ISSUE 6
NOVEMBER 2025

NEWSLETTER

Focus on scientific articles published by WAVE in 2025

IN THIS ISSUE

Central And West African Virus Epidemiology
WAVE
For Food Security

EDITORIAL

Excellence in plant health.

How can cutting-edge science address the phytosanitary challenges that threaten food security in sub-Saharan Africa? A clear answer is given by our recent publications, which set new standards in plant pathology. Indeed, to tackle this issue, The WAVE Regional Centre of Excellence conducted field surveys in Central and West Africa to identify existing
and potential threats to plant health.

The year 2025 was a significant one for WAVE, with a series of major publications in renowned scientific journals such as Scientific Reports, Briefings in Bioinformatics, Virology Journal and Frontiers. The various research projects underway are advancing our understanding of the emergence of plant diseases.

At the same time, the alerts issued by WAVE demonstrate the operational effectiveness of our epidemiological surveillance networks, showcasing our predictive health risk models as innovative tools for crop protection.

These scientific contributions firmly establish WAVE as a key player in plant health research in sub-Saharan Africa. Our cross-disciplinary approach, combining molecular biology, pathosystem ecology, bioinformatics, socioeconomics and innovative green biotechnology solutions, is shaping a new era in plant protection. The international recognition of our work by our peers attests to its scientific accuracy and impact on food and income security.

The emerging vision is of an African science of excellence that is not only skilled in deciphering the fundamental mechanisms of plant diseases, but also in co-developing sustainable solutions with farming communities.

Uncover solutions to phytosanitary challenges by diving into the publications featured in this special issue!

The WAVE Team

01

scientific reports

Journal metrics
Two-year impact factor 3.9 (2024) Third most cited journal in the world, with over 834,000 citations in 2024.* 2024 Journal Citation Reports® Science Edition (Clarivate Analytics, 2025)

scientific reports Impact factor: 3.9

Improving the diagnosis of cassava mosaic begomoviruses using Oxford Nanopore Technology sequencing

Mariam Combala[1,2], Ezechiel B. Tibiri[1,3], Justin S. Pita[1,2], Angela O. Eni[1], Seydou Sawadogo[1,3], Pakyendou E. Name[1,3], Saïdou Zongo[1,3], Poupouanou Kouhoumouri[1,3], Adama Sagnon[1,3], Oghenevwairhe P. Efekemo[4], Olabode Onile-ere[4], Allen Oppong[5], Cyrielle Ndougonna[1] & Fidèle Tiendrébéogo[1,3]

[1]Central and West African Virus Epidemiology (WAVE) for Food Security Program, Pôle Scientifique et d'Innovation,
Université Félix Houphouët-Boigny, Bingerville, Côte d'Ivoire.
[2]UFR Biosciences, Université Félix Houphouët-Boigny, Abidjan, Côte d'Ivoire.
[3]Laboratoire de Virologie et de Biotechnologies Végétales (LVBV), Institut de L'Environnement et de Recherches Agricoles (INERA), 04 BP 8645 Ouagadougou, Burkina Faso.
[4]Central and WestAfrican Virus Epidemiology Program, Covenant University Hub (WAVE-CU), Km.
10 Idiroko Road, Canaan Land, Ota, Ogun State, Nigeria.
[5]CSIR-Crops Research Institute, P.O. Box 3785, Kumasi-GhanaKumasi, Ghana.

email: fidele.tiendrebeogo@wave-center.org

ABSTRACT

Cassava mosaic disease (CMD), caused by begomoviruses such as African cassava mosaic virus (ACMV) and East African cassava mosaic virus (EACMV), poses a threat to food security in sub-Saharan Africa. Conventional PCR assays often fail to detect viral strains in symptomatic plants due to high genetic variability and recombination. In this study, we used Oxford Nanopore Technology (ONT) sequencing on 12 cassava leaf samples that had previously tested negative by PCR. We compared two strategies: direct sequencing of total plant DNA and sequencing after rolling circle amplification (RCA-MinION). Across the samples, we obtained 7,800–36,000 reads, of which 1,327–11,749 were viral reads after host filtering. While direct sequencing of total DNA detected CMD-associated reads without yielding full genomes, RCA-MinION enabled de novo assembly of complete ACMV and EACMV genomes (two to 14 contigs, N50 up to 22.2 kb). This revealed high genetic diversity, mixed infections and recombination. Building on these genomic datasets, we performed computational analyses to identify conserved genomic regions and palindromic motifs, which guided the rational design of new primers. These primers, which target the AV1, AC2, BV1 and BC1 regions, were validated in silico and by PCR. They achieved detection rates of up to 98% across diverse isolates and successfully amplified viral DNA in samples that had previously been undetected by standard primers. Palindromic motif analysis further reduced the risk of secondary structures, ensuring efficient primer binding. Sanger sequencing of the PCR products confirmed the specificity and robustness of the assays. Our findings suggest that ONT combined with RCA is a powerful tool for CMD diagnostics and surveillance, improving detection and providing the genomic insights that are critical for disease management and food security in West Africa.

ARTICLE INFO

Keywords:

motifs, Specific primers Cassava mosaic disease, Begomovirus, Oxford Nanopore Technology sequencing, Palindromic

02

Briefings in Bioinformatics

25 years

Journal metrics

Journal impact factor 2024 (Clarivate) 7.7 Five-year impact factor in 2024 (Clarivate) 8.7 Mathematical and computational biology (Clarivate) 2/67 Biochemical research methods (Clarivate) 3/86 CiteScore 2024 (Scopus) 15.8Information Systems (Scopus) 25/474Molecular Biology (Scopus) 33/410Half-life cited in 2024 (Clarivate) 3.4 yearsImmediacy Index 2024 (Clarivate) 1.52024 Eigenfactor Score (Clarivate) 0.04824Article Influence Score 2024 (Clarivate) 2.5212024 Standardised Impact per Source and per Article (SNIP) (Scopus) 1.718

Briefings in Bioinformatics **Impact factor: 6.8**

Challenges and opportunities of developing bioinformatics platforms in Africa: the case of Burkina Bioinfo at Joseph Ki-Zerbo University, Burkina Faso

Ezechiel B. Tibiri[1,*], Palwende R. Boua[2,3,4], Issiaka Soulama[5], Christine Dubreuil-Tranchant[6‡], Ndomassi Tando[6‡], Charlotte Tollenaere[7], Christophe Brugidou [7], Romaric K. Nanema [8], Fidèle Tiendrébéogo[1,9]

[1] Laboratoire de Virologie et de Biotechnologies Végétales, Institut de l'Environnement et de Recherches Agricoles (LVBV/INERA), Centre National de la Recherche Scientifique et Technologique (CNRST), 01BP476 Ouaga 01, Ouagadougou, Burkina Faso

[2] Clinical Research Unit of Nanoro, Institut de Recherche en Sciences de la Santé, CNRST,42 Avenue Kumda-Yonré, 218 Ouaga CMS11, Nanoro, Burkina Faso

[3] MRC Unit The Gambia, London School of Hygiene and Tropical Medicine, Atlantic Boulevard, Fajara, POBox273, Banjul, the Gambia

[4] Sydney Brenner Institute for Molecular Biosciences (SBIMB), University of the Witwatersrand, The Mount, First Floor, Office109, 9 Jubilee Road, Parktown, Johannesburg, South Africa

[5] Institut de Recherche en Sciences de la Santé, Biomedical and Public Health Department, CNRST, Rue 29.13 Wemtenga 03BP 7047, Ouagadougou, Burkina Faso

[6] DIADE, University of Montpellier, CIRAD, IRD, 911 Avenue Agropolis, Montpellier, Cedex 534934, France French Institute of Bioinformatics (IFB) — South Green Bioinformatics Platform, Bioversity, CIRAD, INRAE, IRD, F-34398 Montpellier, France

[7] PHIM, Plant Health Institute of Montpellier, Univ. Of Montpellier, IRD, CIRAD, INRAE, Institut Agro, 911 Av. Agropolis, 34394 Montpellier, France

[8] Genetic and Plant Breeding Team (EGAP), Biosciences Laboratory, Doctoral School of Science and Technology, Joseph KI-ZERBO University, avenue Pr Yembila Abdoulaye Toguyeni,03 BP7021, Burkina Faso

[9] Central and West African Virus Epidemiology (WAVE), Pôle scientifique et d'innovation de Bingerville, Université Félix Houphouët-Boigny (UFHB), Bingerville BP V34 Abidjan, Côte d'Ivoire

*Corresponding author. Ezechiel B.Tibiri, Laboratoire de Virologie et de Biotechnologies Végétales, Institut de l'Environnement et de Recherches Agricoles (LVBV/INERA), Centre National de la Recherche Scientifique et Technologique (CNRST), 01BP 476 Ouaga01, Ouagadougou, Burkina Faso. E-mail: ezechiel.tibiri@ujkz.bf

‡Christine Dubreuil-Tranchant and Ndomassi Tando contributed equally to this work.

ARTICLE INFO

Keywords:

bioinformatics, Burkina Bioinfo, challenges, training

Scan to read full article

ABSTRACT

Bioinformatics, an interdisciplinary field combining biology and computer science, enables meaningful information to be extracted from complex biological data. The exponential growth of biological data, driven by high-throughput omics technologies and advanced sequencing methods, requires robust computational resources. Worldwide, bioinformatics skills and computational clusters are essential for managing and analysing large-scale biological data sets across health, agriculture, and environmental science, which are crucial for the African continent. In BurkinaFaso, the establishment of bioinformatics infrastructure has been a gradual process. Initial training initiatives between 2015-2016, including bioinformatics courses and the establishment of the BurkinaBioinfo (BBi) platform, marked significant progress. Over 250 scientists have been trained at diverse levels in bioinformatics, 105 user accounts have been created for high-performance computing access. Operational since 2019, this platform has significantly facilitated training programs for scientists and system administrators in west Africa, covering data production, introductory bioinformatics, phylogenetic analysis,and metagenomics. Financial and technical support from various sources has facilitated the rapid development of the platform to meet the growing need for bioinformatics analysis, particularly in conjunction with local 'wet labs'. Establishing a bioinformatics cluster in Burkina Faso involved identifying the needs of researchers, selecting appropriate hardware and installing the necessary bioinformatics tools. At present, the main challenges for the BBi platform include ongoing staff training in bioinformatics skills and high-level IT infrastructure management in the face of growing infrastructure demands. Despite these challenges, the establishment of a bioinformatics platform in Burkina Faso offers significant opportunities for scientific research and economic development in the country.

03

BMC Virology Journal

Journal metrics
Journal impact factor 3.8 (2024) 5-year journal impact factor 3.7 (2024) Downloads 2.8M (2024)

Virology Journal Impact factor: 3.8 BMC

Improvement of Nanopore sequencing provides access to high quality genomic data for multi-component CRESS-DNA plant viruses

Daniel H. Otron[1,2,3], Denis Filloux[4,5], Andy Brousse[4], Murielle Hoareau[2], Babbitha Fenelon[2], Cécile Hoareau[2], Emmanuel Fernandez[4,5], Fidèle Tiendrébéogo[1], Jean-Michel Lett[2], Justin S.Pita[1,3], Philippe Roumagnac[4,5] and Pierre Lefeuvre[2,6*]

[1]The Central and West African Virus Epidemiology (WAVE) for Food Security Program, Pôle Scientifique et d'Innovation, Université Félix Houphouët-Boigny (UFHB), Abidjan , 22 BP 582, Côte d'Ivoire

[2]CIRAD, UMR PVBMT, St Pierre, La Réunion, F-97410, France

[3]UFR Biosciences, Université Félix Houphouët-Boigny (UFHB), Abidjan , 22 BP 582, Côte d'Ivoire

[4]PHIM Plant Health Institute, University Montpellier, CIRAD, INRAE, Institut Agro, IRD, Montpellier, F- 34398, France

[5]CIRAD, PHIM, Montpellier, F-34398, France

[6]Department of Plant Protection, College of Agriculture, CIRAD, UMR PVBMT, Can Tho University, Can Tho city, Vietnam

*Correspondence: Pierre Lefeuvre, pierre.lefeuvre@cirad.fr

ARTICLE INFO

Keywords:

CRESS-DNA viruses,
Rolling circle amplification,
Nanopore sequencing,
Tandem repeat

Scan to read full article

ABSTRACT

Background: Faced with the recrudescence of viral CRESS-DNA plant diseases, the availability of efficient and cost-effective tools for routine diagnosis and genomic characterisation is vital. As these viruses possess circular single-strand DNA genomes, they have been routinely characterised using rolling circle amplification (RCA) coupled with Sanger sequencing. However, while providing the basis of our knowledge of the diverse CRESS-DNA viruses, this approach is laboratory-intensive, time-consuming and ultimately ineffective faced with co-infection or viruses with multiple genomic components, two common characteristics of these viruses. Whereas alternatives have proved effective in some applications, there is a strong need for next-generation sequencing methods suitable for small-scale projects that can routinely produce high quality sequences comparable to the gold standard Sanger sequencing.
Results: Here, we present an RCA sequencing diagnostic technique using the latest Oxford Nanopore Technology flongle flow cells. Originally, using the tandem-repeat nature of RCA products, we were able to improve the quality of each viral read and assemble high-quality genomic components. The effectiveness of the method was demonstrated on two plant samples, one infected with the bipartite begomovirus African cassava mosaic virus (ACMV) and the other infected with the nanovirus faba bean necrotic stunt virus (FBNSV), a virus with eight genomic segments. This method allow us to recover all genomic components of both viruses. The assembled genomes of ACMV and FBNSV shared 100% nucleotide identity with those obtained with Sanger sequencing. Additionally, our experiments demonstrated that for similar-sized components, the number of reads was proportional to the segment frequencies measured using qPCR.
Conclusion: In this study, we demonstrated an accessible and effective Nanopore-based method for high-quality genomic characterisation of CRESS-DNA viruses, comparable to Sanger sequencing. Face with of increasing challenges posed by viral CRESS-DNA plant diseases, integrating this approach into routine workflows could pave the way for more proactive responses to viral epidemics.

Virology Journal Impact factor: 3.8 BMC

A ribodepletion and tagging protocol to multiplex samples for RNA-seq based virus detection: application to the cassava virome

Daniel H. Otron[1,2,3], Justin S. Pita[1,3], Murielle Hoareau[2], Fidèle Tiendrébéogo[1], Jean-Michel Lett[2] and Pierre Lefeuvre[2,4*]

[1]The Central and West African Virus Epidemiology (WAVE) for Food Security Program, Pôle Scientifique Et d'Innovation, Université Félix Houphouët-Boigny (UFHB), Abidjan, 22 BP 582, Côte d'Ivoire

[2]CIRAD, UMR PVBMT F-97410, St Pierre, La Réunion, France

[3]UFR Biosciences, Université Félix Houphouët-Boigny (UFHB), Abidjan, 22 BP 582, Côte d'Ivoire

[4]CIRAD, UMR PVBMT, Department of Plant Protection, College of Agriculture, Can Tho University, Can Tho City, Vietnam

*Correspondence: Pierre Lefeuvre
pierre.lefeuvre@cirad.fr

ARTICLE INFO

Keywords:

Cassava, Virome, Ribodepletion, RNaseH, Multiplexing, High-throughput sequencing, Virus discovery

Scan to read full article

ABSTRACT

Background: Cassava (*Manihot esculenta*, Crantz), is a staple food and the main source of calories for many populations in Africa, but the plant is beset by several damaging viruses. So far, eight families of virus infecting cassava have been identified; the *Geminiviridae* (ssDNA viruses responsible for cassava mosaic disease, CMD) and *Potyviridae* (ssRNA + viruses responsible for cassava brown streak disease, CBSD) families being the most damaging to cassava in Africa. In several cassava-growing regions, the co-existence of species and strains from these two families results in a complex epidemiological situation making it difficult to correctly identify the viruses in circulation and delaying the implementation of disease management schemes. Nevertheless, the development of next generation sequencing (NGS) methods has revolutionized plant virus detection and identification. One NGS method that has been successfully used in virus detection and identification is ribodepleted RNA sequencing. Unfortunately, the relatively high cost makes it difficult to upscale this method to large epidemiological surveys and limits its adoption as a diagnostic tool.

Results: Here, we develop a high-throughput sequencing protocol, named Ribo-M-Seq, that combines plant rRNA ribodepletion, cDNA synthesis, tagging with a 96 multiplexing scheme and Illumina sequencing. We evaluated the protocol on a series of cassava samples with a known assemblage of viruses. After confirming that the protocol was suitable for ribodepletion, we demonstrated it was possible to detect RNA and DNA viruses via identification of near full-size genomes. Additional phylogenetic analyses confirmed the presence of begomoviruses and ipomoviruses responsible for CMD and CBSD, respectively. We also detected a recently described ampelovirus (Manihot esculenta-associated virus) that was not detected in previous analyses.

Conclusions: The use of the Ribo-M-Seq protocol will pave the way for large-scale sample analyses of collections with potentially complex viromes, such as those collected in the West African cassava integrated pest management program.

04

frontiers

Journal metrics
Articles published with Frontiers have been viewed and downloaded 4 billion times and cited 12 million times, demonstrating the power of open research. Articles published in Frontiers journals achieve international visibility with over 308,000 mentions in major media outlets around the world, including the BBC, Newsweek, and Time. They have been mentioned 3.4 million times on social media. They have also received 13,000 mentions in policy documents and 18,000 in patents, demonstrating the real impact of your research around the world.

frontiers

Impact factor: 4.1

Frontiers in Plant Science

Emergence of begomoviruses and DNA satellites associated with weeds and intercrops: a potential threat to sustainable production of cassava in Côte d'Ivoire

Aya Ange Naté Yoboué [1,2*], Bekanvié S. M. Kouakou[1,2], Justin S. Pita[1,2*], Boni N'Zué[3], William J.-L. Amoakon[2,4], Kan Modeste Kouassi[1,2], Linda Patricia L. Vanié-Léabo[1,2], Nazaire K. Kouassi[1,2], Fatogoma Sorho[1] and Michel Zouzou[1]

[1]UPR de Physiologie et Pathologie Végétales, Laboratoire de Biotechnologie, Agriculture et Valorisation des Ressources Biologiques, UFR Biosciences, Université Félix Houphouët-Boigny (UFHB), Abidjan, Côte d'Ivoire,

[2]The Regional Center of Excellence, Central and West African Virus Epidemiology (WAVE) for Transboundary Plant Pathogens, Pôle Scientifique et d'Innovation, Bingerville, Université Félix Houphouët-Boigny (UFHB), Abidjan, Côte d'Ivoire,

[3]Centre National de Recherche Agronomique (CNRA), Bouaké, Côte d'Ivoire,

[4]UFR Sciences de la Nature, Université Nangui Abrogoua (UNA), Abidjan, Côte d'Ivoire

*Correspondence: Aya Ange Naté Yoboé, angenate60@gmail.com,
Justin S. Pita, justin.pita@wave-center.org

ABSTRACT

ARTICLE INFO

Keywords:

weeds, alternative hosts, cassava mosaic begomoviruses, West African Asystasia begomovirus (WAAV), alphasatellites

Scan to read full article

Cassava (*Manihot esculenta* Crantz) plays a significant role in the livelihoods of people in Africa, particularly in Côte d'Ivoire. However, its production is threatened by begomoviruses which cause huge yield losses. Some weeds and food crops intercropped with cassava act as reservoirs, thereby facilitating the sustenance and propagation of Cassava mosaic begomoviruses (CMBs), along with other begomoviruses. To effectively manage these diseases, it is imperative to enhance our understanding of the various hosts of cassava viruses in Côte d'Ivoire. Thus, a comprehensive nationwide survey was conducted in 2017 in cassava fields across Côte d'Ivoire, and molecular analyses were performed on the samples collected. The results obtained from this survey indicated that 65 plant species belonging to 31 families were potential alternative hosts for CMBs in Côte d'Ivoire. The molecular analyses revealed that four species, *Capsicum annuum, Solanum melongena, Centrosema pubescens, and Asystasia gangetica* exhibited differential affinities for both African cassava mosaic virus and East African cassava mosaic Cameroon virus. Additionally, other begomoviruses and new alphasatellites were identified. Soybean chlorotic blotch virus was isolated from C. pubescens while West African Asystasia virus 1, West African Asystasia virus 2, and a new Asystasia yellow mosaic alphasatellite were isolated from A. gangetica which appears to be a plant species that could favor the emergence of new viral species harmful to cassava cultivation. This study offers insights that will inform the development of more effective control methods for sustainable cassava production in Côte d'Ivoire.

frontiers Impact factor: 3.1 Frontiers in Sustainable Food Systems

Artificial intelligence tool for cassava viral diseases diagnosis using participatory surveillance in Burkina Faso

Seydou Sawadogo[1,2], Fidèle Tiendrebeogo[1,2,3*], Ezechiel B. Tibiri[1,2], Pakyendou E. Name[1,2], Florencia Djigma[2], Lassina Traoré[2], Justin S. Pita[3] and Angela O. Eni[3]

[1]Laboratoire de Virologie et de Biotechnologies Végétales, Institut de l'Environnement et de Recherches Agricoles (INERA), Ouagadougou, Burkina Faso,

[2]Laboratoire de Biologie Moléculaire et de Génétique (LABIOGENE), Université Joseph Ki-Zerbo, Ouagadougou, Burkina Faso,

[3]Central and West African Virus Epidemiology (WAVE), Pôle Scientifique et d'Innovation, Université Félix Houphouët-Boigny (UFHB), Bingerville, Côte d'Ivoire

*Correspondance : Fidèle Tiendrebeogo, fidele.tiendrebeogo@wave-center.org

ABSTRACT

ARTICLE INFO

Keywords:

participatory surveillance,
artificial intelligence,
cassava virus diagnosis,
smartphone,
Burkina Faso

In the area of plant health, there has been little work using participatory approaches to control emerging infectious diseases such as cassava mosaic disease (CMD) and cassava brown streak disease (CBSD). These diseases cause significant yield losses in Sub-Saharan Africa. The current study provided low cost and early detection method of cassava viral diseases surveillance, based on participatory approaches using an AI tool (Plantvillage nuru app). The study involved farmers, agricultural extension agents (AEA), and cassava diseases diagnosis experts. Farmers were made aware of CMD and CBSD damage through a national campaign, while AEA received training to identify CMD, CBSD, and cassava green mite (CGM) symptoms using an AI-based diagnostic tool. Sixty trained AEA, equipped with smartphones running the AI tool, conducted fields surveillance either through visual inspection or with AI tool. The participation rate of the AEA and the diagnostic accuracy of the AI tool and visual assessments were evaluated and compared to experts perception validated by molecular analysis. Workshops and smartphones allocation enhanced AEA participation rate to 60%, and increased surveyed fields number to 132. CMD detection revealed no significant difference between users of AI tool (p-value = 0.709) and visual inspection (p-value = 0.997). The mean scores of CMD detection were 29.83 ± 12.99% for AI tool, 37.12 ± 12.78% for experts, and 36.10 ± 12.74% for molecular analysis among AI tool users. With visual inspection users, the mean scores detection were 46.07 ± 13.00% for AEA and experts perception, and 43.87 ± 12.07% for molecular analysis. The AI tool misdiagnosed 5% of CMD as CBSD, but molecular analysis confirmed it as CMD. The CMD infected fields was 31.06%, with a predominantly African Cassava Mosaic Virus (93.33%) detected. The results demonstrated that participatory approaches could be effective in the plant pathogens early management.

Scan to read full article

frontiers Impact factor: 4.8

Frontiers in Plant Science

Removing recalcitrance to the micropropagation of five farmer-preferred cassava varieties in Côte d'Ivoire by supplementing culture medium with kinetin or thidiazuron

John Steven S. Seka[1,2]*, Modeste K. Kouassi [1,2], Edwige F. Yeo[3], Flavie M. Saki[2], Daniel H. Otron[1,2], Fidèle Tiendrebeogo[2]*, Angela Eni[2], Nazaire K. Kouassi [1,2] and Justin S. Pita[1,2]

[1]Unité de Formation et de Recherche Biosciences, Université Félix Houphouët-Boigny (UFHB), Abidjan, Côte d'Ivoire,

[2]The Central and West African Virus Epidemiology (WAVE) for Food Security Program, Pôle Scientique et d'Innovation, Université Félix Houphouët-Boigny (UFHB), Abidjan, Côted'Ivoire,

[3]Unité de Formation et de Recherche (UFR) d'Ingénierie Agronomique forestière et Environnementale, Université de Man (UMAN), Man, Côte d'Ivoire

*Correspondance : Fidèle Tiendrébeogo fidele.tiendrebeogo@wave-center.org, John Steven S. Seka, steveseka7@gmail.com

ABSTRACT

In vitro micropropagation is a rapid method of multiplying healthy planting material to control Cassava mosaic disease (CMD), one of a major constraint to cassava production in Africa. However, some cassava varieties have a low propagation ratio under in vitro conditions. The main objective of this study was to improve the in vitro propagation rate of five difficult to grow, farmer- preferred cassava varieties using plant growth regulators. Microcuttings from in vitro plantlets of five recalcitrant cassava varieties (A bablé 3, Ampong, Bayé rè, Bocou 5, Olé kanga) were evaluated for their capacity to rapidly regenerate plantlets. Time to root or leaf formation, number of nodes, number of roots, and the in vitro plantlet length were evaluated on nine culture media combinations. We found that among all the cassava varieties studied, the shortest times for leaf (4 to 7 days) or root (9 to 14 days) formation were recorded when the two types of MS media were supplemented with kinetin and thidiazuron as well as on the medium contain half-strength MS without these plant growth regulators. These two hormones evaluated were better for regeneration of leaves, nodes and elongation of in vitro plantlets with optimum concentration of 5 and 10 nM or thidiazuron, and 0.12 or 0.24 µM for KIN. A survival rate between 85-91% was recorded under tunnel conditions and the plantlets appeared to be morphologically normal. The information obtained during this study will be useful for mass multiplication programs of elite cassava varieties.

ARTICLE INFO

Keywords:

in vitro propagation, recalcitrant cassava varieties, thidiazuron, kinetin, virus-free plantlets

Scannez pour consulter l'article dans son intégralité

05

Journal metrics
Research areas Agricultural and biological sciences (General) Impact 7.5
CiteScore 6.2

Impact factor: 6.2

Towards sustainable management of cassava mosaic disease : The impact of awareness campaigns in Benin

Dèwanou Kant David Ahoya[a,b,*], Jacob Afouda Yabi[a], Jerome Anani Houngue[b], Serge Sètondji Houédjissin[b], Martine Zandjanakou-Tachin[c], Ettien Antoine Adjei[d], Eveline Marie Fulbert Windinmi Sawadogo-Compaore[e], Justin Simon Pita[d], Corneille Ahanhanzo[b]

[a]Laboratory for Analysis and Research on Economic and Social Dynamics (LARDES), University of Parakou (UP), Benin
[b]Central Laboratory of Plant Biotechnology and Plant Improvement (LCBVAP), University of Abomey-Calavi (UAC), Benin
[c]Research Unit in Horticultural Production and Green Space Management (URPHGEV) of the School of Horticulture and Green Space Management (EHAEV), National University of Agriculture (UNA), Benin
[d]Central and West African Virus Epidemiology (WAVE), Scientific and Innovation Hub of Bingerville, Félix Houphouët-Boigny University (UFHB), Bingerville, Côte d'Ivoire
[e]Department of Natural Resource Management and Production Systems, Institute of Environment and Agricultural Research (INERA), Burkina Faso

Corresponding author. Laboratory for Analysis and Research on Economic and Social Dynamics (LARDES), University of Parakou (UP), Benin.
E-mail addresses: davidahoya13@gmail.com (D.K.D. Ahoya), ja_yabi@yahoo.com (J.A. Yabi), hounanje@gmail.com (J.A. Houngue), sergesth01@yahoo.fr (S.S. Hou´edjissin), mtachin@yahoo.com (M. Zandjanakou-Tachin), ettienadjei31@gmail.com (E. Antoine Adjei), compeve@yahoo.fr (E.M.F.W. Sawadogo-Compaore), justin.pita@wave-center.org (J.S. Pita), corneille.ahanhanzo@wave-center.org (C. Ahanhanzo).

ARTICLE INFO

Keywords:

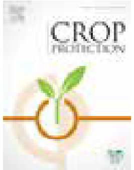
Awareness campaign
Cassava mosaic disease,
Impact assessment,
Propensity score matching (PSM) Benin

Scan to read full article

ABSTRACT

Transboundary diseases, such as cassava mosaic disease (CMD), represent a significant risk to food security and the livelihoods of millions of households in sub-Saharan Africa. To address this issue, awareness campaigns have been conducted targeting farmers and stakeholders within the cassava secor. The objective of this study is to quantify the impact of these awareness campaigns on the knowledge of CMD, the adoption of management practices, and the incidence of the disease in cassava fields. A random sample of 305 farmers and 77 cassava fields in Benin was selected for data collection. To account for potential selection bias associated with observable characteristics, we applied Propensity Score Matching (PSM). The results indicate that farmers who participated in the training demonstrated significantly higher levels of CMD knowledge and were more likely to adopt a greater number of management practices, which ultimately led to a reduction in the prevalence of the disease in their fields. However, CMD symptoms were still prevalent in the majority (61,04) of cassava farms, regardless of participation in the campaigns, due to the lack of healthy planting material and the abundance of whiteflies. These findings suggest that awareness campaigns can significantly improve farmers' knowledge and encourage behavioural changes in the identification and adoption of sustainable CMD management practices. It also shows the need to provide famers with healthy cuttings for more effective disease management.

Impact factor: 2.5



Cassava Mosaic Disease persistence: evidence from farmer adoption patterns of management practices in Benin

Dewanou Kant David Ahoya[a,b], Ettien Antoine Adjei[c], Serge Setondji Houedjissin[b], Jerôme Anani Houngue[b], Martine Zandjanakou-Tachin[d], Jacob Afouda Yabi[a], Eveline Marie Fulbert Windinmi Sawadogo-Compaore[e], Modeste Kan Kouassi[c], Fidèle Tiendrebeogo[c], Ousmane Ndoye[f], Justin Simon Pita[c], Corneille Ahanhanzo[b]

[a] Laboratory of Analysis and Research on Economic and Social Dynamics (LARDES), University of Parakou (UP), Parakou P.O. Box 123, Benin

[b] Central Laboratory of Plant Biotechnology and Crop Improvement (LCBVAP), University of Abomey-Calavi (UAC), Cotonou 01 B.P. 4521, Benin

[c] Central and West African Virus Epidemiology (WAVE), Scientific and Innovation Hub of Bingerville, Felix Houphouët-Boigny University (UFHB), Abidjan BP V34 Bingerville, the Republic of Côte d'Ivoire

[d] Research Unit in Horticultural Production and Green Space Management (URPHGEV), School of Horticulture and Green Space Development (EHAEV), National University of Agriculture (UNA), K´ etou P.O. Box 43, Benin

[e] Department of Natural Resource Management and Production Systems, Institute of Environment and Agricultural Research (INERA), Ouagadougou BP 7047, Burkina Faso

[f] CORAF, BIORISKS Project, 7, Avenue Bourguiba-B.P.48 Dakar, CP, 18523, Senegal

* Corresponding author. Laboratory of Analysis and Research on Economic and Social Dynamics (LARDES), University of Parakou (UP), Parakou P.O. Box 123,Benin. E-mail address: davidahoya13@gmail.com (D.K.D. Ahoya).

ARTICLE INFO

Keywords:

Cassava Mosaic Disease
Adoption
Management practices
Farmer behaviour
Benin

Scan to read full article

ABSTRACT

Cassava Mosaic Disease (CMD) remains a major constraint to cassava production in Sub-Saharan Africa despite extensive promotion of management practices. This study investigates the adoption and intensity of adoption of CMD management practices among 305 cassava farmers in southern Benin, using descriptive statistics and a Tobit regression model. Results show low overall adoption: only 9.84 % of farmers fully implemented all three recommended practices—use of certified disease-free cuttings, removal of infected plants, and adherence to optimal planting density. Key factors positively influencing adoption include participation in CMD-related training, disease knowledge, intercropping practices, larger farm size, and farmer age, while larger household size negatively affects adoption intensity. These findings highlight the need for integrated interventions combining farmer training, improved access to certified planting materials, intercropping promotion, and decentralized advisory services. Strengthening farmers' decision-making capacity and addressing economic constraints are critical for the sustainable management of CMD and the improvement of cassava productivity in Benin.

06

MDPI

Journal metrics

The Journal was founded in 2009. 16,805 articles published 8,030 articles cited 10 times or more 3.5 Current impact factor 3.7 5-year impact factor 7.7 CiteScore

Impact factor: 3.5

Insights into Novel Viral Threats in Sweetpotato from Burkina Faso: Characterisation of Unexplored Pathogens

Pakyendou E. Name [1,2], Florencia Djigma [2] , Ezechiel B. Tibiri [1,2], Fidèle Tiendrébéogo [1,2,3,*], Lassina Traoré [2], Angela O. Eni [3] and Justin S. Pita [3]

[1] Laboratoire de Virologie et de Biotechnologies Végétales, Institut de l'Environnement et de Recherches Agricoles (INERA), Ouagadougou 01 BP 476, Burkina Faso
[2] Laboratoire de Biologie Moléculaire et de Génétique (LABIOGENE), Université Joseph KI-ZERBO, Ouagadougou 03 BP 7021, Burkina Faso
[3] Central and West African Virus Epidemiology (WAVE), Pôle Scientifique et d'Innovation de Bingerville, Université Félix Houphouët-Boigny (UFHB), Bingerville 01 BP V34, Côte d'Ivoire

* Correspondence: fidele.tiendrebeogo@wave-center.org

ARTICLE INFO

Keywords:

alternative hosts; nanopore sequencing; sweetpotato; circular DNA viruses; satellites; Burkina Faso

Scan to read full article

ABSTRACT

Sweetpotato is a key staple crop in tropical and subtropical regions. Its vegetative propagation makes it a persistent reservoir, facilitating the emergence and spread of complex infections. Understanding its virome is crucial for disease management and food security. We investigated the sweetpotato virome in Burkina Faso using rolling circle amplification and Oxford Nanopore sequencing. Eight symptomatic leaf samples, previously undiagnosed using conventional methods, were analysed. Bioinformatic pipelines were employed followed by phylogenetic comparisons. Two viruses known to infect sweetpotato, namely sweet potato leaf curl virus (SPLCV) and sweet potato leaf curl deltasatellite 3 (SPLCD3), were consistently detected in all samples. Additionally, pepper yellow vein Mali virus (PepYVMV), cotton leaf curl Gezira alphasatellite (CLCuGeA) and cotton leaf curl Gezira betasatellite (CLCuGeB) were identified for the first time in this crop. Phylogenetic analysis confirmed their genetic proximity to isolates from tomato, okra and pepper. Their co-occurrence with SPLCV and SPLCD3 indicates a complex viral landscape that could influence disease severity. This study highlights the underestimated role of sweetpotato as a viral reservoir, influencing virus evolution and transmission. Further studies should assess their pathogenicity, co-infection dynamics and vector-mediated transmission to improve crop productivity.

Impact factor: 3.5

Identification and Full-Genome Characterisation of Genomoviruses in Cassava Leaves Infected with Cassava Mosaic Disease

Olabode Onile-ere [1,2,*], Oluwagboadurami John [2], Oreoluwa Sonowo [2], Pakyendou Estel Name [3]

Ezechiel Bionimian Tibiri [3], Fidèle Tiendrébéogo [3,4] , Justin Pita [4], Solomon Oranusi [1] and

Angela O. Eni [2,4,*]

[1] Department of Biological Sciences, Covenant University, Km 10 Idiroko Road, Ota 12212, Ogun State, Nigeria

[2] Central and West African Virus Epidemiology Program, Covenant University Hub, Km 10 Idiroko Road,
Canaan Land, Ota 12212, Ogun State, Nigeria

[3] Laboratory of Virology and Plant Biotechnology, Institute for the Environment and Agricultural
Research (INERA), Ouagadougou 01 BP 476, Burkina Faso

[4] WAVE Regional Center of Excellence for Transboundary Plant Pathogens,
Université Felix Houphouët-Boigny (UFHB), Abidjan 01 BPV 34, Côte d'Ivoire

* Correspondence: olabode.onile-ere@stu.cu.edu.ng (O.O.-e.); angela.eni@wave-center.org (A.O.E.)

ARTICLE INFO

Keywords:

Genomovirius;
CRESS-DNA virus;
viromics

ABSTRACT

This study identified and characterised three Genomoviruses during a circular DNA enriched sequencing project aimed at assessing the evolution of Cassava mosaic begomoviruses in Nigeria. Using a combination of rolling circle amplification, Oxford Nanopore Sequencing and targeted amplicon sequencing, three full-length Genomovirus genomes were recovered. The recovered genomes ranged from 2090 to 2188 nucleotides in length, contained two open reading frames (Rep and CP) in an ambisense orientation and shared between 84.81 and 95.37% nucleotide similarity with isolates in the NCBI GenBank repository. Motif analyses confirmed the presence of conserved rolling circle replication (RCR) and helicase motifs in all three isolates; however, one isolate lacked the RCR II motif. Phylogenetic inference using Rep and CP nucleotide sequences suggested that the isolates belonged to a divergent lineage within the Genomovirus family. These findings expand current knowledge of Genomovirus diversity and highlight the potential of cassava as a source for identifying novel CRESS-DNA viruses.

MDPI

Impact factor: 3

horticulturae

Detection of Cassava Mosaic Disease and Assessment of Selected Agronomic Traits of Cassava *(Manihot esculenta)*

Musa Decius Saffa [1,*], Alusaine Edward Samura [1], Mohamed Alieu Bah [2,*], Angela Obiageli Eni [3], Ezechiel Bionimian Tibiri [4], Adama Sagnon [4], Fidèle Tiendrébéogo [3], Justin Simon Pita [3], Prince Emmanuel Norman [5] and Raymonda Adeline Bernardette Johnson [1]

[1] Department of Crop Protection, School of Agriculture and Food Sciences, Njala University, Njala Campus, Njala 1313, Sierra Leone; alusaine.samura@wave-center.org (A.E.S.); raymonda.johnson@yahho.com (R.A.B.J.)

[2] Department of Crop Science, School of Agriculture and Food Sciences, Njala University, Njala Campus, Njala 1313, Sierra Leone

[3] Regional Center of Excellence for Transboundary Plant Pathogens, Central and West African Virus Epidemiology (WAVE), Pôle Scientifique et d'Innovation, Université Félix Houphouët-Boigny, Abidjan BPV 34, Côte d'Ivoire; angela.eni@wave-center.org (A.O.E.);
fidele.tiendrebeogo@wave-center.org (F.T.); justin.pita@wave-center.org (J.S.P.)

[4] Laboratoire de Virologie et de Biotechnologies Végétales, Institut de l'Environnement et de Recherches Agricoles (LVBV/INERA), CNRST, Ouagadougou 7047, Burkina Faso; ezechiel.tibiri@ujkz.bf (E.B.T.);
sagnonyadama@gmail.com (A.S.)

[5] Germplasm Enhancement and Seeds System, Sierra Leone Agricultural Research Institute (SLARI), Tower Hill, Freetown PMB 1313, Sierra Leone; norman.prince64@gmail.com

* Correspondence: m.saffa21@yahoo.com (M.D.S.); abah@njala.edu.sl (M.A.B.)

ABSTRACT

A study was conducted in Sierra Leone to identify cassava plants that are asymptomatic and symptomatic to cassava mosaic disease (CMD) and collect planting materials for field trial establishment; determine the prevalence of CMD caused by African cassava mosaic virus (ACMV) and East African cassava mosaic virus (EACMV) using the Nuru App and virus indexing techniques; and assess selected agronomic traits in cassava. A total of 80 cassava farms spanning four provinces (Southern, Eastern, Northern, and North-West) were surveyed in April 2022. Findings showed that the cassava variants of the experiment and locations significantly ($p < 0.001$) affected CMD incidence, severity, growth, and fresh storage root yield traits. The CMD incidence (87.0%) and whitefly abundance (144.8) were highest, and the CMD severity was moderate (4.0) for the plants derived from cuttings obtained from symptomatic Cocoa mother plants, while plants derived from cuttings of improved mother plants exhibited no visible symptoms of the disease and the lowest population (45.1) of whiteflies. The Nuru app is inefficient for phenotypically detecting CMD at 3 months after planting (MAP), while at 6, 9 and 12 MAP, the app efficiently detected the disease using a molecular analysis technique. Resistant, non- diseased plants derived from cuttings obtained from SLICASS 4 mother plants produced the highest fresh storage root yield (54.9 t ha −1). The highest storage root yield loss was recorded in the plants obtained from cuttings of symptomatic variety Cocoa mother plants harvested at Matotoka grassland ecology, Bombali District (90.2%), while those harvested from cuttings of asymptomatic variety Cocoa mother plants grown at the four test environments had a similar storage root yield loss ranging from 40.3 to 46.2%. Findings suggest the importance of genetic variability, environmental adaptation, utilization of diseased-free materials, and phytosanitation as disease management strategies for increased production. These findings provide important insights into the distribution, impact, and spread of CMD and whitefly abundance in the studied areas in Sierra Leone that could be exploited for cassava production, productivity, conservation, and population improvement.

ARTICLE INFO

Keywords:

disease detection; whitefly; agronomic traits; yield loss; cassava genotypes

Scan to read full article

Impact factor: 4.1

plants

Identification and Distribution of Begomoviruses Infecting Cassava Fields in Sierra Leone

Musa Decius Saffa [1,*] , Alusaine Edward Samura [1] ,Ezechiel B. Tibiri [4], Saïdou Zongo [4], William J.-L. Amoakon [3] ,Prince Emmanuel Norman [5] , Mohamed Alieu Bah [2], Angela Obiageli Eni [3], Fidèle Tiendrébéogo [3] , Justin Simon Pita [3]

[1] Department of Crop Protection, School of Agriculture and Food Sciences, Njala University, Njala Campus, Njala 1313, Sierra Leone; alusaine.samura@wave-center.org (A.E.S.); raymonda.johnson@yahho.com (R.A.B.J.)

[2] Department of Crop Science, School of Agriculture and Food Sciences, Njala University, Njala Campus, Njala 1313, Sierra Leone

[3] Regional Center of Excellence for Transboundary Plant Pathogens, Central and West African Virus Epidemiology (WAVE), Pôle Scientifique et d'Innovation, Université Félix Houphouët-Boigny, Abidjan BPV 34, Côte d'Ivoire; angela.eni@wave-center.org (A.O.E.);

fidele.tiendrebeogo@wave-center.org (F.T.); justin.pita@wave-center.org (J.S.P.)

[4] Laboratoire de Virologie et de Biotechnologies Végétales, Institut de l'Environnement et de Recherches Agricoles (LVBV/INERA), CNRST, Ouagadougou 7047, Ouagadougou 04 BP 8645, Burkina Faso; ezechiel.tibiri@ujkz.bf (E.B.T.);

zongosaidou642@gmail.com (S.Z.)

[5] Germplasm Enhancement and Seeds System, Sierra Leone Agricultural Research Institute (SLARI), Tower Hill, Freetown PMB 1313, Sierra Leone; norman.prince64@gmail.com

* Correspondence: m.saffa21@yahoo.com (M.D.S.); abah@njala.edu.sl (M.A.B.)

ABSTRACT

A dearth of knowledge exists on identifying the begomoviruses and distributing cassava mosaic viruses across key cassava-growing regions of Sierra Leone. The study aimed to identify and map the distribution of cassava mosaic disease (CMD)-associated viruses in farmers' fields in Sierra Leone. Cassava (Manihot esculenta Crantz) leaf samples were collected in 109 smallholder farms during a geo-referenced survey conducted from 10th May to 5th June 2024. Molecular diagnostics were carried out to identify the viral strains associated with CMD. Findings revealed that infection by stem cutting was more pre- dominant in the south, east, north, and northwest regions than in the west region. In contrast, infection by whitefly was predominant in the west, north, and northwest regions. PCR screening of 426 samples coupled with sequence analysis revealed the presence of African cassava mosaic-like (ACMV-like) viruses, and East African cassava mosaic-like (EACMV-like) viruses as single infections at 78.1% and 1.3%, respectively. Co-infections of ACMV-like and EACMV-like viruses were detected in 20.6% of the tested samples. In addi- tion, 70.6% of the samples positive for EACMV-like virus (single and mixed infections) were found to be positive for East African cassava mosaic Cameroon virus (EACMCMV). The ACMV and co-infection of ACMV and EACMV viruses were present in all regions, while EACMCV was detected in all regions except the western area. The results indicate more prevalence of the EACMCMV variant in Sierra Leone. This study suggests utilization of participatory surveillance and good agronomic practices to manage CMD in Sierra Leone.

ARTICLE INFO

Keywords:

epidemiology; viruses; East African cassava mosaic (EACMV); African cassava mosaic virus (ACMV); Manihot esculenta

Impact factor: 3.5

viruses

Reinfection Dynamics of Disease-Free Cassava Plants in Three Agroecological Regions of Côte d'Ivoire

John Steven S. Seka [1,2,*] , Justin S. Pita [1,2], Modeste K. Kouassi [1,2], William J. -L. Amoakon [2], Bekanvié S. M. Kouakou [1,2] , Mariam Combala [1,2], Daniel H. Otron [1,2] , Brice Sidoine Essis [3], Konan Evrard B. Dibi [3], Angela O. Eni 2, Nazaire K. Kouassi [1,2] and Fidèle Tiendrébéogo [2],*

[1] Laboratoire d'Innovation Pour la Santé des Plantes, UFR Biosciences, Université Félix Houphouët-Boigny, Abidjan 22 BP 582, Côte d'Ivoire

[2] The Central and West African Virus Epidemiology (WAVE) for Food Security Program, Pôle Scientifique et D'innovation, Université Félix Houphouët-Boigny, Bingerville 22 BP 582, Côte d'Ivoire

[3] Centre National de Recherche Agronomique (CNRA), Bouaké 01 BP 1740, Côte d'Ivoire

* Correspondence: steveseka7@gmail.com (J.S.S.S.); fidele.tiendrebeogo@wave-center.org (F.T.)

ABSTRACT

ARTICLE INFO

Keywords:

cassava; begomovirus; virus-free plantlets; reinfection dynamics; whiteflies; cassava mosaic disease

Cassava mosaic disease (CMD) is caused by begomoviruses and can result in yield losses of up to 90% in susceptible varieties. Using disease-free planting material from in vitro cultures is one of the most effective ways of controlling this disease. A CMD epidemiological assessment was conducted in fields established with disease-free plantlets in Bouaké, Dabou, and Man, selected for their contrasting agroecological and CMD prevalence conditions. Virus and whitefly species characterisation was performed using PCR and sequencing. CMD incidence and severity were lowest at the Man site and highest at the Dabou site. Although whitefly abundance was relatively low at the Man and Bouaké sites compared to the Dabou site, they were a significant factor in the spread of the disease. While all resistant varieties remained asymptomatic, susceptible and tolerant varieties became infected, and some tolerant varieties were able to recover from the disease. Molecular analyses revealed the presence of two viral species: Begomovirus manihotis (ACMV) and Begomovirus manihotiscameroonense (EACMCMV). No viral infection was detected 4 weeks after planting (WAP). Cases of single infection and double infection were observed at 12 and 20 WAP. Also, no double infections were found at the Man site, in contrast to the Bouaké site (12 WAP: 2.36%) and Dabou site (12 WAP: 2.59%; 20 WAP: 5.76%). EACMCMV was found in a single infection in Bouaké (12 WAP: 1.39%) and Man (20 WAP: 0.66%). The whitefly species Bemisia tabaci and Bemisia afer were most commonly found feeding on all cassava varieties. A high diversity of whitefly species was observed in Bouaké and Dabou compared to Man. Furthermore, the Bemisia tabaci species identified in this study was found to be able to transmit ACMV and EACMCMV viruses. These highlights would contribute to improving CMD management and control strategies.

MDPI Impact factor: 3.5 viruses

Molecular Identification of the Viruses Associated with Sweetpotato Diseases in Côte d'Ivoire

El Hadj Hussein Tapily [1,2], Justin S. Pita [1,2], William J.-L. Amoakon [2] ,Nazaire K. Kouassi [1,2] and Fidèle Tiendrébéogo [2,*]

[1] Laboratoire d'Innovation pour la Santé des Plantes, UFR Biosciences,
Université Félix Houphouët-Boigny (UFHB), Abidjan 22 BP 582, Côte d'Ivoire
[2] The Central and West African Virus Epidemiology (WAVE) for Food Security Program,
Pôle Scientifique et d'Innovation, Université Félix Houphouët-Boigny (UFHB),
Abidjan 22 BP 582, Côte d'Ivoire

* Correspondence: fidele.tiendrebeogo@wave-center.org

ABSTRACT

Sweetpotato (Ipomoea batatas) is a staple crop of strategic importance in West Africa, particularly in Côte d'Ivoire. However, its productivity is increasingly under threat due to viral diseases. Given the lack of updated epidemiological data over the past three decades, a nationwide survey was conducted in September 2023 across 94 fields in 83 locations covering seven agroecological zones of the country. A total of 221 symptomatic and asymptomatic leaf samples were analyzed using PCR for DNA viruses and RT-PCR for RNA viruses. The overall viral incidence rate calculated was 65.61%, with significant regional variations (35–97.18%, $p < 0.001$) and notable differences in the severity of symptoms ($p = 0.0095$). Agroecological zone I was the most affected, while agroecological zones IV and V were the least impacted. Four viruses were identified: cucumber mosaic virus (CMV), sweet potato leaf curl virus (SPLCV), sweet potato feathery mottle virus (SPFMV), and sweet potato chlorotic stunt virus (SPCSV). No badnaviruses were found. CMV was the most common virus found in single infections (43.44%), followed by SPLCV (5.43%). SPFMV and SPCSV were only observed in mixed infections, particularly CMV/SPLCV (14.03%) and CMV/SPFMV (1.81%). Two triple infections were also detected: SPFMV/SPCSV/CMV and SPFMV/SPLCV/CMV. In total, 34 partial coat protein sequences were obtained (28 SPLCV, 4 SPFMV, 1 CMV, 1 SPCSV). Phylogenetic analysis revealed a high similarity between SPLCV isolates characterized in Côte d'Ivoire and those from Burkina Faso, Europe (Spain, Italy), and the Americas (USA, Puerto Rico) with nucleotide identity values ranging from 98% to 100%. The Côte d'Ivoire SPCSV sequence showed 97.92% nucleotide identity with European isolates, whereas SPFMV sequences exhibited greater diversity (77–89% identity) but clus- tered within the West African lineage. Sweetpotato viral diseases were detected mostly in mixed-cropping fields (66.85%). This work provides the first epidemiological update on sweetpotato viral diseases since 1987 and the first molecular evidence of the nationwide presence of SPLCV and SPCSV in Côte d'Ivoire.

ARTICLE INFO

Keywords:
Ipomoea batatas; nationwide survey; viruses; epidemiology; Côte d'Ivoire

Scan to read full article

Impact factor: 3.1

BioTech

Enhancing In Vitro Regeneration in Three Sweet Potato Genotypes: Interplay Between Disinfectant, Explant Age, and Genotype

El Hadj Hussein Tapily [1,2,*], Kan Modeste Kouassi [1,2,*], Marius Konan Kouassi [2], John Steven S. Seka [1,2], Fidèle Tiendrébéogo [2] and Justin S. Pita [1,2]

[1] Unité de Formation et de Recherche Biosciences, Université Félix Houphouët-Boigny (UFHB), Abidjan 22 BP 582, Côte d'Ivoire; steveseka7@gmail.com (J.S.S.S.); justin.pita@wave-center.org (J.S.P.)

[2] The Central and West African Virus Epidemiology (WAVE) for Food Security Program, Pôle Scientifique et d'Innovation, Univesité Félix Houphouët-Boigny (UFHB), Bingerville 01 BP V34, Côte d'Ivoire; marius.kouassi@wave-center.org (M.K.K.); fidele.tiendrebeogo@wave-center.org (F.T.)

* Correspondence: hussein_tapily@yahoo.fr (E.H.H.T.); modeste.kouassi@wave-center.org (K.M.K.)

ARTICLE INFO

Keywords:

ipomea batatas; sodium hypochlorite; mercuric chloride; genotype variability

Scan to read full article

ABSTRACT

Regenerating sweet potato from field-derived plant material requires careful management of several critical factors, including the effectiveness of the disinfectant, the age of the explant, and the genotype used. In this context, establishing a reliable aseptic protocol is essential for successful in vitro culture. This study aimed to assess the effects of two disinfectants (sodium hypochlorite and mercuric chloride), three sweet potato genotypes (Nakabo, Boyapleu, and Irene), and three explant ages (2, 3, and 4 weeks) on clean culture establishment and regeneration efficiency from nodal explants. The findings revealed that regeneration success is significantly influenced by the type and concentration of disinfectant, explant age, and genotype. Treatment with 10% sodium hypochlorite markedly reduced contamination, achieving clean culture and regeneration rates of 75.72 ± 3.36% and 86.83 ± 3.02%, respectively, regardless of explant age. In contrast, higher concentrations of mercuric chloride induced necrosis in the explants. The highest clean culture rate (93.82 ± 1.16%) was observed in 3-week-old explants, which also showed a regeneration rate of 54.93 ± 3.19%. Furthermore, the Boyapleu and Irene genotypes demonstrated good suitability for in vitro culture, whereas the Nakabo genotype performed poorly under the tested conditions.

Impact factor: 3.6

agriculture

Enhancing Farmers' Capacity for Sustainable Management of Cassava Mosaic Disease in Côte d'Ivoire

Ettien Antoine Adjéi [1,2,*], Kassoum Traoré [1,3], Eveline M. F. W. Sawadogo-Compaore [4], Bekanvié S. M. Kouakou [2], John Steven S. Séka [2], Dèwanou Kant David Ahoya [5], Kan Modeste Kouassi [2], Nazaire K. Kouassi [2] and Justin Simon Pita [2,*]

[1]UFR Sciences Sociales, Département de Sociologie, Université Peleforo GON COULIBALY,
Korhogo BP 1328, Côte d'Ivoire; traorekassfr@yahoo.fr
[2]Regional Center of Excellence for Transboundary Plant Pathogens, Central and West African Virus
Epidemiology (WAVE), Pôle Scientifique et D'innovation, Université Félix Houphouët-Boigny (UFHB),
Abidjan 22 BP 582, Côte d'Ivoire; bekanviemarie@yahoo.fr (B.S.M.K.); steveseka7@gmail.com (J.S.S.S.);
modeste.kouassi@wave-center.org (K.M.K.); nazaire.kouassi@wave-center.org (N.K.K.)
[3]Centre Ivoirien de Recherches Economiques et Sociales (CIRES), Abidjan 08 08 BP 1295, Côte d'Ivoire
[4] Institut de l'Environnement et de Recherches Agricoles (INERA),
Ouagadougou 04 04 BP 8645, Burkina Faso; compeve@yahoo.fr
[5] Laboratory for Analysis and Research on Economic and Social Dynamics (LARDES), University of
Parakou (UP), Parakou P.O. Box 123, Benin; davidahoya13@gmail.com

* Correspondence: ettienadjei31@gmail.com (E.A.A.); justin.pita@wave-center.org (J.S.P.);
Tel.: +225-0749107525 (E.A.A.); +225-0544825605 (J.S.P.)

ARTICLE INFO

Keywords:

awareness campaign; CMD knowledge; impact assessment; PSM; Tobit

ABSTRACT

Cassava Mosaic Disease (CMD) is a major constraint to cassava production in Côte d'Ivoire, causing significant yield and income losses for smallholder farmers. Despite its high prevalence, farmers' knowledge and understanding of the disease remain limited. To address this issue, the Central and West African Virus Epidemiology (WAVE) Regional Center of Excellence provided capacity building for farmers in the major cassava growing regions. This study assesses the impact of the WAVE's trainings and awareness campaigns on farmers' knowledge of the disease and the management methods they adopted. Mixed socio-agronomic data were collected from 290 farmers, and CMD epidemiological parame- ters were assessed in 82 farms. Data were analysed using propensity score matching (PSM), followed by a Tobit regression model to assess the determinants and intensity of adoption of CMD management practices, using Stata. The results showed that trained farmers had a better understanding of CMD compared to untrained farmers. On average, trained farmers adopted 2.36 disease management practices (DMPs) compared to 1.55 DMPs for untrained farmers. Participation in WAVE's training sessions and a sound knowledge of CMD positively influenced both the adoption and intensity of adoption of DMPs. However, there was no significant difference in CMD incidence between beneficiary areas (54.55%) and non-beneficiary areas (54.95%), likely due to the unavailability of disease-free planting material, inadequate agricultural practices, and high populations of whiteflies (Bemisia tabaci). This study shows the importance of awareness campaigns in the sustainable management of crop diseases in general and CMD in particular and suggests the need to train farmers on disease management and provide them with healthy planting materials.

Impact factor: 1.6

International Journal of Plant Biology

Genetic Characterization and Variability of Cassava (Manihot esculenta) Accessions Cultivated in Southwest and North Central Nigeria Using Agromorphological Markers

Isaac O. Abegunde [1,2,*], Oghenevwairhe P. Efekemo [1,3], Olabode Onile-Ere [1,3],

Folashade Otitolaye [1,3], Olusegun A. Oduwaye [4], Thomas O. Fabunmi [5], Emmanuel O. Idehen [1,4] ,

Justin S. Pita [6], Fidèle Tiendrébéogo [6], Titus Alicai [7] and Angela O. Eni [1,6,*]

[1] Central and West African Virus Epidemiology Program, Covenant University Hub, Km. 10 Idiroko Road, Canaan Land, P.M.B 1023, Ota 112233, Ogun State, Nigeria
[2] Centre of Excellence in Agricultural Development and Sustainable Environment, Federal University of Agriculture, Alabata Road, P.M.B 2240, Abeokuta 110115, Ogun State, Nigeria
[3] Department of Biological Sciences, Covenant University, Km. 10, Idiroko Road, P.M.B 1023, Ota 112233, Ogun State, Nigeria
[4] Department of Plant Breeding and Seed Technology, Federal University of Agriculture, Alabata Road, P.M.B 2240, Abeokuta 110115, Ogun State, Nigeria
[5] Department of Plant Physiology and Crop Production, Federal University of Agriculture, Alabata Road, P.M.B 2240, Abeokuta 110115, Ogun State, Nigeria
[6] Regional Center of Excellence for Transboundary Plant Pathogens (Central and West African Virus Epidemiology, WAVE), Université Felix Houphouët-Boigny (UFHB), Abidjan 01 BPV 34, Côte d'Ivoire
[7] National Agricultural Research Organization (NARO), National Crops Resources Research Institute, Kampala P.O. Box 7084, Uganda

* Correspondence: ioabegunde@gmail.com (I.O.A.); angela.eni@wave-center.org (A.O.E.)

ABSTRACT

Understanding the genetic variability among Nigerian cassava accessions is a crucial prerequisite for its improvement. The objective of this study was to estimate the genetic variability among 477 cassava accessions and to classify them based on their genetic simi- larities for effective utilization in breeding programs. The accessions were evaluated at the Federal University of Agriculture, Abeokuta experimental site from 2023–2024, using an augmented randomized complete block design with two checks (TME 419 and NR 87184). Agromorphological descriptors were collected at 3-month intervals for 12 months. Broad sense heritability and genetic advance as percent of mean (GAM) were high, indicating that the overall phenotypic expressions observed were largely influenced by genetic factors. Multiple correspondence analysis (MCA) showed that petiole color, number of leaf lobes, color of leaf veins, and parenchyma contributed the most to the overall variability observed in the study population. Principal component analysis (PCA) identified petiole length, length of leaf lobe, width of leaf lobe, and plant height as primary contributors to the overall phenotypic variations observed in the population. Hierarchical clustering of accessions using Euclidean distance revealed two and three clusters based on qualitative and quantitative traits respectively. This study has shown the existence of wide genetic variations in several cassava traits, providing a valuable resource for breeding programs.

ARTICLE INFO

Keywords:

genetic diversity; morphological identification; food security; climate-smart crops; crop improvement

07

SPRINGER NATURE Link

Journal metrics
Submission to first decision (median) 17 days
Downloads 110.4k (2024)

SPRINGER NATURE Link

Cassava mosaic disease in Burkina Faso: epidemiological aspects and disease management perspectives

Seydou Sawadogo[1,2], Fidèle Tiendrébéogo[1,2,3*], Ezechiel B. Tibiri1,2, Pakyendou E. Name[1,2], Florencia Djigma[2], Lassina Traoré[2], Justin S. Pita[3] and Angela O. Eni[3]

[1]Laboratoire de Virologie et de Biotechnologies Végétales, Institut de l'Environnement et de Recherches Agricoles (INERA), Ouagadougou, Burkina Faso
[2]Laboratoire de Biologie Moléculaire et de Génétique (LABIOGENE), Université Joseph Ki-Zerbo, Ouagadougou, Burkina Faso
[3]Pôle scientifique et d'innovation de Bingerville, Central and West African Virus Epidemiology (WAVE), Université Félix Houphouët-Boigny (UFHB), Bingerville, Côte d'Ivoire

*Correspondence: Fidèle Tiendrébéogo fidele.tiendrebeogo@wave-center.org

ABSTRACT

ARTICLE INFO

Keywords:

Cassava mosaic begomoviruses, Classical surveillance, Surveillance limitations, Incidence, Burkina faso

Cassava Mosaic Disease (CMD) is the main biotic constraint to cassava production in West Africa. In Burkina Faso, efforts are underway to manage it sustainably using classical surveillance, including field monitoring and laboratory diagnosis. However, this method has significant limitations that make it difficult to address early management. The aim of this study was to provide recent epidemiological data on CMD, while highlighting the limitations of classical surveillance. Fields monitoring and laboratory diagnosis took 14 months for the 2020 survey and 6 months for the 2022 survey year. A total of 4,680 plants from 156 fields were assessed in 2020 and 3,810 plants from 127 fields in 2022. The overall mean incidences were 9.46% and 3.33% in 2020 and 2022, respectively. The highest incidences were found in the Centre-Ouest region (23.13%) in 2020 and in the Plateau-Cetral region (32.38%) in 2022. The Plateau-Central region was identified as a CMD new outbreak. In 2020 survey, African cassava mosaic virus (ACMV) rate was 93.95%, while East African cassava mosaic virus (EACMV) was 3.69%. In the 2022 survey, ACMV alone was detected in 75.95%, in double infection with EACMV in 16.46%, and triple infection with EACMV and East African cassava mosaic Cameroon virus (EACMCMV) in 5.06%. This study showed that classical surveillance is a robust method, but extremely time consuming to anticipate early management of CMD. Similarly, classical surveillance required significant financial resources for its implementation. Given these constraints, the implementation of participatory surveillance involving farmers, extension agents, breeders, plant protection services, and researchers could help in CMD management efforts.

Scan to read full article

08

WILEY Online Library

Métriques de la revue
Publication
2024 Vues de texte intégral : 110 713
2024 Nombre total d'articles publiés : 85

WILEY Online Library

Impact factor: 4.1

New Disease Reports

First report of sugarcane white streak virus infecting sugarcane *(Saccharum spp.)* in Côte d'Ivoire

M. L. Kouman[1,2], Justin S. Pita[1,2], E. B. Tibiri[3], M. B. Boua[4], M. Ouattara[4], G. Yeo[5], N. K. Kouassi[1,2], A.O. Eni[1], Fidèle Tiendrébéogo[1]

[1]The Central and West African Virus Epidemiology (WAVE) for Food Security Program, Pôle Scientifique Et d'Innovation, Université Félix Houphouët-Boigny (UFHB), Abidjan, 22 BP 582, Côte d'Ivoire

[2]Laboratoire de Biotechnologie, Agriculture et Valorisation des Ressources Biologiques, UFR Biosciences, Université Félix Houphouët-Boigny, Bingerville, Côte d'Ivoire

[3]Laboratoire de Virologie et de Biotechnologies Végétales, Institut de l'Environnement et de Recherches Agricoles, Centre National de la Recherche Scientifique et Technologique,Ouagadougou, Burkina Faso

[4]SUCAF-CI, Ferkessédougou, Côte d'Ivoire

[5]National Centre for Agronomic Research, Sugarcane Programme, Phytopathology Laboratory, Ferkessédougou, Côte d'Ivoire

* Correspondence: fidele.tiendrebeogo@wave-center.org

ABSTRACT

ARTICLE INFO

Keywords:

disease surveys,- mastrevirus, nanopore sequencing

Scan to read full article

Sugarcane ***(Saccharum spp.)*** is an important interspecific hybrid crop grown for sugar and ethanol production in tropical and subtropical regions around the world. However, its vegetative propagation makes it vulnerable to viral diseases which pose a serious threat to crop yield and quality. Several viruses belonging to species in the genus ***Mastrevirus***, family ***Geminiviridae*** are known to infect sugarcane including maize streak virus, saccharum streak virus, sugarcane chlorotic streak virus, sugarcane streak Egypt virus, sugarcane streak Reunion virus, sugarcane streak virus, sugarcane striate virus and sugarcane white streak virus (SWSV), (Boukari et al., 2020).

In Côte d'Ivoire, sugarcane streak mosaic virus (SCSMV; ***genus Poacevirus***, family ***Potyviridae***) is reported as an emerging virus affecting a wide range of sugarcane varieties in the country (Daugrois et al., 2020; Sorho et al., 2020). With the aim of developing a holistic method for controlling its spread on areas cultivated by SUCAF-CI (a sugar company in Côte d'Ivoire), we undertook an inventory of the viruses present on its sites. Twenty-four samples were collected from SUCAF-CI germplasm collections and nurseries, and leaves were analysed by rolling circle amplification with random hexamers followed by nanopore sequencing using a MinION device as described by Ben Chehida et al. (2021). One sugarcane leaf sample (SC_BC38) with peculiar symptoms (Figure 1) collected in a sugarcane field of the Centre National de Recherche Agronomique of Côte d'Ivoire, located c. 50 kilometers from SUCAF-CI, was also screened.

09

UNIVERSITAS LAMPUNG

in collaboration with:

Assessment of cassava mosaic disease (CMD) intensity and whitefly *(Bemisia tabaci)* population in Cameroon based on field surveys

Joseph Aime Lauryn Bahoya[1,4], Lewis Dopgima Levai[1], Patrick Fogang Kenfack[1,2], Ekwa Yawa Monono[1], Desmond Neba Ngwa[1], Fidèle Tiendrebeogo[5], François Tchoumbougnang[4], Nicolas Niemenak[3], Angela Obiageli Eni[5], Justin Simon Pita[5] & Oumar Doungous[1]

[1]The Central and West African Virus Epidemiology (WAVE), Biotechnology Laboratory, Ekona Regional Research Centre, Institute of Agricultural Research for Development, Buea, Cameroon 25

[2]Central Entomology Laboratory, Mbalmayo Regional Research Centre, Institute of Agricultural Research for Development, Yaoundé, Cameroon 2123

[3]Plant Physiology and Biochemistry Laboratory, Department of Biological Science, Higher Teachers Training, College of Yaoundé,Yaoundé, Cameroon 47

[4]Biochemistry Laboratory, Faculty of Science, University of Douala, Douala, Cameroon 24157

[5]Regional Center of Excellence for Transboundary Plant Pathogens, Central and West African Virus Epidemiology (WAVE), Pôle Scientifique et d'Innovation, Université Félix Houphouët-Boigny, Abidjan BPV 34, Côte d'Ivoire

Corresponding author:
Oumar Doungous (doungous.oumar@wave-center.org)

ABSTRACT

ARTICLE INFO

Keywords:

Bemisia tabaci, cassava mosaic geminivirus, CMD symptoms, epidemiology

Cassava mosaic disease (CMD) remains a major constraint to cassava (***Manihot esculenta*** Crantz) production in Cameroon. This study aimed to generate updated epidemiological data on CMD across the country. Surveys were conducted in 342 fields across the ten administrative regions of Cameroon between January and September 2022, following a standardized protocol adopted by all fourteen countries participating in the Central and West African Virus Epidemiology for Food Security (WAVE) program. In each field, 30 plants were assessed for CMD incidence, severity, whitefly population, and mode of infection. CMD symptoms were observed in all ten regions. The overall mean CMD incidence was 54.72%, with a mean severity score of 2.39. Incidence, severity, and whitefly populations varied significantly among regions. The South Region recorded the highest mean incidence (74.34%), while the Far North had the lowest (18.97%). The Adamawa Region exhibited the highest mean severity (2.63), whereas the South West Region had the lowest (2.19). Whitefly abundance per plant was greatest in the South West (21.44) and lowest in the Far North (0.40). PCR amplification and sequencing confirmed the presence of cassava mosaic geminiviruses (CMGs) in leaf samples. A positive correlation was detected between mean whitefly abundance and CMD incidence, while altitude was negatively correlated with whitefly numbers. Both CMD incidence and whitefly populations were higher in intercropped fields than in monocropped fields. Notably, intercropping cassava with maize reduced whitefly populations, while intercropping with sweet potato lowered CMD incidence. The primary source of CMD infection was the use of infected cuttings. These findings provide valuable insights for the development of targeted interventions and improved management strategies for CMD in Cameroon.

Scan to read full article

wave-center.org

Central And West African Virus Epidemiology

WAVE

For Food Security