**INTRODUCTION**

Cassava (Manihot esculenta Crantz) is a perennial plant, also known as “Maravalli” in Tamil, and “Manioc” in Sinhala is belongs to the family Euphorbiaceae. Although Cassava is native to South America, it remains an important vegetable crop in tropical and subtropical regions of Africa, Asia, and Latin America for its tuberous starchy root. (Reynolds, 2017). Cassava occupies 4th rank in the world as a rich source of carbohydrates followed by rice, corn, and wheat. The potential of the Cassava plant to grow under a wide range of climatic conditions and poor soil, paved a way for food security over a century, for over 500 million people throughout the world.

Cassava was introduced to Sri Lanka during the Dutch period. It is being cultivated in dry, wet, and intermediate zones of Sri Lanka including Jaffna, Trincomalee, Anuradhapura, Gampaha, Matara, Ratnapura, and Kurunegala districts, approximately in an area of 20, 592 hectares with an annual production of 281, 075 tonnes for human consumption and industrial purposes. In 2019, the export value of Cassava was 2.82 million USD. (Sri Lanka Cassava Market Insights, 2020). The raw Cassava tuber is reserved with energy (3200 kcal/kg) (Egena, 2006), and it can be consumed after boiling or processed into a variety of products including floor, cassava chips, bioethanol, pasta, etc. (Kenneth et al., 2000). As cassava leaves contain Cyanogens, it’s restricted in the human diet, but it can feed animals because of its high protein, vitamins, and mineral nutrients. (Morgan and Choct, 2016 and Cock, 1982).

Although Cassava cultivation is affected by various pests and diseases, the Cassava Mosaic Disease (CMD) has emerged as a serious threat that leads to yield losses. (Calvert and Thresh, 2002 and Sseruwagi et al., 2004). CMD is caused by Cassava mosaic viruses (Family: Geminiviride; Genus: Begomovirus) transmitted by whitefly vector Bemisia tabaci. (Storey and Nichols, 1938). Cassava mosaic virus genome is encapsulated with circular, single-stranded two DNA components, which are DNA A and DNA B. (Stanley and Gay, 1983). CMD produces a complex of varying symptoms typically include, an irregular yellow and green chlorotic mosaic pattern, twisted and misshapen leaflets, puckering, reduction of leaf size, and overall stunted plant growth. According to the previous reports, twenty different viruses are associated with this CMD. (Thresh et al., 1994). Among these, in Sri Lanka, Cassava mosaic disease is caused by two Begomo viruses, such as Sri Lankan Cassava mosaic virus and Indian cassava mosaic virus. (Emmanuel et al., 2019).

Unfortunately, after 2016, the Cassava production has been drastically reduced by CMD than earlier in the Trincomalee district. (Conversation with Deputy Director, Agriculture, Trincomalee district). However, because of less awareness and background knowledge about the disease, mode of virus transmission, and disease control measures, most of the farmers abandoned Cassava cultivation and moved to other vegetable crops. So, the present study aimed to understand the status of cassava cultivation in the Trincomalee district and to confirm the causative agent of the disease by using virus specific primers, and yield losses in plants affected by CMD.

**MATERIALS AND METHODS**

**Survey to the study the present status of Cassava Mosaic disease in Trincomalee district**

The Survey was conducted from May to July 2021 to determine the Cassava Mosaic Disease (CMD) incidence and to study the present status of CMD. Field visits were arranged to three different D.S divisions of Trincomalee district namely, Padavisripura, Muthur, and Nilaveli. The pre-prepared questionnaires with queries related to Cassava cultivation and CMD were randomly provided to 80 selected farmers of all fields and required information was gathered.

**Assessment of Disease incidence, disease severity, and mode of transmission**

In each field, six plots of 10 m2 area were selected and the number of diseased plants (n) showing typical symptoms and total plants. The percentage of CMD incidence per field was calculated by using the following equation.

% Disease incidence = n x 100

N

The CMD severity was scored for each plant in all five plots of the selected fields on a scale ranging from 1 to 5, where 1 = no visible symptoms; 2=mild chlorosis of the entire leaflet or mild distortion at the base of the leaflet, but overall green and healthy leaves; 3=moderate mosaic patterns throughout the leaf, and narrowing and distortion of the lower one-third of the leaflet; 4 = severe mosaic and distortion of two-thirds of the leaflets, with a general reduction in leaf size; and 5 = Very severe mosaic symptoms on most of the leaves, with distortion, twisting and puckering with severe leaf reduction of most of the leaves, subsequently leads to stunting of plants. (Hahn et al., 1980). Based on the mode of transmission CMD was characterized as either cutting-borne (lowest earliest-formed leaves showing symptoms) or whitefly–borne (uppermost leaves showing symptoms)

**Sample collection**

Foliar samples with Cassava Mosaic symptoms were collected in June 2021 from five different regions of Trincomalee district where Cassava was cultivated to a large extent namely, Padavisripura (L1), Muthur (L2), Nilaveli (L3), Kuchchaveli (L4), and Kinniya (L5). Each field is situated approximately 20-25 km away from the other. The sampled CMD infected leaves from above five fields were categorized based on the disease severity. The infected leaves with three different range of symptoms (A – entire leaves with moderate mosaic symptoms, B – Curled leaves, and C – Deformed leaves showing puckering symptom) from above fields were separated and packed in polythene bags and stored at -20oC.

**Total Genomic DNA extraction from infected leaf samples**

The sampled and stored CMD infected leaves from different regions were subjected to total DNA extraction by using modified CTAB extraction method. (….). DNA extracts were preserved at -20OC the virus identification using PCR techniques.

**Detection of Virus by PCR**

PCR reactions were carried out to the DNA extracts collected from different regions by using the Deng A and Deng B primers (Deng et al., 1994) that amplifies the partial sequence (530 bp) of Coat protein gene (CP – gene) specific of DNA- A component of Begomo virus. The PCR reaction was performed in a volume of 20 µL containing 3 µL of extracted DNA, 0.4 µL of Taq Polymerase (Bio mix), and 0.4 µL of Master mix (Biomix), 0.1 µL of each primer the reaction buffer provided by the manufacturer. The PCR conditions are as followed: a 94°C initial denaturation step of 4 min followed by 30 cycles of 1 min at 94°C, 45 sec at 60oC, and 1 min at 72°C and then a final extension step of 5 min at 72°C.

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