Detection and Diversity of Viruses Affecting the Production of Dioscorea Rotundata in West Africa-A Review

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DOI: https://doi.org/10.51244/IJRSI.2025.120500039

Received: 23 April 2025; Accepted: 30 April 2025; Published: 31 May 2025

ABSTRACT

Yam (Dioscorea spp.) is recognized as one of the most important staple crops in West Africa, to the extent where descendants of southeastern Nigeria refer to it as the “King of Tuber Crops.” However, research reports over the decades have shown that the destructive activities of yam pathogens, particularly viruses, pose a serious threat to its production and exchange in West Africa. To identify and ensure propagation of clean germplasm, there is a vital need for the development and deployment of robust, rapid, highly sensitive, and cost-effective molecular diagnostic tools. This review, thus, provides insight into the advances in yam viruses’ detection methods, their efficacy, and their efficiency. Furthermore, to provide an overview of the diverse management strategies used to mitigate the impact of these diseases on yam (Dioscorea rotundata) growers in West Africa.

Keywords: yam viruses; molecular diagnostic tools; Dioscorea rotundata; clean germplasm

INTRODUCTION

Yam is a main staple for millions of people globally and especially in West Africa. Approximately, there are about 600 species of yam of which an estimated 10 species are consumed and cultivated worldwide. Interestingly, the “yam belt” zone of West Africa which comprises Nigeria, Cote d’Ivoire, Benin, Ghana and Togo account for 95% of this global yam production. Ranked as the fourth most important root and tuber crop behind potato, sweet potato and cassava truly confirms the role yam plays in food security and the socio-economic fortunes of the people. (Tostain et al., 2007; Jonathan et al.,2011;Toualy et al., 2014; ; Tamiru et al., 2017Azeteh et al., 2019; FAOSTAT, 2021; Ita et al., 2020).

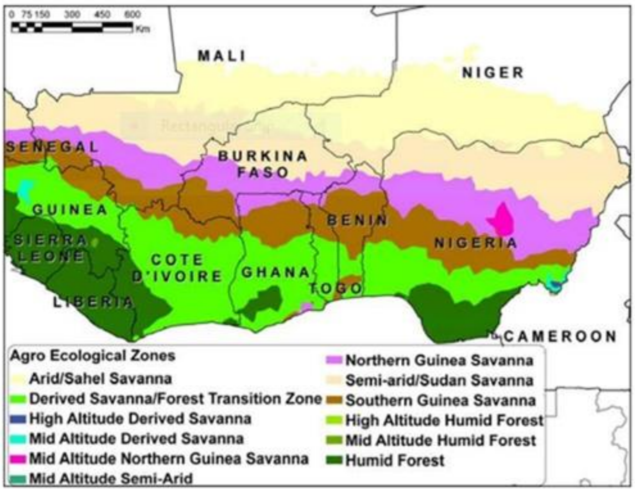


Figure 1. Map showing the key agro-ecologies of major yam producing countries in West Africa. Robert Asiedu et al., 2010.

Table 1. Shows 5 major yam producing countries in “Yam-Belt Zone of West Africa” ranked by 2006 production data (FAO, 2007).

S/N	COUNTRY	PRODUCTION QUANTITIES (Tonnes)	AREA HARVESTED (Hectares)
1	Nigeria	36720000	3035000
2	Côte d'Ivoire	4800000	540000
3	Ghana	3600000	300000
4	Benin	2239757	195747
5	Togo	621055	60246

Taxonomically, yam belongs to the family Dioscoreaceae of the order Dioscoreales (Liliflorae) and genus Dioscorea. (Jonathan,2019). One of the Dioscorea species, D. rotundata, fondly known as “white yam or Guinea yam,” is native to West Africa. It is actually the most important food yam and accounts for 79% of the world’s total food yam production (IITA, 1995;Jonathan et. al.,2025;). Interestingly, Nigeria produces 70% of this total (31.5 million tonnes annually) (Ezulike et al., 2006). To date, this record positions Nigeria as the largest producer of D. rotundata in the world. D. rotundata is the most famous and favoured yam variety among farmers and end consumers. Its advantageous potentials, which include exceptional agronomic traits, notable resistance to critical pests and diseases, adaptability to a variety of environmental conditions, and culinary attributes, make it eligible for agricultural improvement initiatives, commercial expansion, and international trade (Nwankwo, 2012; Singh, 2016).

According to Touré et al. (2013), yam is the most valuable staple crop in Côte d'Ivoire, with over 7.2 million tonnes produced in 2018. It is reported that D. rotundata accounts for 75% of the yam trade in the country.

Because yams are vegetatively propagated, the primary means of easily spreading plant diseases, particularly viruses, is through infected propagules. The endemic activities of these yam viruses result in "after effects" such as reduced quality of harvested tubers and gross yield losses. It is noteworthy that insect vectors, including aphids (vectors for YMV and CMV) and mealybugs (vectors for Badnavirus), have been shown to facilitate the activities and spread of yam viruses through mechanical transmission in a non/semi-persistent manner (Odu et al., 2004; Odu et al., 1999; Phillips et al., 1999; Thouvenel et al., 1990). In contrast to other pests and pathogens, including nematodes, bacteria, fungi, and insects, yam viruses are also the hardest to control.

In general, colossal losses have been documented on D. rotundata, specifically due to the devastating impact of YMV (Adeniji et al., 2012). This grim reality is typically due to the combined effects of biotic and abiotic forces.

Figure 2. Yam tubers stored in a barn (Aighewi et al., 2014).

Detection methods of yam viruses

The diagnostic methods for identifying yam viruses in D. rotundata have gained significant attention, regardless of the valuable information that may be gleaned from symptom manifestations alone. The sensitivity, specificity, speed, ease of use, reliability, reproducibility, and even price of these diagnostics are crucial indicators that may help in selecting the most appropriate technique in a certain circumstance. To achieve the best study results, these techniques could be applied separately or in combination, as in the case of Immunocapture-PCR (IC-PCR). In this succinct review, molecular-based and serological methods will be discussed.

In West Africa, many viruses have been routinely indexed and shown to cause either moderate or severe infections in yams. These viruses include the following: potyviruses (yam mosaic virus, YMV, and yam mild mosaic virus, YMMV), cucumoviruses (cucumber mosaic virus, CMV), badnaviruses (Dioscorea alata bacilliform virus), potexviruses (Dioscorea latent virus), and sadwaviruses (Dioscorea mosaic-associated virus, DMaV). Consequently, yam growers in Nigeria and Côte d'Ivoire have reported disastrous crop losses. Common viral symptoms were also noted, including mosaic, leaf distortion, leaf banding, interveinal chlorosis, necrosis, puckering, mottling, stunted growth, and brown spots on the leaves (Bakayoko et al., 2021; Eni et al., 2008; Odedara et al., 2012; Odu et al., 2004; Séka et al., 2009; Silva et al., 2015; Toualy et al., 2014).

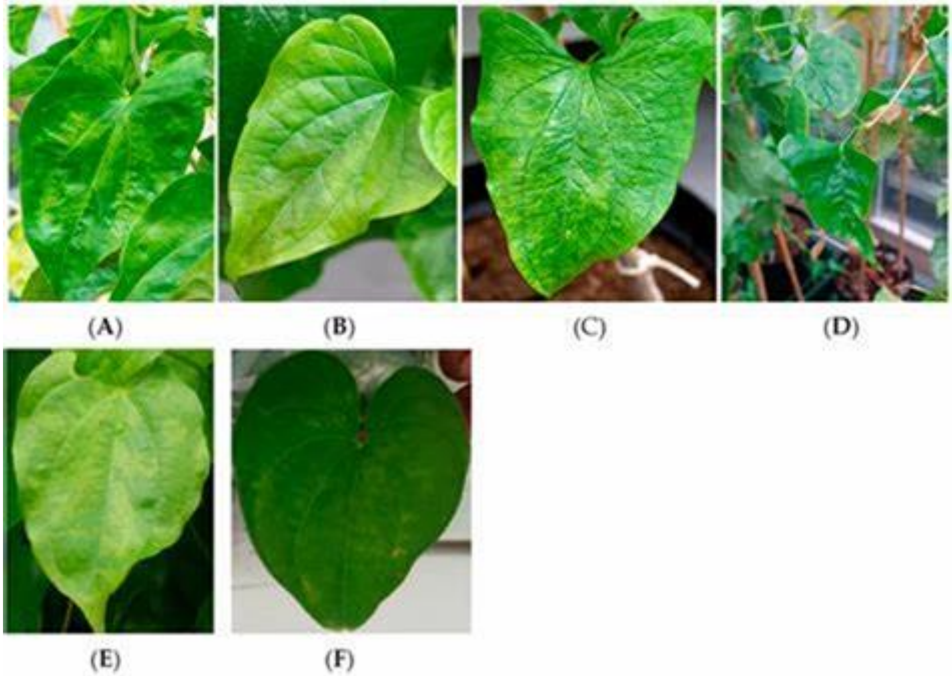


Figure 3. Typical virus symptoms on yam. (A) D. rotundata TDr 99/02674 showing mosaic symptoms; (B) D. rotundata cv. Adaka showing chlorotic leaf discoloration, and (C) mottling; (D) D. rotundata TDr 00/00168 showing leaf deformation ((A–D) source G.R.E. Silva (NRI) [20]); (E) D. rotundata leaf discoloration (Source: Stephen Winter, DSMZ); (F) D. alata showing diffused mottling.

For example, yam virus symptoms in D. rotundata were reported in Nigeria (Jonathan,2019). Aside from the reduction in the photosynthetic activity of the infected plant and the evident yield losses triggered by these symptoms, the plant may eventually die (Odu et al., 2001.

Seological based methods (Immunoassays)

Immunoassays as a technique is used for routine diagnosis of plant viruses, including those infecting yam. Dot blot immunoassay, precipitation and agglutination tests, immuno-electron microscopy, lateral flow assays, western blotting, enzyme-linked immunosorbent assay (ELISA) are several examples of commonly used serological methods.

Enzyme-linked Immunosorbent Assay, ELISA is the most popularly used serological test for detection of yam viruses because of its simplicity, versatility, adaptability and sensitivity in screening a huge number of samples within a short time (Jonathan,2019). It operates on a principle that allows an antigen (virus protein) from extracted sap to be captured by specific antibodies (could be monoclonal or polyclonal) and probing with specific immunoglobulins bearing an enzyme label. A suitable substrate added to the mixture is then converted to a product, with a detectable colour change, if it is in a case of positive reaction. The reaction stays colourless in the absence of the virus protein. Procedures used in ELISA can be direct or indirect.

Nucleic Acid Based Methods

Polymerase chain reaction, PCR is a highly sensitive molecular technique that is useful in detecting plant pathogens, particularly viruses, by amplifying exponentially a specific but short DNA sequence of the virus genome. Interestingly, PCR in combination with serological procedures has tremendously enhanced the detection of yam viruses. For instance immunocapture-PCR (IC-PCR) has been used in the detection of yam potyviruses (Mumford et al., 1997).

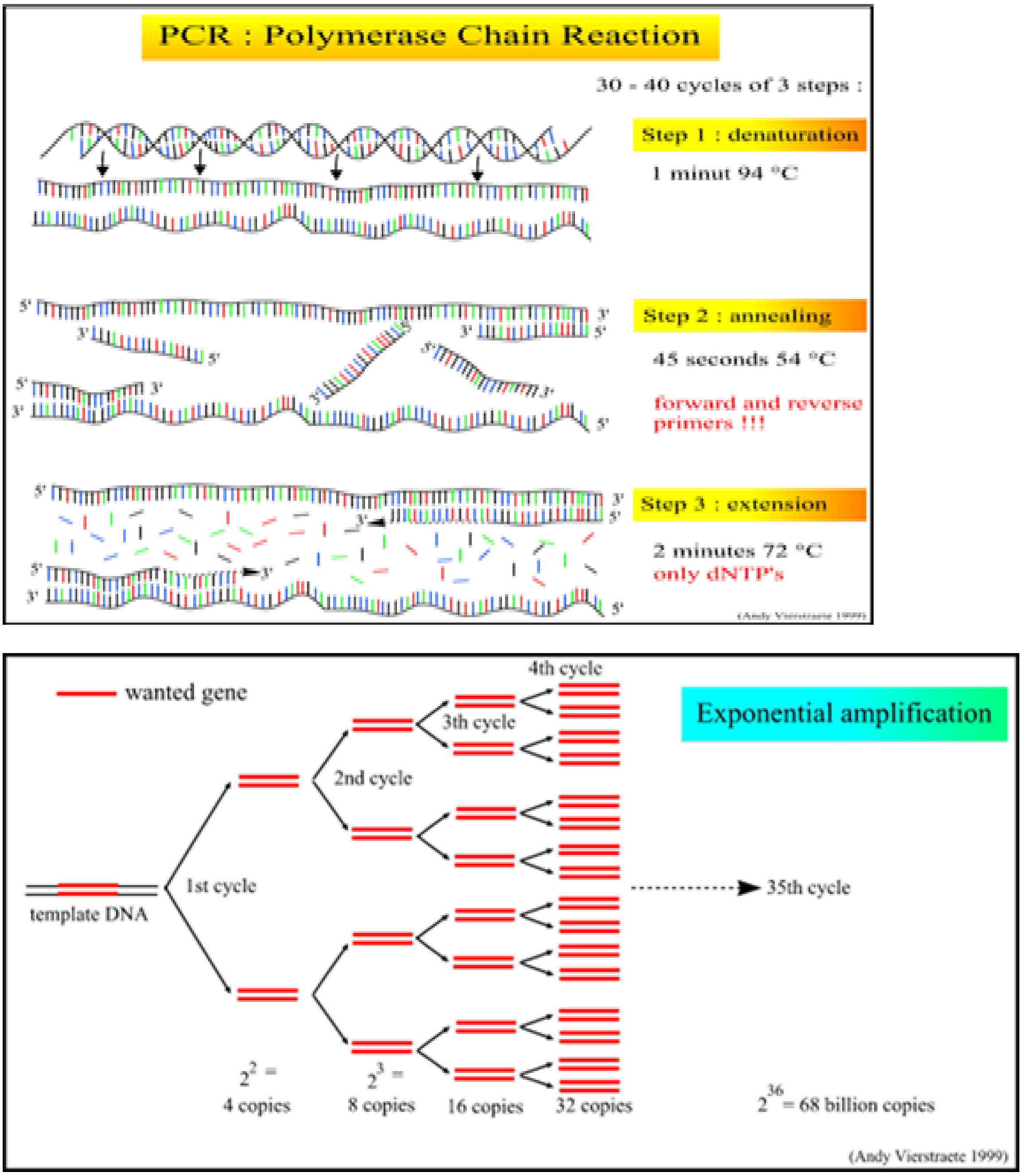
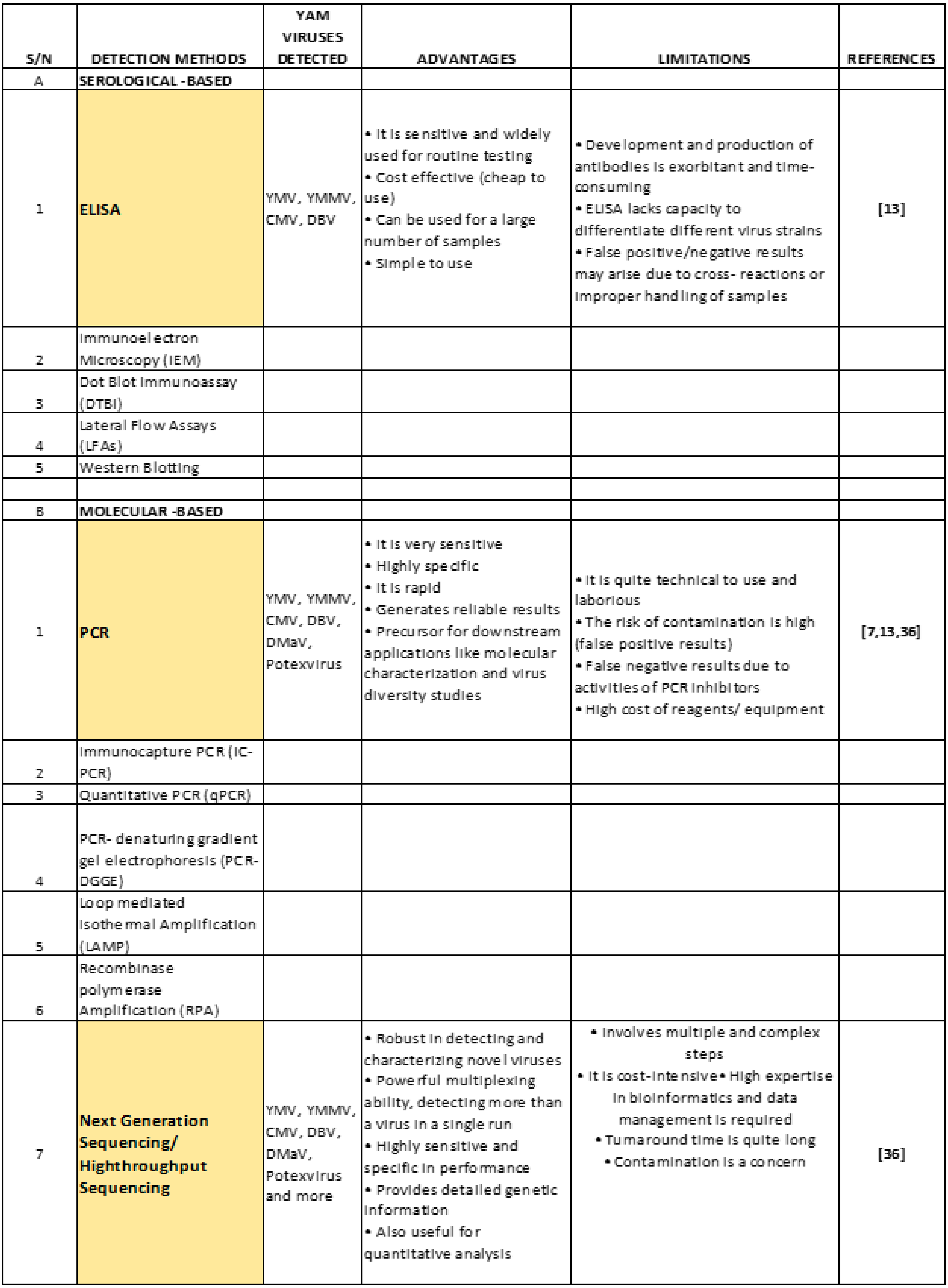


Figure 4. Steps of Polymerase chain reaction (Andy Vierstraete 1999).

Table showing a list of techniques for yam virus detection.



S/N	DETECTION METHODS	YAM VIRUSES DETECTED	ADVANTAGES	LIMITATIONS	REFERENCES
A	SEROLOGICAL -BASED				
1	**ELISA**	YMV, YMMV, CMV, DBV	• It is sensitive and widely used for routine testing • Cost effective (cheap to use) • Can be used for a large number of samples • Simple to use	• Development and production of antibodies is exorbitant and time-consuming • ELISA lacks capacity to differentiate different virus strains • False positive/negative results may arise due to cross- reactions or improper handling of samples	[13]
2	Immunoelectron Microscopy (IEM)				
3	Dot Blot Immunoassay (DTBI)				
4	Lateral Flow Assays (LFAs)				
5	Western Blotting				
B	MOLECULAR -BASED				
1	**PCR**	YMV, YMMV, CMV, DBV, DMaV, Potexvirus	• It is very sensitive • Highly specific • It is rapid • Generates reliable results • Precursor for downstream applications like molecular characterization and virus diversity studies	• It is quite technical to use and laborious • The risk of contamination is high (false positive results) • False negative results due to activities of PCR inhibitors • High cost of reagents/ equipment	[7,13,36]
2	Immunocapture PCR (IC-PCR)				
3	Quantitative PCR (qPCR)				
4	PCR- denaturing gradient gel electrophoresis (PCR-DGGE)				
5	Loop mediated Isothermal Amplification (LAMP)				
6	Recombinase polymerase Amplification (RPA)				
7	**Next Generation Sequencing/ Highthroughput Sequencing**	YMV, YMMV, CMV, DBV, DMaV, Potexvirus and more	• Robust in detecting and characterizing novel viruses • Powerful multiplexing ability, detecting more than a virus in a single run • Highly sensitive and specific in performance • Provides detailed genetic information • Also useful for quantitative analysis	• Involves multiple and complex steps • It is cost-intensive• High expertise in bioinformatics and data management is required • Turnaround time is quite long • Contamination is a concern	[36]

Yam virus diversity

There are currently 25 viruses that infect yams, according to the International Committee for the Taxonomy of Viruses (ICTV). These viruses are classified into eight families (Alphaflexiviridae, Betaflexiviridae, Bromoviridae, Caulimoviridae, Closteroviridae, Potyviridae, Secoviridae, Tombusviridae) and twelve genera (Aureusvirus, Ampelovirus, Badnavirus, Carlavirus, Cucumovirus, Dioscovirus, Fabavirus, Macluravirus, Potexvirus, Potyvirus, Sadwavirus, Velarivirus) (Silva et al., 2019).

Broadly, the diversity of viruses that affect yam, especially D. rotundata, is largely determined by several key factors. These factors comprise yam varieties, vector transmission mechanisms, host range, environmental influences, virus evolution, agricultural practices, co-infection with numerous viruses, climatic change, etc. Molecular characterization studies demonstrate that these variables contribute to the rapid evolution of yam viruses, such as YMV, YMMV, and Badnaviruses, into new pathogenic strains in different genotypes of D. rotundata.

Bousalem et al. (2000), for instance, highlighted that a lot of diversity studies on YMV have been conducted globally. Of all yam viruses, YMV is the most prevalent and economically significant, which is why it is the focus of attention.

Yam mosaic virus (YMV), a potyvirus that infects D. rotundata across Africa and other yam species is a single stranded RNA virus and is transmitted both mechanically and by different species of aphid vectors in a non-persistent manner (Odu et al., 2004; Thouvenel et al., 1979). In 1996, Aleman et. al., reported the first complete nucleotide sequence in YMV- Cote d'Ivoire isolate with 9608 nucleotides (nt). This when compared with the complete genome sequence of YMV- NG isolate consisting of a nucleotide length of 9594, shared 85% sequence identity. The basis for the reported high genetic variations among YMV isolates can be linked with the differential accumulation of mutations and recombination activities (Bousalem et al., 2000; Aleman-Verdaguer et al., 1997).

To lessen the detrimental impact and spread of YMV, virus-free planting materials and resistant cultivars must be used.

Yam mild mosaic virus (YMMV), another potyvirus, is the second most important virus infecting yam after YMV (Atiri et al., 2003). YMMV however, does not constitute a major threat on production of D. rotundata and yam generally even though it is more prevalent in D. alata. Results from the analysis of the nucleotide sequences of the coat protein of YMMV confirms that it is extremely different from YMV regardless the amino acid (aa) sequence identity between the two viruses being 57.1% (Fuji et al., 1999). The complete genome sequences of YMMV isolates range from 9521 and 9538 nucleotides in length, without the Poly (A) tail.

Badnaviruses are a group of viruses composed of a single circular double stranded DNA genome encapsulated in non-enveloped bacilliform particles of approximately 130 x 29-30nm in size (Phillips et al., 1999). They are known to infect a vast collection of crops of economic value besides yam. Taking a cue from complete nucleotide sequences of two badnaviruses- the Nigerian isolate of DaBV (Dioscorea alata Bacilliform Virus) and the Benin isolate of DsBV (Dioscorea sansibarensis Bacilliform Virus), a 61.9% nucleotide identity was determined from the analysis (Phillips et al., 1999).

Although many of the viruses that infect yam have been identified and characterized (Goudou-Urbino et al., 1996; Odu et al., 1999; Thouvenel et al., 1979), knowledge about their geographic distribution across West Africa is minimal and undetailed. The only countries where this is known to occur are Nigeria and Côte d'Ivoire (Gumedzoe et al., 2001; Hughes et al., 1997; Odu et al., 2001).

The introduction of these novel yam virus strains creates serious research gaps in understanding their etiology, symptomatology, pathogenicity, epidemiology, and even potential effects on D. rotundata production in West Africa. These disparities undoubtedly make it more difficult to implement the phytosanitary controls and efficient disease management programs that are required to enable the smooth exchange of disease-free germplasm between partnering countries.

Until the aforementioned elements are sufficiently tracked and regulated, efforts to mitigate the adverse impact of these yam viruses will persist.

Future Perspectives

The application of fit-for-purpose and highly sensitive diagnostics for early detection of viruses (including established and emerging viruses) infecting D. rotundata production together with molecular characterization of detected viruses for diversity studies are essential in establishing an effective plant health management program for the crop. In achieving this, most of the gaps identified including insufficient data available in the yam virus database and delayed reporting of virus incidence due to poorly executed disease surveillance and monitoring programs must be addressed by engaging all stakeholders in the value-chain as well as smallholder farmers through awareness programs, advocacy campaigns and capacity development workshops.

In addition, advanced surveillance involving the use of remote sensing tools, drones and other relevant AI methods linked with a real-time reporting platform (ICT) can be explored. In the same vein, the absence of a sustainable yam seed system can be solved through the use of digital tools like the “cassava seed tracker” that aims to unite various stakeholders (researchers, breeders, Yam seed producers, Certification Institutions etc.) statutorily for decision-making and advisory functions, on how certified disease-free yam seeds can be easily accessed [16]. Research funding agencies and government institutions must play a huge financial role in transforming the yam (D. rotundata) research landscape in West Africa.

Implementing these few approaches and others, will establish a better insight on the etiology, symptomatology, incidence, pathogenicity and epidemiology of these viruses that will in effect, enhance good policy-making and strengthen the yam seed system.

CONCLUSION

Propagation of clean planting materials and resistant varieties remain the best method for tackling the transmission and spread of yam viruses infecting D. rotundata (McQuaid et al., 2017). Furthermore, best agricultural and cultural practices with standardized disease management strategies will equally play a substantive role in ensuring increased production of the crop. It is also essential that National Quarantine Service workforce in all the dominant yam-producing countries in West Africa are frequently trained and properly sensitized to know the dangers of permitting the illicit movement and/or exchange of uncertified yam seeds across the region.

Indeed, the food security agenda, and improved socio-economic livelihood of the West African people can be actualized, provided that government parastatals at all level and prominent philanthropists continue to make sufficient funding available in order to sustain the ongoing research in the yam production industry, with emphasis on D. rotundata being the most important yam crop in West Africa.

DECLARATION OF CONFLICT INTEREST

None

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