

The Global Journey of Cassava Mosaic Disease: Understanding Its Origin to Impact and Solutions

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Cassava (*Manihot esculenta* Crantz) is a woody shrub that belongs to the Euphorbiaceae family. Cassava was originated along the southern edge of the Brazilian Amazon and was domesticated by indigenous South Americans approximately 12,000–17,000 years ago (Olsen & Schaal, 1999) and also commonly known Brazilian arrow root, manioc, tapioca, or yucca. The crop was introduced to Africa by Portuguese traders in 1558 and brought to Asia by Europeans from South America between the late eighteenth century and early nineteenth century and extensively cultivated in the 20th century in the Philippines, India, Indonesia and later to the rest of Asia (i.e., Malaysia, Thailand, Vietnam and China) (Malik et al., 2020). Cassava is highly efficient in carbohydrate produc-

tion, yielding 250×10^3 calories/ha/day, which surpasses other staple crops such as rice (176×10^3), wheat (110×10^3), maize (200×10^3), and sorghum (114×10^3) (Adebayo, 2023). Cassava is grown on about 29.95 million hectares worldwide, with the majority cultivated in Africa (60.9%), followed by Asia (29.4%) and America (9.6%), yielding over 319 million tons of fresh roots. In India, cassava is grown on roughly 1.66 lakh hectares, producing about 59.38 lakh tonnes, with an average yield of 35.77 tonnes per hectare (FAOSTAT, 2023). It is an essential raw material for starch and sago industries and is also used in animal, poultry, and fish feed. Recognized as a crucial food security crop, its global production has significantly increased from around 124 million tons in 1980 to 278 million tons in 2018 (Bhargava et al., 2024). Cassava is often referred to as a "famine crop" due to its ability to thrive in poor soils and tolerate drought and acidity. However, the increasing prevalence of diseases and pests poses a serious threat to its productivity and the overall competitiveness of the cassava industry. Among these challenges, plant viruses significantly impact global crop yields.

Amongst all the viral diseases of cassava, Cassava mosaic disease caused by Cassava mosaic virus is one of the significant among them. Cassava mosaic disease is caused by several Cassava mosaic Geminiviruses across the world, which belong to the family Geminiviridae and genus Begomovirus.

Origin of Cassava mosaic virus in World and India:

Cassava mosaic disease (CMD) was first identified in 1894 in the Usambara Mountains of north-east Tanzania, with its symptoms documented by Warburg (Warburg, 1894). Initially called "krauselkrankheit", it was later

recognized as a viral disease by Zimmermann in 1906. The pathogen, originally named Cassava latent virus was sequenced and reclassified as African cassava mosaic virus (ACMV) in the early 1980s. Over time, CMD spread across Africa, Madagascar, Seychelles and parts of Asia, including Java and India.

In India, CMD was first reported in Kerala in 1956 (Abraham, 1956) and was later confirmed by Malathi et al. in 1985. Since then, the disease has spread across Southern India wherever cassava is grown. In 1993, scientists successfully cloned and sequenced the virus, naming it Indian cassava mosaic virus (ICMV). Later, in 2002, a distinct variant called Sri Lankan cassava mosaic virus (SLCMV) was identified in Sri Lanka, and by 2005, it was detected in Kerala as well. Researches in Tamil Nadu has revealed infections with SLCMV, with some plants showing mixed infections of SLCMV and ICMV, raising concerns about its continued impact on cassava production in India.

Cassava Mosaic Geminivirus Species Worldwide:

Cassava mosaic disease is caused by a group of about eleven Cassava mosaic geminivirus (CMG) species, with nine occurring in Africa and two in India, such as

- African cassava mosaic virus (ACMV)
- East African cassava mosaic virus (EACMV)
- South African cassava mosaic virus (SACMV)
- East African cassava mosaic Cameroon virus (EACMCV)
- East African cassava mosaic Malawi virus (EACMMV)
- East African cassava mosaic Zanzibar virus (EACMZV)
- East African cassava mosaic Kenya virus (EACMKV)
- Cassava mosaic Madagascar virus (CMMGV)

- African cassava mosaic Burkina Faso virus (AC-MBFV)
- Indian cassava mosaic virus (ICMV)
- Sri Lankan cassava mosaic virus (SLCMV).

Regardless of the viral species involved, CMD manifests through distinct symptoms that severely impact plant health and yield. Cassava mosaic disease (CMD) causes characteristic symptoms such as mottling, yellow mosaic coloration, leaf deformation, reduced leaflet size, crumpled leaves, and overall stunting of the plant. CMD infection can be seen in the cassava plants, illustrating its effect in the field, as depicted in the Figure.



Cassava plants infected with Cassava mosaic disease on the field

The Spread of Cassava Mosaic Disease (CMD) Over Time

A) Early History and Spread in East Africa (1894–1940s)

Following the first report of Cassava Mosaic Disease (CMD) in 1894 in the Usambara Mountains of northeast Tanzania, scattered observations of the disease continued in the early 1900s, suggesting its gradual spread within East Africa. By 1910s, symptoms resembling CMD were noted in other parts of East Africa, likely spreading through infected cassava cuttings and whitefly (*Bemisia tabaci*) transmission. In the 1920s, CMD was officially recorded in Uganda, marking its expansion beyond Tanzania and

raising concerns about its impact on cassava production in the region, followed by a regional epidemic in the 1930s and early 1940s.

B) Global Expansion and Scientific Understanding (1950s–1990s)

By the 1950s, Cassava Mosaic Disease (CMD) had spread from its East African origins into West and Central Africa, establishing itself as a major agricultural threat. In 1956, India reported its first CMD case in Kerala, caused by the Indian cassava mosaic virus (ICMV), marking the disease's expansion beyond Africa. During the 1970s, the African cassava mosaic virus (ACMV) was first identified in Nigeria and soon became the most widespread cassava mosaic begomovirus across West and Central Africa, affecting countries like Ghana, Togo, Cameroon, Ivory Coast, and extending as far south as Zambia and Angola. Around the same time, scientific breakthroughs in the 1970s and 1980s confirmed that CMD was caused by geminiviruses, leading to the identification of multiple strains. In the early 1990s, the East African cassava mosaic virus (EACMV) emerged in Kenya and Tanzania, and rapidly spread to Uganda, Mozambique, Rwanda, and Burundi. A severe epidemic in Uganda during the 1990s was linked to a highly virulent recombinant strain, EACMV-Ug, which accelerated the disease's spread across East and Central Africa. The East African cassava mosaic Kenya virus (EACMKV) was first reported in 1997, primarily in Kenya and Tanzania, while the East African cassava mosaic Malawi virus (EACMMV) was identified in Malawi in 1998. Around the same time, the South African cassava mosaic virus (SACMV) was reported in South Africa, signalling CMD's growing footprint in Southern Africa. East African cassava

mosaic Zanzibar virus (EACMZV) was identified in Uguja Island, Zanzibar in 1998 and later found in coastal Kenya, recognized as a distinct strain responsible for CMD in the region.

C) Further Spread and Emerging Strains (2000s–Present)

A distinct strain, East African cassava mosaic Cameroon virus (EACMCV), was first detected in Cameroon in 2000 and later spread to Gabon, Equatorial Guinea, and Nigeria, contributing to the growing diversity of CMD-causing viruses in Central and West Africa. The Sri Lankan cassava mosaic virus (SLCMV), a begomovirus causing CMD, was first identified in Colombo, Sri Lanka in 2002, and later spread to India and Southeast Asia, co-existing with Indian cassava mosaic virus (ICMV).

The 2000s witnessed a further intensification of CMD spread, with EACMV-Ug reaching the Republic of Congo in 2002, and more aggressive strains appearing in countries like Nigeria and Ghana by 2008–2010. In West Africa, the Indian cassava mosaic virus (ICMV) was detected in Togo in 2008, its first confirmed presence outside Asia. By 2012, Cassava mosaic Madagascar virus (CMMGV) was reported in Madagascar as a distinct virus limited to the island, and African cassava mosaic Burkina Faso virus (ACMBFV) was also first reported in Burkina Faso in 2012, adding to the region's viral complexity. Meanwhile, CMD began spreading in Asia, starting with the detection of a cassava mosaic geminivirus on *Jatropha curcas* in Singapore (2013). Sri Lankan cassava mosaic virus (SLCMV) emerged in Cambodia in 2015 and rapidly expanded across Vietnam, China, and Thailand by 2019, and into Laos in 2020. Its identification in Australia in 2022 marked a global warning for cassava production, intensifying concerns over

CMD's impact on food security and agriculture worldwide.

Yield and economic Losses:

Cassava Mosaic Disease (CMD) is not just a plant pathology issue—it's an economic disaster affecting millions of farmers worldwide. Cassava Mosaic Disease (CMD) has been a major agricultural concern for over a century, with its first identification in 1894. Over time, the disease spread across Africa and beyond, causing severe economic losses. In 2009, a CMD pandemic devastated 2.6 million hectares across East and Central Africa, causing estimated losses of \$1.97–\$2.7 billion annually. By 2011, the disease was wiping out 15%–24% of cassava yields in Africa, translating into financial losses of \$1–\$2.3 billion every year. A study in Zambia in 2015 revealed that CMD had infected 57.4% of cassava fields, resulting in a 34% yield loss and annual financial damages of \$51.7 million, a crisis that continued into 2017.

In India, CMD has been a growing challenge, with its impact becoming more evident over the past two decades. A survey in 2008 in West Bengal recorded an incidence rate between 61% and 92%, with symptoms ranging from mild chlorotic patterns to severe mosaic and leaf distortion. By 2011, Tamil Nadu witnessed infection rates exceeding 90%, signalling a severe outbreak in the region. In 2018, research highlighted that the use of infected planting materials was a major contributor to crop losses, reducing cassava root yields by 16%–33% and starch content by 22%–38%. By 2019, estimates suggested that CMD was causing a 30% yield loss in India, raising significant concerns for food security and rural economies. Tackling this crisis requires urgent action through disease-free planting materials, resistant cassava varieties, and

effective disease management strategies.

Integrated Strategies for Managing Cassava Mosaic Disease (CMD)

Cassava Mosaic Disease (CMD) threatens global cassava production, endangering millions of smallholder farmers, especially in Africa, Asia and Australia. The disease causes major yield losses, leading to billions in economic damages annually. Its rapid spread is driven by new recombinant virus strains, rising whitefly (*Bemisia tabaci*) populations, and climate change. Unchecked, CMD could severely impact food security, disrupt local economies, starch and sago industries, and push farmers into financial hardship by reducing both their income and access to affordable food.

To effectively tackle Cassava Mosaic Disease (CMD), a holistic and science-driven approach is crucial. CMD management relies on a combination of sound farming practices, the use of disease-resistant varieties, and targeted control of whitefly vectors. Cultural methods such as rouging (removal of infected plants), intercropping cassava with maize or legumes, and the application of reflective mulches are widely practiced to disrupt whitefly activity and minimize disease spread. Promoting the use of certified, virus-free planting material is another critical step in preventing CMD transmission through vegetative propagation.

The ICAR-Central Tuber Crops Research Institute (ICAR-CTCRI) in Thiruvananthapuram has played a leading role in the development of CMD-resistant cassava varieties, including Sree Reksha, Sree Sakthi, Sree Suvana, and Sree Kaveri, all of which are now widely adopted by farmers. Furthermore, biological solutions such as *Piriformospora indica*, a beneficial microorganism, have shown great

potential in both promoting plant growth and offering biocontrol against CMD. Integrated strategies that combine phytosanitation, vector control, conventional breeding, and advanced genetic techniques like CRISPR-Cas9 and marker-assisted selection are being actively employed to build long-term resilience.

With whiteflies (*Bemisia tabaci*) identified as the primary carriers of the CMD virus, controlling their population is essential. Promising tools like RNA interference (RNAi) are being explored to block virus transmission at the molecular level. At the same time, biological control methods involving natural predators are being used to keep whitefly numbers in check. Technology is also stepping in to support farmers—machine learning (ML) and deep learning (DL) are now being harnessed for real-time CMD detection, using innovations such as drone-based surveillance, satellite imaging, and AI-powered mobile applications. These tools enable early disease diagnosis and swift management interventions. The future of CMD management lies in a comprehensive, integrated strategy that combines resistant varieties, clean planting material, vector suppression, improved agronomic practices, and technology-driven surveillance. This multi-layered approach not only strengthens the fight against CMD but also ensures the sustainability of cassava cultivation and the livelihoods that depend on it.

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