

Cassava Mosaic Disease (CMD): Host- Virus- Vector relationship

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Cassava is the fifth-largest source of carbohydrates in food in the tropics, after rice, wheat, potato and maize, making it an important staple; more than 700 million people depend on it. *Manihot esculenta*, commonly called cassava, manioc, or yuca, is a woody shrub of the spurge family, Euphorbiaceae native to South America from Brazil. Although a perennial plant, cassava is extensively cultivated in tropical and subtropical regions as an annual crop for its edible starchy tuberous root. Cassava is a monoicous, diploid species having 36 chromosomes. In India, cultivated in Kerala, Tamil Nadu, Andhra Pradesh and Maharashtra states. In Tamil Nadu, the cassava used in industrial purpose for making sago, starch and used for animal feed. The major constrain in cassava production is affected by cassava mosaic disease (CMD) and due to CMD, about 12-90% yield lose is recorded, that's approximately equal to 1.9-2.7 billion US dollars per annual. The CMD disease is caused by cassava mosaic virus belongs to geminivirus group and this disease is transmitted by whitefly feeding on healthy cassava plant. The disease can be effectively managed by utilizing host-plant resistance that has been introgressed from *Manihot glaziovii* into cultivated cassava. The interrelationship among CMV virus, the host-plant resistance, and the whitefly vector is explained below.

a) Cassava Mosaic Virus (CMV)

The CMV viruses are members of the family Geminiviridae and the genus Begomovirus. The first report of cassava mosaic disease (CMD) was from East Africa in 1894. Initially named as cassava latent virus. Based on the characteristics of genome sequences, named as African cassava virus or ACMV. There are total twelve CMV virus reported, such as African cassava mosaic virus (ACMV), African cassava mosaic Burkino faso virus (ACMBFV), Cassava mosaic Madagascar virus (CMMGV), East African cassava mosaic Cameroon virus (EACMCV), East African cassava

mosaic Kenya virus (EACMKV), East African cassava mosaic Malawi virus (EACMMV), East African cassava mosaic virus (EACMV), East African cassava mosaic virus Ugandan variant (EACMUG), East African cassava mosaic Zanzibar virus (EACMZV), South African cassava mosaic virus (SACMV), Indian cassava mosaic virus (ICMV), and Sri Lankan cassava mosaic virus (SLCMV).

These Gemini viruses are, small plant virus having two circular single stranded DNA. These replicated by rolling circular mechanism in the plant cell nucleus. They are possessing two DNA molecule DNA-A & DNA-B (Fig.1). In DNA-A, there are five open reading frames (ORF's), genes on DNA-A, code for (i) coat protein AV1 (CP) (ii) replication associated protein AC1 (Rep) (iii) protein associated with movement AV2 (MP) (iv) trans activation of AV1 & BV1 (AC2, TrAP) and (v) replication enhancement AC3 (REN). They encode all the viral protein necessary for replication and encapsulation of both components. While DNA-B component encodes for two proteins necessary for efficient systematic spread of the virus through all the plant. The genes are in DNA-B, are BV1, NSP for nuclear transport, BC1 MP for cell-cell movement. These have role of symptoms producing in plants.

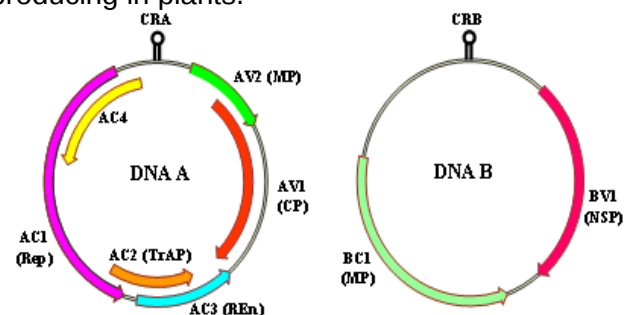


Fig.1 DNA structure of cassava mosaic virus (CMV)

b) Host-Plant Resistance

In 1971, a resistant line of cassava, the predominant host of the pathogen, was established and used by the International Institute

of Tropical Agriculture in Nigeria. This resistance breeding is as an effective control CMD disease. However, in the late 20th century, a more virulent virus broke out in Uganda and quickly spread to East and Central Africa. The highly virulent strain was later discovered to be a chimera of two distinct Begomovirus species. CMV virus transmitted through a vector called whitefly (*Bemisia tabaci*). ICMV, SLCMV found in cassava growing states of India, but SLCMV more prevalent in Kerala.

Cassava Mosaic Disease (CMD)

One of the major problems in cassava is CMD or Cassava mosaic disease. CMD is mainly spread by infected cuttings and transmitted by whitefly. There are three CMD associated resistance gene was identified namely CMD1, CMD2, CMD3. CMD1 is consisting of polygenic and recessive, CMD2 is monogenetic dominant and CMD3 is quantitative trait loci-QTL. CMD considered as most serious disease of cassava causing severe yield loss to the crop.

CMD symptoms

Initially following infection of a cassava geminivirus, systemic symptoms develop. These symptoms include chlorotic mosaic of the leaves, leaf distortion, and stunted growth. Leaf stalks have a characteristic S-shape and reduced root development. Infected plants may also exhibit mosaic patterns on their leaves. CMD causes two characteristic symptoms of green and yellow mosaic patterns in leaves. Plants affected by green mosaic have leaves with contrasting sectors of dark and light green tissue. While, yellow mosaics are much more conspicuous, as they have leaves with contrasting areas of normal green and yellow tissues. The most severely affected plants are so stunted virtually with no yield of roots and stems not suitable for further propagation.

c) Vector - Whitefly (*Bemisia tabaci*)

Bemisia tabaci commonly called whiteflies are belongs to Aleyrodidae family. Whiteflies are winged insects that usually white in colour (Fig.2). They look very similar to the aphids. In cassava white flies are feeds on the under surface of the leaves, majorly in young leaves and they can also feed on the stems near the new leaves. Whiteflies feed on plants by sucking out the juice from leaves and heavily infected plants restricts photosynthesis forms mosaic pattern in the leaves and yield causes significant losses. The life cycle of whitefly is 6 to 8 weeks. There are many different types of whiteflies, and they feed on different types of plants generally polyphagous. Whiteflies can like citrus plants, flowering plants such as Allamanda, Begonia, Chrysanthemum, garden roses, Petunia, Salvia, Primula. They also like many greenhouse

crops such as tobacco, sweet potatoes, cucumber and Solanaceae crops like tomato, potato, brinjal, potato.



Fig.2 Whitefly

The Gemini virus is transmitted by whiteflies through a non-propagative, circulate mode. Adult whiteflies require approximately three hours for acquiring the virus. After a latent period of about eight hours, the virus can be transmitted to healthy plants during a feeding period of less than ten minutes, leading to the development of cassava mosaic disease (CMD) in cassava.

CMD Resistance Breeding:

Resistance breeding at IITA

The use of resistant varieties has obvious advantages in seeking to decrease the losses due to virus. This was appreciated by early workers on CMD in Africa in the 1920s and 1930s, when cassava production expanded rapidly in many areas and CMD became increasingly important. The first CMD-resistant varieties, developed by IITA in Nigeria, were hybrids obtained with *M. glaziovii*, found in Brazil, which conferred multigenic resistance (CMD1). Among these varieties, three have been largely popularized and have shown a very high CMD resistance with low or no yield losses. CMD2-associated resistance, discovered in landraces across West Africa, is a dominant, single genetic locus located on Chromosome 12. The gene responsible for this resistance remains unknown. Quantitative Trait Loci (QTLs) associated with resistance to CMD were identified using F1 progeny derived from a cross between the CMD resistant (TMS30572) and the susceptible landrace (TME117) and confirms polygenic nature of this resistance

In East Africa, local and introduced cassava varieties were evaluated and cassava was crossed with *M. glaziovii*. Varieties with a high level of resistance to CMD with roots having a satisfactory starch content were obtained by backcrossing *M. esculenta* × *M. glaziovii* hybrids to cassava. Some of the varieties selected for resistance in this way proved suitable for East African conditions and were released to farmers. Seeds from promising selections were also sent to Nigeria in the 1950s for use in the national breeding programme. Nigerian clonal selection 58308, which originated from East African seed, has since featured prominently as a parent in resistance breeding at

the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria.

Since the 1970s, the most comprehensive and influential cassava breeding programme in Africa has been at IITA where, resistance to CMD was one of the main objectives along with yield. Clones viz., TMS30001, TMS4(2)1425, TMS30337, TMS30395 and TMS30572 were raised at IITA in 1973 and they were the first improved varieties with resistance to CMD. Among the five lines, TMS30001 was found to be the best with inconspicuous symptoms of restricted distribution of virus when infected. Some of the tropical *M. esculenta* (TME) from Nigeria and west African which is associated with CMD2 resistance gene, crossed with TMS, which is associated with CMD1 resistance gene.

In the latest phase of the IITA resistance breeding programme, considerable use of cassava landraces collected in Nigeria and West Africa has been made. Some of these tropical *Manihot esculenta* (TME) types are highly resistant to infection and are seldom infected, even when exposed at sites of very high inoculum pressure. Moreover, the high resistance of some TME clones is attributed to a single dominant gene that was designated CMD2. The TME resistance differs from that of TMS (Tropical Manihot Selection) varieties, which is considered to be polygenic, recessive and associated with gene CMD1 derived from *M. glaziovii*. Thus, the two types of resistance are complementary in their effects, and can be combined by inter crossing TME and TMS parents. Several of the TME × TMS hybrids produced in the IITA breeding programme have given very high yields and additional attributes of many landraces involved. The progenies of these crosses have the erect growth habit with tuberous roots of good taste and quality preferred by many farmers. Several of the landraces and progenies derived from crosses with TMS clones are already being grown in Nigeria.

Resistance breeding at CTCRI, Trivandrum

In Central Tuber Crops Research Institute, Thiruvananthapuram, cassava cultivar MNga-1 and wild *M. caerulescens* were identified as resistant to ICMV. MNga-1 is a breeding line from IITA, designated as TMS30001. Intensive resistance breeding programme was undertaken through inter-varietal and interspecific hybridization programmes. In inter-varietal hybridization programme, MNga-1 (Sree Padmanabha) was used as a donor for ICMV resistance and crosses were made with released varieties and promising selections from indigenous germplasm. Evaluation of seedling population of MNga-1 for ICMV showed that open pollinated

populations showed lesser ICMV incidence (15-34%) than the crosses with promising selections (37%) Similarly, hybrid progenies obtained from crosses CMD susceptible Ambakadan with MNga-1, showed resistance to ICMV at seedling and first clonal stage. Among the crosses, one interspecific hybrid cassava with *M. caerulescens* (CMC-1) showed complete resistance to ICMV for the past twelve years of evaluation while other field tolerant interspecific hybrids showed varying degrees of incidence during the same periods. Backcross derivative of *M. caerulescens* exhibited high level of resistance and were used as donor parents for transferring resistance to elite Indian cultivars. Among the crosses, one interspecific hybrid cassava with *M. caerulescens* showed complete resistance to ICMV for the past twelve years of evaluation while other field tolerant interspecific hybrids showed varying degrees of incidence during the same periods. This hybrid is now being back crossed with elite cassava cultivars for recovering quality attributes.

From ICAR-CTCRI, a total of five resistant varieties were released Sree Padmanabha, Sree Reksha, Sree Suvarna, Sree Sakthi and Sree Kaveri.

1. Sree Padmanabha: Released in 2006. Growing in rainfed areas of Kerala & Andhra-Pradesh; irrigated plains of Tamil Nadu, yielding about 38 t ha⁻¹. Pedigree: Exotic germplasm - (TMS 30001) from IITA, Nigeria Introduced through CIAT, Cali, Colombia. It is a tall, late branching variety with greyish green stem and light green emerging leaves. Its tuber shape long cylindrical, skin colour silvery white. Tubers have 25.8% starch, 38.2 µg/100g cyanogen and excellent cooking quality. Resistant to cassava mosaic disease, shows cupping of leaves under drought conditions.

2. Sree Reksha: Released in 2017. It is grown in rainfed areas of Kerala and Tamil Nadu. Yield is 45-50t ha⁻¹. Pedigree: CM79515 x C-18. Tall (275-325 cm), non-branching variety with brown stem and light brown emerging leaf, completely resistant to cassava mosaic disease caused by both Indian cassava mosaic virus and Sri Lankan cassava mosaic virus. It is also tolerant to post-harvest physiological deterioration. It has medium starch (27-31%) and low sugar (1.10%) content. Suitable for planting in rainfed and irrigated conditions especially in regions with high incidence of cassava mosaic disease



3. Sree Suvarna: Released in 2018. It is grown in rainfed areas of Kerala, Tamil Nadu and Andhra Pradesh. Yield is 45-50 t ha⁻¹. Pedigree: SM1741 x C33. It is an erect top branching variety with brown stem, conical to cylindrical tubers with brown skin. Cream rind and white flesh colour. It has medium starch, 25-27% (range: 24-29.8%). It is completely resistant to cassava mosaic disease caused by both Indian cassava mosaic virus and Sri Lankan cassava mosaic virus. It is suitable for planting in regions with high incidence of cassava mosaic disease.



4. Sree Sakthi: Released in 2018. It is grown in rainfed areas of Kerala, Tamil Nadu, Andhra Pradesh and Maharashtra under irrigated/rainfed upland conditions. Yield is 45-50 tha⁻¹. Pedigree: C33 x CM4574-7. It is non-branching variety with dark brown stem, brownish green pubescent. Long cylindrical tubers with brown skin, cream rind and white flesh colour. It is completely resistant to cassava mosaic disease caused by both Indian cassava mosaic virus and Sri Lankan cassava mosaic virus. Also tolerant to post harvest physiological deterioration. It has high starch content of 29% (range: 26-32%) It is an industrial variety.



5. Sree Kaveri: Released in 2023. It is grown in rainfed areas of Kerala, Tamil Nadu, Andhra Pradesh. Yield is 45-50 t ha⁻¹. It is resistant to cassava mosaic disease, high nutrient use efficiency and drought tolerance. It is tall, top-branching variety with silver grey stem, light green petiole, cylindrical tubers with cream skin, cream rind and white flesh.

