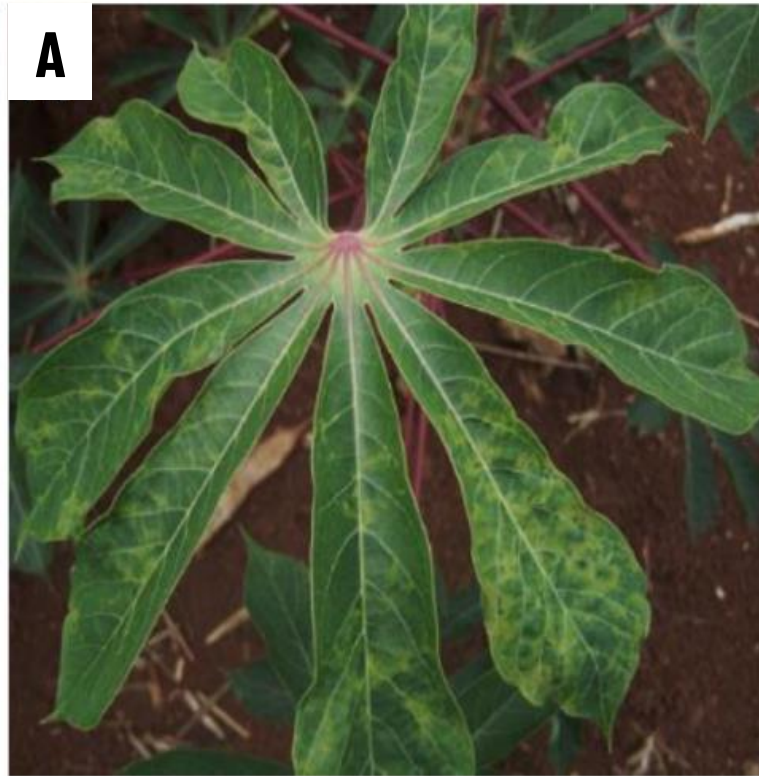




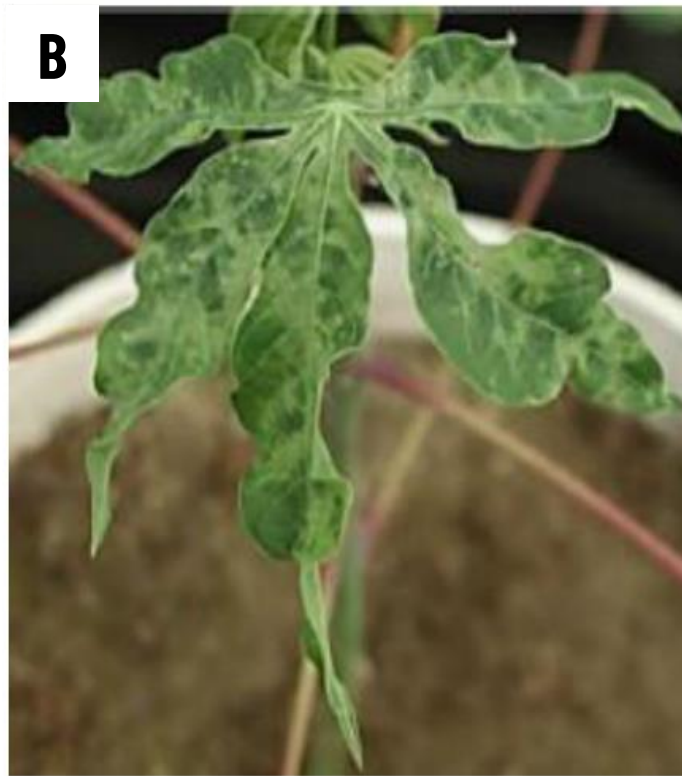
Maintaining productivity in mainland Southeast Asia by addressing CMD

Wilmer Cuellar
Cassava Program Retreat - Colombia
February - 2023

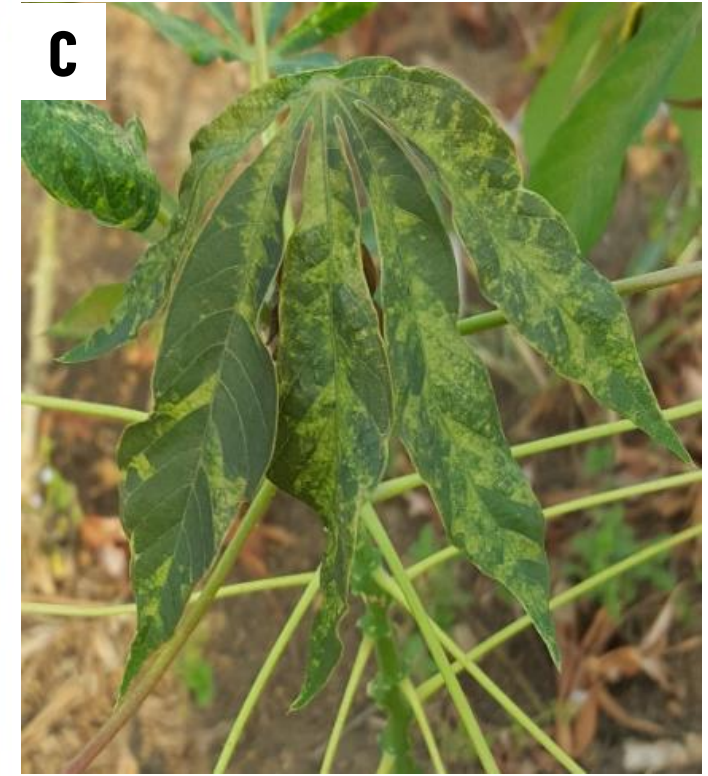
Mosaic Diseases of cassava



Mosaico común
(virus de ARN)
LAC



Mosaico 'Caribeño/Cuero de Sapo'
(infecciones mixtas)
LAC



Mosaico 'Africano'/Mosaico Asiático
(virus de ADN)
Africa y Asia

LAC = Las Americas y el Caribe

CMD in SEA emerged after a 'first wave' of CWBD

- 2010: CWBD incidence ~80% in Yen Bai, Quang Ngai and Dong Nai (north, central and south Vietnam)
- 2012: CWBD incidences of 30-40% in Cambodia in the provinces of Kampong Cham, Kratie and Prey Veng.
- 2012: field surveys in Chachoengsao and Rayong in southern Thailand, report similar "high incidences" of CWBD.
- 2014: average incidence of CWBD in SEA 32% (highest in Cambodia, 46%)
- High impact on planting material for next season



KU50 the most important cassava variety in the world
(shows tolerance to CMD but is susceptible to CWBD)

Cassava Mosaic Disease

Nucleotide sequence of cassava latent virus DNA

Ann. appl. Biol. (1982) **101**, 33–42
With 1 plate
Printed in Great Britain

33

Serological studies on cassava latent virus

By J. C. SEQUEIRA* AND B. D. HARRISON

Scottish Crop Research Institute

Particles of cassava latent virus were detected in extracts from infected cassava plants kept at 15 °C or 30 °C. The concentration of virus in the extracts was comparable to that in leaves with fluorescent antibody.

Trop. Sci. 1994, **34**, 3–14

African cassava mosaic virus disease: an under-estimated and unsolved problem

J. M. Thresh, L. D. C. Fishpool, G. W. Otim-Nape* and D. Fargette†

Natural Resources Institute, Chatham Maritime, Kent, ME4 4TB, UK. *Namulonge Agricultural and Animal Production Research Institute, PO Box 7084, Kampala, Uganda; †ORSTOM/LPRC/CIRAD, BP 5035, 34032, Montpellier, France

Abstract A brief history is presented of research on African cassava mosaic disease, which is caused by a whitefly-borne geminivirus. Particular attention is given to epidemiology, control and effects on yield. It is estimated that mosaic disease in Africa causes crop losses of 28–40% totalling 28–49 million tonnes per annum. Attention is drawn to the opportunity for considerable increases in production by using virus-resistant varieties and sanitation, although it will be difficult to ensure the adoption of these control measures on a sufficiently wide scale.

“The disease now known as African cassava mosaic (ACMD) was first reported in 1894 in Tanzania”

“No virus was detected in or transmitted from infected plants until 1975”

“Bock et al. (1978), found that the virus is widespread in mosaic-affected cassava growing in East Africa to the west of the Rift Valley but could not detect it in mosaic-free plants from the same fields”

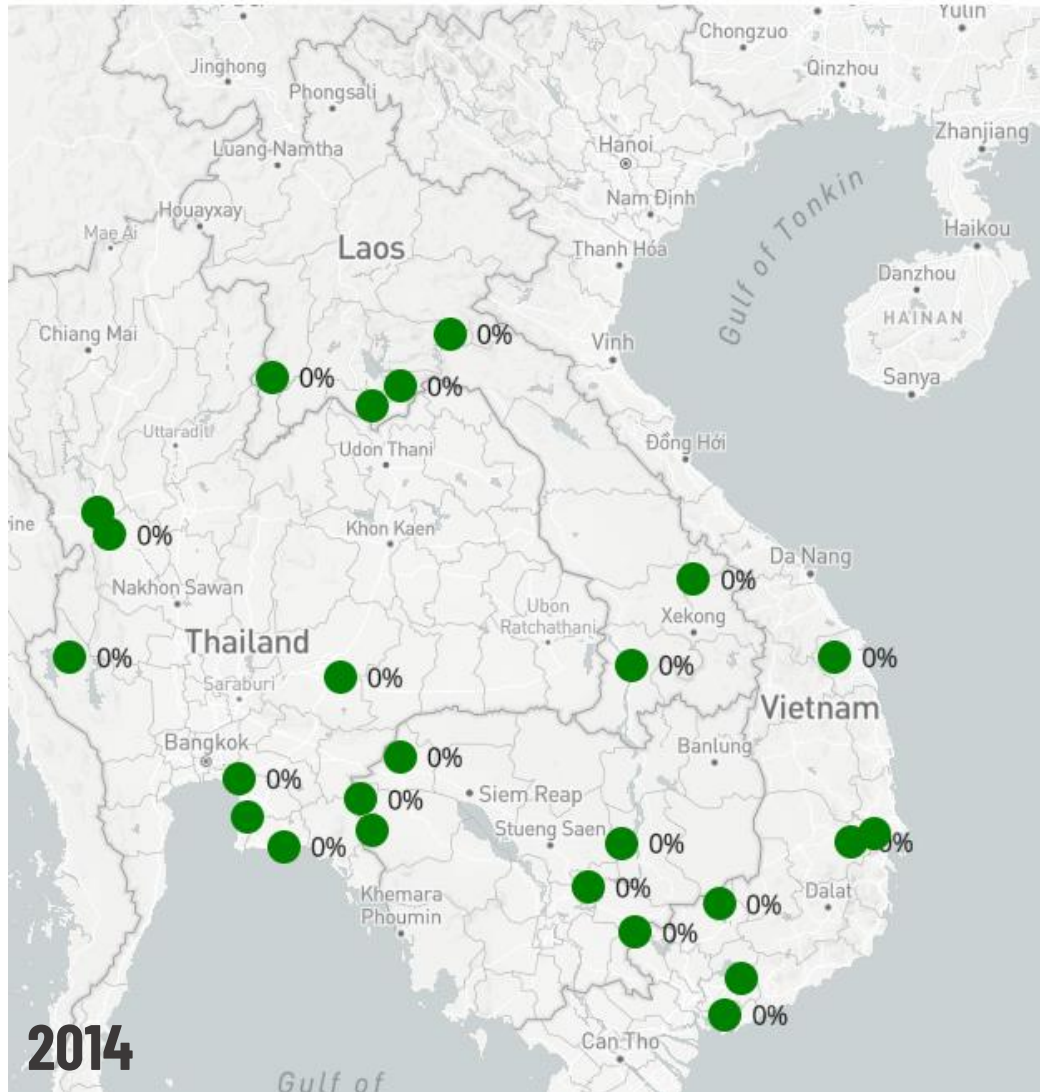
“Cassava latent virus (CLV) is almost entirely confined in East Africa to upland cassava-growing areas west of the Rift Valley, where it is often associated with cassava mosaic disease. However, it is not the causal agent, because it was not recovered from any of 31 mosaic-diseased plants in coastal districts”

Diagnosics – Symptoms vs PCR

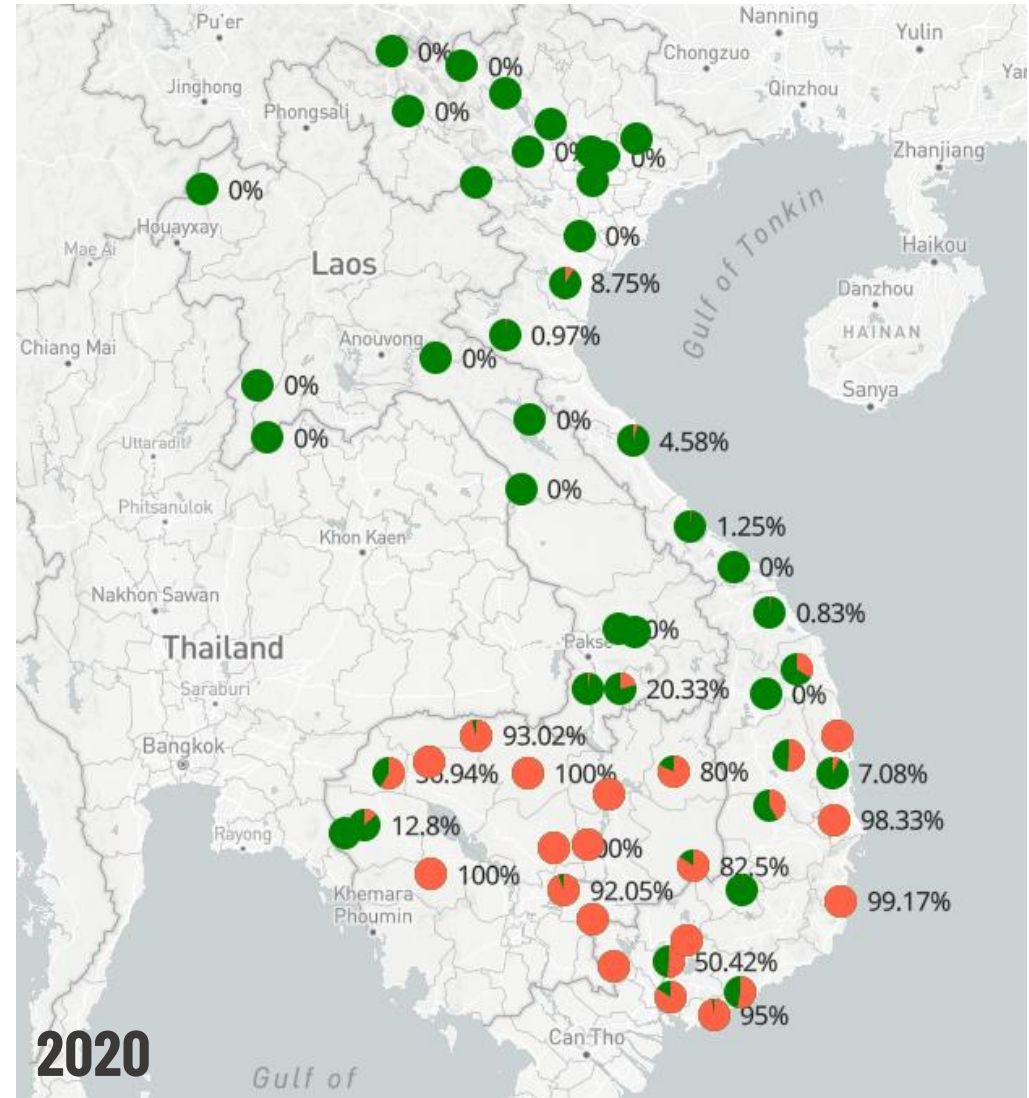
Symptoms start 3-5 months after planting

Phenotype	CWBD			CMD		
	No of samples	PCR (-)	PCR (+)	No of samples	PCR (-)	PCR (+)
Asymptomatic	20	19	1	284	244	40
Symptomatic	31	0	31	76	1	75
Other symptoms	3	3	0	0	0	0
Total	54 (1 field; one country)			360 (8 fields; 2 countries)		

Incidence maps (Province level) – standard protocols



Transect sampling, 50 observations per field; 3-5 months plants

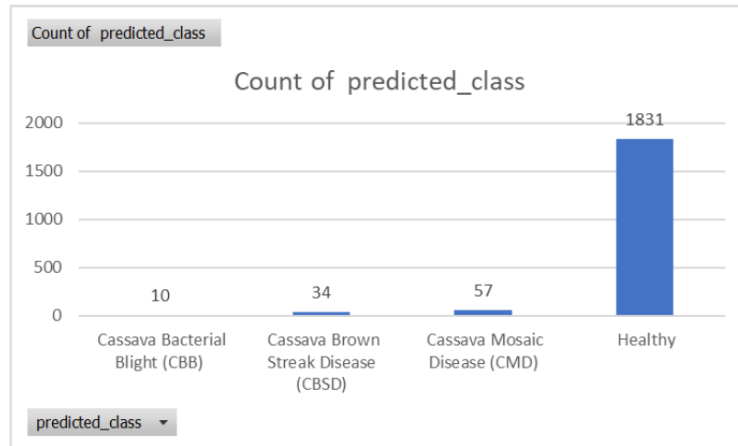


Transect sampling, 60 observations per field; 4-6 months plants

Use of AI for bulk classification of CMD symptoms

Healthy plants

This first evaluation was carried out with 1932 images previously identified by an expert as healthy (or no-CMD). The tool classified those images in the following way:

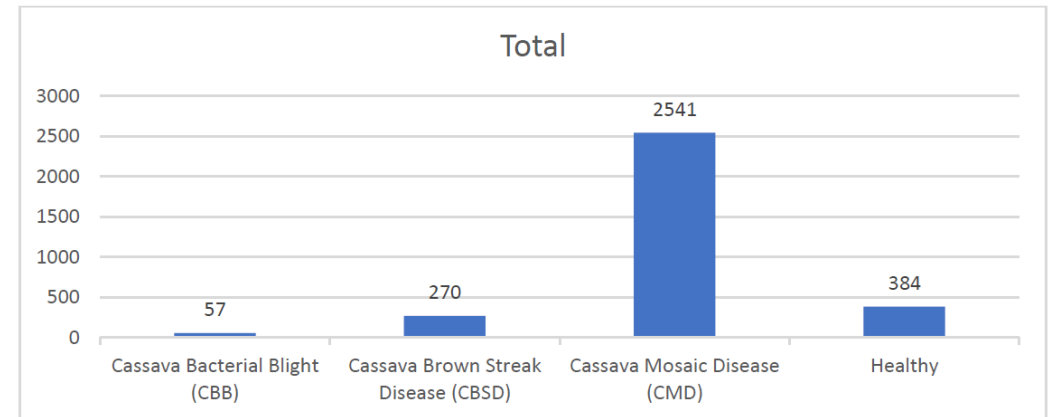


1831 images were classified as 'Healthy', which corresponded to 94% of the images. 57 images

94%

CMD symptoms

The following evaluation corresponded to a dataset of 3252 images of CMD symptoms identified by an expert. The results were as follows:



In this case a 78% of the images (2541) were rightly classified as CMD by the tool, but the 22% restante was classified as other disease (or as Healthy).

78%

CMD in the world – 12 virus species

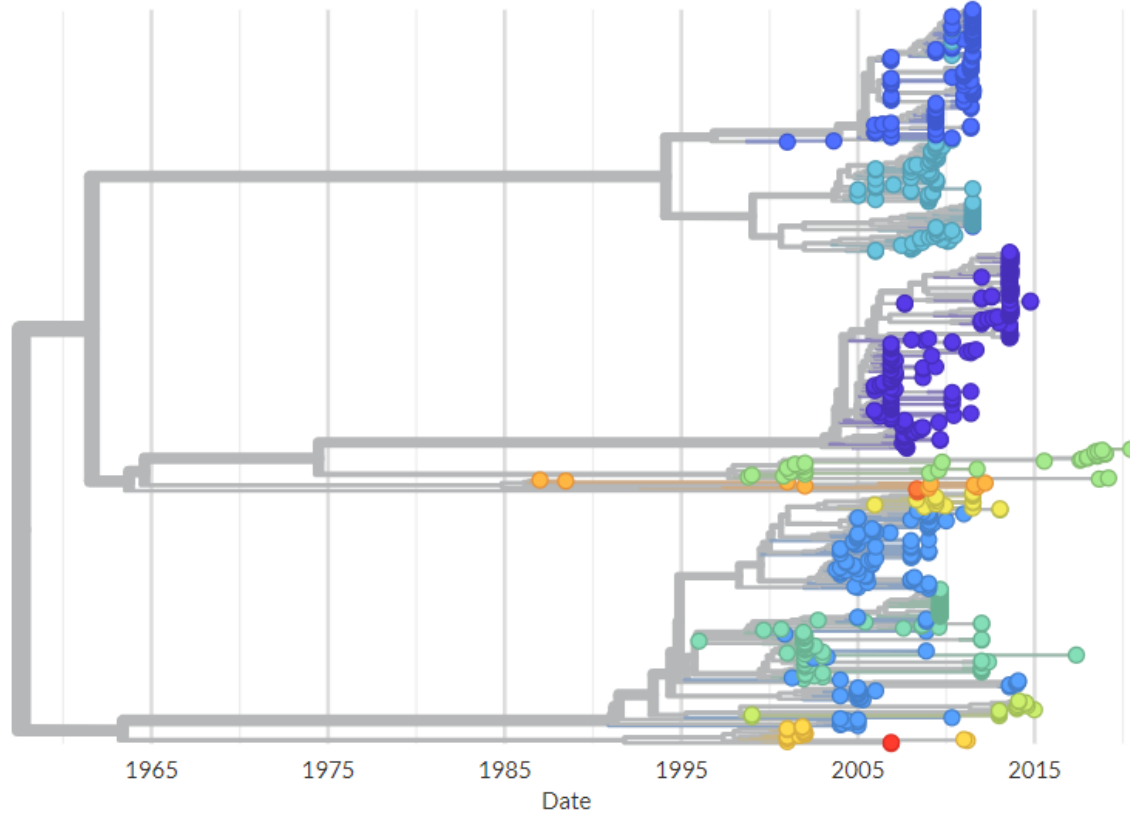
Built with [pestdisplace/Geminivirus](#). Maintained by [PestDisPlace](#).

Showing 739 of 739 genomes sampled between Dec 1986 and Jun 2020.

Phylogeny

Virus ▾

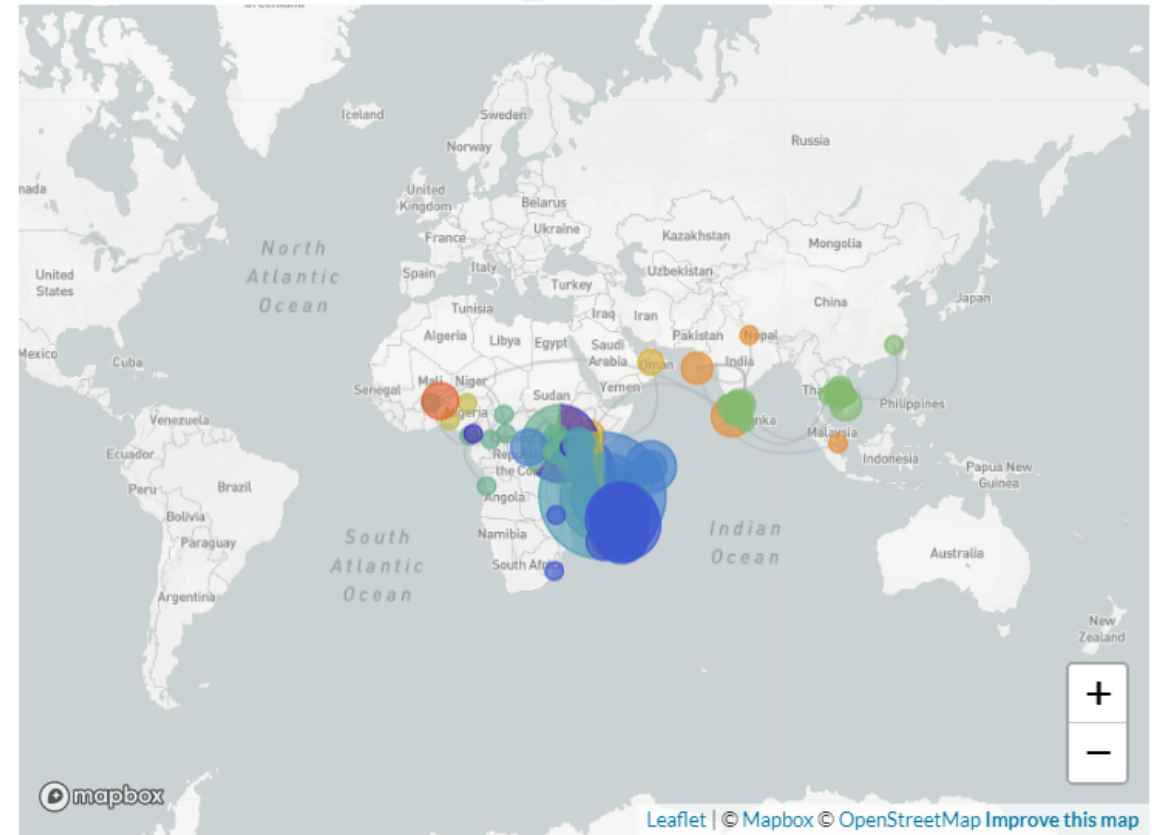
🔍 ZOOM TO SELECTED RESET LAYOUT










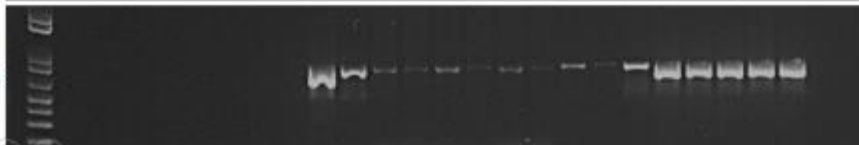


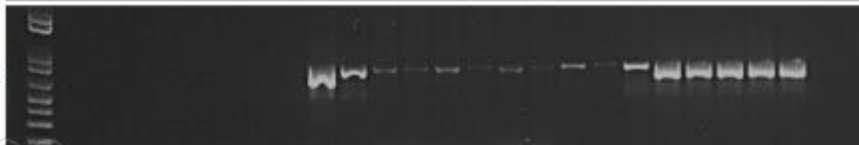
Virus ^

- ACMV
- SACMV
- EACMV
- EACMKV
- EACMV UG
- SLCMV
- EACMMV
- EACMCV
- EACMZV
- ICMV
- ACMBFV
- CMMGV

Transmissions



PCR and LAMP versus Genome Sequencing

Samples	Not infected	Asymptomatic	Symptomatic
			
	Extraction	Washing	Elution
Process			
	Not infected	Asymptomatic	Symptomatic
DipSticks			
	CTAB		

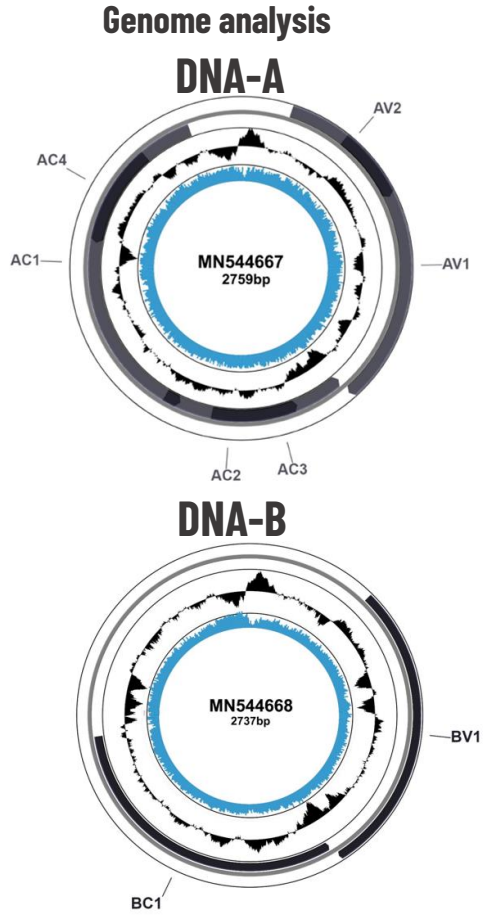


Coffee cup droid

UQueensland



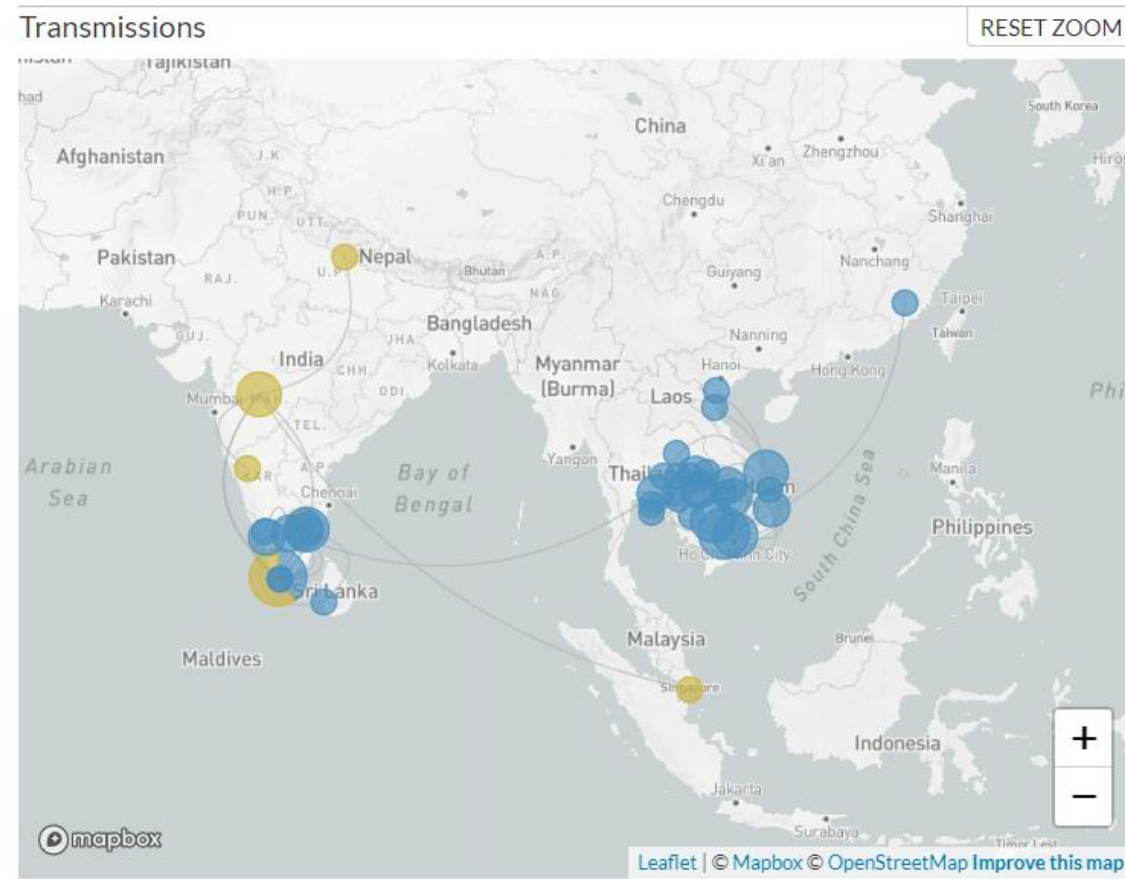
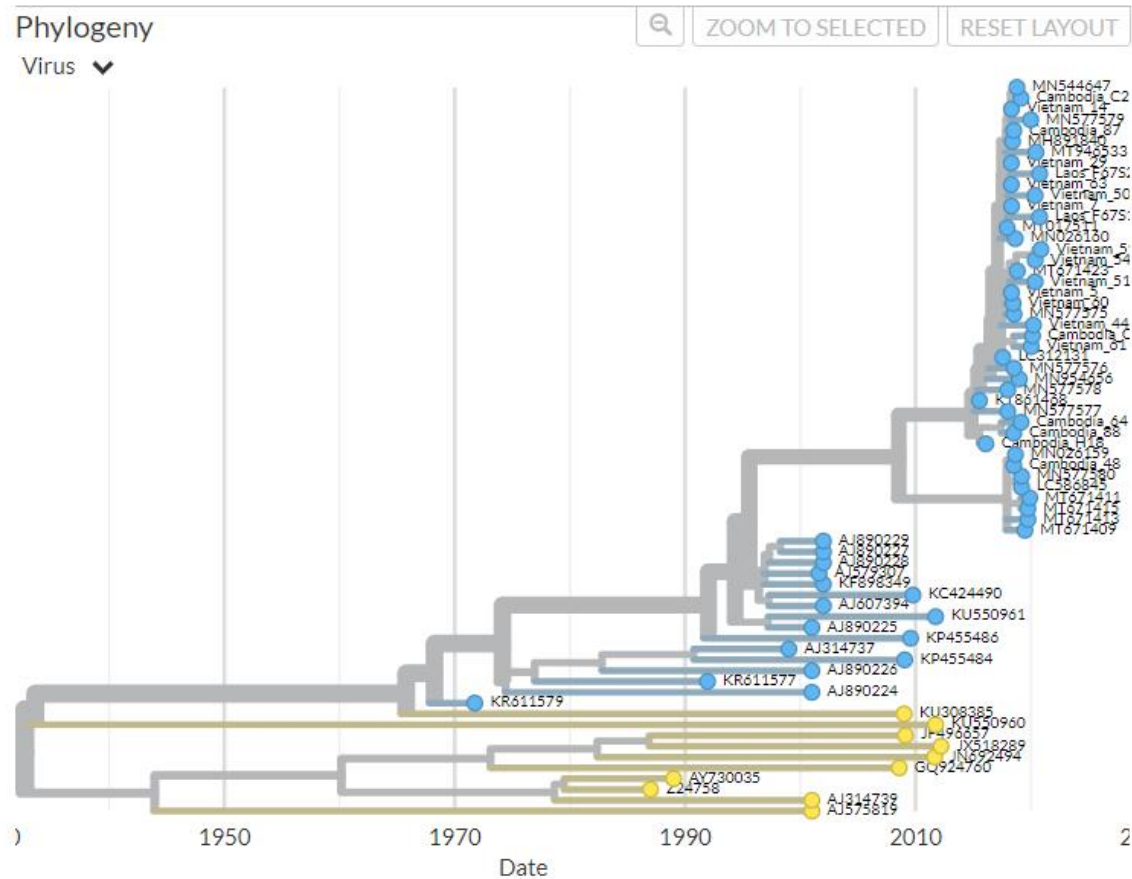
Nanopore



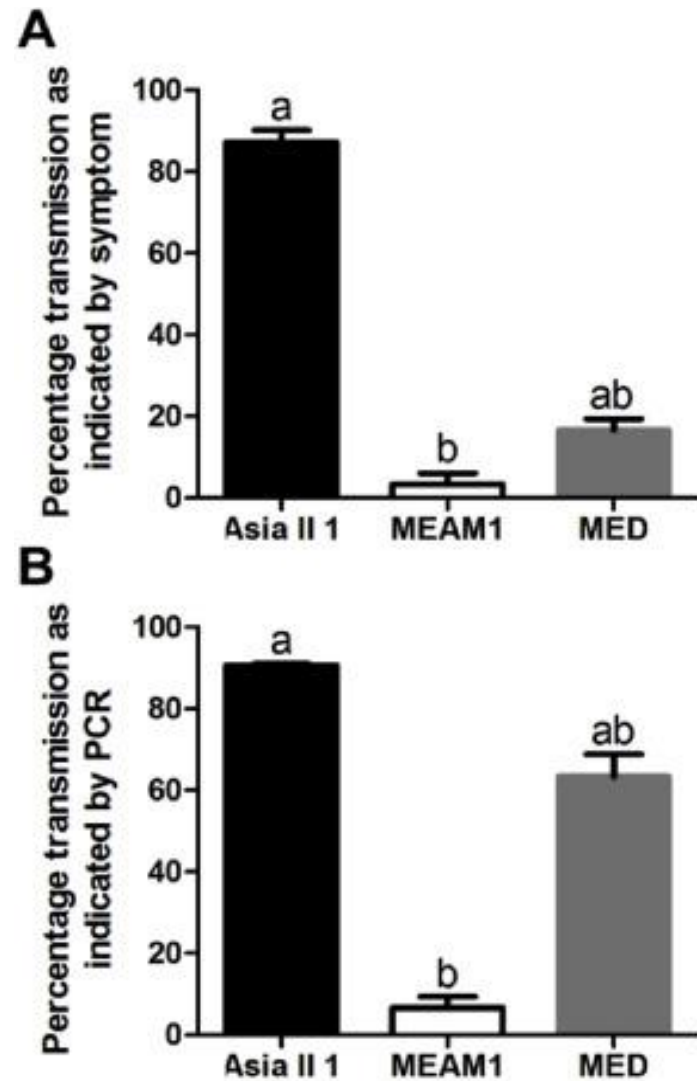
CMD in Asia – One virus species (so far)

 Built with pestdisplace/CMDASIA1. Maintained by PestDisPlace.

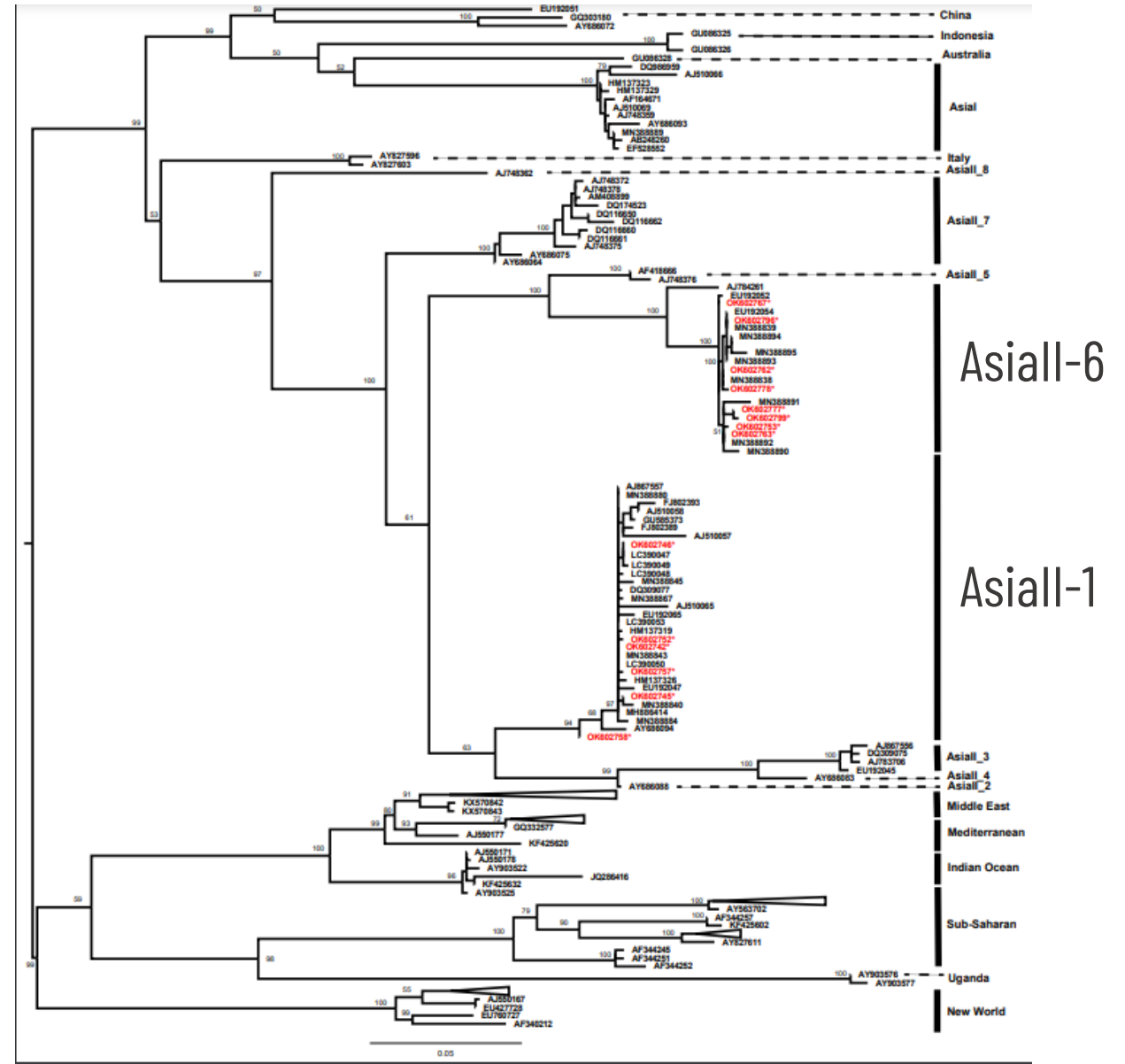
Showing 68 of 68 genomes sampled between Sep 1971 and Nov 2020.



Whiteflies (WF)



Chi et al., 2020



Leiva et al., 2022

Relative abundance of the insect vector

Table 1. List of surveyed provinces and abundance data for whiteflies associated to cassava in Lao PDR. Comparative whitefly abundance data from Tanzania and Nigeria is included. SD = standard deviation. The asterisks indicate provinces where CMD was observed. Asia II 1 and its haplotypes are indicated in red.

Country	Province	No. of Fields	Abundance (Per Leaf)	SD	Cryptic Species	Haplotype	Ref.
Lao PDR	LaoungNamTha	2	0.150	0.012	Asia II 1	H1	This work
	Saiyabouly	9	0.041	0.021	Asia II 1	H1	
	Vientiane	5	0.014	0.012	Asia II 1/Asia II 6	H1, H2, H3, H14, H17	
	Xaysomboun	3	0.078	0.040	Asia II 1	H1	
	Borlikhamsai	11	0.145	0.034	Asia II 1/Asia II 6	H1, H5, H20, H13	
	Khammoun	1	0.166	0.000	Asia II 1	H1	
	Salavan	7	0.129	0.031	Asia II 1/Asia II 6	H12, H17, H15, H16	
	Sekong	1	0.167	0.000	Asia II 6	H18	
	Champasack *	25	0.177	0.043	Asia II 1/Asia II 6	H1, H2, H6, H17, H16, H14, H21	
Attapue *	6	0.233	0.072	Asia II 1/Asia II 6	H1, H17, H16		
Tanzania			2.35–71.99 (14.3)	0.86–22.07	SSA1-SG1-SG2-SG3	ND	[47]
Nigeria		24	2.34–265.5		SSA1-SG5, SSA3, SSA1-SG1-Bemisia afer, MED-ASL	ND	[48]

Strengthen existing networks



Awareness raising leads to early detection and rapid response



Notes

- Identifying tolerant/resistant varieties against CMD in the current context (i.e. consider CWBD)
- Timely detection of resistance-breaking strains (e.g. African geminiviruses)
- Raise awareness on other cassava transboundary pests and diseases
- Monitoring of whitefly abundance
- Harmonize quarantine and seed movement protocols
- Establish disease models (biological and epidemiological) for risk and impact analyses
- Access to Biosafety Level 2-3 facilities?



Thanks!