Diagnostics for Sustainable Cassava Productivity in Africa project

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Introduction

CMD-infected cassava

In Kenya, cassava is mainly grown in Coast, Western, Eastern and Nyanza regions. Few crop stands are found in Eastern and Rift Valley regions. Most farmers use their old landraces for planting. Due to the lack of a formal seed system for this crop, farmers obtain planting materials from previous crops thereby perpetuating diseases. A major constraint to production of cassava are viral diseases infecting the crop. Cassava mosaic disease (CMD) is considered the most important due to its spread in cassava growing regions and cassava brown streak disease (CBSD) which has gained importance due to its continued spread.

CMD causes up to 100% reduction in yield, while CBSD causes up to 70% yield losses. The viruses are spread by use of infected cuttings or are transmitted by white flies (*Bemisia tabaci*) . CMD express a range of symptoms which depend on the virus species/strain, prevailing environmental conditions, and the sensitivity of the cassava host.

Cassava brown streak disease is caused by two different viruses, namely Uganda Cassava Brown streak Virus (UCBSV) and Cassava brown streak virus (CBSV). Common symptoms due to CBSD include chlorotic mottles on the leaves and development of dry, brown, corky necrotic lesions on the roots. Brown necrotic streaks occur on the stems. The necrotic browning of roots makes them inedible and unmarketable.

CBSD-infected cassava roots showing necrotic browning

Cassava infected with CBSD showing mosaic and streaks on leaves and stems, respectively

Key project objectives

Objective 1. Disease distribution (country surveys)
Cassava viruses and vector surveys are to be conducted in Eastern, Western, Nyanza and Coast regions to determine incidence and severity of CMD and CDSDs. Potential vectors to be identified, collected and population densities determined.

Objective 2. Characterization of emerging viruses
This activity involves laboratory detection of cassava viruses, purification of PCR products and sequencing of short fragments in order to determine their diversities.
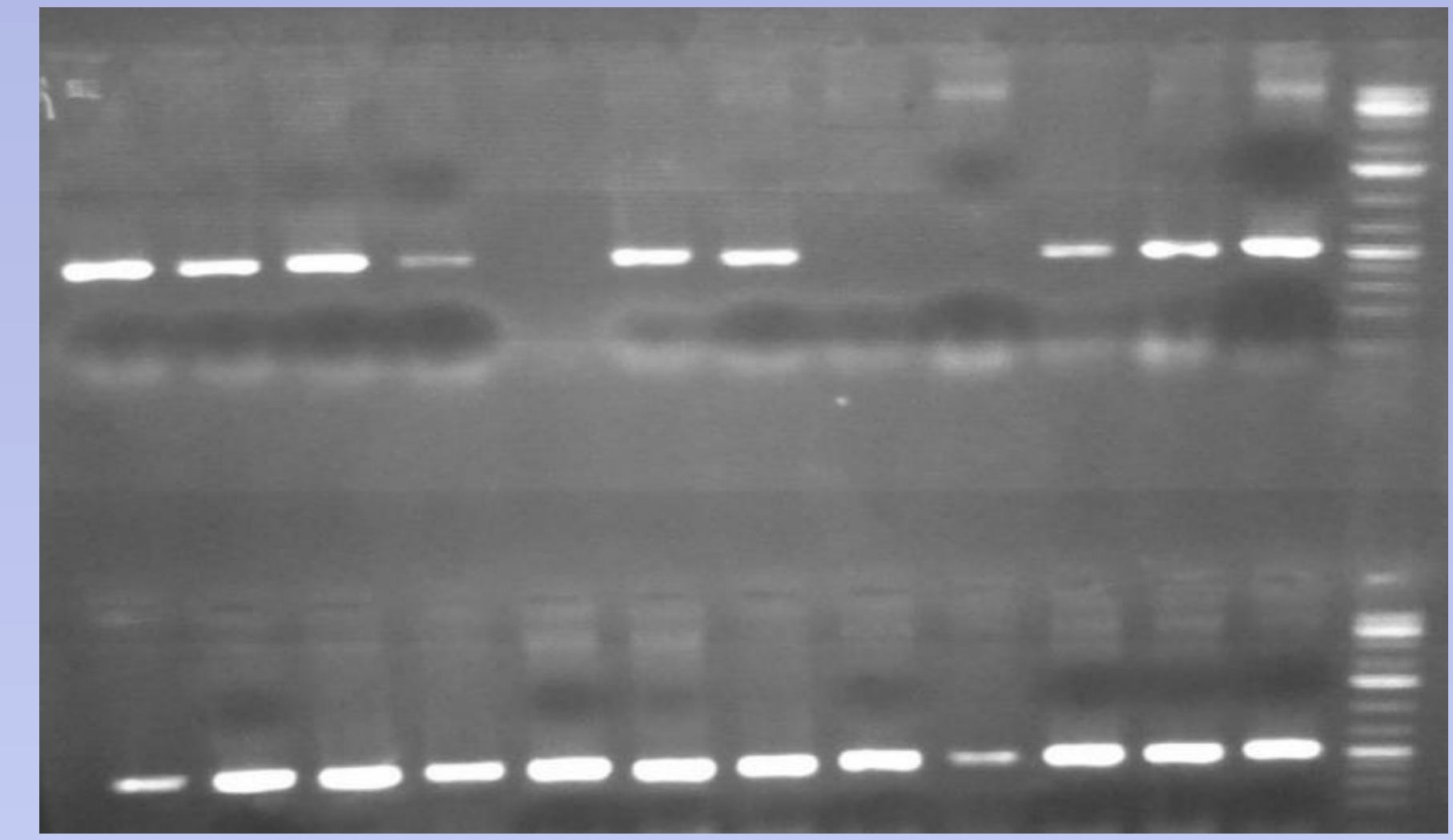
Improved cassava viruses diagnostics capacity at JKUAT

Objective 3.Characterization of vectors
Whiteflies populations will be collected across the 4 regions and characterized using mtCO1 gene primers. PCR products will be sequenced followed by phylogenetic analysis for genetic diversity.

Objective 4. Development of diagnostic tools
The project intends to develop methods for field detection of CBSV and CMGs.

Objective 6. Conventional breeding support
The project team will work with cassava breeders in the country. Specifically, the project will help with indexing of materials and determining the viral load of CBSD and CMD in promising varieties.

Objective 7. Reaching farmers directly
The project intends to train farmers on how to identify symptoms and manage the diseases in major cassava regions. This will be achieved by setting up demonstrations fields in Coast, Western, Eastern and Nyanza. This will also be achieved through participation in Agricultural fairs.

Expected outputs
• The distribution of viruses and strains will be determined and disseminated through disease prevalence maps

•Framers will be trained on preventive measures such as using disease free planting material
•Development of resistant varieties by the collaborating breeders

• Develop rapid and accurate detection and diagnosis and contribute in generating knowledge to address CMD and CBSVs infections in cassava.

•Create knowledge base in farmers on symptoms recognition during on farm demonstration and diagnostic clinics.

•To strengthen partnerships with stakeholders in cassava research and regulators towards a sustainable cassava seed system.
•Improved physical and human resource capacities in the country

•Contribute to increased cassava production in Kenya.