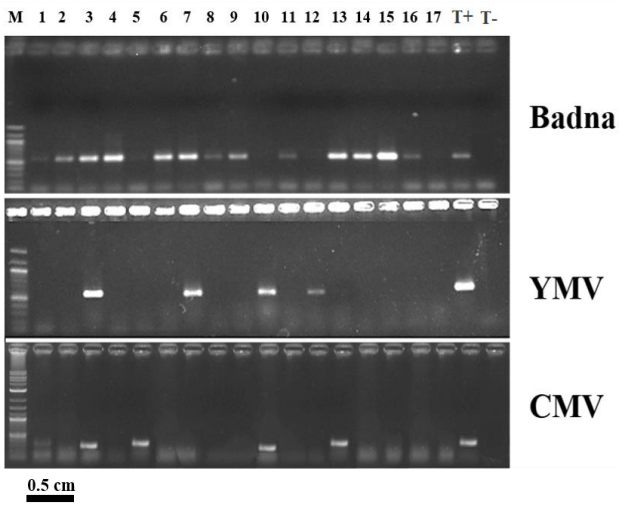

Fig. 4: Agarose gel electrophoresis (1%) of PCR products for the detection of cucumber mosaic virus CMV (500 bp), yam mosaic virus YMV (586 bp) and *Badnavirus*es (579 bp). M: 100 bp DNA ladder.

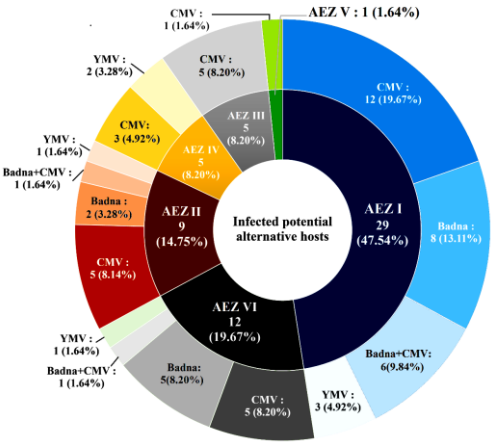

Fig. 5: Incidence of viruses on yam alternatives hosts across agro-ecological zones (AEZs); Circular diagram showing the incidence of virus in six agroecological zones (ZAE I–VI). Outer segments indicate the proportion of each viral infection type detected: *Badnavirus* (Badna), cucumber mosaic virus (CMV), yam mosaic virus (YMV), and Badna+CMV. Sector size reflects the proportion of infected hosts in each zone.

Table 2: List of species of potential alternative hosts of yam viruses: *Badnavirus*es (Immuno-capture-PCR) and YMV, YMMV, CMV (DAS-Elisa and RT-PCR) in Côte d'Ivoire

			IC-PCR	DAS-ELISA / RT-PCR		
Family	Species (AEZs)	Samples (n)	Badna	CMV	YMMV	YMV
Malvaceae	*Abelmoschus esculentus*	8	-	+	-	-
Alchorneae	*Alchornea cordifolia*	1	-	-	-	-
Amaranthaceae	*Amaranthus viridis*	1	-	-	-	+
Araceae	*Anchomanes difformis*	1	-	-	-	-
Acanthaceae	*Asystasia gangetica*	2	-	-	-	-
Moraceae	*Broussonetia papyrifera*	1	-	-	-	-
Solanaceae	*Capsicum annuum*	20	-	+	-	-
Caricaceae	*Carica papaya*	1	-	-	-	-
Fabaceae	*Centrosema pubescens*	7	-	+	-	-
Fabaceae	*Colocasia esculenta*	2	+	-	-	-
Commelinaceae	*Commelina benghalensis*	1	-	-	-	+
Euphorbiaceae	*Croton hirtus*	1	-	-	-	+
Polygonaceae	*Fallopia convolvulus*	3	-	-	-	-
Moraceae	*Ficus exasperata*	1	-	-	-	-
Asteraceae	*Chromolaena odorata*	1	-	-	-	+
Cucurbitaceae	*Lagenaria siceraria*	2	-	+	-	-
Euphorbiaceae	*Manihot esculenta*	5	-	-	-	-
Euphorbiaceae	*Mareya micrantha*	1	-	-	-	-
Phyllantaceae	*Margaritaria discoidea*	1	-	-	-	-
Cucurbitaceae	*Momordica charantia*	1	-	-	-	-
Fabaceae	*Mucuna pruriens*	2	-	-	-	-
Oxalidaceae	*Oxalis barrelieri*	1	-	-	-	-
Fabaceae	*Phaseolus lunatus*	2	-	+	-	-
Fabaceae	*Phaseolus vulgaris*	11	+	+	-	-
Fabaceae	*Pueraria phaseoloides*	3	-	-	-	+
Apocynaceae	*Rauvolfia vomitoria*	2	-	-	-	-
Poaceae	*Setaria chevalieri*	1	-	-	-	-
Solanaceae	*Solanum aethiopicum*	2	-	-	-	-
Solanaceae	*Solanum lycopersicum*	11	+	+	-	-
Solanaceae	*Solanum macrocarpon*	1	-	-	-	-
Solanaceae	*Solanum melongena*	12	+	+	-	-
Solanaceae	*Solanum torvum*	4	-	+	-	-
Poaceae	*Zea mays*	18	-	+	-	-

Tabel 3: Viruses detected in leaf samples of potential alternative hosts collected in Côte d'Ivoire, by AEZs: *Badnavirus*es (Immuno-capture-PCR) and YMV, YMMV, CMV (DAS-Elisa and RT-PCR) in Côte d'Ivoire

AEZ	Total	Healthy	Infection	YMV	Badna	CMV	Badna+ CMV
I	54	25 (46.30%)	29 (53.70%)	3 (5.56%)	8 (14.81%)	12 (22.22%)	6 (11.11%)
II	20	11 (55%)	9 (45%)	1 (5%)	2 (10%)	5 (25%)	1 (5%)
III	16	11 (68.75%)	5 (31.25%)	0	0	5 (31.25%)	0
IV	12	7 (58.33%)	5 (41.67%)	2 (16.67)	0	3 (25%)	0
V	5	4 (80%)	1 (20%)	0	0	1 (20%)	0
VI	24	12 (50%)	12 (50%)	1 (4.17%)	5 (20.83%)	5 (20.83)	1 (4.17%)
Total	131 (100%)	70 (53.44%)	61 (46.56%)	7 (5.34%)	15 (11.45%)	31 (23.66%)	8 (6.11%)
p-value		<0.001	0.0005	0.32	0.0005	0.021	0.001

YMV: yam mosaic virus; CMV: cucumber mosaic virus, Badna, *Badnavirus*es. Statistical significance was calculated using the khi2 test at 0.5 threshold (α = 0.05). AEZs: Agro-ecological zones (I, II,III, IV, V, VI).

were visualized by agarose gel electrophoresis (Fig. 4). Around 46.56% of potential alternative hosts were positive for one or more viruses after DAS-ELISA and PCR. There were three cases of single infections, one mixed infection case (Badna and CMV) (Table 3; Fig. 5). CMV single infection was the most prevalent throughout the country, with a general predominance 23.66% in the potential hosts in all AEZs, followed by *Badnavirus*es infection (11.45%) and YMV infection (5.34%). YMV was not detected in mixed infection in the alternative hosts. Mixed infection Badna and CMV was present in 6.11% of the samples collected (Table 3). The AEZ I alone account for 6 out of 8 cases of mixed infections. YMMV was not detected in all the samples and the regions. Also, the mixed infection was reported in *Phaseolus vulgaris*, *Solanum lycopersicum*, and *Solanum melongena* in AEZ I, II, and VI. Single *badnavirus* infection and mixed *Badnavirus*es and CMV infection was not detected in AEZs III, IV, and V. The AEZ I and VI had the highest viral infection rates (53.70% and 50%), while AEZ V had the lowest (20%), as shown in Table 3. These zones are characterized by increased viral diversity and the frequent presence of viral co-infections, making them critical points for epidemiological surveillance.

Interaction between AEZs, Hosts and Yam Viruses

The Fig. 6 illustrates the interactions between agro-ecological zones (AEZs), alternative host plants and the yam viruses studied (YMV, CMV, and *Badnavirus*es). It clearly shows that AEZ I and VI harbour the highest number of infected hosts, while AEZ V contains the lowest number of symptomatic hosts with one sample of *Zea mays* infected. The most represented alternative host species include *Solanum lycopersicum, Solanum melongena*, and *Phaseolus vulgaris*. *Solanum lycopersicum* was found in AEZs I and II, while *Solanum melongena* is located in AEZs I and III. On the other hand, *Pueraria phaseoloides* spread in three zones: AEZs I, II, and VI. These three species were essentially infected with *Badnavirus*es, and CMV. Only *Badnavirus*es were reported in *Colocasia esculenta*. The CMV group accounts for the majority of viral detections, with 39 cases of

infection, followed by *Badnavirus*es (23 occurrences), while yam mosaic virus remains minor with only 7 occurrences and are widely distributed across all agro-ecological zones and plant species. *Solanum lycopersicum* is the host most infected by *Badnavirus*es, and CMV. *Capsicum annuum* and *Abelmoschus esculentus* were infected only by CMV. Also, CMV was detected in many hosts but remains the most widespread in *Solanaceae*. YMV was detected the most in *Pueraria phaseolides* (3 occurences) in AEZs I, II, and VI, then in *Amaranthus viridis, Croton hirtus, Commelina benghalensis, and Chromoleona odorata*. The diversity of hosts and their distribution in the AEZs highlights the essential role of non-yam plants in the maintenance and spread of the viruses, underlining the need for in-depth monitoring and management of alternative hosts in yam in the AEZs.

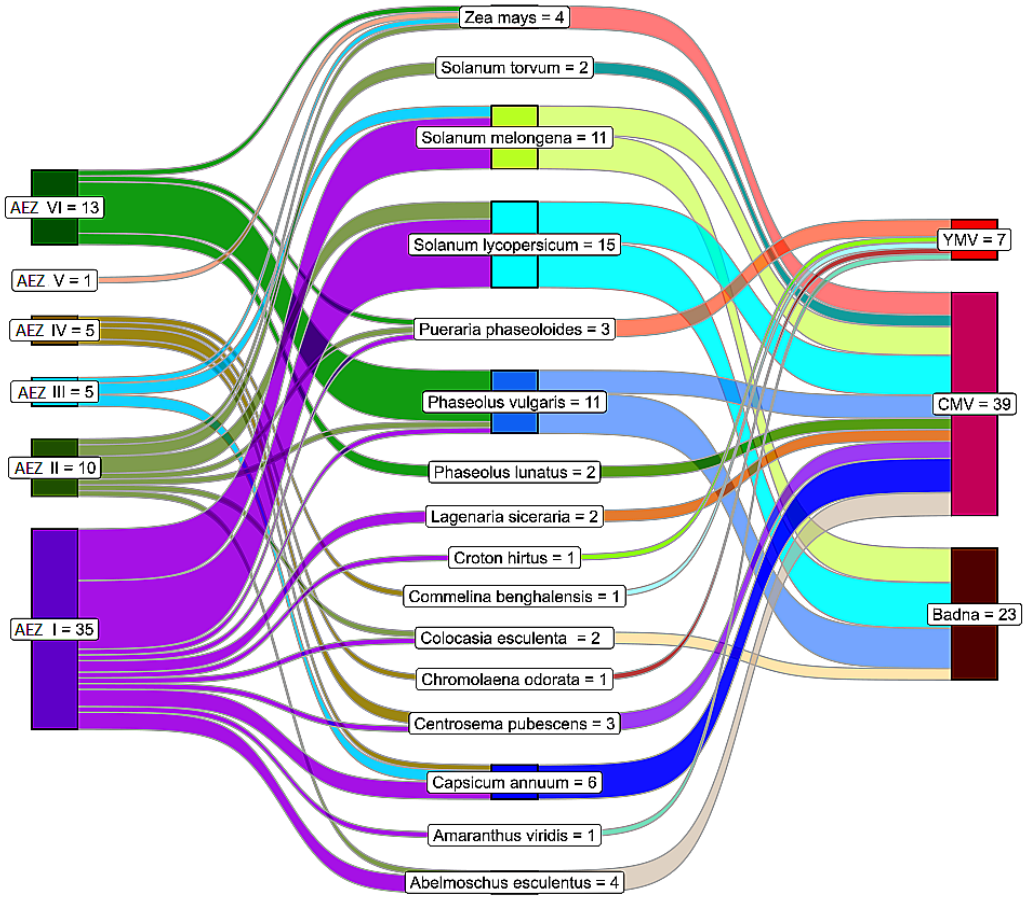

Fig. 6: Interaction between viruses circulating in alternative hosts according to agro-ecological zones (AEZs); YMV: yam mosaic virus; YMMV: yam mild mosaic virus; Badna, *Badnavirus*es. AEZs: Agro-ecological zones (I, II,III, IV, V, VI).

Phylogenetic Analysis

After sequencing of PCR products, only the sequences of DNA viruses (*Badnavirus*es) were good for phylogenetic analysis. None of the RNA virus sequences (CMV, YMV, and YMMV) presented good quality. RT-RNase H sequences alignment from Côte d'Ivoire obtained in this study showed that all the sequences are most closely related to isolates from Côte d'Ivoire, Ghana, Benin and Nigeria (Fig. 7). The sequences are from *Phaseolus vulgaris,* which represent food crops in visited fields. The phylogenetic tree generated in Fig. 7 presents the relationship between these sequences and those from this study. The nucleotide sequences generated in this study have been deposited in the GenBank database under accession numbers LC899256 to LC899259.

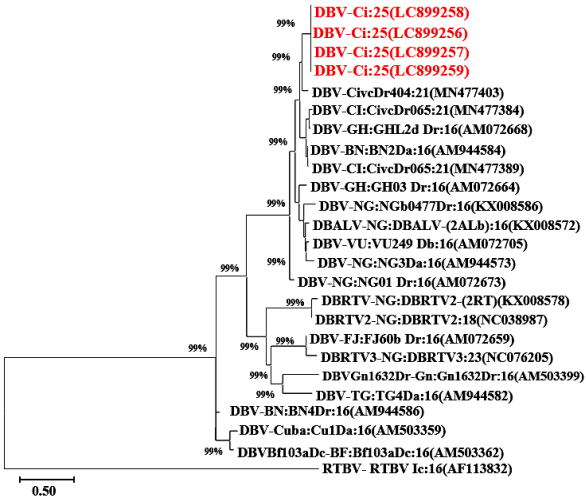

Fig. 7: Maximum-likelihood phylogenetic tree indicating the relationships between four partial RT-RNase H domain of badnaviruses and diverse representatives of the badnaviruses. The tree is rooted using Rice Tungro bacilliform virus (RTBV-Ic, GenBank accession AF113832) as an outgroup. The sequences from GenBank are coloured black, and the sequences from this study are in red. Bootstrap analysis was performed with 1000 replicates, and the horizontal scale indicates the genetic distance.

DISCUSSION

The study reported a high incidence of common yam viruses in alternative hosts collected from yam fields. Both single and mixed infections of *Badnavirus*es, YMV, and CMV were detected across the AEZs. YMMV was not

detected at all in the samples. The six AEZs showed the presence of at least one virus in 46.56% of tested samples. CMV (23.66%) was the most prevalent virus, occurring in all AEZs, followed by *Badnavirus*es and mixed infections, while YMV was the least frequent. These findings differ from previous reports by Diouf et al. (2022) who found that YMMV infected mostly several annual weed species that are widespread in yam fields in Guadeloupe. The discrepancy may be explained by the abundance of Solanaceae (food crops) in the collected samples. Our findings complement earlier reports that identified several weed species as reservoirs of YMV in yam fields in Nigeria (Asala et al., 2014; Aliyu et al., 2021).

The proportions of infected plants were the most important in AEZ I, comparing to the others zones. The variations in virus occurrence between the six AEZs can be explained by factors including the host species, vectors, and initial inoculum sources that exist in each place (Aliyu et al., 2021). The Solanaceae, Fabaceae, and Poaceae families were the most widespread across surveyed fields. In fact, more than 70% of the visited fields were intercropped with tomato, pepper, and maize. Farmers in Côte d'Ivoire often introduce these crops, such as tomato, chilli, and eggplant, into or around yam fields to diversify food production and generate income, as they require little effort to establish. A study of Kouakou et al. (2019) in some localities of the country similarly reported that yam is usually grown in mixed crop with other crops, mainly, corn, cassava and vegetables. This common practice of intercropping may accentuate virus transmission between cultivated species and weeds on a larger scale, potentially leading to more virulent strains. The presence of mixed infection (6.11%) in the sample is not an isolated case in fields. Co-infection can increase the replication or viral load of the co-infecting virus, often through the joint suppression of the RNA silencing pathway (Moreno & López-Moya, 2020), which is plants' primary antiviral defensive mechanism. This interaction may result in more severe symptoms, enhance transmission efficiency, and ultimately a higher risk of viral epidemic outbreaks. Laboratory analysis confirmed that virus infection was most prevalent in Solanaceae and Fabaceae species. This contrasts with the findings of Ekanayake & Asiedu (2003), who reported that weeds in yam-growing areas were mainly grasses (Poaceae). Aliyu et al. (2021) also observed Poaceae and Asteraceae as the most common alternative hosts in Nigerian yam fields. In our study, although Poaceae (represented by *Zea mays*) were relatively common (14%), they were not significantly infected by yam viruses, although CMV was detected in maize.

Among the collected samples, 75.56% were food crops cultivated by farmers. The persistence of weeds was also notable, with 75% of perennial plants identified as weeds. Because weeds can withstand drought and persist in yam fields during fallow periods, they provide a continuous reservoir for viruses in the absence of the preferred host. Weeds thus play a critical role in maintaining viral inoculum, which can later spread to yam and other crops when growth resumes (Asala et al., 2014). Specific hosts were particularly important. *Solanum lycopersicum*, *Phaseolus vulgaris*, and *Solanum melongena* were among the most infected by *Badnavirus*es and CMV. Tomato and common bean have already been reported as hosts for *Badnavirus*es (Staginnus et al., 2007; Wainaina et al., 2019; Serfraz, 2021; Chiquito-Almanza et al., 2021) and CMV, while *Badnavirus*es were also observed in *Solanum melongena* (Serfraz et al., 2021) and *Colocasia esculenta*. *Phaseolus vulgaris* was found in up to three zones and represents a serious threat as a potential inoculum source of CMV and *Badnavirus*es, as this species is particularly vulnerable to viral infection within the Leguminosae family (Ferreira et al., 2024). *Pueraria phaseoloides* also deserves particular attention, since it harbors YMV and is widespread in three AEZs. A similar observation was recorded in the previous studies in Nigeria Asala et al. (2014).

This study further revealed CMV infection in *Zea mays*, *Abelmoschus esculentus*, *Capsicum annuum*, *Solanum lycopersicum*, *Amaranthus viridis*, *Lagenaria siceraria*, *Phaseolus lunatus*, and *Solanum torvum*. The predominance of CMV in these hosts is not surprising, as this virus is known for its wide host range (Salaudeen et al., 2018; Abirami et al., 2022; Zohoungbogbo et al., 2024). Mixed infections were detected mainly in *Solanum lycopersicum*, *Phaseolus vulgaris*, and *Solanum melongena*, with 75% of such cases occurring in AEZ I. Co-infections are of particular concern, as they may enhance viral accumulation, promote synergistic interactions, and increase transmission efficiency by insect vectors in these species. As a result, plants carrying double infections may act as stronger reservoirs, thereby amplifying the risk of virus spread and causing more severe outbreaks in yam fields. As reported by Groves et al. (2002) and Aliyu et al. (2021), plant viruses need different hosts to keep the virus-host-vector relationship going. In this case, biological carriers are important for the spread and survival of most plant viruses that threaten crops. This indicates that the plant species identified as positive for *Badnavirus*es, YMV and CMV may act as alternative hosts for these viruses, potentially serving as inoculum sources for secondary viral spread and diminishing yam production.

Sequence analysis showed high similarity between the viruses detected in the reservoirs and yam *Badnavirus*es sequences from Côte d'Ivoire and neighboring countries, confirming their role as alternate hosts and their contribution to the epidemiology of yam viruses in the region. Since there are presently no viable therapies for plant viral infections, risk-reducing techniques are crucial. One of the most efficient and long-lasting strategies is still the introduction of genetic resistance in crop plants. Other tactics include using healthy, certified planting materials to stop the spread of infections, limiting the exchange of plant materials and requiring certification testing before introducing them into new environments, and maintaining field hygiene by eliminating weeds and alternate hosts to break the cycles of virus transmission (Tatineni & Hein, 2023; Devi et al., 2024; Andrade-Piedra et al., 2025).

Conclusion

This work is the first to be carried out on alternative

hosts in yam fields in Côte d'Ivoire. The study shows that numerous weeds and cultivated plants can be identified as substitute hosts of Badnavivrus, YMV, and CMV, sustaining the viral inoculum in the absence of yam crops in the field and facilitating the virus's survival for ongoing infection in the six AEZ. The survey's findings allow the development of practical preventive measures, such as more stringent weed control and restrictions on the use of imported tubers as planting material. Implementing these measures together with the use of certified virus-free planting material by farmers is expected to enhance yam production in Côte d'Ivoire. To encourage long-term, disease-free production, agricultural research centers and the Government should also enforce adherence to these measures. A substantial amount of work is still needed to clarify the implication of vector in the epidemiology of yam viruses and their relation with the alternate's hosts. This will first require identifying the potential vectors involved, as such crucial information is currently lacking.

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