

Agricultural Productivity Program for Southern Africa (APPSA)

CASSAVA COMMODITY

(3rd Cycle- 2017)

Jamisse Amisse



Government of Malawi



Government of Mozambique



Government of Zambia

**END OF PROJECT
CONFERENCE**

27-29 November 2019, Johannesburg, South Africa

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Importance of Cassava in the world

- 20th most produced food
- 6th most consumed in the world (Africa, Asia and Latin America).
- consumed as root an important carbohydrate and leaf as vitamin and protein source.

- transformation from the subsistence to cash crop due the emergence of industries that use cassava derivate as a raw material



- Cassava has the potential to increase farm incomes, reduce rural and urban poverty and help close the food gap.

Introd...

In Mozambique

- In Mozambique: 2nd most important staple food after maize,
- Mozambique ranks among the top five cassava producers in Africa and
- the 10th in the world, with 6149897 ton per year (FAO, 2000; FAO, 2004).

- Approximately 2.5 million farmers
- almost 12 million people ($\approx 50\%$) use cassava for consumption (MIC, 2005 and FAO, 2007).
- Cassava is used not only for consumption but also as source of income (farmers' association supply beer factory)

Without question, cassava holds great promise for feeding Africa's growing population with more emphasis in Mozambique.

However

Gaps/Research area and objective

- Despite its importance, cassava production in Mozambique is limited by several pest/diseases. **Epidemiology study in order to determine the disease occurrence and associated pathogens, its extent and severity and identify higher risk cultivation areas, is of high importance as strategy to control the disease (CV-P01-2016)**

- Cassava is tolerant to stress hydric, however the yield could be affected when the plant is under stress (more than 3 months). Climatic events, such as extended drought has been observed in the country (Southern Mozambique). **Identification of drought tolerant cassava genotypes suitable for utilization by farmers living in drought zones (CV-P04-2016)**

- Due the transformation of cassava for different uses, it is important to **map out the various physical and chemical properties of existing and most used cassava cultivars as well the new released cassava varieties and test them for selected types of final utilization (INDUSTRIES, CONSUMPTION)- (CV-P05-2016)**

KEY OUTPUTS

Project Code	Technology Generated/Disseminated	Descriptions
CV-P01-2016	Three cassava varieties selected by the farmers based on the disease resistance/tolerance, yield and adaptability. Under farmer's field multiplication (5 districts)	Disease resistance/tolerance (CBSD/CMD), Yield (20-23 ton/ha), Dry matter and adaptability
	Main disease (most occurrence) recorded	Cassava disease and pest identified at least in two province surveyed
	<ul style="list-style-type: none"> • 2 protocols (RNA; DNA extraction) optimized 	Two (2) protocols optimized are been used in the lab (routine test of the diseases)
	<ul style="list-style-type: none"> • 1 primer set designed to detect the presence of viruses 	

ZAMBIA	17 of 77 accessions selected and included in the cross block for CASSAVA breeding program	- Selection of 17 Landraces were based on the morphological and agronomic performance. Currently included in the cross block for breeding activities
	Selected 4 cassava clones based on the performance (GxE)	Four varieties selected based on the adaptability of southern Mozambique environment conditions.
	Identified two varieties (for utilization and processing for industries) 20 cassava genotypes evaluated for resistance to CBSD with results showing varying response levels	Two (Phora and Chinhembwe) cassava landraces were selected based on the root quality (low cyanete and Fiber content)

Zambia

Protocol validation

- One modified protocol validated and used in detection of DNA and RNA pathogens

Survey

- Survey and sample collection from seven provinces of Zambia completed. CBB, CLS, CBSD and CMD mapped

Characterization of cassava pathogens

- CBB and CLS causal pathogens PCR detected
- One CBSD virus fully sequenced and a complete genome deposited in the GenBank

Evaluation of cassava genotypes

- 20 cassava genotypes evaluated for resistance to CBSD with results showing varying response levels

Main traits/Characteristic of varieties Disseminated

Variety	Orera	Eyope	Colicanana
CBSD	Resistant	Resistant	Tolerant
Mosaic	Tolerant	Resistant	Tolerant
Yield	23.0	20.0	20.0
DM	30-36	28-36	26-37
Cycle	12.0	12.0	12.0
Use	Flour	Fresh/Flour	Fresh/Flour

OTHER ACHIEVEMENTS -Mozambique

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210 farmers & 28 extension agents trained (Cassava Disease identification, management and control)



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- **Human capacity: 5 laboratory technicians trained on DNA/RNA extraction and disease diagnostic using molecular tools**



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▶ **CASSAVA CUTTINGS DISTRIBUTION (BEST 3 SELECTED VARIETIES)**

▶ **FIVE DISTRICTS / 245 FARMERS BENEFITED**



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Other Achievement-ZAMBIA

- One paper published
- A paper presented at the ICPP, Aug-2018 in Boston, USA

Plant Disease • 2018 • 102:1410-1418 • <https://doi.org/10.1094/PDIS-11-17-1707-RE>

e-Xtra*

Cassava Brown Streak Disease and *Ugandan cassava brown streak virus* Reported for the First Time in Zambia

Rabson M. Mulenga, Zambia Agriculture Research Institute, Mount Makulu Central Research Station, Chilanga, Lusaka, Zambia; **Laura M. Boykin**, The University of Western Australia, ARC Centre of Excellence in Plant Energy Biology and Molecular Sciences, Crawley, Perth 6009, Western Australia, Australia; **Patrick C. Chikoti**, **Suwilanjji Sichilima**, and **Dickson Ng'uni**, Zambia Agriculture Research Institute, Mount Makulu Central Research Station; and **Olufemi J. Alabi**,[†] Department of Plant Pathology & Microbiology, Texas A&M AgriLife Research and Extension Center, Weslaco 78596

Abstract

A diagnostic survey was conducted in July 2017 in two northern districts of Zambia to investigate presence or absence of cassava brown streak disease (CBSD) and its causal viruses. In total, 29 cassava fields were surveyed and cassava leaf samples were collected from 116 plants (92 symptomatic and 24 nonsymptomatic). CBSD prevalence was approximately 79% (23 of 29) across fields. Mean CBSD incidence varied across fields but averaged 32.3% while mean disease severity was 2.3 on a 1-to-5 rating scale. Reverse-transcription polymerase chain reaction screening of all 116 samples with one generic and two species-specific primer pairs yielded DNA bands of the expected sizes from all symptomatic plants with the generic (785 bp) and Ugandan cassava brown streak virus (UCBSV)-specific (440 bp) primers. All 24

nonsymptomatic samples were negative for UCBSV and all samples tested negative with primers targeting *Cassava brown streak virus*. The complete genome of a representative isolate of UCBSV (WP282) was determined to be 9,050 nucleotides in length, minus the poly A tail. A comparative analysis of this isolate with global virus isolates revealed its nature as a sequence variant of UCBSV sharing 94 and 96% maximum complete polyprotein nucleotide and amino acid identities, respectively, with isolates from Malawi (MF379362) and Tanzania (FJ039520). This is the first report of CBSD and UCBSV in Zambia, thus expanding the geographical distribution of the disease and its causal virus and further reinforcing the need to strengthen national and regional phytosanitary programs in Africa.

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Key Lessons

- Worked: Involvement/participation of the farmers from the first establishment of the fields was crucial for their own decision on which cassava varieties was best based on their traits preferences and performance on disease resistance
- Knowledge on disease identification transmitted was fundamental, because most of the members of farmers association were able to identify the main disease in their field and report to research

Did not work:

The interruption of the projects before pre-established time, has affected most activities, thus some objectives were not reached

Way forward

In order to increase accessibility, availability, of technologies is necessary

- Source of funds to continue with activities of the program,
- Find alternative funds to follow up with activities

Thank you

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