





Establishing sustainable solutions to cassava disease in mainland Southeast Asia

Objective 3: Develop and deploy diagnostic protocol, tools and information platforms fit for purpose in monitoring, surveillance, and certification applications

Presented by Le Thi Hang

Plant Protection Research Institute (PPRI – Vietnam) Email: <u>Hanglee.ppri@gmail.com</u> Project final review 3 October 2023 Conduct training and capacity building of scientists/staff in the plant production institutes in key diagnostic tools, sampling design, and data management platforms

Develop and deploy diagnostic protocol, tools and information platforms fit for purpose in monitoring, surveillance, and certification applications Design and implement regional surveillance for CMD and CWBD in Vietnam, Cambodia, Lao PDR, Myanmar and Thailand with results shared in a common platform

Understand the distribution and diversity of whitefly populations throughout the cassava production regions of Vietnam, Cambodia, Lao PDR, Myanmar, and Thailand

Evaluate new technologies of rapid field diagnostic for CMD and CWBD with particular applications in seed systems

Develop protocols for screening cassava clones and the biological characterization of diseases, particularly CWBD

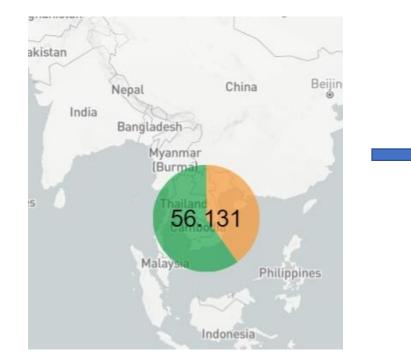
Develop and evaluate the effectiveness of communication products and awareness raising strategies utilising different public and private sector stakeholders

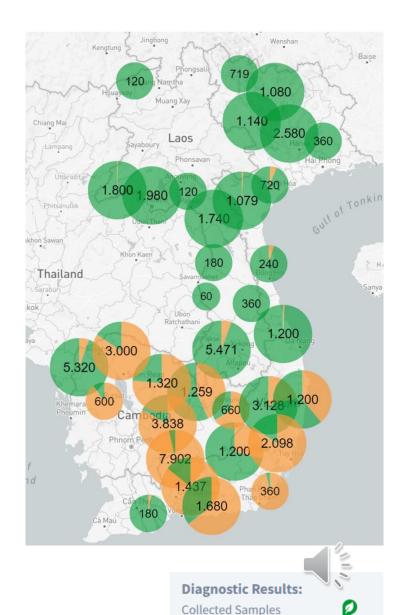


Surveillance 2020-2022

CASSAVA MOSAIC DISEASE (CMD) and CASSAVA WITCHES' -BROOM DISEASE (CWBD)

 37,980 observations were shared on PestDisPlace that were conducted by PPRI teams during 3 years





Suspected

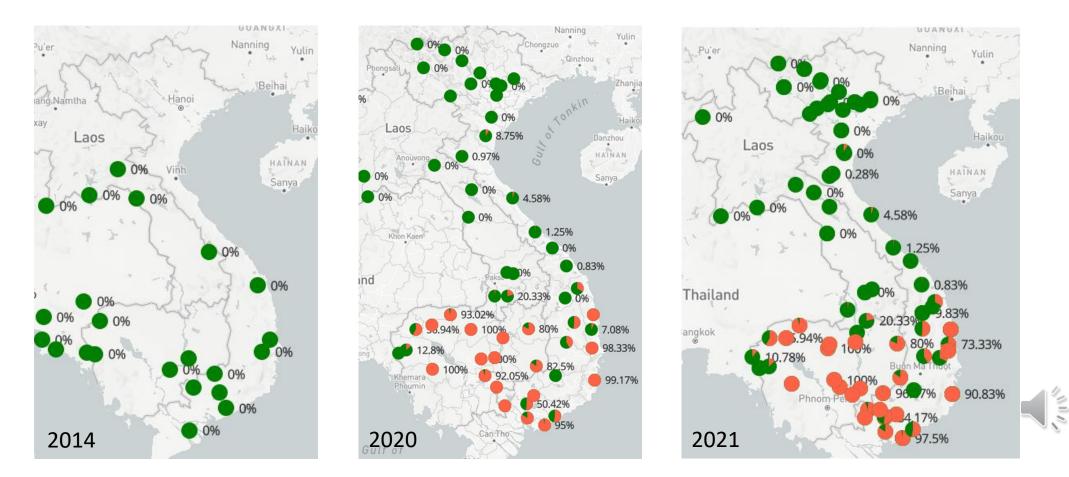
Confirmed Diagnostics

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Incidence Maps of CMD

In the three years from 2020 to 2022, a total of **633 fields** were surveyed The hotspots of the disease are in the *southern, central highland,* and *south-central coast* It has rapidly spread to the central and northern provinces in just 3 years



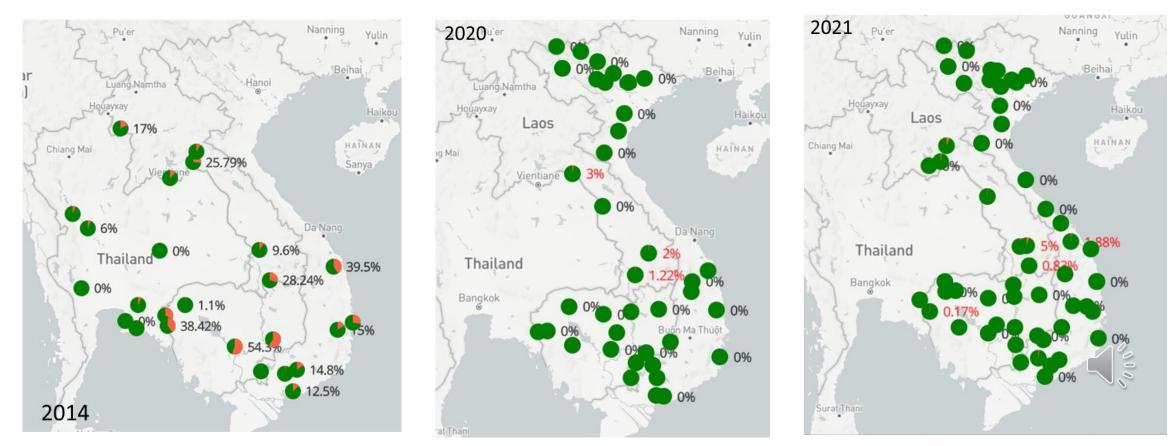
Incidence Maps of CWBD

"First wave" of CWBD in Vietnam in 2010-2015.

Field surveys in 2020 - 2021 identified 1 location.

In 2022, no symptoms were detected during the sampling process (however, they were subsequently found in sideline activities).

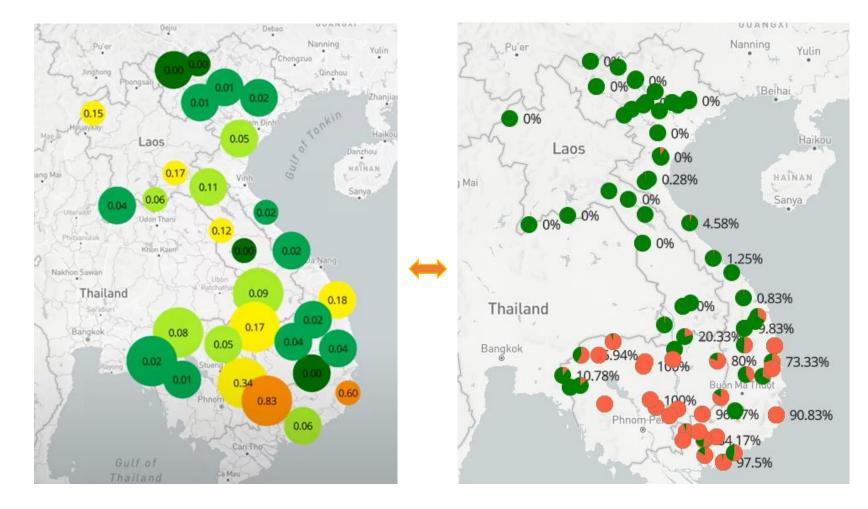
In 2023, CWB symptoms were recorded in many cassava cultivation regions.



Incidence Maps of Whitefly

Incidence in the southern, central highland, and central coast regions is higher than those in the north. Regions that are severely affected by CMD tend to have higher whitefly incidence.

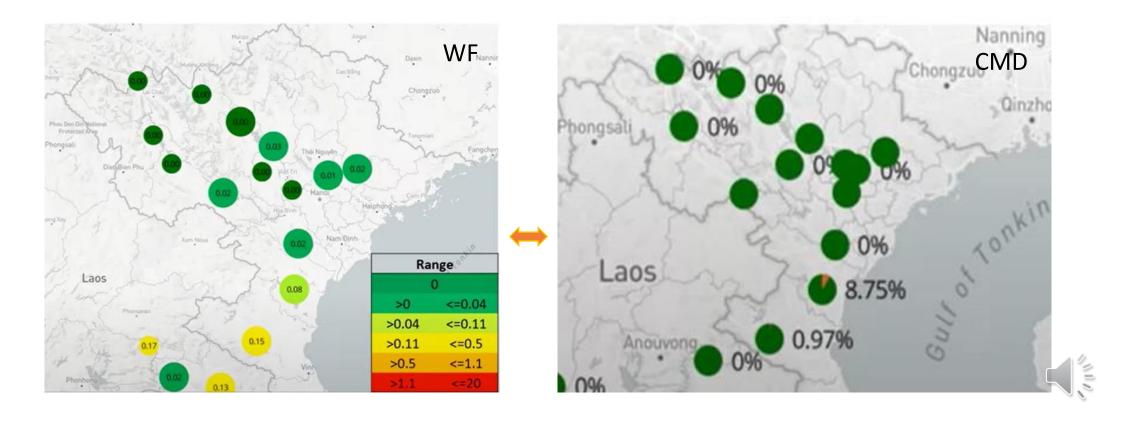
=> The correlation with the CMD



Whitefly relative abundance 2020-2022

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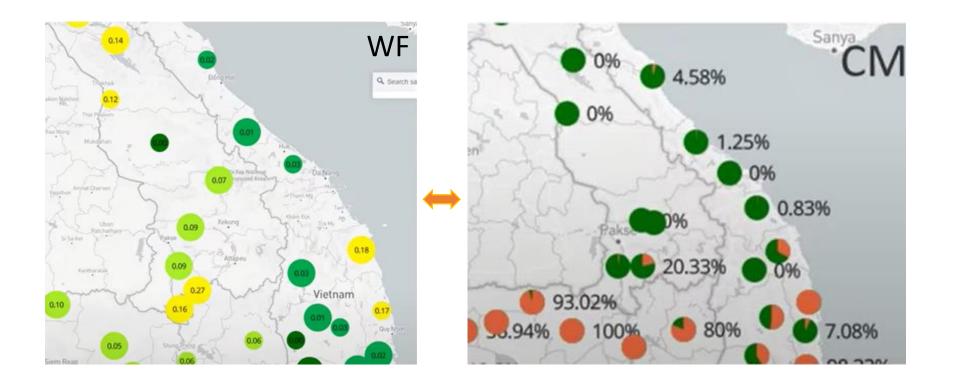
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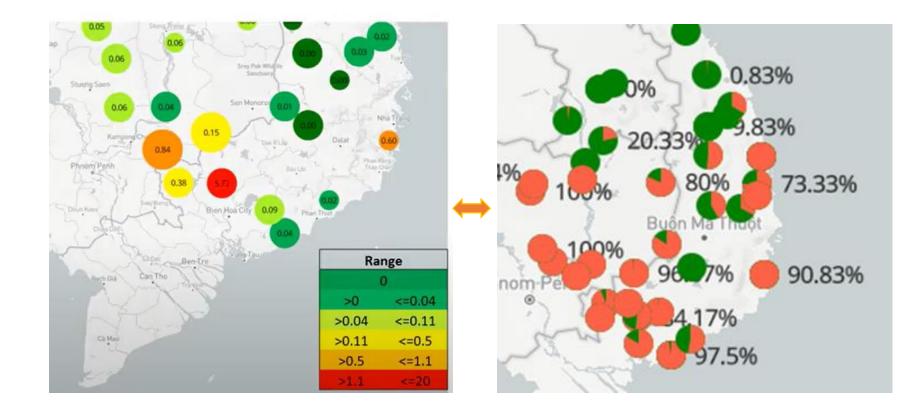




Whitefly relative abundance 2020-2022

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=> The correlation with the CMD





- 1. Sampling of whiteflies designed during surveys
- 2. Update data (photos) of whitefly density sampling fields.

3. Evaluate the correlation between the cassava leaves and whiteflies in Vietnam by determining the density of whiteflies on the first 5 youngest leaves

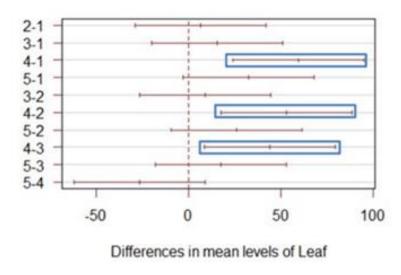
4. Sequencing of 73 whitefly samples collected during 2020-2021 surveys for phylogenetic analysis based on mtCOI gene to sequence characterize the identify a different populations.and identify a different population

- Determine the density of whiteflies by taking a picture of the first fully expanded leaf and then collecting whiteflies for diversity analysis in SEA.
- Evaluate the correlation between the cassava
 leaves and whiteflies in Vietnam by determining
 the density of whiteflies on the first 5 youngest
 leaves from 30 plants from different fields

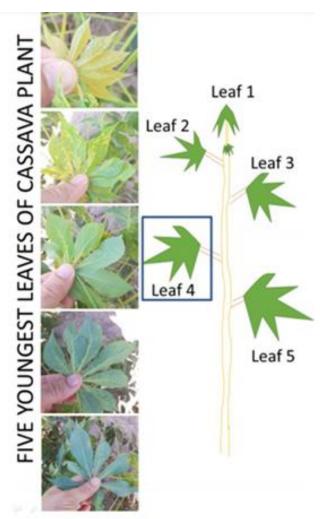
=> The preference of WF is the fourth leaf

Vietnam-Chon Thanh-Binh Phuoc Whitefly species *Bemisia tabaci* pos. Asia II-1

95% family-wise confidence level

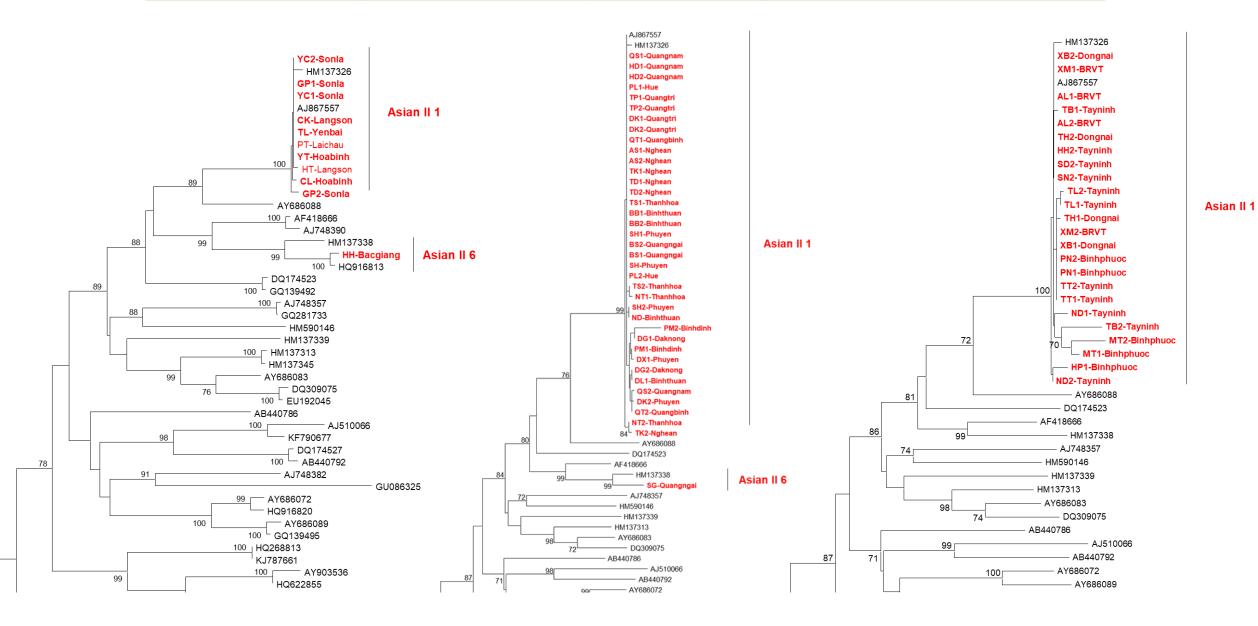


Tukey HSD test



Sequencing of 73 whitefly samples collected during 2020-2021 surveys for phylogenetic analysis based on mtCOI gene to sequence characterize the identity and different populations.





Sequencing of 73 whitefly samples collected during 2020-2021 surveys for phylogenetic analysis based on mtCOI gene to sequence characterize the identity and different populations.

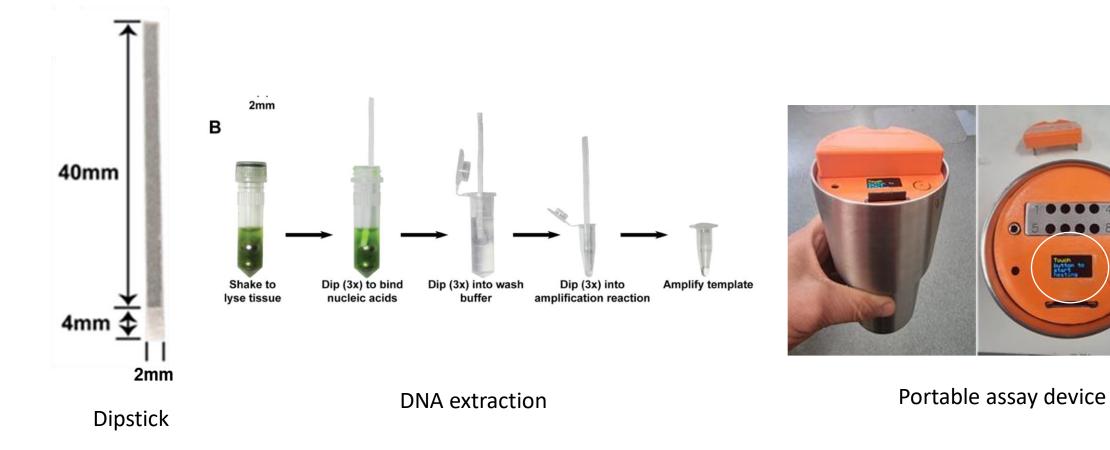
Location	No. of samples	Biotype
Northern zone	11	Asian II 1, Asian II 6
Middle zone	38	Asian II 1, Asian II 6
Southern zone	24	Asian II 1



Evaluate new technologies of rapid field diagnostic for CMD



Evaluate new technologies of rapid field diagnostic for CMD



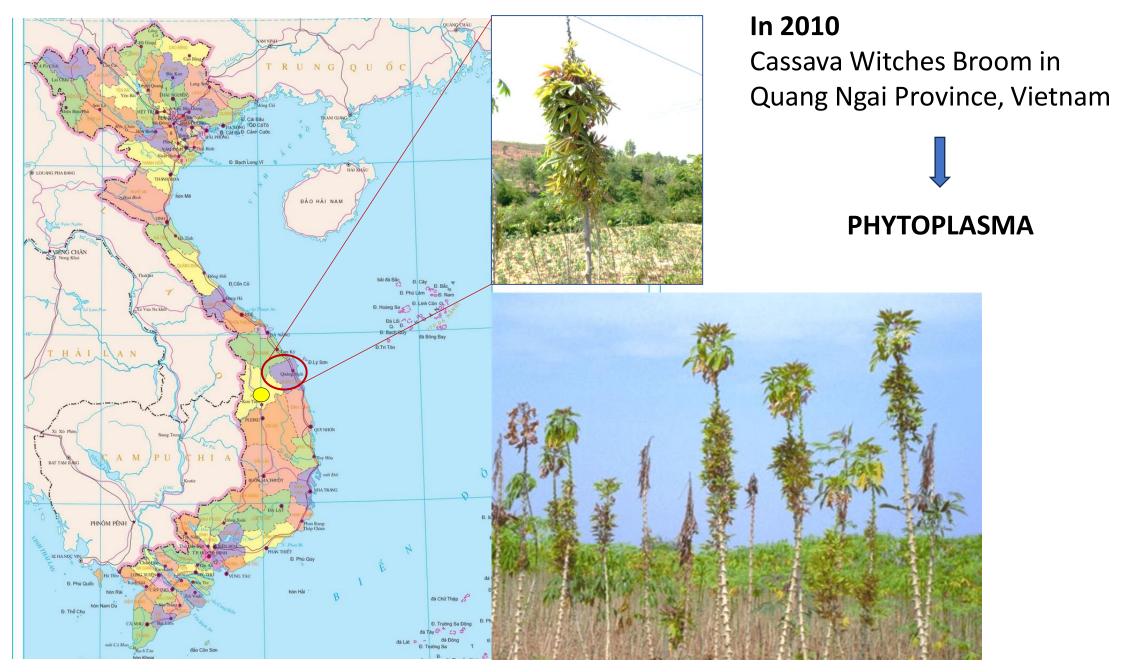
CWBD IN VIETNAM 2023



CWBD activities 2023

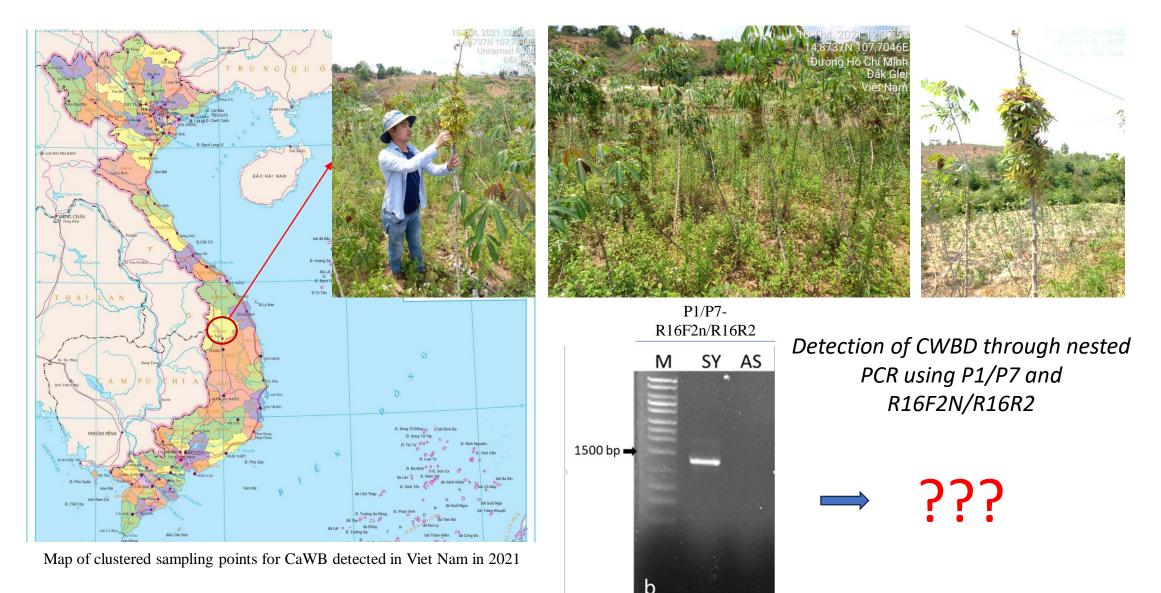
✓ Surveillance activities for CWBD in cassava growing region Vietnam

✓ Detection of agents on CWBD



Map of clustered sampling points for CWB detected in Viet Nam in 2010

Field surveillance was carried out in late April **2021** in the southern province - Kontum. The result has notably shown that CWB was coming back after a long absence.

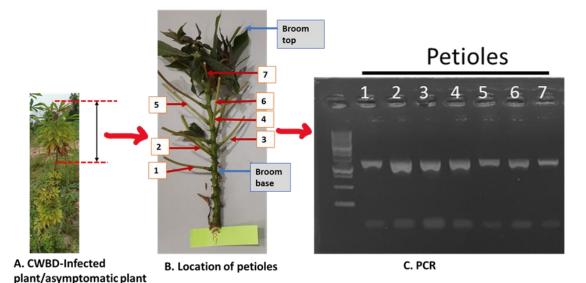


Sign of disease

Surveillance activities

- Field survey and sampling in 7 southern growing cassava provinces (Kontum, DakLak, Gia Lai, Tay Ninh, Dong Nai)
- Sampling protocol by CIAT's

Which petioles to collect?





Detection of agents on CWBD cassava

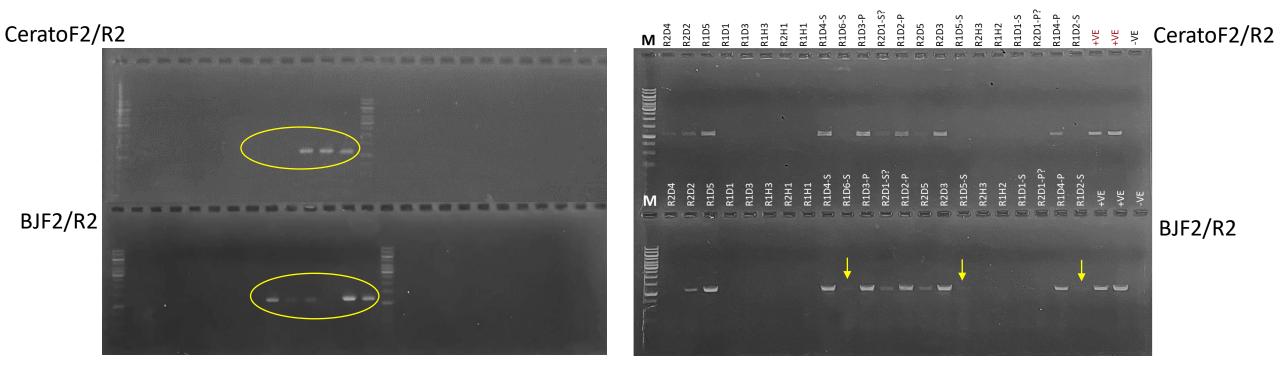
Check the accuracy of the Cerato primer



No of samples	PCR+	PCR -	Accuracy rate (%)	sensitivity[TP/(TP+FN)*100]	specificity [TN/(TN+FP)*100]
47	39	8	83	83	100
5	0	5	100		
2	2	0			
54	41	13	2		
	5 2	47 39 5 0 2 2	47 39 8 5 0 5 2 2 0	47 39 8 83 5 0 5 100 2 2 0 100	47 39 8 83 83 5 0 5 100 2 2 0

Detection of agents on CWBD cassava

Check the accuracy of pairs of primer detecting Ceratobasidium



Surveillance activities

CWBD symptoms

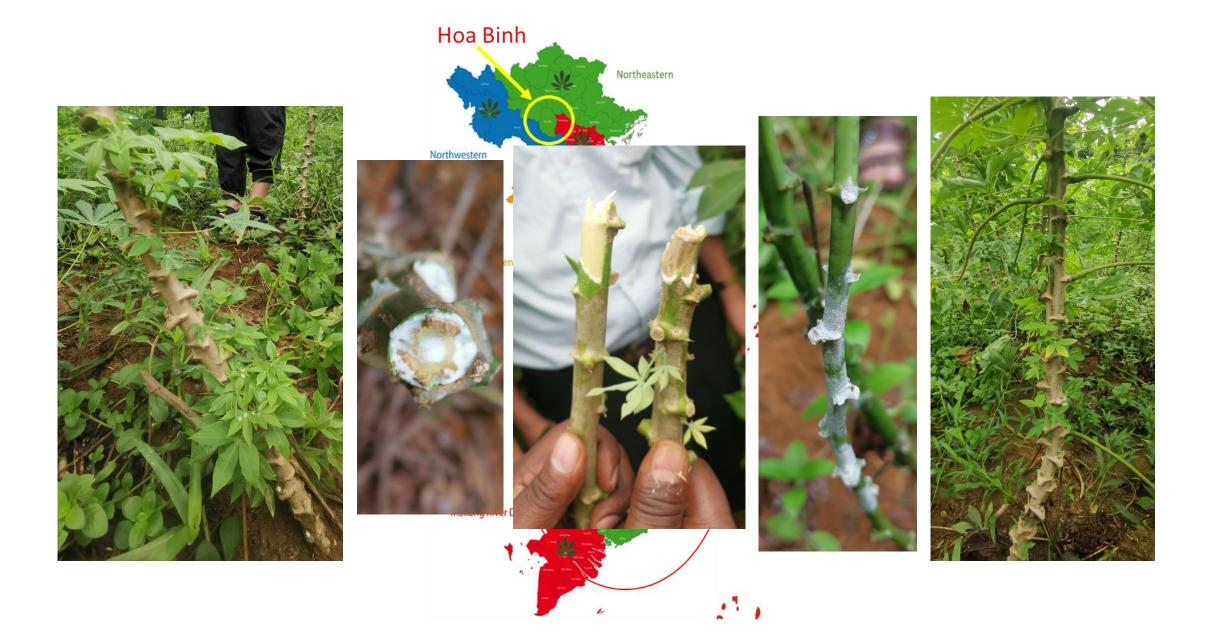


Surveillance activities

Symptom confusion



Expanding the scope of disease survey to northern provinces



Expanding the scope of disease survey to northern provinces



Expanding the scope of disease survey to northern provinces

M	R2D4	R2D2	R1D5	R1D1	R1D3	R1H3	R2H1	👢 R1H1	R1D4-S	R1D6-S	R1D3-P	R2D1-S?	R1D2-P	R2D5	R2D3	R1D5-S	R2H3	R1H2	R1D1-S	R2D1-P?	R1D4-P	R1D2-S	+VE	+VE	-VE
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	4	2	2	Ļ	8	3	1	,	4-S	6-S	3-P	1-S?	2-P	Δ	3	5-S	3	2	1-S	1-P?	4-P	2-S	•	-	
M	R2D4	R2D2	 R1D5 	R1D1	Į R1D3	R1H3	R2H1	R1H1	R1D4-S	R1D6-S	R1D3-P	R2D1-S?	1 R1D2-P	1 R2D5	I R2D3	. I R1D5-S	R2H3	I R1H2	R1D1-S	R2D1-P?	R1D4-P	👬 R1D2-S	11 +VE	J/+ /	1 -VE
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THANK YOU

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