**<tentative>** Phylogenetic analysis of Sri Lankan Cassava Mosaic Virus (SLCMV) causing Cassava Mosaic Disease (CMD) in Trincomalee, Sri Lanka based on their DNA-A sequences.

**Introduction**

Cassava (*Manihot esculenta* Crantz*)* is a perennial woody shrub belonging to family Euphorbiaceae, that is cultivated primarily for its tuberous roots in tropical and neotropical nations around the world. It’s native to southern edge of Brazilian Amazon and was domesticated by indigenous South Americans roughly 15,000 years ago *(Allem, 1994); (Oslen and Schaal, 1999)* Sri Lanka being a tropical island, has had cassava growing on its soils since time immemorial, and cassava has become a well-integrated element in the Sri Lankan culinary landscape. Sri Lankan Department of Agriculture lists the following eight varieties: Shani, Suranimala, Suwarne, HORDI Mu – 01, Kirikawadi, Mu 51, HORDI 06 and CAR5 555 as customarily planted cassava cultivars in Sri Lanka. A diverse array of products is prepared from cassava tubers e.g., curries, porridges, crispy snacks, boiled tubers, ground powder of dried tubers and **<what not>** which eloquently decorate cuisines of Sri Lankan households. It even served as an alternative staple food source when Sri Lankans faced severe shortages of imported wheat flour in the1970s, which highlights the historical and dietary significance of cassava tubers in Sri Lankans’ subsistence.

However, cassava plantations in Sri Lanka have been suffering from the Cassava Mosaic Disease (CMD) caused by Sri Lankan Cassava Mosaic Virus (SLCMV) for a long time. The first known academic report studying CMD in Sri Lanka comes from *Salim, N. and Bandumala S. H (2001).* The causal agent is a closely related variant of Indian Cassava Mosaic Virus (ICMV) and infects both commercially cultivated cassava cultivars and wild cassava plants (*Manihot carthaginensis* subsp. *glaziovii*, also known as Ceara rubber)*(Salim. N 2001)*. Since then, this disease and its ravages have been studied sporadically by academics, both Sri Lankan and outsiders. Alongside the efforts of the local academic community and researchers, SLCMV also seems to have merited academic attention from international researchers from Vietnam, Loas, India and Cambodia as the virus spread over to their nations. **<list the symptoms>**

SLCMV is a bipartite plant virus belonging to the family Geminiviridae, genus *Begomovirus.* The genome of SLCMV is composed of two circular ssDNAs, namely DNA-A (approximately 2,760 bp long) and DNA-B (approximately 2,737 bp long) each of which are encapsulated in separate twinned icosahedral capsids *(Stanley and Gay, 1983)*. DNA-A encodes six genes (AC1, AC2, AC3, AC4, AV1 and AV2), that play vital roles in replication, defense, transcription and the synthesis of capsids. DNA-B encodes two genes (BC1 and BV1) that facilitate intercellular and systemic movement of virus particles *(Hareesh et al., 2023)*. DNA-A and DNA-B of SLCMVs also share a common region (~200 bases long) that encodes elements involved in replication and transcription *(Saunders et al., 2002)*. And the sizes of these two DNAs show only a minute difference, whereby DNA-A happens to be 21 to 23 bases longer than its DNA-B counterpart.

This study aims to sample diseased *M. esculenta* leaves from a select set of fields in Trincomalee district, Sri Lanka and compare the SLCMV viral DNA-A sequences with that of other viral pathogens affecting *M. esculenta* plants in Sri Lanka as well as all internationally known variants of CMV, in a quest to discern the evolutionary relationships between them and to deduce the possible events that might have paved way for this genetic diversity to come into existence.

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