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Overview of research on viruses infecting bananas, roots and tubers in sub-Saharan Africa

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Abstract

Studying phytoviruses is crucial to understand their dynamics and design effective disease management strategies. This study seeks to present an overview of the current state of virological research pertaining to banana, cassava, potato, sweet potato, taro, and yam within sub-Saharan Africa over the past 25 years. To accomplish this, an extensive literature review was performed, concentrating on peer-reviewed articles published in English. Key data were extracted for each crop, including the year of publication, the sub-Saharan country where the study was conducted, and the virus name, genus, and family. Six hundred and seventy-two articles were identified in the literature. All crops under study have been subjected to virological studies at least once in the selected geographic location. Studies on cassava were conducted in most countries and were by far the most published among all the other crops. Taro had the fewest publications. Uganda is the only country in sub-Saharan Africa to have published articles on viruses infecting all six crops. Viruses infecting banana root and tuber crops belong to 23 genera across 14 families. This analysis underscores cassava as the most comprehensively studied crop from a virological standpoint and highlights the pressing need to expand research efforts to encompass viruses affecting other crops.

Keywords: Cassava, potato, sweet potato, taro, yam, food security, research and development, plant virology

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Abbreviations

The following abbreviations are used in this manuscript:

BSV	Banana streak virus
BBTV	Banana bunchy top virus
Cas	CRISPR-associated proteins
CBSIs	Cassava brown streak ipomoviruses
CMBs	Cassava mosaic begomoviruses
CRISPR	Clustered regularly interspaced short palindromic repeats
DRC	Democratic Republic of Congo
ELISA	Enzyme-linked immunosorbent assay
HTS	High-throughput sequencing
ICTV	International Committee on Taxonomy of Viruses
kb	kilobases
LAMP	Loop-mediated isothermal amplification
PCR	Polymerase chain reaction
PLRV	Potato leafroll virus
PTGS	Post-transcriptional gene silencing
PVY	Potato virus Y
qPCR	Quantitative polymerase chain reaction
RNA	Ribonucleic Acid
SCBV	Sugarcane bacilliform virus
SPCSV	Sweet potato chlorotic stunt virus
SPFMV	Sweet potato feathery mottle virus
SPPV	Sweet potato pakakuy virus
SPVD	Sweet potato virus disease
TaBV	Taro bacilliform virus
TaBCHV:	Taro bacilliform CH virus
YMV:	Yam mosaic virus

1. INTRODUCTION

Root and tuber crops are plants from diverse botanical families that produce edible carbohydrates in underground organs, such as subterranean stems, swollen roots, rhizomes, corms, and tubers (Chandrasekara et al., 2016). They constitute the second most important source of carbohydrates to humans worldwide. Although their use extends beyond human nutrition, root and tuber crops are widely recognized as the predominant food source in sub-Saharan Africa (Gregory and Wojciechowski, 2020). Major roots and tubers consumed in that region include cassava (*Manihot esculenta* Crantz), yam (*Dioscorea* spp.), sweet potato (*Ipomoea batatas* (L.) Lam.), and potato (*Solanum tuberosum* L.), as well as edible aroids like cocoyam (*Xanthosoma sagittifolium*) and taro (*Colocasia esculenta* (L.) Schott). These roots and tubers, together with bananas, are a crucial group of staple crops for food security, income generation, and sustainable development across the continent (Sharma and Kaushal, 2016).

Cassava is a dicotyledonous plant belonging to the family *Euphorbiaceae*. This perennial woody shrub, indigenous to Latin America, was brought to Africa by the Portuguese traders in 1558 (Mohidin et al., 2023). Nowadays, cassava on the continent has transcended from being a cash and subsistence crop to become an industrial crop useful in human nutrition, beverages, animal feed, detergents, textiles, cosmetics, paperboard, and ethno-nutraceutical industries (Li et al., 2017; Tonukari et al., 2015; Mbanjo et al., 2020) as well as in the production of bioenergy (Padi et al., 2021). Given cassava's significant contribution to the livelihoods of African farmers and its potential for transforming African economies, it has been listed among the six strategic crops in the continent (Feleke et al., 2016). Production-wise, sub-Saharan Africa has been the world's leading cassava producer, contributing more than 60% since 2019 (Food and Agriculture Organization of the United Nations, 2025). Nigeria is the world's leading cassava producer. The Democratic Republic of the Congo, Ghana, and Angola have consistently ranked among the top 10 African cassava-producing countries (Food and Agriculture Organization of the United Nations, 2025).

"Yam" is a vernacular name for any of the 600 species of the genus *Dioscorea* in the family *Dioscoreaceae* worldwide (Diouf et al., 2022). They are monocotyledonous climbing and twining vines that are either annual or perennial (Tariq et al., 2024). Vines sprout from the rhizome or tuber, which later often serve as photosynthetic sinks for starch and other secondary metabolites (Obidiegwu et al., 2020). Yam species native to Africa include *Dioscorea rotundata* (white yam) (Scarcelli et al., 2019), *D. cayenensis* (yellow yam) (Salehi et al., 2019), *D. praehensilis* (POWO, 2025), *D. bulbifera* (air potato) (Salehi et al., 2019), and *D. dumetorum* (bitter yam) (POWO, 2025). *D. bulbifera* is also native to Asia and Australia (Salehi et al., 2019; POWO, 2025). In sub-Saharan Africa, yam is the fourth most important crop after cassava, sugarcane, and maize (Food and Agriculture Organization of the United Nations, 2025). Moreover, sub-Saharan Africa has accounted for 98% of global yam production over the past five years (Food and Agriculture Organization of the United Nations, 2025). Yams are mainly produced in the "yam belt," a region that includes the Republic of Côte d'Ivoire, Ghana, Togo, Benin, Nigeria, and Cameroon (Food and Agriculture Organization of the United Nations, 2025; Scarcelli et al., 2019). Yams have become important not only for their nutritional properties but also for their enormous medicinal properties (Salehi et al., 2019).

Sweet potato is a herbaceous liana plant with alternating leaves and tubular flowers [17]. This root vegetable crop, belonging to the family *Convolvulaceae*, originated in tropical South America, where it was domesticated about 5000 years ago. Its edible tuberous roots may vary in shape and color depending on the variety cultivated and the environmental conditions. The roots are usually long, with skin colors ranging from white to red, including cream, yellow, orange, pink, and purple. Their flesh's color varies from white or various shades of cream, yellow, orange, or even purple (Sapakhova et al., 2023; Motsa et al., 2015; Alam et al., 2021). Portuguese explorers are believed to have introduced sweet potato to Africa in the 16th century (Motsa et al., 2015).

Sweet potato is the eighth-most-produced commodity in Africa, ahead of potatoes and bananas. Its production in sub-Saharan Africa rose from 28 million tonnes in 2019 to 31 million tonnes in 2023, contributing to 32% of the world's production. Key producing countries include Malawi, Nigeria, Angola, Uganda, Ethiopia, and Rwanda (Food and Agriculture Organization of the United Nations, 2025). Sweet potato is primarily used for human consumption and occasionally for animal feed. Sweet potato is used mainly for human consumption and occasionally for animal feed. In addition to their nutritional value, sweet potato leaves have been found to contain various bioactive compounds with potential health-promoting benefits. These include high levels of polyphenols, flavonoids, and carotenoids, which have antioxidant, anticancer, antimutagenic, immunomodulatory, and hepatoprotective properties (Nguyen et al., 2021).

The potato plant belongs to the family *Solanaceae*, a family of flowering plants. It is a dicotyledonous, tuberous, herbaceous plant, perennial by its tubers but grown as an annual plant (VIB|IPBO, 2025). The edible, fleshy tubers develop at the ends of underground stolons. The origin of the potato was tracked to the Andes Mountains of South America, where its wild relatives can still be found. Its cultivation started about 8000 years ago in Peru's Central Andes (Lutaladio et al., 2009). European Christian missionaries brought potatoes to Africa at the end of the 17th century (VIB|IPBO, 2025). In sub-Saharan Africa, for the period 2019-2023, eastern Africa contributed 58.3%

of total production, while southern, western, and middle Africa accounted for 19.4%, 15.3%, and 7%, respectively (Food and Agriculture Organization of the United Nations, 2025). Potatoes are primarily used as a staple food crop, providing crucial calories for food security, and as a valuable cash crop for smallholder farmers, offering income generation and employment opportunities.

Taro is a tropical monocotyledonous, vegetatively propagated, perennial crop of the family *Araceae*. It is the most commonly cultivated species in the genus *Colocasia*, primarily for its starchy corm, or underground stem. It is regarded as one of the world's oldest food crops, domesticated over 9000 years ago in Southeast Asia (Oladimeji et al., 2022). Taro is an essential crop for millions of people in sub-Saharan Africa. It is widely found in backyards and in intercropping systems. It is commonly used for human nutrition, as a medicinal plant source of valuable bioactive compounds, and as an ornamental or fodder plant (Oladimeji et al., 2022; Matthews et al., 2021). Despite its proven high nutritional value and considerable trade as a fresh and processed crop, taro has been listed as an orphan crop (Matthews et al., 2021). Africa accounted for 83% of global taro production between 2019 and 2023 (Food and Agriculture Organization of the United Nations, 2025). Nigeria is by far the largest producer, averaging 8 million tonnes. China is the second with an average of 1.9 million tonnes. Other sub-Saharan African countries in the top ten include Cameroon, Ethiopia, Ghana, Madagascar, Rwanda, and the Central African Republic (Food and Agriculture Organization of the United Nations, 2025).

Banana is a monocotyledonous herbaceous perennial plant with an underground stem and pseudostem that is vegetatively propagated (Mathew et al., 2017). They also refer to the elongated and curved fruits of the plant. The edible banana, identified as plantain and dessert banana, belongs to the genus *Musa* in the family *Musaceae*. Plants of this family originated in the hot, tropical regions of Southeast Asia/Oceania. Its domestication began more than 7,000 years ago, likely in New Guinea (Beránková et al., 2024; Sardos et al., 2022). Bananas and plantains are cultivated in different environments. Nigeria, with an average of 7 million tonnes, was the largest banana producer in sub-Saharan Africa between 2019 and 2023 (Food and Agriculture Organization of the United Nations, 2025). Angola and the United Republic of Tanzania were among the top ten banana producers, with 4.4 and 3.5 million tonnes, respectively. Millions of people in sub-Saharan Africa rely on bananas for daily food and income. Bananas are consumed in various forms, including raw, cooked, baked, fried, as baby food, and as sweet and alcoholic beverage products (Marimo et al., 2020). Moreover, several studies have demonstrated the potential of banana as an industrial crop with applications in the nutraceutical, textile, bioenergy, and biofertilizer industries (Emmanuel et al., 2025).

Roots, tubers, and banana production have been plagued by low agricultural yield across sub-Saharan Africa. Diseases and pests are among several factors that have contributed to this alarming situation. Plant-infecting viruses are a group of obligate intracellular parasites of plants. They are smart entities consisting of one or more nucleic acid molecules enclosed in a protein shell. They enter host cells passively through microscopic wounds or via their vectors. Upon successful entry into a susceptible host plant cell, they induce various symptoms as a result of their multiplication and propagation throughout the host (Suman et al., 2023). Plant virus diseases have long been a significant concern for farmers, researchers, and policymakers because they cause substantial yield losses in many economically important crops (Sharma et al., 2023). This study aimed to provide an overview of virology research conducted on banana, cassava, potato, sweet potato, taro, and yam in sub-Saharan Africa from 2000.

2. MATERIALS AND METHODS

2.1 Study Design

This study was conducted as a **scoping review** to map and summarize published research on viruses infecting banana, cassava, potato, sweet potato, taro, and yam in sub-Saharan Africa over a 25-year period. A scoping review approach was selected because of the broad research questions addressed and the objective of capturing trends in research activity rather than evaluating intervention effectiveness.

2.2 Literature Search Strategy

Peer-reviewed journal articles published between January 2000 and June 2025 were identified through searches conducted in **Google Scholar**, **ScienceDirect**, and **Wiley Online Library**. These databases were selected to ensure broad coverage of plant virology, plant pathology, and agricultural research.

Search terms combined crop names, virus-related keywords, and geographic identifiers. Typical search strings included combinations of crop names (e.g., "cassava," "banana," "yam," "sweet potato," "potato," "taro"), virus-related terms ("virus," "viral disease," "plant virus"), and geographic descriptors ("sub-Saharan Africa" or individual country names). Only articles published in English were considered.

2.3 Eligibility Criteria

Studies were included if they:

1. Reported original research on viruses infecting at least one of the six target crops;
2. Focused on plant material originating from sub-Saharan African countries;
3. Were published in peer-reviewed journals between 2000 and 2025.

Studies were excluded if they:

1. Did not involve plant viruses;
2. Focused exclusively on crops outside the scope of this review;
3. Lacked a clear link to sub-Saharan African plant material or virus isolates;
4. Are review articles, conference abstracts, theses, or non–peer-reviewed publications.

2.4 Study Selection and Data Extraction

Titles and abstracts of retrieved articles were screened to assess relevance, followed by full-text evaluation of eligible studies. In cases where experiments were conducted outside sub-Saharan Africa using plant material or virus isolates originating from the region, the country of origin of the material was used for geographic attribution.

For each included study, the following data were extracted:

- Year of publication
- Crop studied
- Sub-Saharan African country involved
- Virus species name
- Virus genus and family

Extracted data were compiled and curated to allow descriptive analysis of publication trends, geographic distribution, and virus diversity.

2.5 Data Analysis and Visualization

The extracted data were analyzed descriptively to summarize trends across crops, countries, years, and virus taxonomic groups. Bar graphs, pie charts, and maps were used to visualize results. Graphs and tables were generated using WPS Sheet (https://fr.wps.com/), while geographic distribution maps were produced using MapChart (https://www.mapchart.net/africa.html).

Given the scoping nature of the review, no formal assessment of study quality or risk of bias was conducted. However, variability in study focus, methodology, and depth is acknowledged and discussed as a limitation.

3. RESULTS

1.1. Articles on virological research conducted on banana, cassava, potato, sweet potato, taro and yam in sub-Saharan Africa

Six hundred and seventy-two articles on viruses infecting banana, cassava, potato, sweet potato, taro, and yam in sub-Saharan Africa have been published in the past 25 years. Articles on viruses infecting cassava were the most published, accounting for 57.6% (Figure 1).

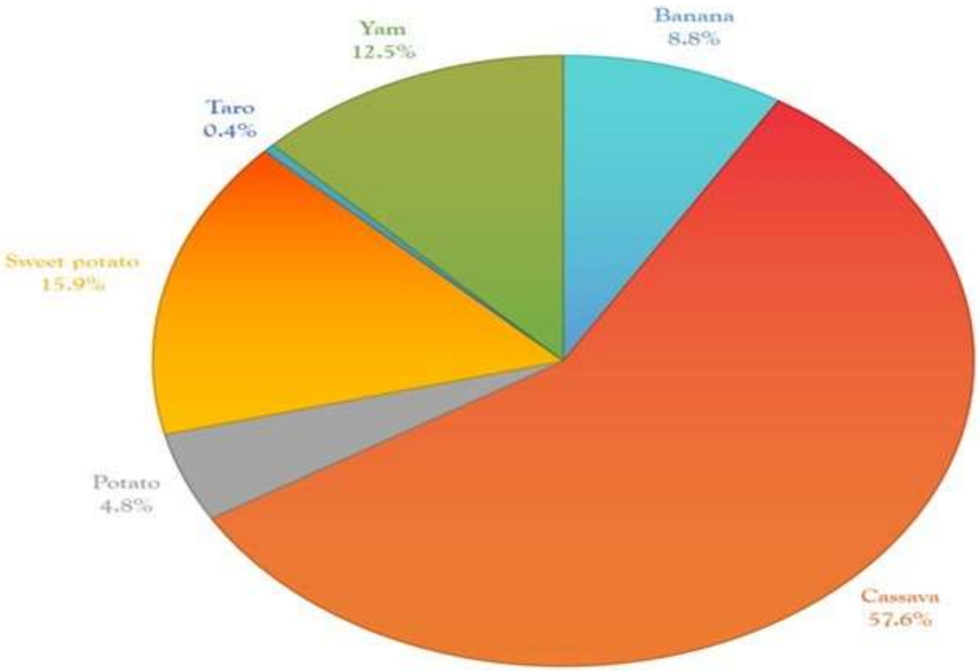

Figure 1: Pie chart of articles published on virology research conducted on banana, cassava, potato, sweet potato, taro and yam in sub-Saharan Africa.

Articles on viruses that infect sweet potatoes accounted for 15.9%. Articles on yams accounted for 12.5%. The percentage of articles on viruses infecting banana, potato, and taro was below 10% for each of these crops, with studies on taro having the least, with 0.4%.

3.1. Articles published over the years

It was observed that there were years without any studies published on viruses infecting banana, potato, sweet potato, taro, and yam (Figure 2). Articles on viruses infecting taro were published only in 2018 and 2022. Potato came next, with 11 years without any publications. No articles on viruses infecting bananas from sub-Saharan Africa were published in 2000, 2003, or 2018. Articles on virus-infecting sweet potato could not be found for the years 2005 and 2025. Articles on viruses infecting yams were missing for 2003 and 2025. Cassava is the only crop under study to have virus studies published every single year since 2000. It was only in 2022 that studies on viruses infecting the six crop understudies were available.

In terms of articles published in a year, the highest number was recorded for studies on viruses infecting cassava, reaching 30 in 2021 (Figure 2). The lowest score for cassava was seven, recorded in 2007 and in 2009. Regarding the other crops under study, the highest number of publications in a year was 9 for studies on viruses infecting sweet potato recorded in 2010 and 2019; 8 for studies on viruses infecting yam in 2024; 6 for studies on viruses infecting banana in 2020; 5 for studies on viruses infecting potato in 2013; and 2 for studies on viruses infecting taro in 2022.

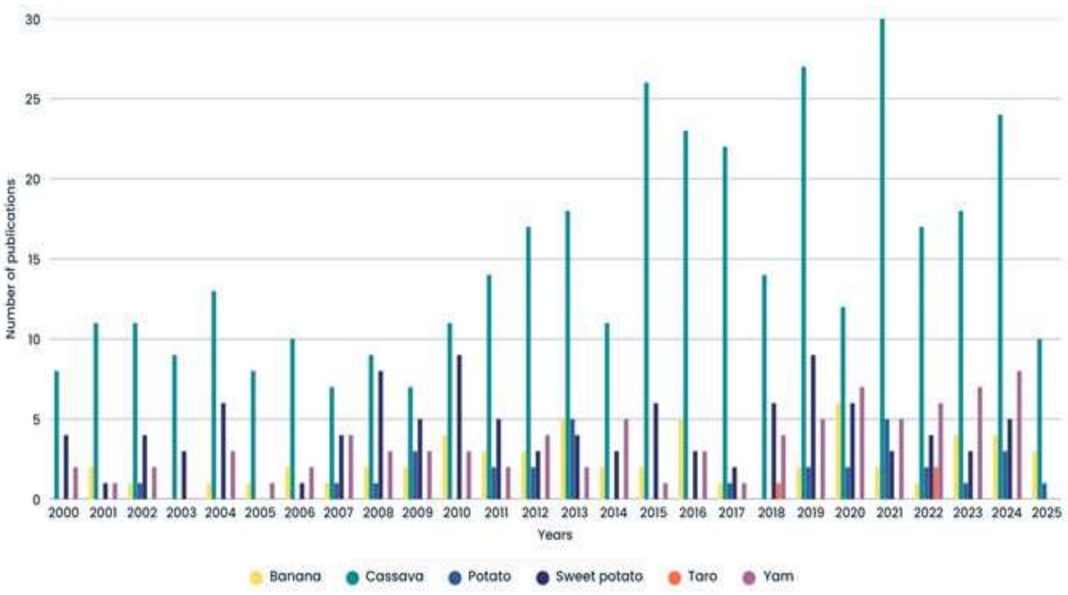

Figure 2: Articles on virological reseach conducted on banana, cassava, potato, sweet potato, taro and yam in sub-Saharan Africa published between 2000 and 2025.

3.2. Articles published per sub-Saharan African country

A comparative study of countries that have conducted virological studies on the crop under study revealed a fairly unique pattern (Figure 3). Uganda is the only country in sub-Saharan Africa to have published articles on viruses infecting all six crops. It is followed closely by Ethiopia, Kenya, Nigeria, and the United Republic of Tanzania, where virological studies have been conducted on five of the six crops under study. Benin, Burkina Faso, Burundi, Cameroon, Ghana, Rwanda, and South Africa come next for publishing virological studies conducted on four crops. Countries where virology studies have been conducted on three crops include Côte d'Ivoire, the Democratic Republic of Congo, Malawi, Mozambique, Togo, and Zambia. Angola, the Republic of the Congo, Gabon, Madagascar, and Zimbabwe have published virological research on two crops. Fourteen sub-Saharan African countries have published virology research on a single crop. However, eleven countries still lack data on viruses infecting the crops under study.

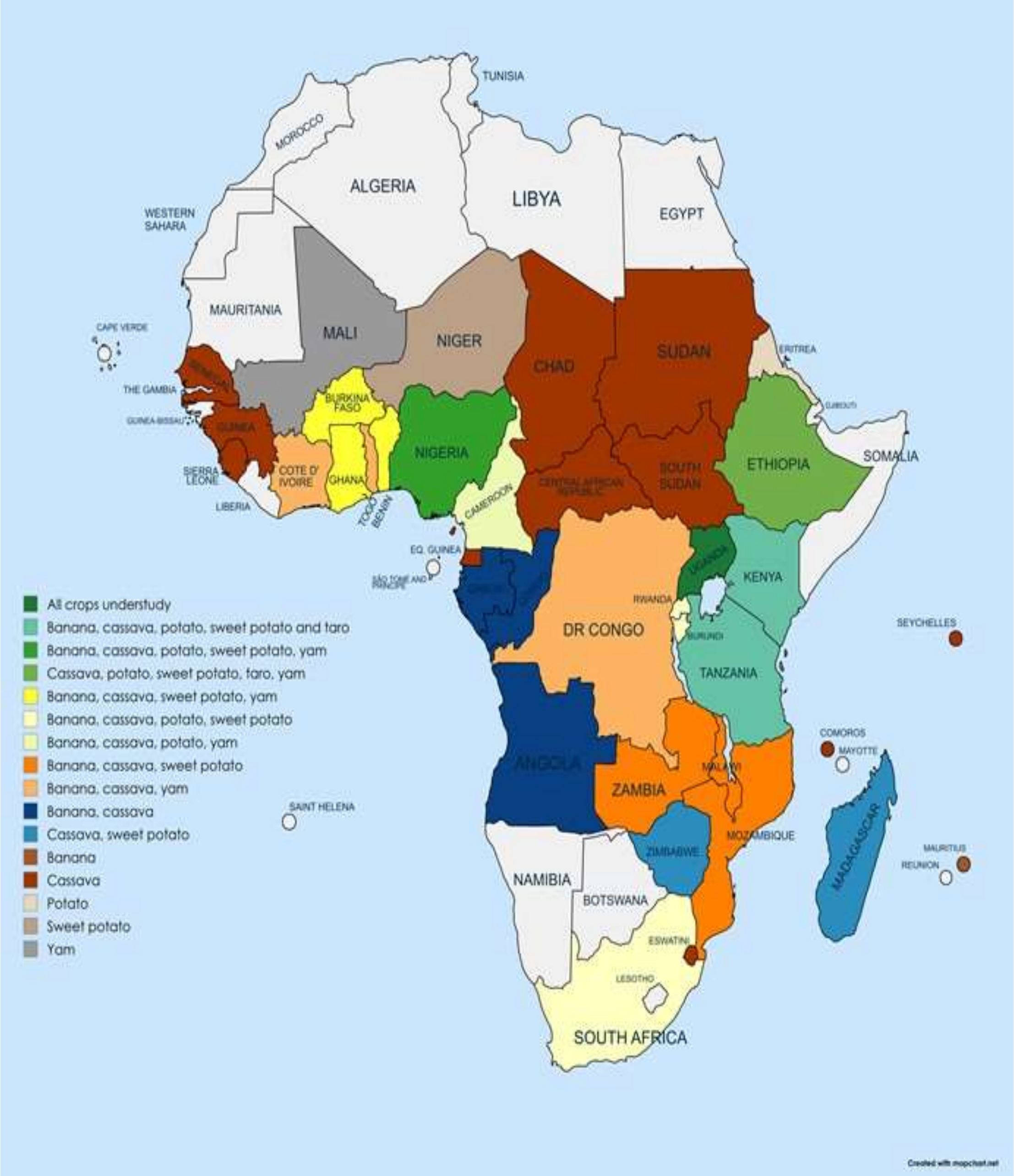

Figure 3: Crops that have been subjected to virological studies in sub-Saharan African countries

Table 1: Number of sub-Saharan African countries where virological research on banana, cassava, potato, sweet potato, taro and yam have been published.

Crops	Banana	Cassava	Potato	Sweet potato	Taro	Yam
Number of sub-Saharan African countries	21	40	10	17	4	11

From a crop perspective (Table 1), research on viruses affecting cassava has been carried out in 40 countries across sub-Saharan Africa. Similarly, studies on viruses impacting bananas have been conducted in 21 countries. For sweet potatoes, research has taken place in 17 countries. In comparison, virology studies concerning yams, potatoes, and taro have been conducted in 11, 10, and 4 countries, respectively.

3.3. Genera and families of viruses infecting banana, cassava, potato, sweet potato, taro, and yam in sub-Saharan African countries

Viruses that infect banana, root, and tuber crops belong to 23 genera spread across 14 families (Table 2). The family *Potyviridae* is particularly noticeable because it includes members that infect all the crops studied. Three families—*Betaflexiviridae*, *Bromoviridae*, and *Caulimoviridae*—include members that infect four of the six crops. Meanwhile, the families *Alphaflexiviridae*, *Closteroviridae*, and *Geminiviridae* have been found to infect three of the six crops under investigation.

Table 2: Genera and families of viruses infecting banana, cassava, potato, sweet potato, taro and yam studied in sub-Saharan Africa.

Family	Genera	Banana	Cassava	Potato	Sweet potato	Taro	Yam
Alphaflexiviridae	*Potexvirus*			+	+		+
Betaflexiviridae	*Banmivirus*	+					
	Carlavirus			+	+		+
Bromoviridae	*Cucumovirus*	+			+	+	+
Caulimoviridae	*Badnavirus*	+			+	+	+
	Cavemovirus				+		
	Dioscovirus						+
	Solendovirus				+		
Closteroviridae	*Ampelovirus*						+
	Crinivirus				+		
Endornaviridae	*Alphaendornavirus*					+	
Geminiviridae	*Begomovirus*		+		+	+	
	Mastrevirus				+		
Nanoviridae	*Babuvirus*	+					
Pospiviroidae	*Pospiviroid*					+	
Potyviridae	*Ipomovirus*		+		+		
	Macluravirus						+
	Potyvirus	+		+	+	+	+
Rhabdoviridae	*Alphanucleorhabdovirus*					+	
	Cytorhabdovirus					+	
Secoviridae	*Comovirus*						+
	Sadwavirus						+
Solemoviridae	*Polerovirus*			+			
Virgaviridae	*Tobravirus*			+			

Key:
+ = Viruses that have been studied.

In terms of specific crops, viruses infecting sweet potato, taro, and yam belong to seven different families. In contrast, bananas and potatoes are infected by viruses from five distinct families, while viruses infecting cassava are primarily from just two families (Table 2).

Among the genera of viruses infecting the crop under study (Table 2), *Potyvirus*, *Cucumovirus*, and *Badnavirus* are readily spotted for their broader host ranges. Potyviruses have been studied on banana, potato, sweet potato, taro, and yam. Cucumoviruses and badnaviruses have both been studied across all crops except cassava and sweet potato. Three other genera, namely, *Potexvirus*, *Carlavirus*, and *Begomovirus*, have host ranges that include three of the six crops under study. Viruses of the genera *Potexvirus* and *Carlavirus* have been found to infect potato, sweet potato, and yam. In contrast, members of the genus *Begomovirus* have been studied on cassava, sweet potato, and taro. *Ipomovirus* is the only genus with members infecting two of the six crops, namely cassava and sweet potato. Members of 17 virus genera infect one crop.

3.4. Economically important virus species of banana, cassava, potato, sweet potato, taro, and yam in sub-Saharan African countries

Banana streak virus (BSV) and banana bunchy top virus (BBTV) are the primary focus of studies on viruses infecting bananas in sub-Saharan Africa. BBTV, with the binomial name *Babuvirus musae*, belongs to the family *Nanoviridae*. It is a non-enveloped, multi-component virus composed of at least six particles, each containing a distinct circular single-stranded DNA (Thomas et al., 2021). It was first reported from the Fiji Islands in 1889, but its causal agent was not identified until the late 1980s (Kumar et al., 2011). The earliest confirmed identification of BBTV in sub-Saharan Africa dates back to the 1950s in the Democratic Republic of Congo, from where it spread to other countries (Kumar et al., 2011). BBTV has since been reported in Rwanda (Gaidashova et al., 2025), Angola (Lava Kumar et al., 2009), Cameroon (Oben et al., 2009), Burundi (Niyongere et al., 2011), Gabon and Malawi (Kumar et al., 2011), Benin (Lokossou et al., 2012), Nigeria (Adegbola et al., 2013), Congo (Stainton et al., 2015), South Africa (Jooste et al., 2016), Côte d'Ivoire (Kouadio et al., 2016), Togo (Kolombia et al., 2021), Uganda (Ocimati et al., 2021), Tanzania (Shimwela et al., 2022), and Mozambique (Barros et al., 2024).

BSV is a member of the family *Caulimoviridae*, a group of non-enveloped reverse-transcribing plant viruses with non-covalently closed circular double-stranded DNA (Teycheney et al., 2020). At the genus level, BSV belongs to *Badnavirus*, characterized by bacilliform virions with parallel sides and rounded ends (Teycheney et al., 2020). The earliest documented report of banana streak disease dates back to 1968 in Côte d'Ivoire; however, the virus was first isolated and characterized in Morocco (Malik et al., 2022). The International Committee on Taxonomy of Viruses (ICTV) has validated four distinct BSV species: *Badnavirus alphavirgamusae*, *Badnavirus deltavirgamusae*, *Badnavirus gammavirgamusae*, and *Badnavirus iotavirgamusae* (Teycheney et al., 2020). Other sub-Saharan African countries where BSV has been detected include Benin, Ghana, and Nigeria (Pasberg-Gauhl, 1996); Cameroon (Gauhl et al., 1997); Uganda and Mauritius (Kubiriba et al., 2001; Jaufeerally-Fakim et al., 2006); South Africa (Jaufeerally-Fakim et al., 2006); Kenya and Burundi (Karanja et al., 2008; Wambulwa et al., 2012); and Burkina Faso (Ouattara et al., 2023a, b).

Cassava mosaic begomoviruses (CMBs) and cassava brown streak ipomoviruses (CBSIs) have been at the center of research on viruses infecting cassava in sub-Saharan Africa. CMBs belong to the family *Geminiviridae*, the largest family of plant-infecting DNA viruses, characterized by twinned icosahedral particles and a bipartite genome composed of DNA-A and DNA-B components of approximately 2.5–2.6 kb each (Fiallo-Olivé et al., 2021). They are the causal agents of cassava mosaic disease, first reported in East Africa in 1894 (Legg & Fauquet, 2004). Although initially considered relatively benign, the disease became a major constraint to cassava production toward the end of the twentieth century due to the emergence of highly virulent recombinant strains (Combala et al., 2024). Currently, eleven CMB species are recognized, nine of which are widespread in sub-Saharan Africa.

CBSIs consist of two virus species, *Ipomovirus brunusmanihotis* (cassava brown streak virus, CBSV) and *Ipomovirus manihotis* (Ugandan cassava brown streak virus, UCBSV). Both belong to the genus *Ipomovirus* within the family *Potyviridae*, the largest group of plant-infecting RNA viruses. Their virions are non-enveloped flexuous filaments containing a single linear positive-sense RNA genome of approximately 9 kb (Inoue-Nagata et al., 2022). CBSIs cause cassava brown streak disease, a devastating disease that can lead to total crop failure. The disease was first detected in 1935 in coastal Tanzania and remained confined to low-altitude coastal areas until the early 2000s, when it spread inland to Uganda, Kenya, Rwanda, Burundi, Malawi, Mozambique, the Democratic Republic of Congo, Zambia, and the Comoros Islands (Robson et al., 2024).

Studies on viruses infecting potatoes in sub-Saharan Africa focus on approximately eight viruses, among which potato leafroll virus (PLRV) and potato virus Y (PVY) are the most intensively studied. PLRV (*Polerovirus PLRV*) belongs to the family *Solemoviridae* and has stable icosahedral virions enclosing a positive-sense monopartite RNA genome (Sõmera et al., 2021). PLRV is one of the most destructive viral pathogens of potato worldwide, causing severe yield and quality losses. It has been reported in South Africa (Murray et al., 2002), Cameroon (Njukeng et al., 2007), Eritrea (Biniam, 2008), Kenya (Muthomi et al., 2009), Ethiopia (Bekele et al., 2011), Tanzania (Chiunga & Valkonen, 2013), Rwanda (Okonya et al., 2021), and Uganda (Byarugaba et al., 2021).

PVY (*Potyvirus yituberosi*) is another member of the family *Potyviridae*, genus *Potyvirus*. The virions consist of flexuous filaments containing a single linear positive-sense RNA genome of approximately 9.7 kb (Inoue-Nagata et al., 2022). PVY was first described in the early 1930s as the causal agent of potato degeneration (Smith, 1931). It has a complex evolutionary history shaped by frequent recombination events, with at least five major parental variants and over 35 recombinant forms identified worldwide (Samarskaya et al., 2025). Mixed infections involving PVY and PLRV result in severe disease symptoms and substantial yield and quality losses (Byarugaba et al., 2020).

Sweet potato virus disease (SPVD) is the most devastating disease affecting sweet potato worldwide, causing yield losses of up to 90% or complete crop failure. SPVD results from the synergistic interaction between sweet potato feathery mottle virus (SPFMV) and sweet potato chlorotic stunt virus (SPCSV) (Zhang et al., 2020). SPFMV (*Potyvirus batataplumei*) belongs to the family *Potyviridae* and was first described in the United States in 1945 before being reported in East Africa in 1957. SPCSV (Crinivirus ipomeae), a phloem-limited virus belonging to the family *Closteroviridae*, possesses a bipartite positive-sense RNA genome and was first identified in West Africa in the 1970s (Fuchs et al., 2020).

Yam mosaic virus (YMV) is the most extensively studied virus infecting yam in sub-Saharan Africa. It belongs to the genus *Potyvirus* under the binomial name *Potyvirus yamtesselati* (Inoue-Nagata et al., 2022). Since its first report in Côte d'Ivoire in 1979, YMV has spread widely and is now the most prevalent and economically important virus of yam, infecting both cultivated and wild species (Luo et al., 2022).

Only three publications have reported viruses infecting taro in sub-Saharan Africa. High-throughput sequencing approaches revealed that taro is infected by at least eleven viruses from six families and one viroid (Kidanemariam et al., 2018; Kidanemariam et al., 2022; Muruu et al., 2022). *Badnavirus* was the most represented genus, with *Badnavirus alphacolocalasiae*, *Badnavirus betacolocalasiae*, *Badnavirus occultipomeae*, and *Badnavirus deltasacchari* detected.

4. DISCUSSION

Plant virology started with the discovery of *Tobamovirus tabaci* (tobacco mosaic virus) in 1892. It seeks to understand and unravel the dynamics underlying the development of plant diseases of viral etiology. This discipline has been gaining ground in sub-Saharan Africa, as evidenced by the growing body of scientific literature on the topic. We focused in this study on peer-reviewed articles on virological studies of banana, cassava, potato, sweet potato, taro, and yam. It was encouraging to note that all crops under study have been subjected to virological studies at least once in the selected geographic location.

A noteworthy finding from this research was the significant disparity in the number of published articles for each crop. Research on viruses that infect cassava significantly outnumbered the total publications for all other crops combined, whereas studies on viruses that affect taro received the least representation. Articles on viruses that infect sweet potatoes ranked second. Looking at the history of viruses infecting these crops, such as CMBs and CBSIs in cassava and SPCD in sweet potato, it becomes evident that they have been a serious threat to food and nutritional security in sub-Saharan Africa (Legg & Fauquet, 2004; Ndunguru et al., 2015; Robson et al., 2024; Zhang et al., 2020). Therefore, it is not surprising to note that most publications in virological research over the past 25 years have focused on viruses infecting cassava and sweet potatoes.

Besides being the subject of most publications, viruses infecting cassava have been studied in most sub-Saharan African countries. These two facts provide enough confidence to conclude that cassava is the most studied crop from a virological perspective. Similarly, cassava-infecting viruses are the most studied in sub-Saharan Africa.

However, this does not eliminate the need for further research on viruses that infect cassava. On the contrary, we must give the other crops under study the same, if not more, attention. Limited knowledge of the viruses infecting the other crops may worsen the situation in the field, causing greater inconvenience. Increasing the effort invested in understanding the viruses of banana, potato, taro, and yams will improve the management of their diseases, with a positive impact on farmers' livelihoods.

Published research on viruses infecting bananas ranked third in quantity but originated from 21 sub-Saharan African countries. In contrast, studies on viruses infecting sweet potatoes ranked second in volume, albeit from fewer countries. Taro scored lowest on both parameters. Studies on viruses infecting taro were the lowest for the crops under study, with only three publications recorded in 2018 (Kidanemariam et al., 2018) and 2022 (Kidanemariam et al., 2022; Muruu et al., 2022), which provide information on the molecular characteristics of viruses present in Ethiopia, Kenya, Tanzania, and Uganda. The limited interest in taro can be a direct consequence of its status as an orphan or underutilized crop. Hopefully, the growing interest in this crop over the past few years, driven by its enormous nutritional and pharmaceutical potential (Aditika et al., 2022), will prompt the need to study the biotic factors limiting its growth in the field.

The high number of publications on viruses infecting cassava, in addition to contributing to the body of knowledge, also covers more aspects of the discipline of plant virology, thereby providing a broader understanding of the life cycles of these viruses. Publications on viruses infecting banana, potato, sweet potato, and yam from sub-Saharan African countries address questions on biological and molecular characteristics, phylogeny of virus isolates, host resistance, detection methods, vector transmission, and, to a lesser extent, epidemiology. In contrast, publications on viruses infecting cassava explore additional topics such as virus–vector interactions, virus–host interactions, virus gene function, and the effects of climate change on virus and vector populations. Not only do studies on cassava address more topics, but they also offer a broader range of methodological approaches. In studies of viruses infecting sweet potato, researchers primarily use grafting as the inoculation method, while for viruses infecting cassava, they employ insect vectors, infectious clones, Agrobacterium, or grafting.

A similar trend can be observed with the technologies employed in plant virus studies. Taking the example of high-throughput sequencing (HTS), which was developed to address the limitations of Sanger sequencing. It was noticed that these technologies have been used in virological studies on cassava (Allie & Rey, 2013; Liu et al., 2014; Maruthi et al., 2014; Allie et al., 2014; Louis & Rey, 2015; Ndunguru et al., 2015; Rogans et al., 2016; Kathurima et al., 2016; Maredza et al., 2016; Kathurima & Ateka, 2016; Ogwok et al., 2016; Alicai et al., 2016; Kuria et al., 2017; Amuge et al., 2017; Tairo et al., 2017; Ateka et al., 2017; Anjanappa et al., 2018; Kyallo et al., 2019; Amisse et al., 2019; Chen et al., 2019; Tomlinson et al., 2019a; Scussel et al., 2019; Kathurima & Ateka, 2019;

Kuon et al., 2019; Tomlinson et al., 2019b; Kwibuka et al., 2021; Kavil et al., 2021; Bizabani et al., 2021; Aimone et al., 2021; Rieux et al., 2021; Dye et al., 2023; Ngazi et al., 2024; Otron et al., 2025; Ngwensang et al., 2025; Sizani et al., 2025), potatoes (Ximba et al., 2017; Okonya et al., 2021; Espach et al., 2025), sweet potatoes (Mbanzibwa et al., 2014; Cuellar et al., 2015; Nhlapo et al., 2018; Wainaina et al., 2018; Mulabisana et al., 2019; Wokorach et al., 2020; Kiemo et al., 2024), taro (Kidanemariam et al., 2022; Muruu et al., 2022), and yams (Bömer et al., 2019; Silva et al., 2019; Marais et al., 2020; Umber et al., 2022). However, while HTS was primarily used as a virus detection tool in potato, sweet potato, taro, and yam, it has also been used in cassava in virus detection and to study host resistance and virus gene functions.

The diagnosis of plant viruses has also benefited from major technological advances, including enzyme-linked immunosorbent assay (ELISA), polymerase chain reaction (PCR), quantitative PCR (qPCR), loop-mediated isothermal amplification (LAMP), and HTS (Massart et al., 2017; Kutnjak et al., 2021). More recently, CRISPR–Cas–based diagnostic assays have been developed (Gootenberg et al., 2017; Kellner et al., 2019). However, unlike the other approaches, CRISPR–Cas technology has not yet been applied for virus detection in any of the crops considered in this study, nor in other crops in Africa. This lack of application is likely attributable to the relative novelty of CRISPR–Cas–based diagnostics and the limited capacity for their deployment on the continent.

Improving plant genetic resistance to viruses can be achieved through breeding or genetic engineering approaches. For the crops under study, post-transcriptional gene silencing technologies and CRISPR-Cas9 genome editing have been employed to create bananas resistant to banana streak virus (Shekhawat et al., 2012), potatoes resistant to potato leafroll virus (Murray et al., 2002), sweet potatoes (Gutiérrez et al., 2016), and cassava resistant to cassava mosaic begomoviruses and cassava brown streak ipomoviruses (Ogwok et al., 2016; Wagaba et al., 2017; Gomez et al., 2019; Beyene et al., 2021).

CONCLUSIONS

Viruses infecting banana, cassava, potato, sweet potato, taro, and yam have been the subject of numerous studies over the past 25 years in sub-Saharan Africa. Our analysis showed that cassava has received significantly more attention. It is essential for the scientific community to actively pursue research in countries where data remain scarce and to continue enriching the body of knowledge regarding viruses infecting the other crops under study.

Collaborative research has played an important role in virological studies conducted on viruses infecting crops in sub-Saharan Africa. De Stefano et al. (2013) define scientific collaboration as a set of informal functions and formal activities among scientists engaged in knowledge production, through participation in research projects. Deeper institutional partnerships must not only maintain but also strengthen this collaborative culture.

Scholarly collaboration closely correlates with research productivity, impact, and innovation performance, according to the literature (Vieira et al., 2023). Research and development are widely acknowledged as critical drivers of economic growth, innovation, and enhanced living standards, particularly in developing countries. Strategic investments in research promote innovation, enhance productivity, and support the development of knowledge-based economies (Acharya and Pathak, 2019; Yu and Jin, 2024). Therefore, we strongly encourage countries in sub-Saharan Africa to design and implement policies that foster a highly conducive environment for scientific research across all disciplines.

RECOMMENDATIONS AND FUTURE DIRECTIONS

Based on the trends and gaps identified in this scoping review, several strategic recommendations emerge to guide future research, policy formulation, and capacity development in plant virology in sub-Saharan Africa.

1. Rebalancing Research Efforts across crops.

While cassava virology research is comparatively advanced, viruses infecting banana, potato, yam, and especially taro remain underexplored despite their importance for food security and rural livelihoods. Targeted funding mechanisms and research calls should prioritize these neglected crops, with particular attention to taro and yam, which remain critically understudied across most of the region.

2. Expanding Geographic Coverage and Surveillance

A significant number of sub-Saharan African countries still lack published data on viruses infecting one or more of the crops examined. Strengthening regional surveillance systems and supporting national plant protection organizations to generate baseline virological data are essential to improve early detection, risk assessment, and outbreak preparedness.

3. Integrating Advanced Genomic and Diagnostic Technologies

Although high-throughput sequencing (HTS) has increasingly been adopted, its use remains uneven across crops and countries. Future research should integrate HTS with conventional diagnostics for routine virus surveillance, diversity assessment, and epidemiological studies. Furthermore, the adaptation and implementation of novel CRISPR-Cas-based diagnostic platforms may provide swift, field-deployable solutions specifically designed for African agricultural systems.

4. Strengthening Epidemiological and Climate-Responsive Research

Most studies remain descriptive or molecular in nature, with limited emphasis on virus epidemiology, vector ecology, and climate-driven disease dynamics. Future research should adopt interdisciplinary approaches combining virology, entomology, climate science, and modeling to anticipate virus emergence and spread under changing environmental conditions.

5. Translating Knowledge into Resistance Breeding and Disease Management

Greater efforts are needed to translate virological knowledge into practical disease management strategies. This includes integrating virus resistance into breeding programs, validating resistant varieties under farmer field conditions, and developing integrated pest and disease management packages adapted to local agroecological contexts.

6. Enhancing Regional Collaboration and Research Capacity

Sustained progress in plant virology will depend on strong regional and international collaborations. Investments in training, infrastructure, and equitable partnerships are critical to building long-term capacity in genomics, bioinformatics, and advanced diagnostics. We should further strengthen regional research networks to foster data sharing, harmonized protocols, and coordinated responses to transboundary viral threats.

7. Informing policies and Agricultural Development Strategies

Finally, policymakers should recognize plant viral diseases as a major constraint to agricultural productivity and food security. Evidence generated from virological research should be systematically integrated into national agricultural strategies, seed certification schemes, and phytosanitary regulations to ensure science-driven decision-making.

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Conflicts of Interest

The authors declare no conflicts of interest. The funders had no part in the study's design, data collection, analysis, or interpretation, manuscript writing, or publication decision.

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