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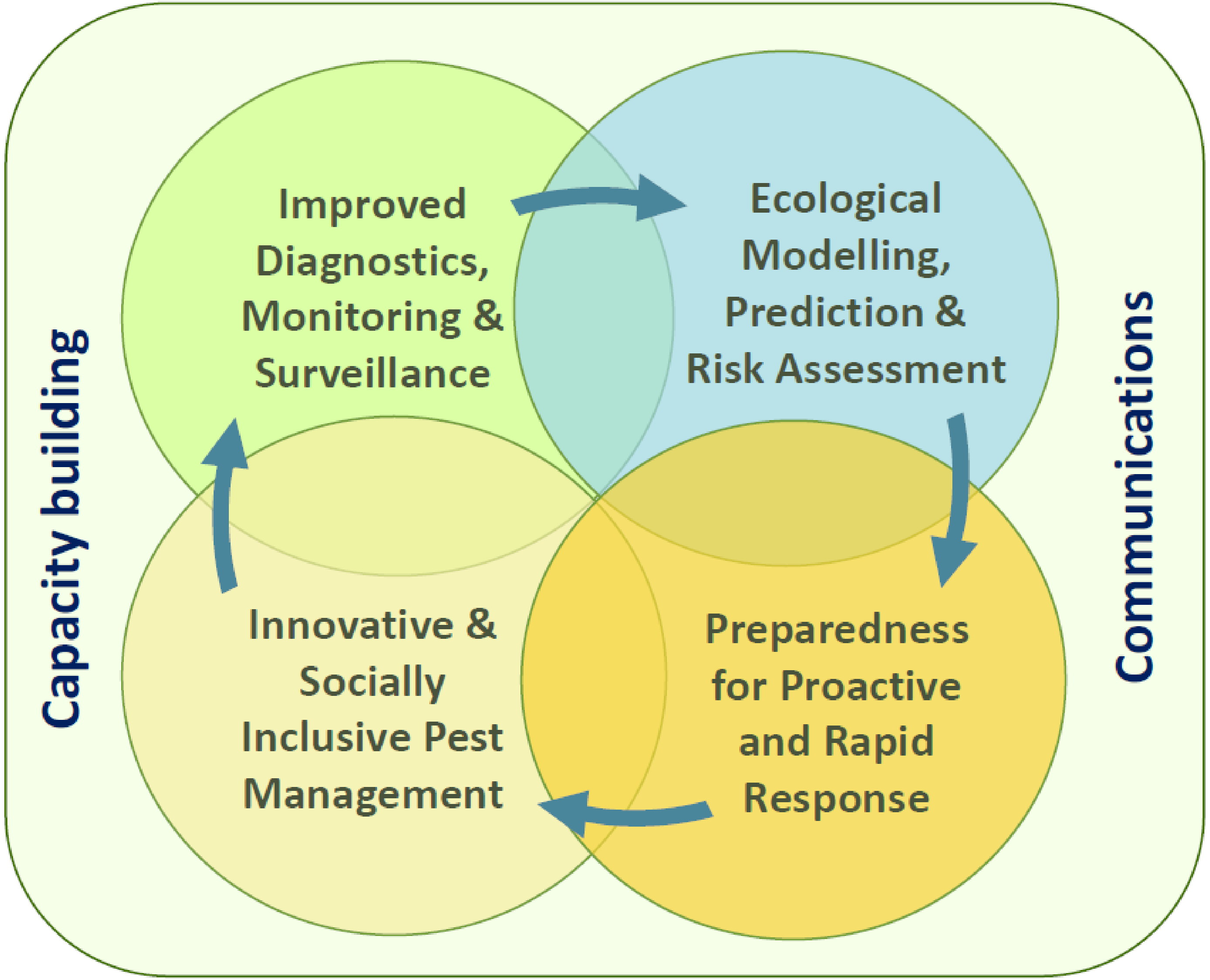
Global Plant Virus Management: Diagnostics, Surveillance, and Modelling

Jan Kreuze, Wilmer J. Cuellar, Lava Kumar, B.M. Prasanna, Aman Omondi

AfricaRice
Alliance Bioversity International CIAT International Center for Tropical Agriculture Since 1967 Science to cultivate change
CIMMYT International Maize and Wheat Improvement Center
CIP International Potato Center
ICARDA Science for resilient livelihoods in dry areas
IITA Transforming African Agriculture
IRRI

Plant Health Management under Changing Climates
Need for a Revitalized Strategy and Innovative Approaches



Next generation diagnostics

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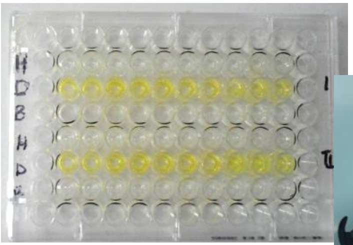
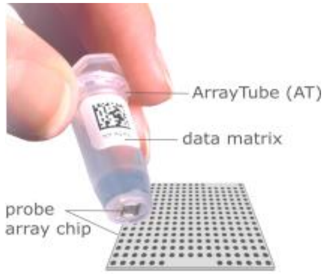
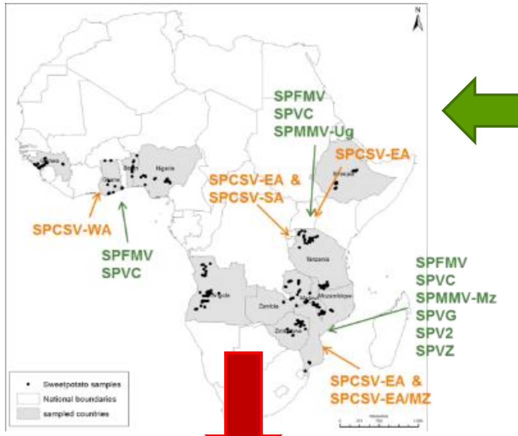
Better understanding of the major diseases contributing to crop losses, their epidemiology and cheap rapid accurate diagnostics

Appropriate diagnostics technologies

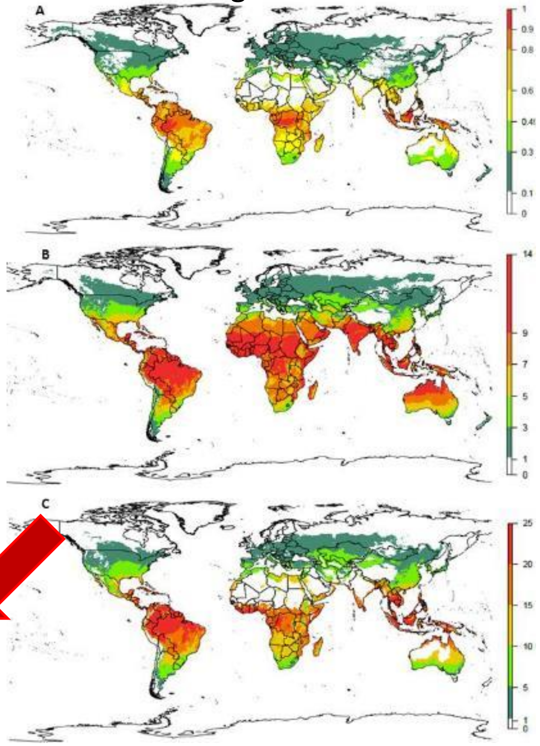




Characterization & surveillance of (new & emerging) pathogens

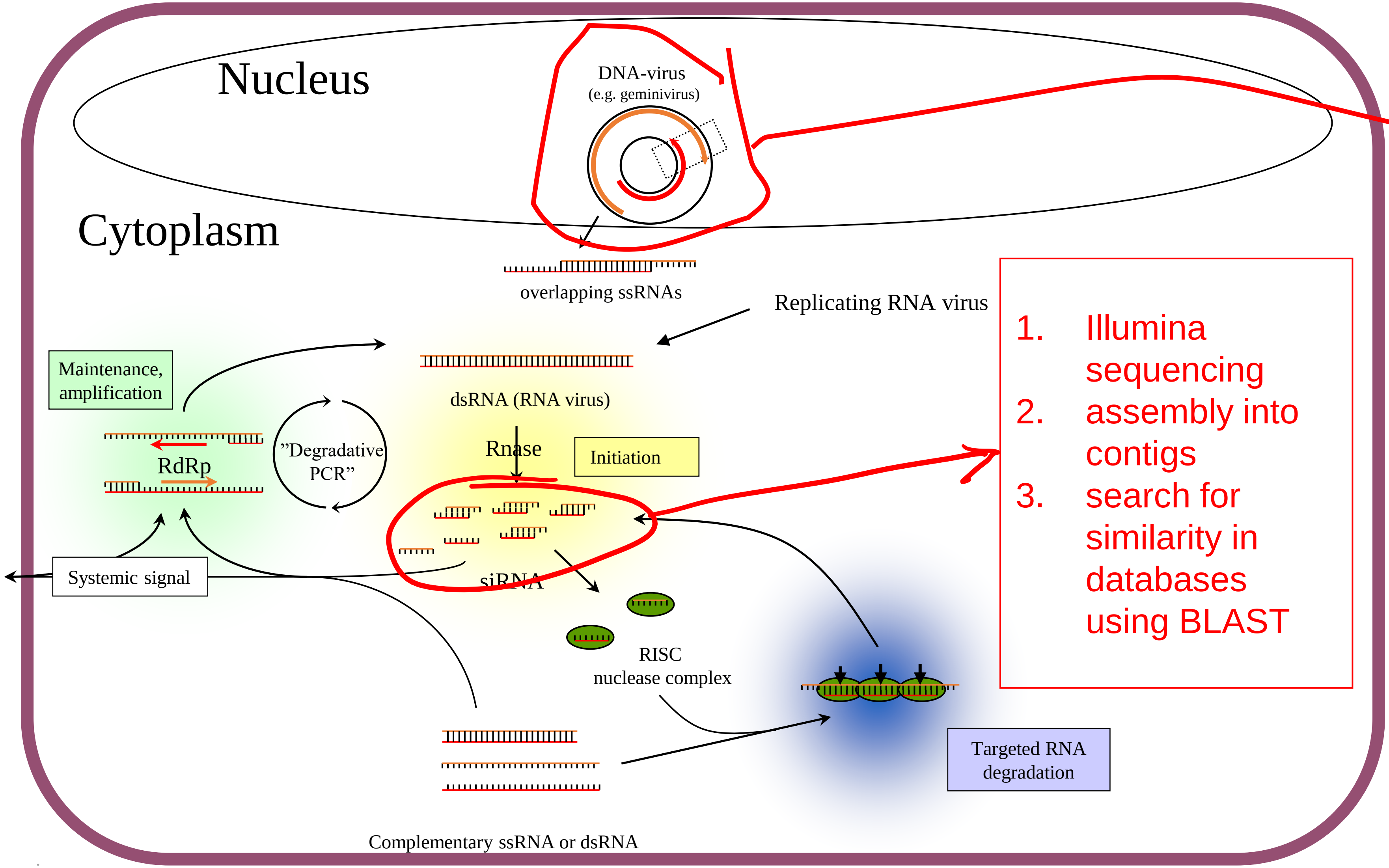


Predicting risk



disease management
germplasm exchange
crop improvement

Surveillance/monitoring using HTS

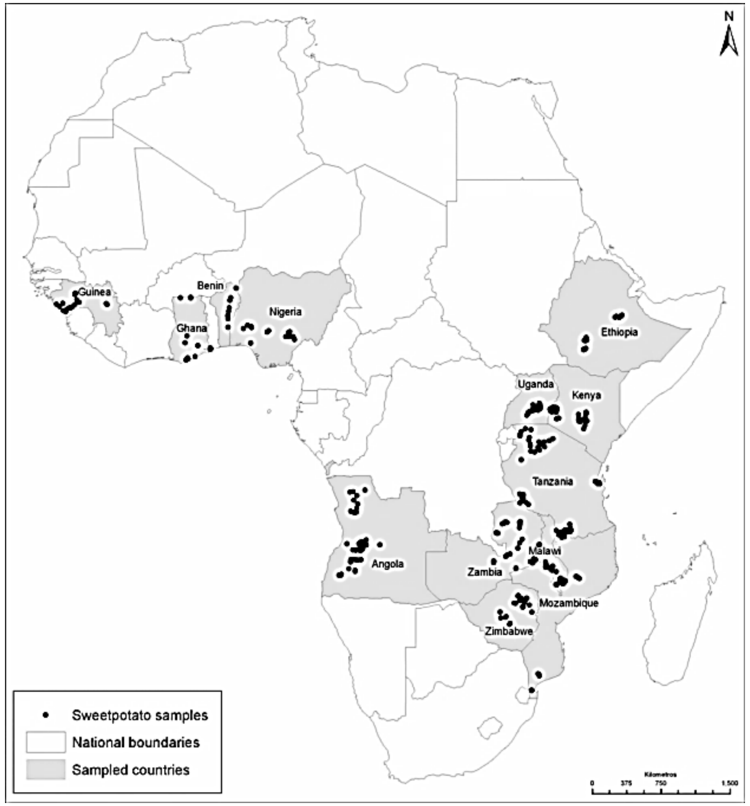


1. Illumina sequencing
2. assembly into contigs
3. search for similarity in databases using BLAST

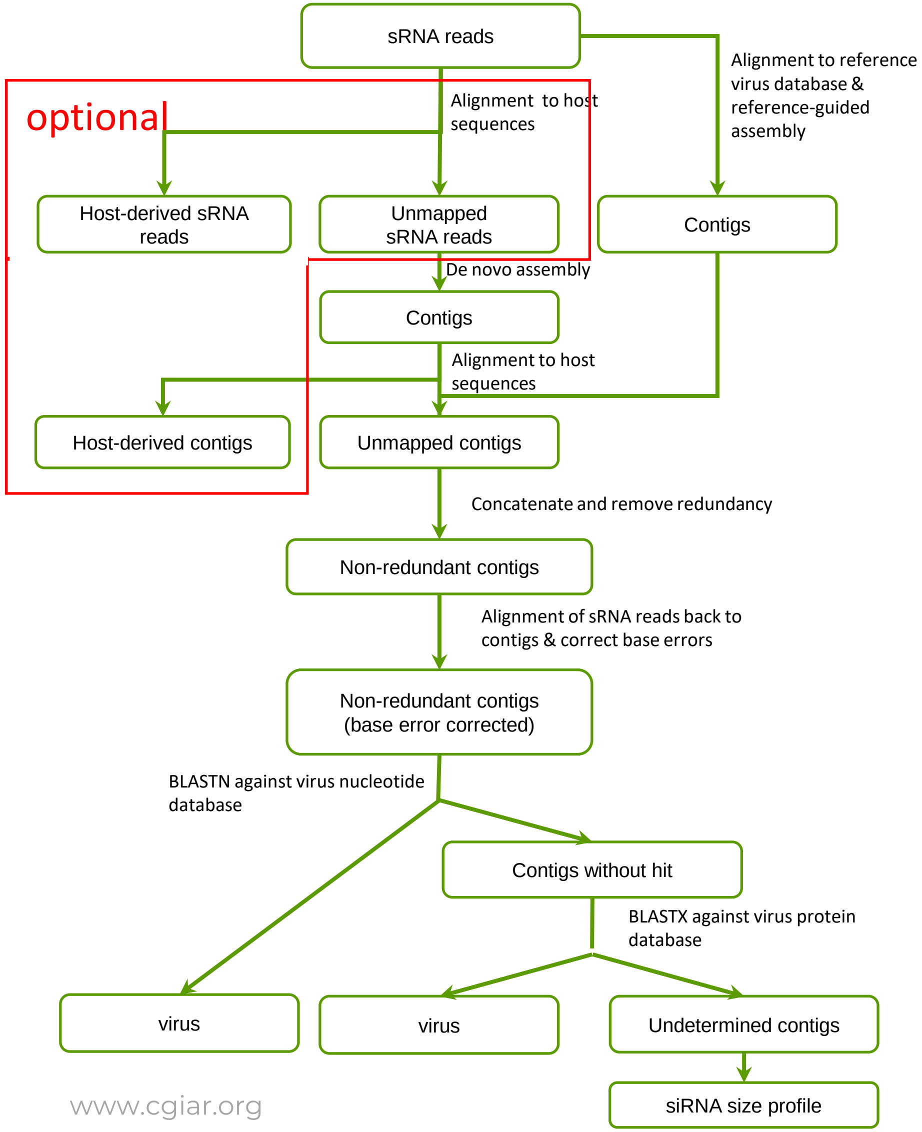
1. Rolling circle amplification
2. Nanopore sequencing

The African sweetpotato virome

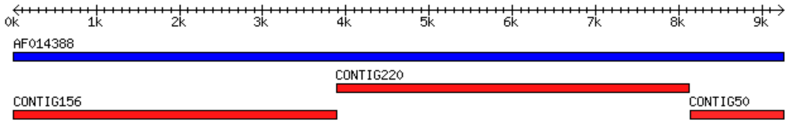
~2000 samples and bioinformatics pipeline for virus identification using siRNA assembly and genome subtraction



Small RNA sequence analysis pipeline: VirusDetect



Reference	Length	Coverage (%)	#contig	Depth	Depth (Norm)	%Identity	%Iden Max	%Iden Min	Genus	Description
FJ150422	4806	4806 (100)	11	675.9	18.5	94.64	96.00	84.82	NA	Drosophila A virus isolate HD, complete genome.
GQ342962	3260	3257 (99.9)	3	524.3	14.4	98.11	98.75	97.03	NA	Drosophila melanogaster birnavirus SW-2009a strain DBV segment A, complete sequence.
GQ342963	3014	3014 (100)	1	854.8	23.4	98.47	98.47	98.47	NA	Drosophila melanogaster birnavirus SW-2009a strain DBV segment B, complete sequence.
KF947078	13534	1773 (13.1)	27	35.2	1.0	99.10	100	97.14	NA	Spodoptera frugiperda rhabdovirus isolate Sf, complete genome.
GQ257737	12333	12333 (100)	6	661.2	18.1	96.87	99.29	91.67	NA	Nora virus isolate Umea 2007, complete genome.
M32779	2225	2112 (94.9)	7	20.4	0.6	99.57	100	97.69	alphabaculovirus	Autographa californica nucleopolyhedrovirus insertion element IFP2.2 genomic sequence.
EF690537	3107	3089 (99.4)	5	654.2	17.9	94.82	96.59	94.12	alphanodavirus	Flock house virus isolate TNCL segment RNA1 protein A mRNA, complete cds.
EF690538	1383	1383 (100)	1	378.8	10.4	94.44	94.44	94.44	alphanodavirus	Flock house virus isolate TNCL segment RNA2 protein alpha mRNA, complete cds.
AF014388	9264	9244 (99.8)	3	1096.2	30.1	98.03	98.21	96.88	cripavirus	Drosophila C virus strain EB, complete genome.



Order	Query ID	Query Start	Query End	Subjct Start	Subjct End	Identity	E value	Strand
1	CONTIG50	1	1121	8144	9264	1086/1121(96%)	0.0	1

Alignment:

```
Query: 1    tgaggttgaatatgctcgtattgttgcgcaagtaatgggtgaagatgtagctattcaaag 60
            |||||||||| ||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct: 8144 tgaggttgaagatgctcgtattgttgcgcaagtaatgggtgaagatttagctattcaaag 8203

Query: 61   aaacgatgctcaacatggtgttcatccaatgaccatagacactcataagattgactcaaa 120
            ||||||||||||||||||||||||||||||||| ||||||||||||||||| ||||||||
Sbjct: 8204 aaacgatgctcaacatggtgttcatccaatgactatagacactcataagatcgactcaaa 8263
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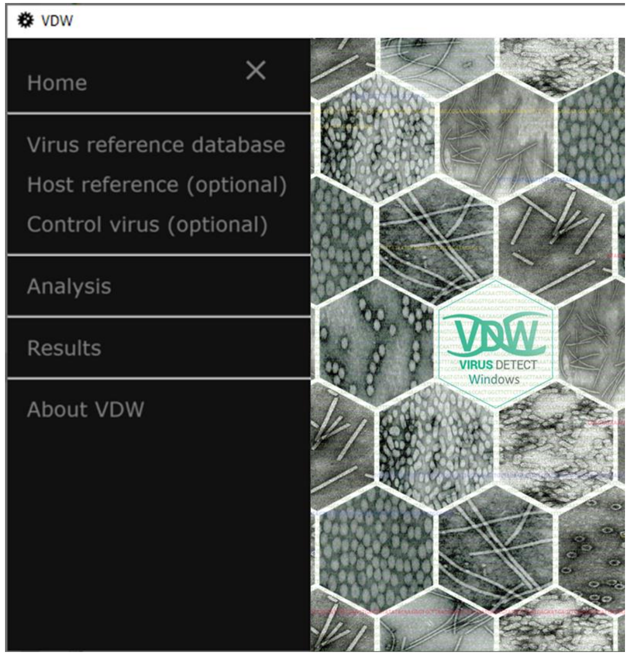
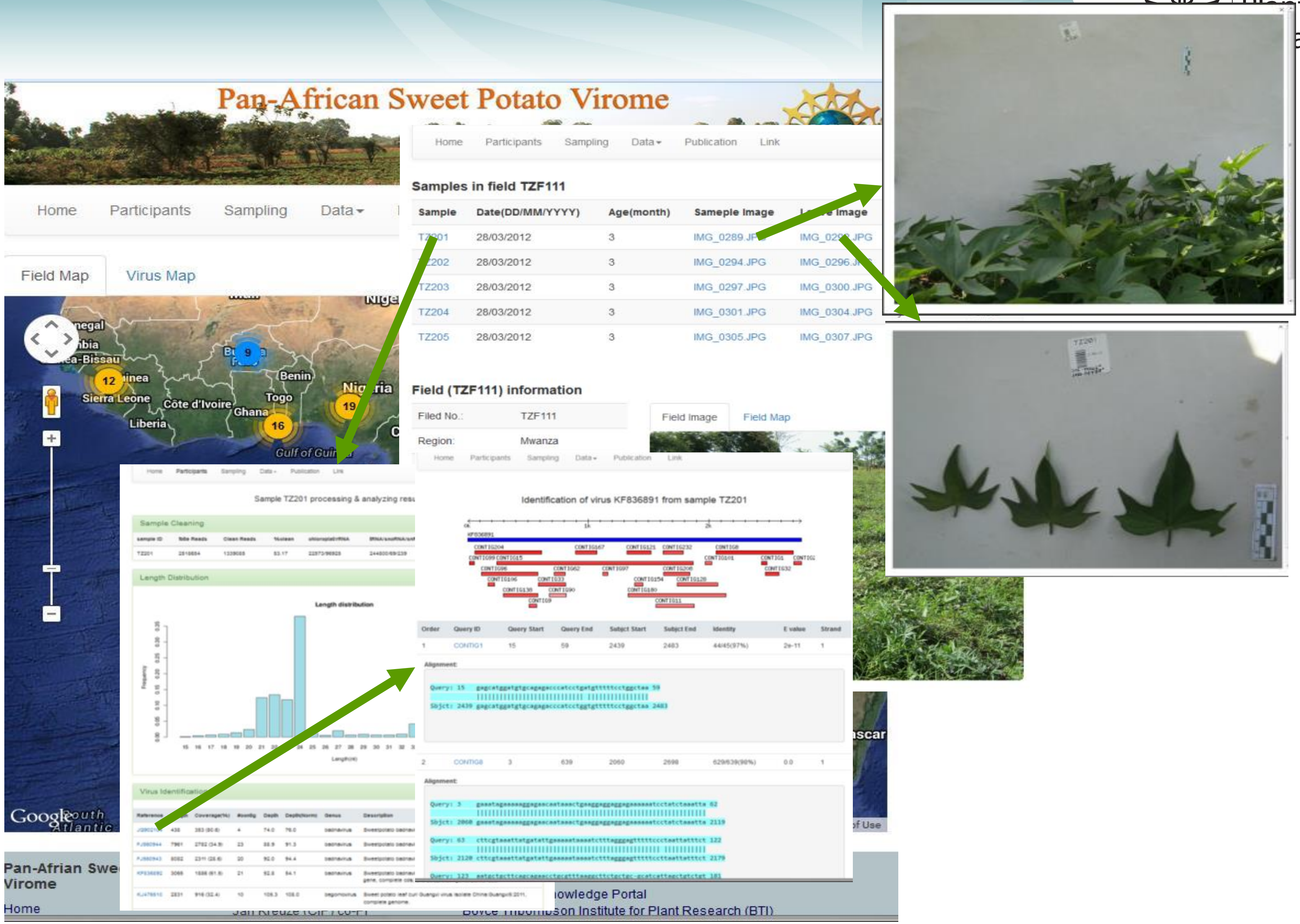
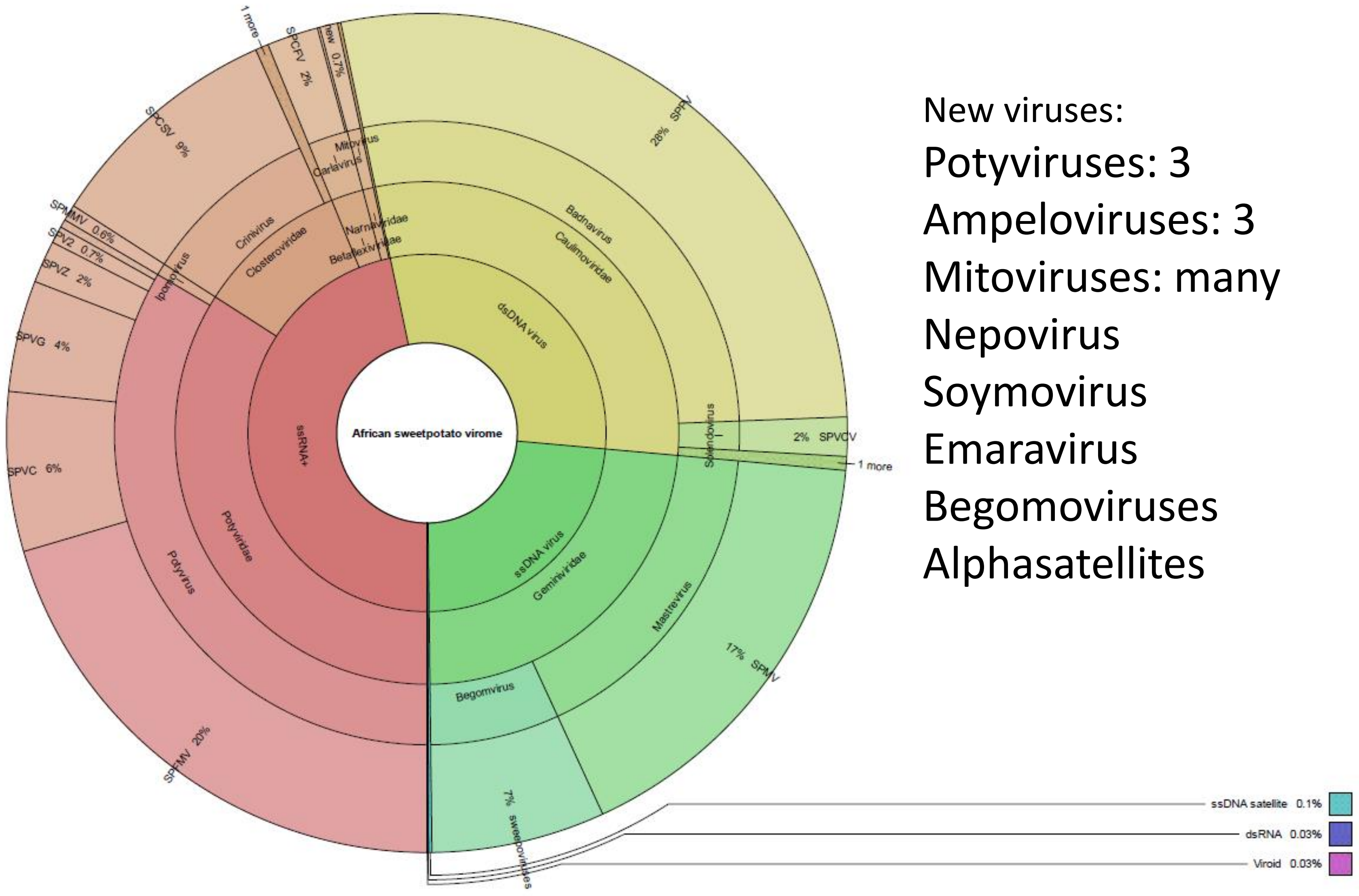


http://bioinfo.bti.cornell.edu/virome/index



Results: the viruses
3193 viruses from 1168 samples



New viruses:

Potyviruses: 3

Ampeloviruses: 3

Mitoviruses: many

Nepovirus

Soymovirus

Emaravirus

Begomoviruses

Alphasatellites

Are all viruses relevant?

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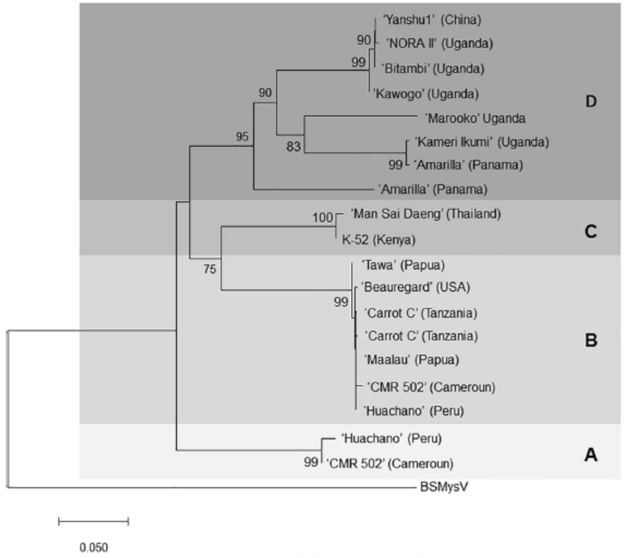
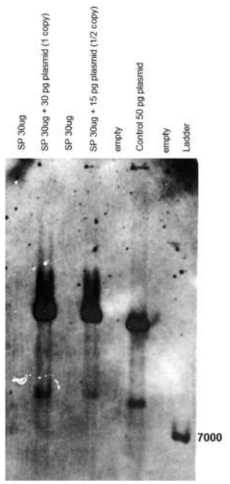
frontiers in Plant Science

ORIGINAL RESEARCH
published: 31 March 2020
doi: 10.3389/fpls.2020.00313

Badnaviruses of Sweet Potato: Symptomless Coinhabitants on a Global Scale

Jan F. Kreuze*‡, Ana Perez‡, Marco Galvez Gargurevich† and Wilmer J. Cuellar†





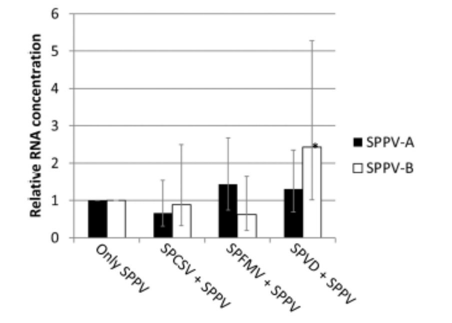


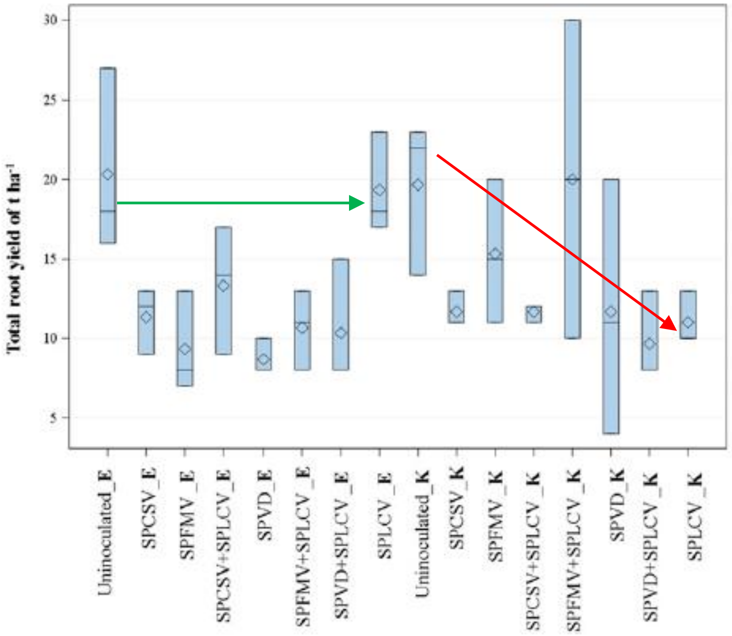
FIGURE 4 | Relative expression for *Badnavirus* SPPV A and B. Bar graph depicting the expression of SPPV-A and SPPV-B in leaves in coinfection with SPFMV, SPCSV, or both viruses (SPVD) relative to plants infected only with SPPV (only SPPV). Error bars indicate standard error of relative expression. *Significantly upregulated as compared to plants infected only by SPPV (only SPPV; $p = 0.001$).

Plant Disease • 2020 • 104:1477-1486 • https://doi.org/10.1094/PDIS-06-19-1196-RE

e-Xtra*

Storage Root Yield of Sweetpotato as Influenced by *Sweetpotato leaf curl virus* and Its Interaction With *Sweetpotato feathery mottle virus* and *Sweetpotato chlorotic stunt virus* in Kenya

Bramwel W. Wanjala,[1,2] Elijah M. Ateka,[2] Douglas W. Miano,[3] Jan W. Low,[1] and Jan F. Kreuze[4,†]



https://doi.org/10.3389/fpls.2020.00313

https://doi.org/10.1094/PDIS-06-19-1196-RE

Can we make predictions about likely occurance beyond evaluated areas?

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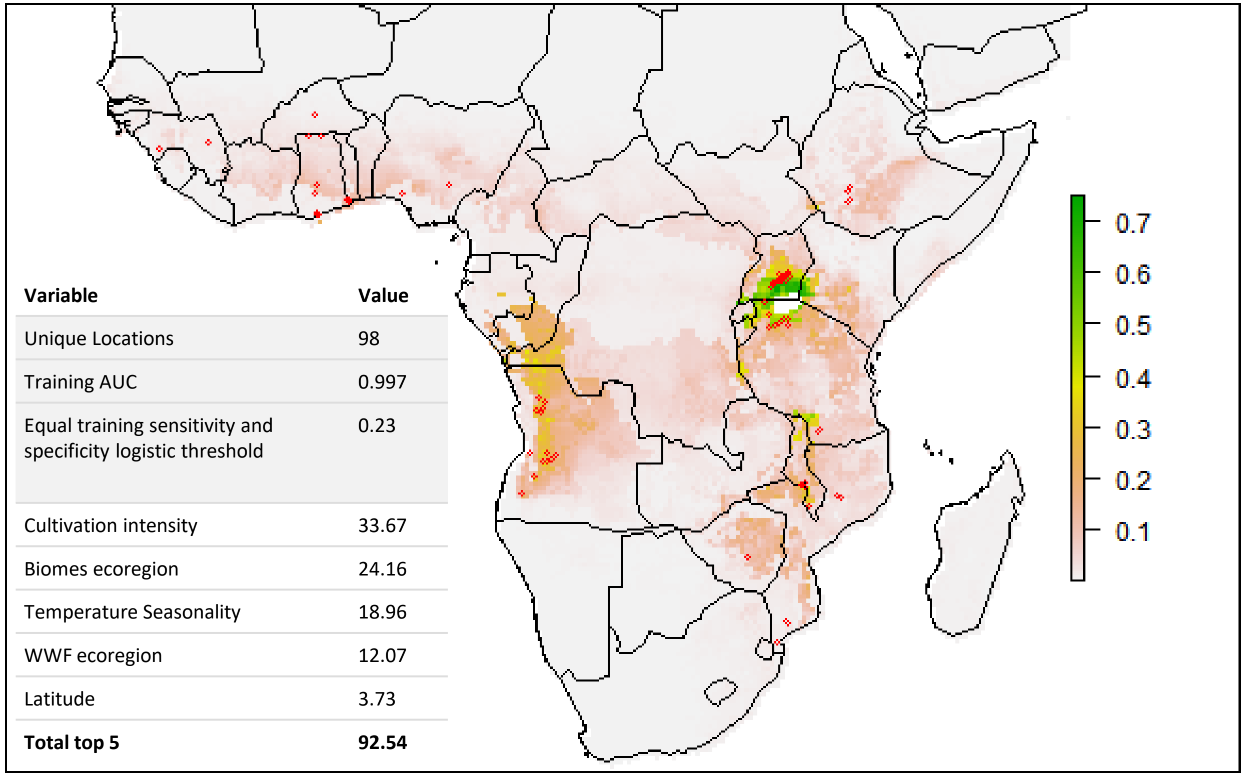
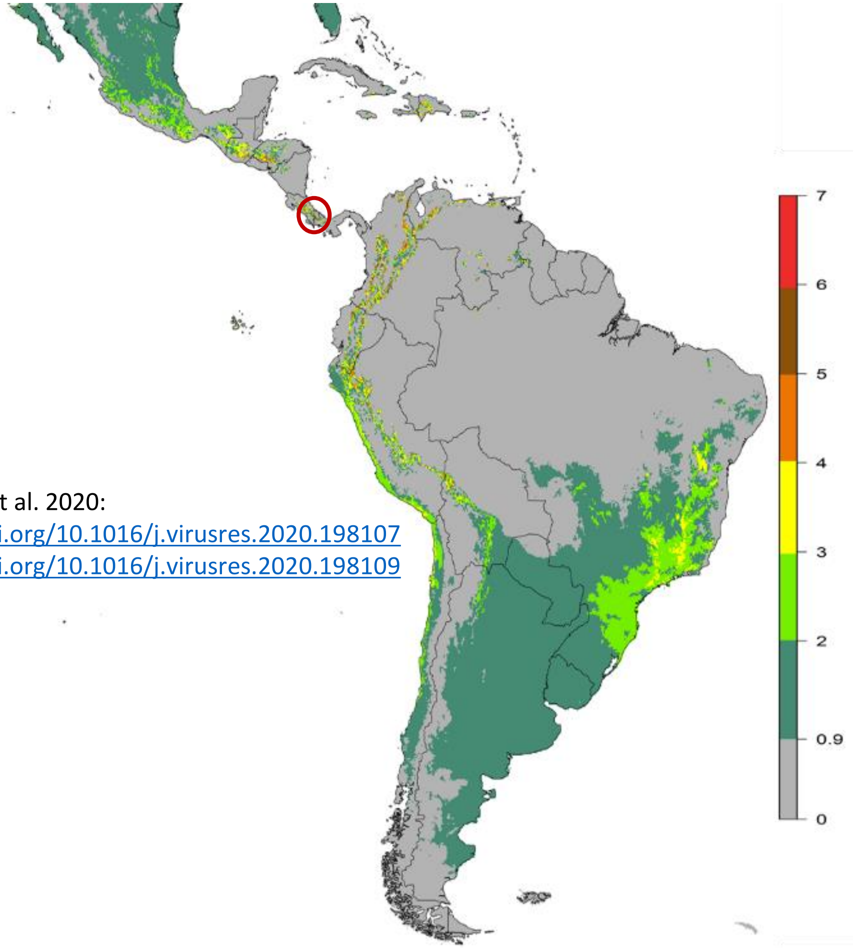
Example for begomoviruses: Niche analysis using MaxEnt modeling and bioclimatic-ecosystem variables



Variable	Value
Unique Locations	98
Training AUC	0.997
Equal training sensitivity and specificity logistic threshold	0.23
Cultivation intensity	33.67
Biomes ecoregion	24.16
Temperature Seasonality	18.96
WWF ecoregion	12.07
Latitude	3.73
Total top 5	**92.54**

Example for PYVV: phenology modeling for surveillance



Gamarra et al. 2020:
https://doi.org/10.1016/j.virusres.2020.198107
https://doi.org/10.1016/j.virusres.2020.198109

Field LAMP kit

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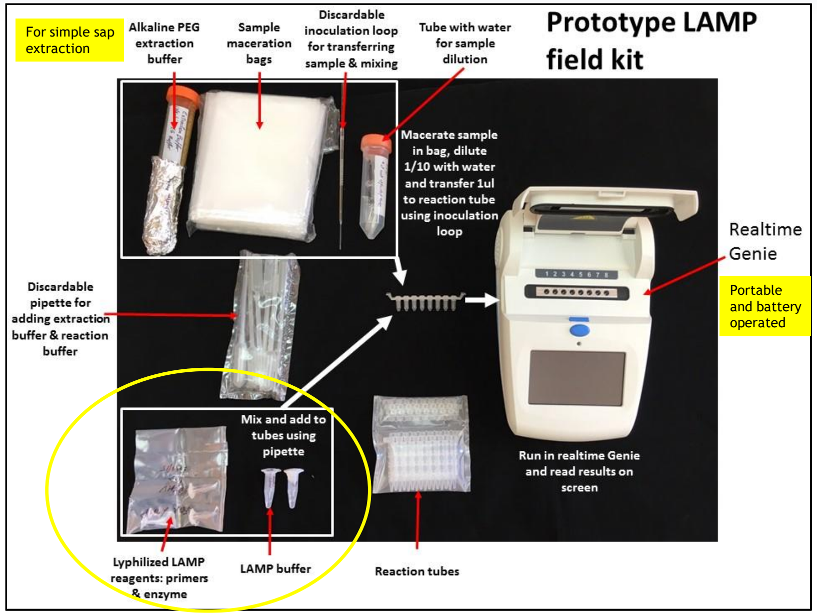
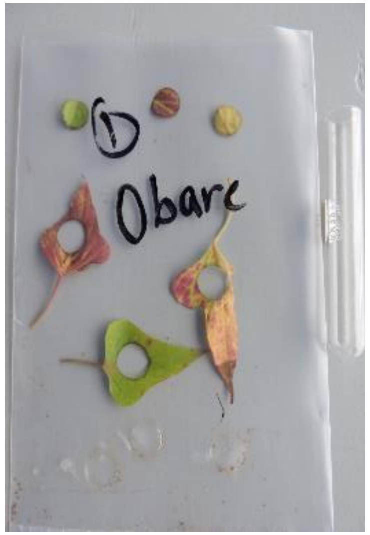
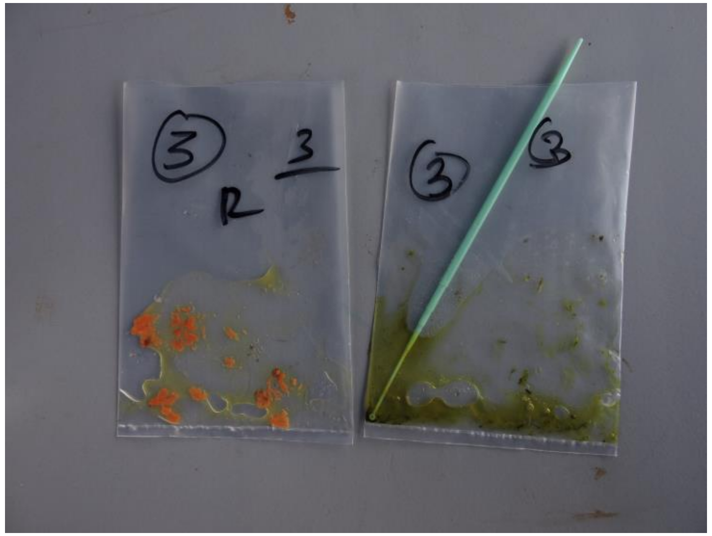
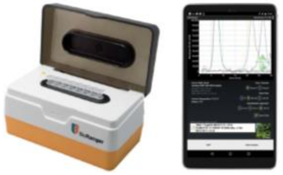




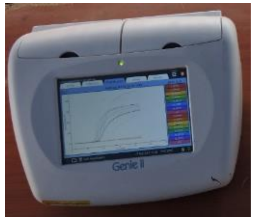


Wanjala et al., 2020: https://doi.org/10.1094/PDIS-06-19-1196-RE

Lyophilized reagents



BioRanger



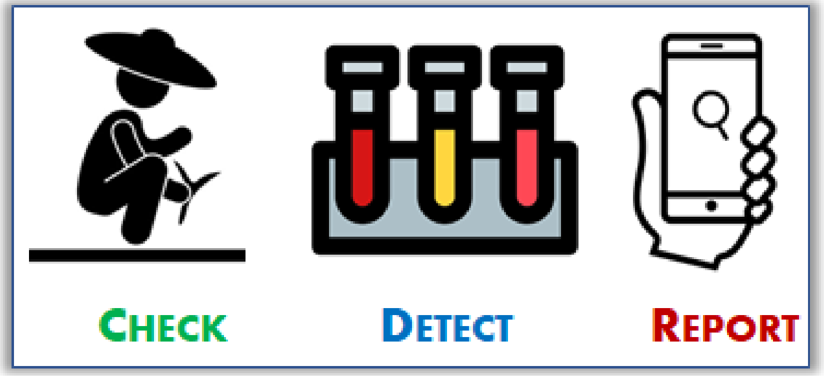
Easy to interpret

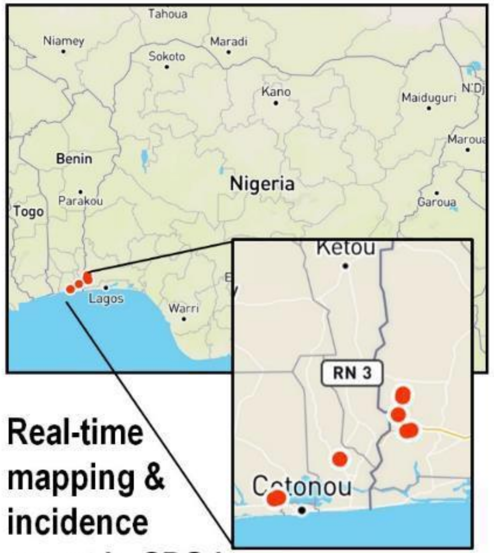
Njere et al., 2018: https://doi.org/10.1007/s00705-018-3706-0

BBTV surveillance system

Step-1. Sample preparation (1 min)

Step-2. Sample loading into premixed BBTV RPA reagent mix (1 min)





Real-time mapping & incidence report in CDS base

Step - 4. Incidence reporting through CDS App

Step - 3. Reaction incubation and real time detection (10 – 15 min)

Real-time

- **Reporting**
- **Mapping**
- **Diagnosis**
- **Control**

Remote Sensing for Disease (risk) Mapping

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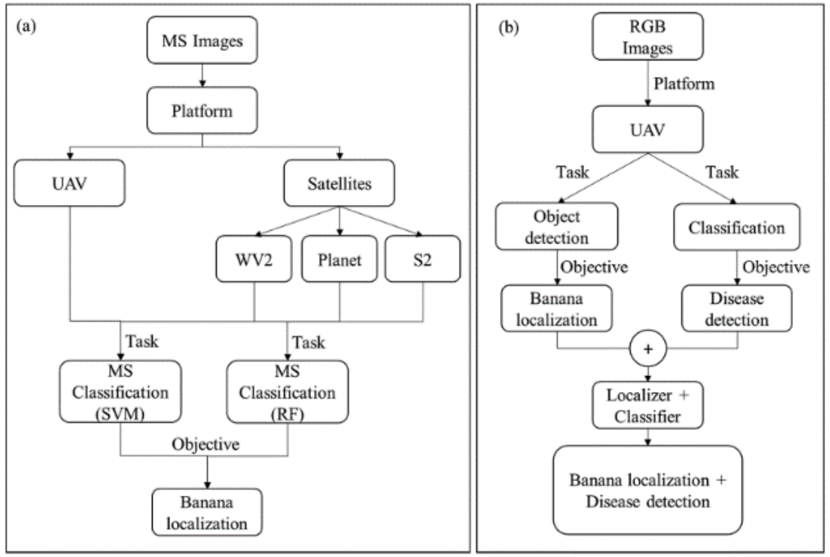

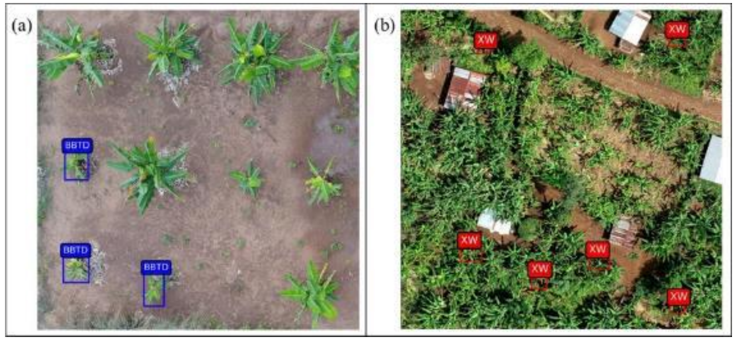

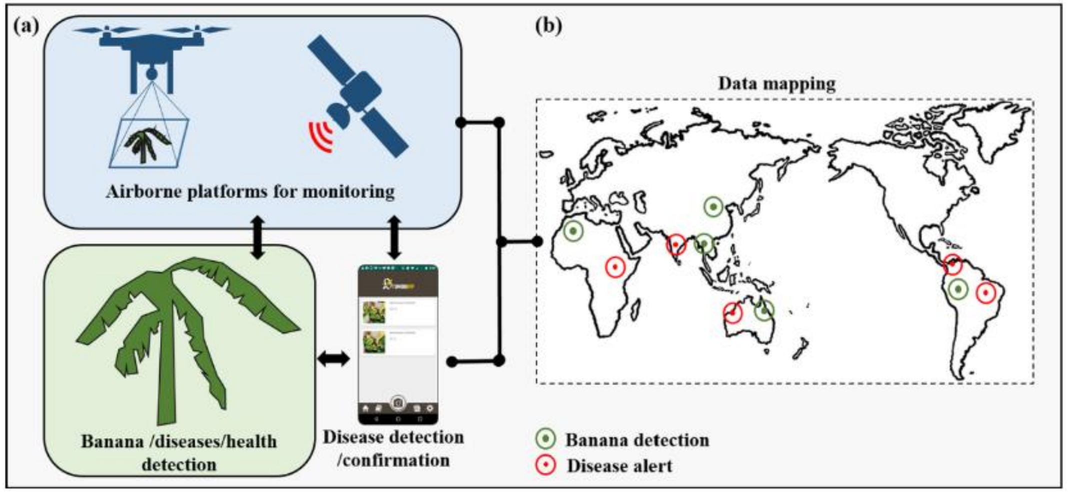

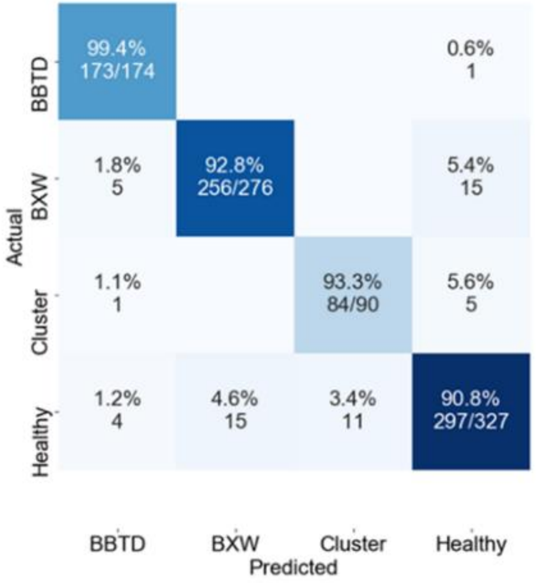

Selveraj et al., 2020: https://doi.org/10.1016/j.isprsjprs.2020.08.025

CMD in SEA: dev. standard protocols

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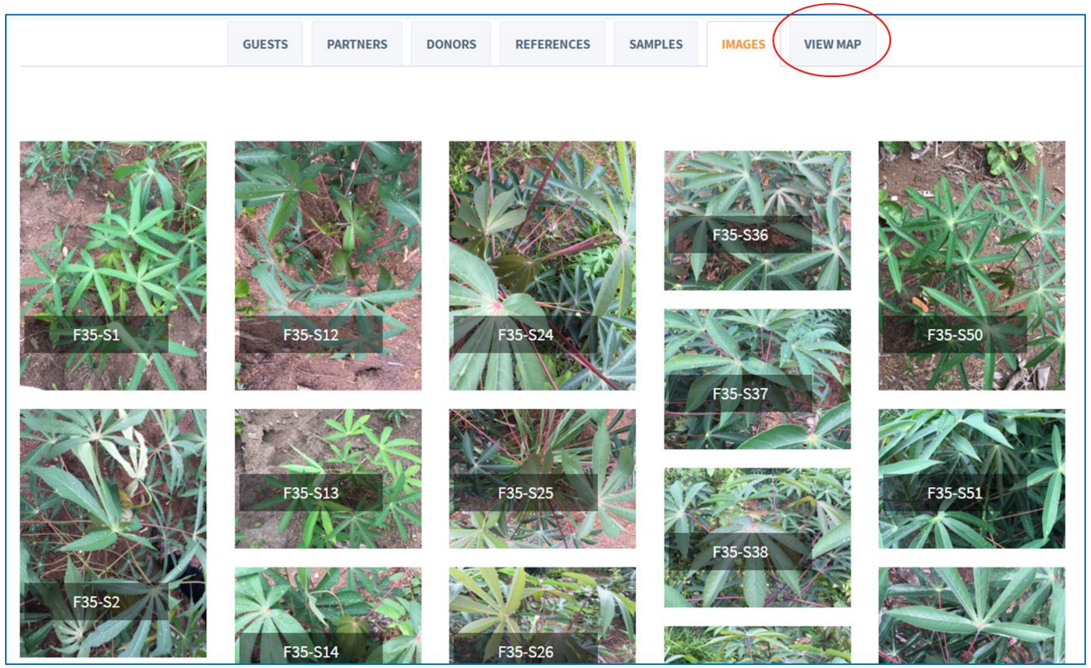
Field

PestDisPlace

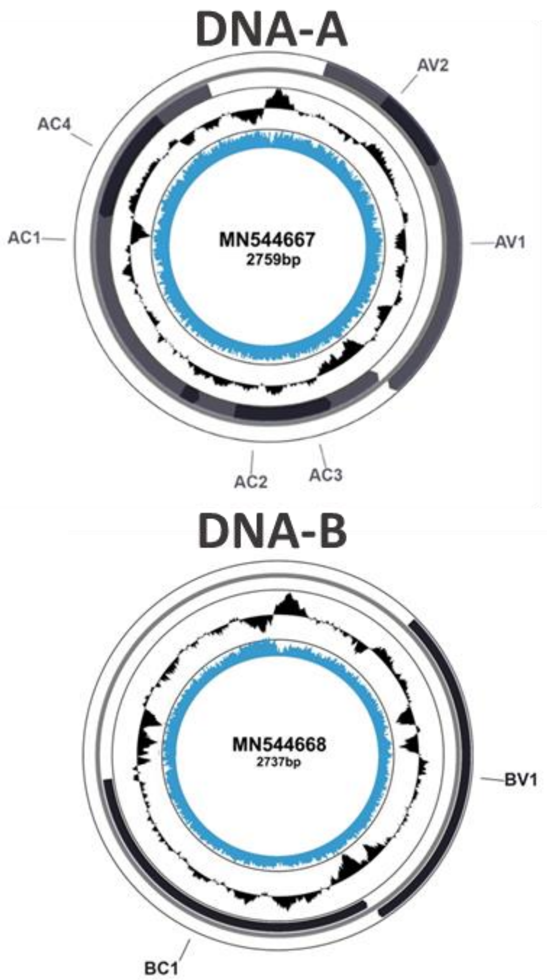


https://pestdisplace.org

Cuellar et al., 2021 https://hdl.handle.net/20.500.11766/67115

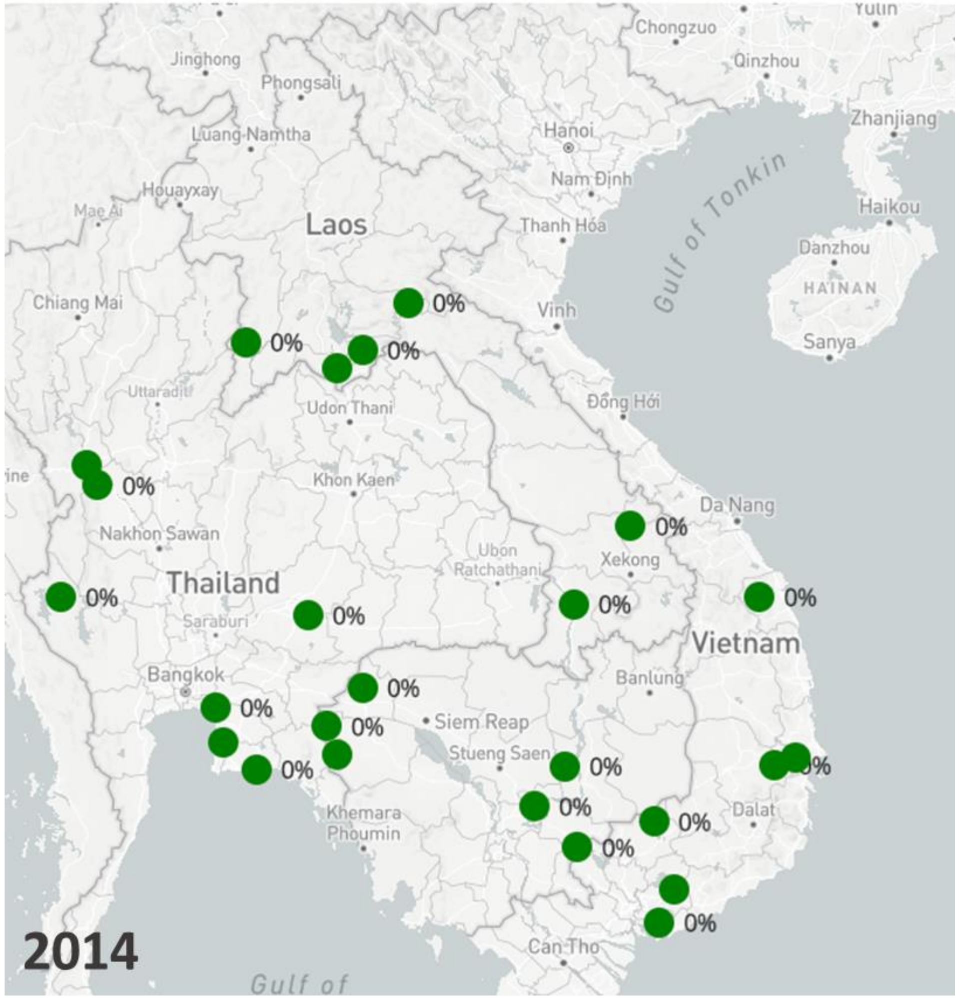
RCA and sequencing of circular DNA: Only 1 (out of 12) species of cassava-infecting begomovirus is present in SEA: Sri Lankan cassava mosaic virus (SLCMV)

Lab

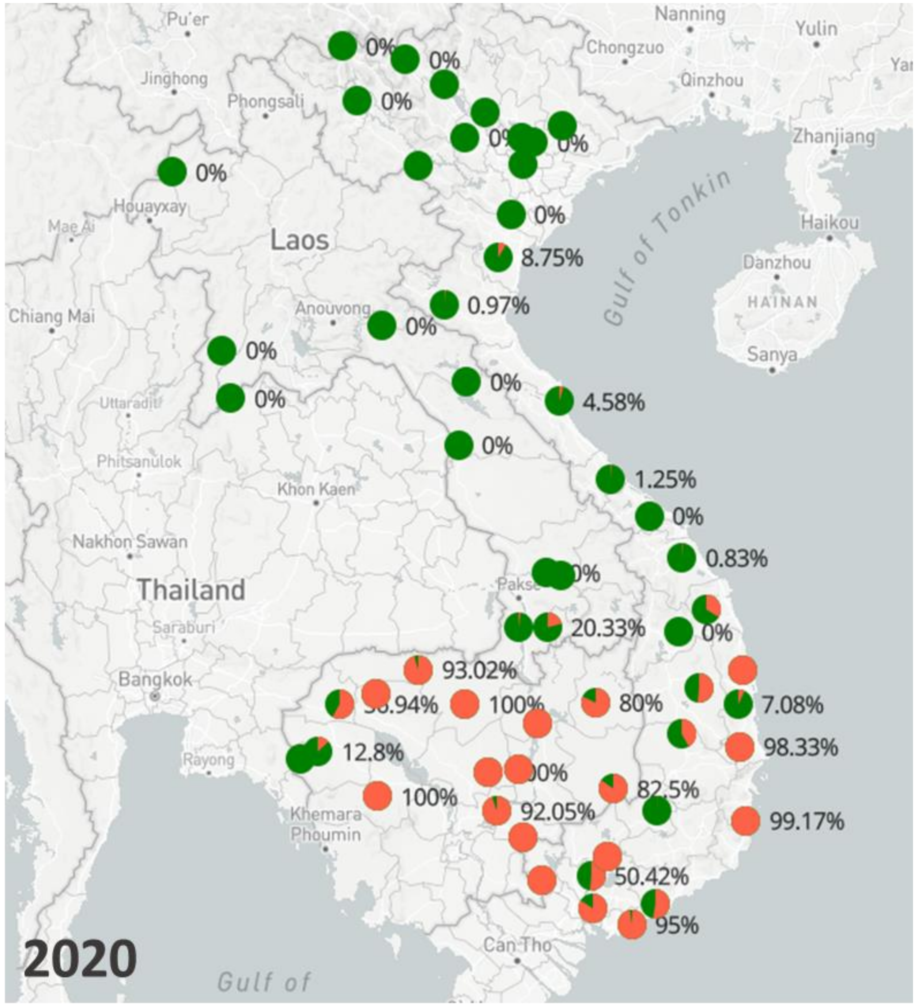


Leiva et al., 2020. https://doi.org/10.1128/MRA.01274-19

Cassava Mosaic Disease in SEA



Graziosi et al., 2016. https://doi.org/10.1002/ps.4250

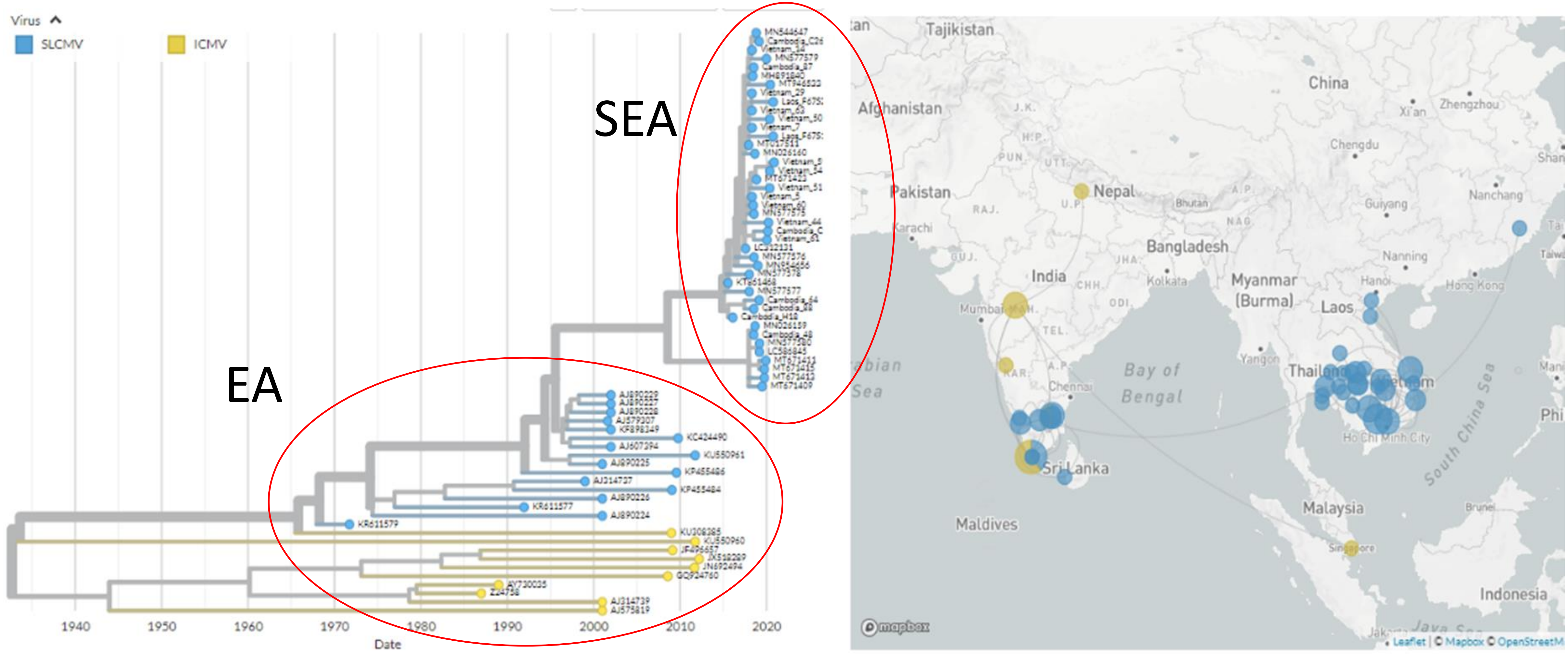


Siriwan et al., 2020. https://doi.org/10.1016/j.virusres.2020.197959

>30,000 observations

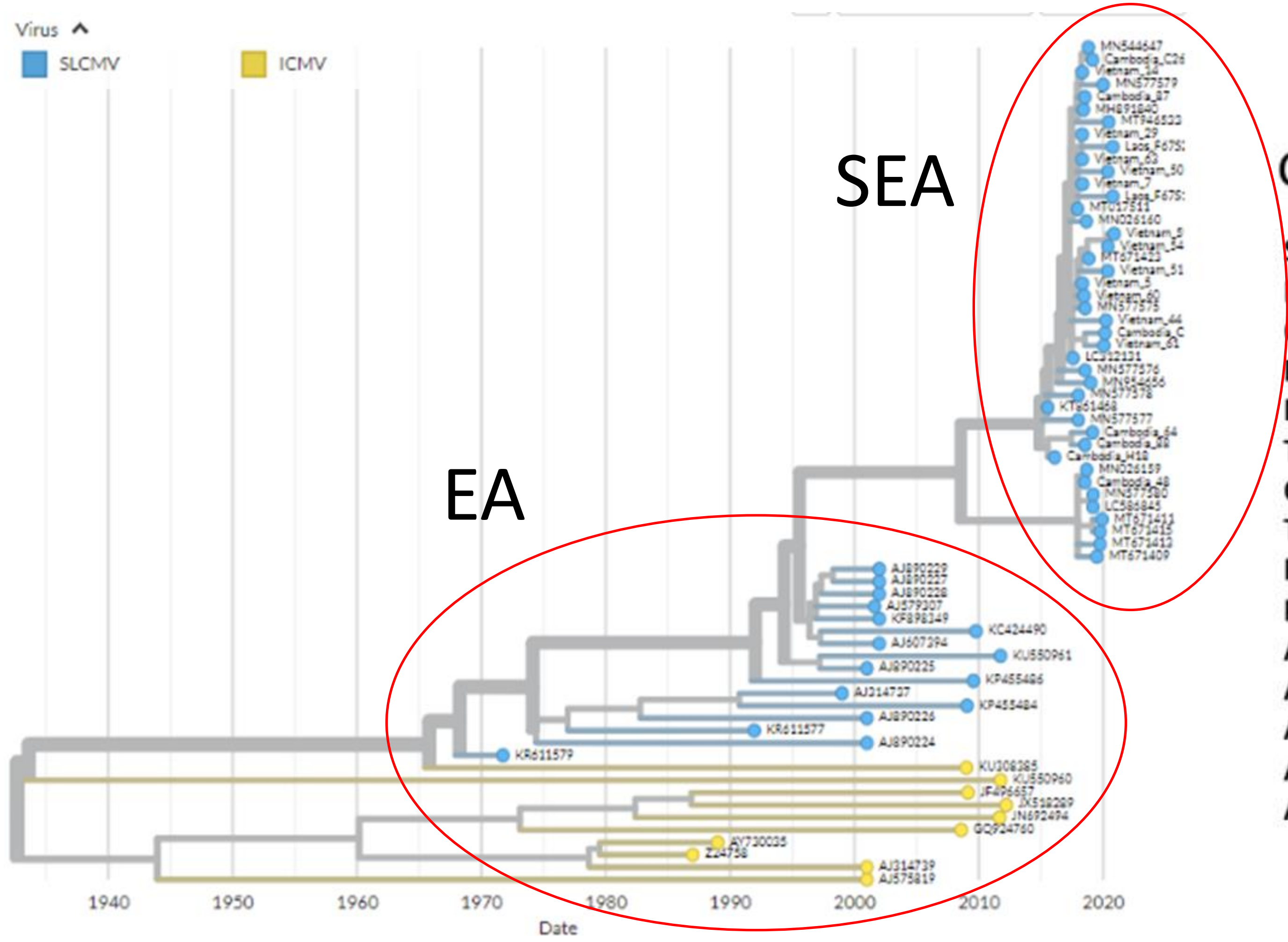
CMD in:
Thailand
Cambodia
Vietnam
Lao PDR
China

Tracking SLCMV genome evolution

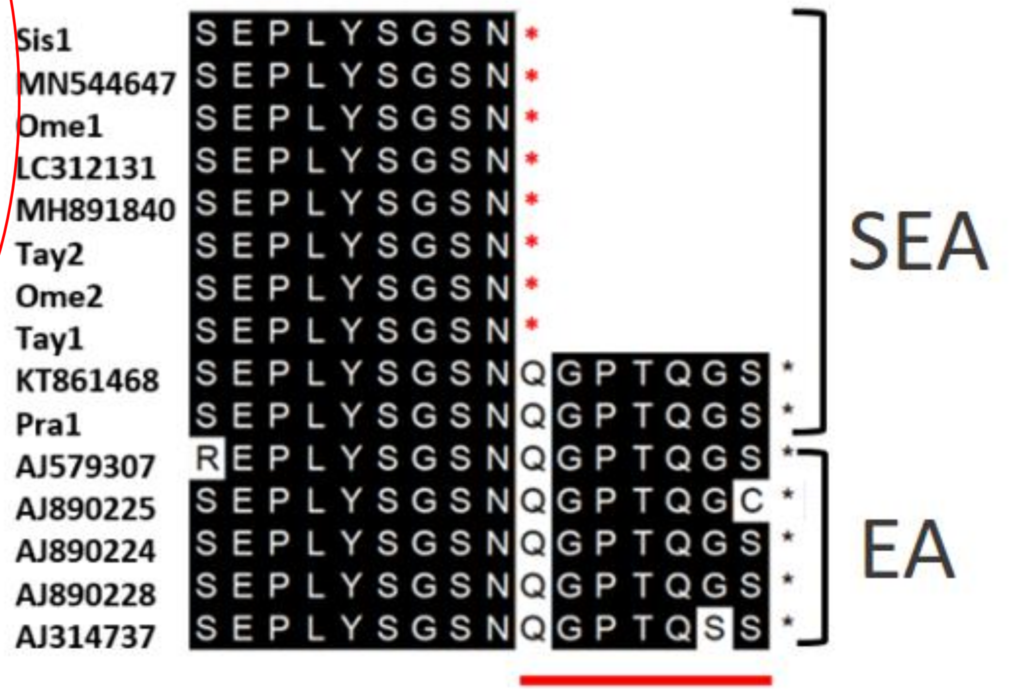


https://nextstrain.org/community/pestdisplace/CMDASIA1?c=virus&r=location

Cuellar et al., 2021



C-terminus of the Rep protein



These extra 7 amino acids are involved in virulence

Siriwan et al., 2020. https://doi.org/10.1016/j.virusres.2020.197959
Wang et al., 2020. https://doi.org/10.1094/MPMI-06-19-0163-FI

The Peruvian potato virome

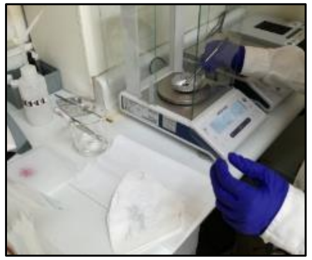
- Sample collection:
  994 geo-referenced potato leaf samples


Field


Plant


Leaves


Drying


Weighting

General results

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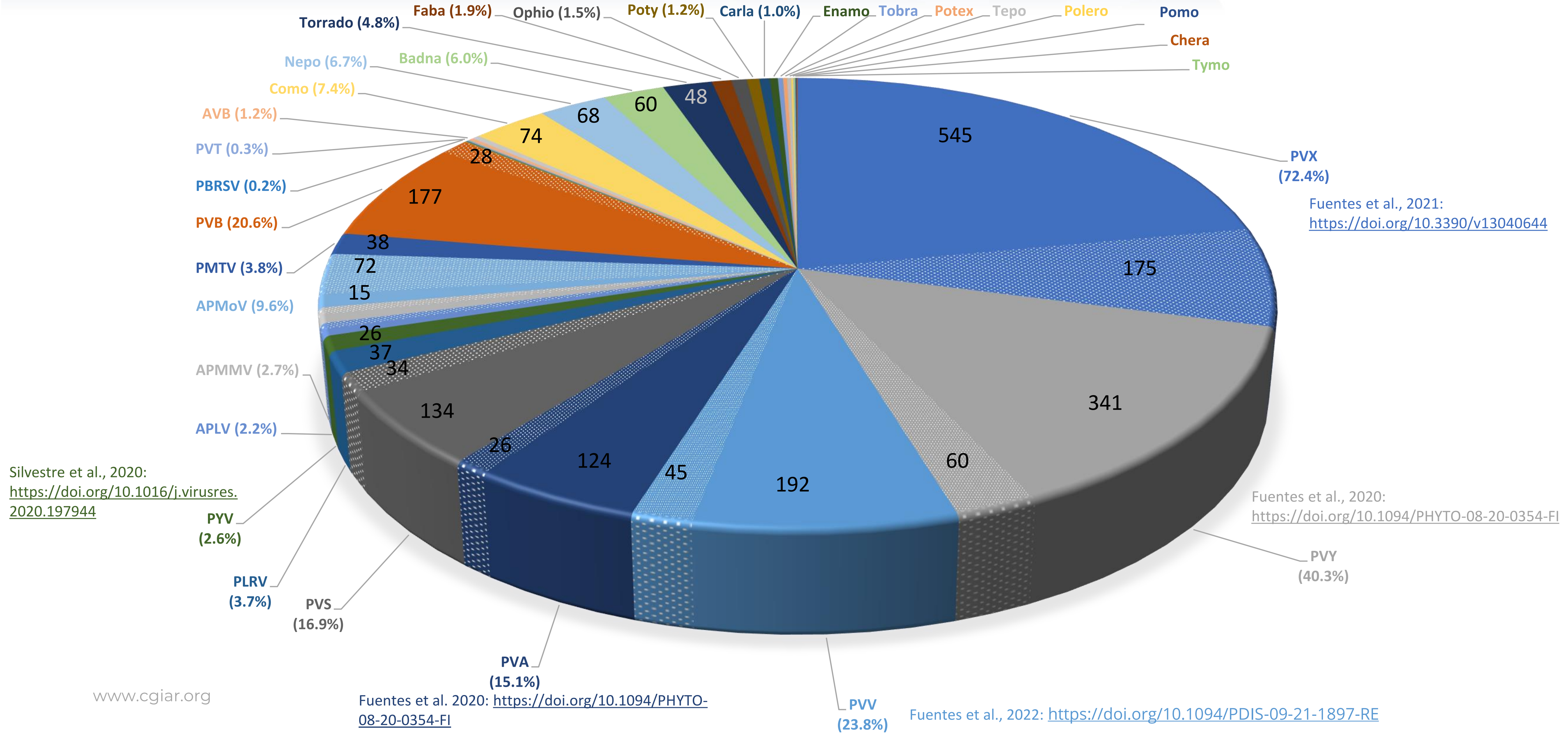
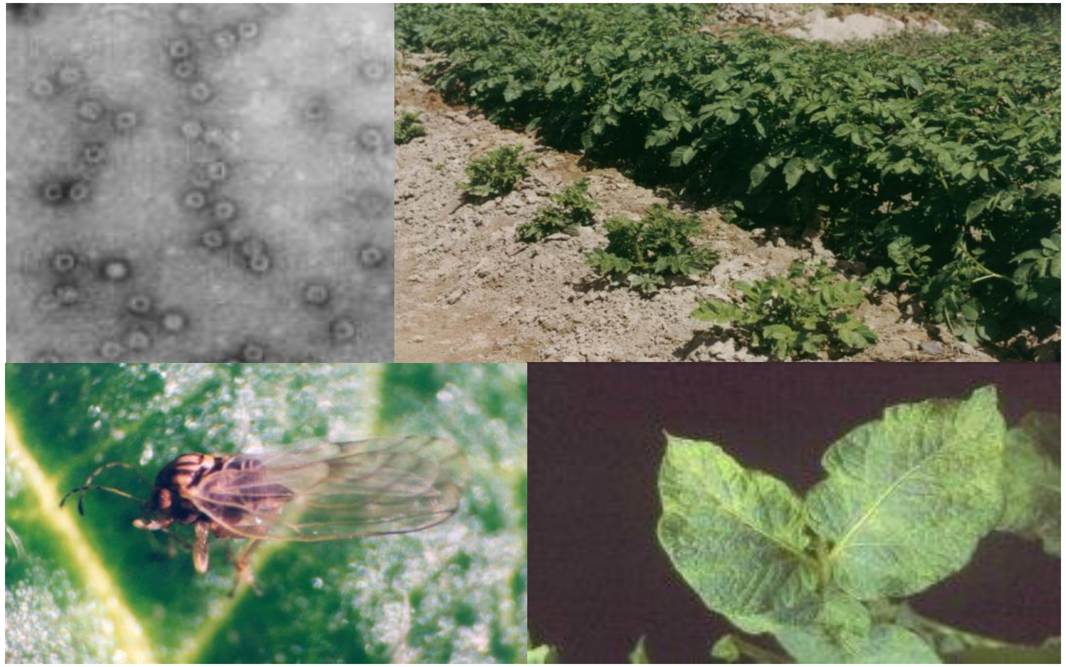


Rugose stunting disease of potato: the history of the emergence and decline of a viral disease

- Observed since 1990 in Arequipa, Moquegua and Tacna and studied as SB26 and SB29
- Isometric virus, two dsRNA sizes, transmitted by South American potato psyllid (*Russelliana solanicola*) and generated losses of between 35-85% depending on the variety
- Farmers changed their planting dates to manage the disease or quit potato al together and it is no longer considered a problem
- It was never determined what type of virus it was



Are any of the new viruses of relevance?

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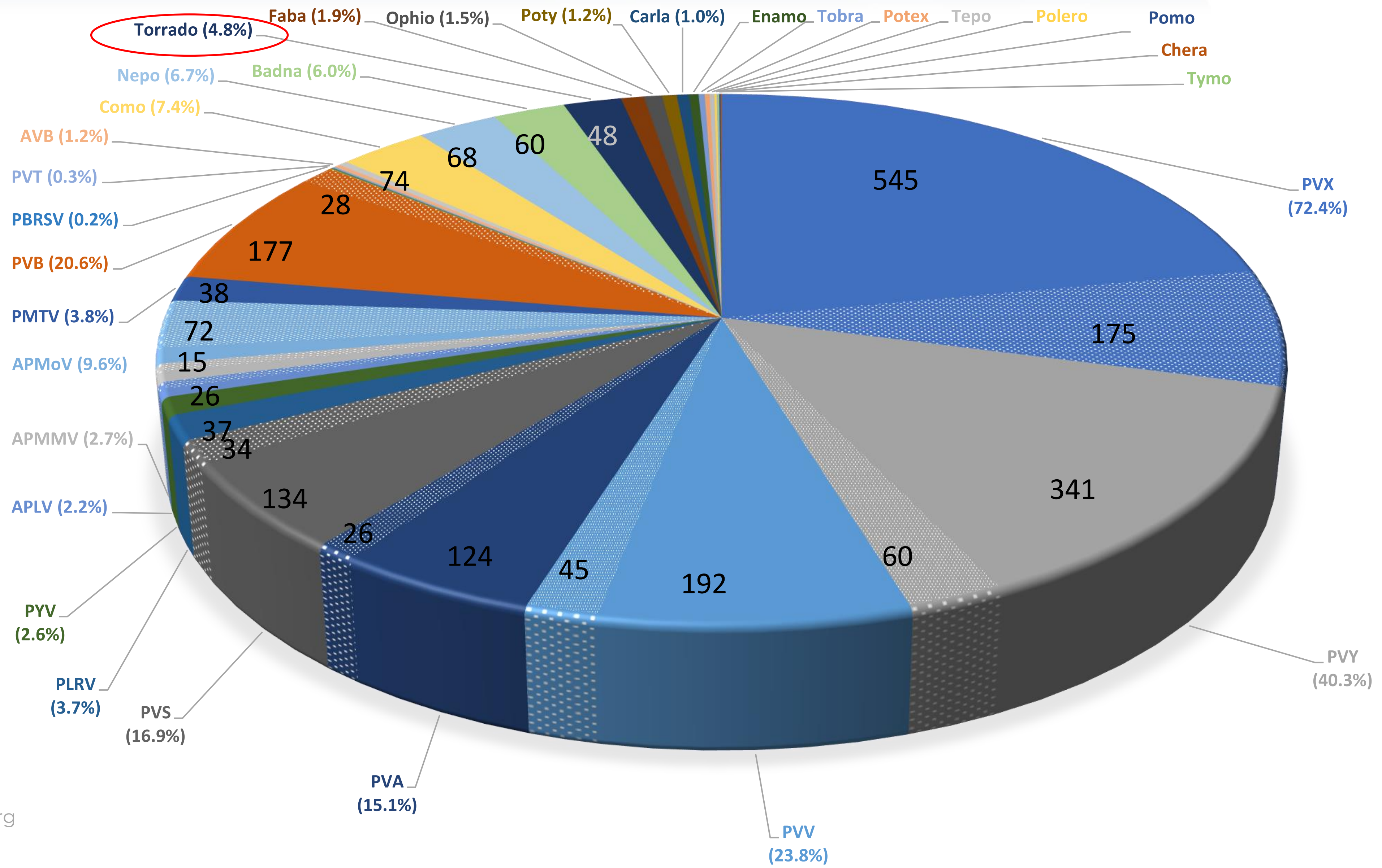

Potato rugose stunting virus is a torradovirus and present in low frequencies in potatoes throughout Peru

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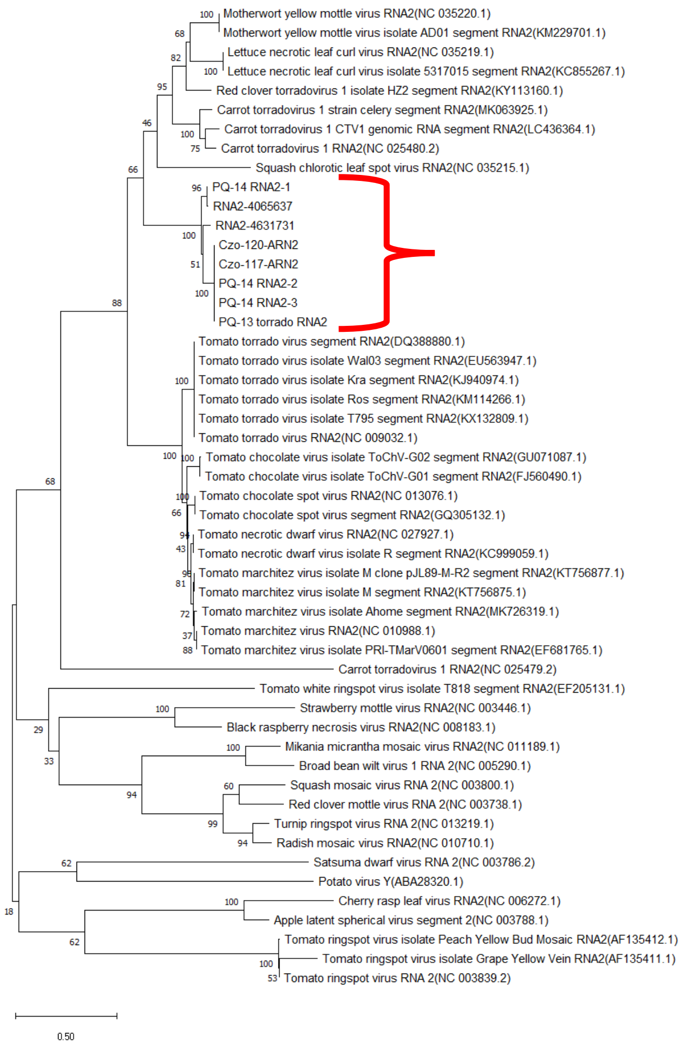
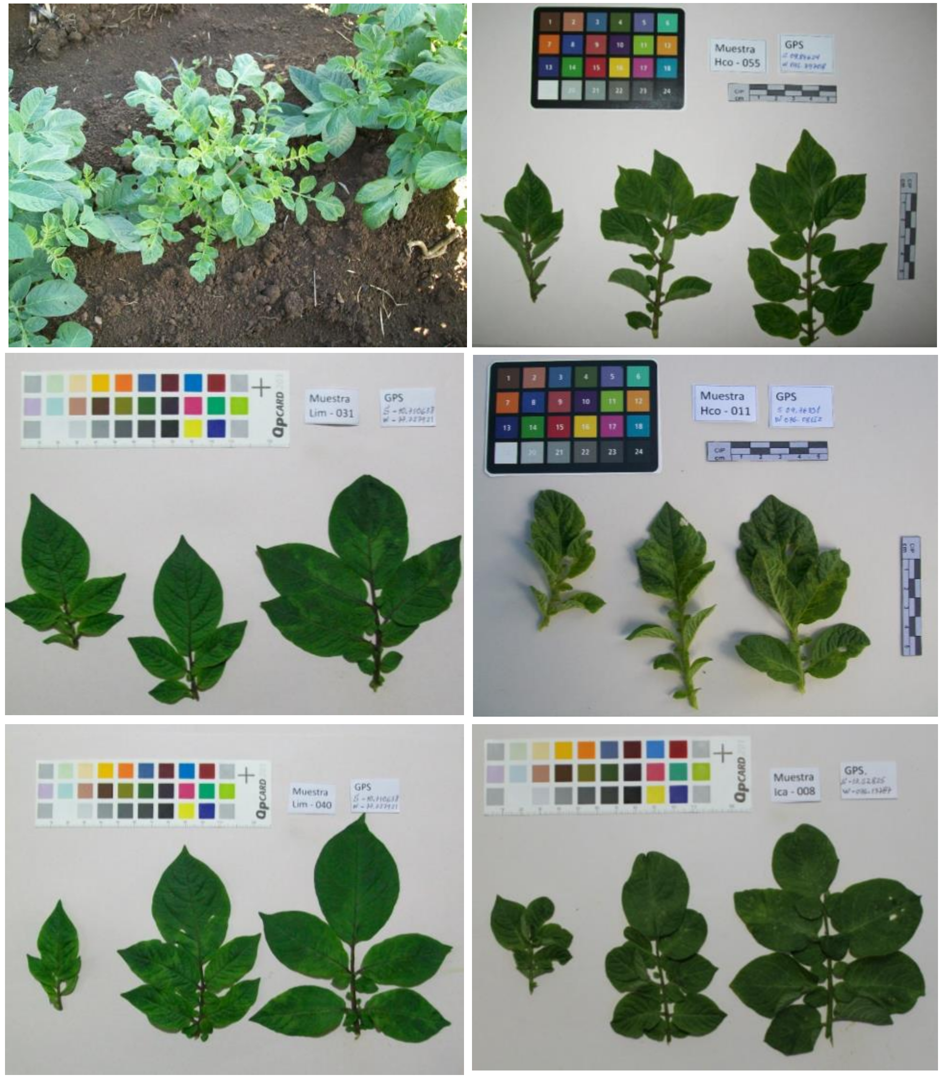
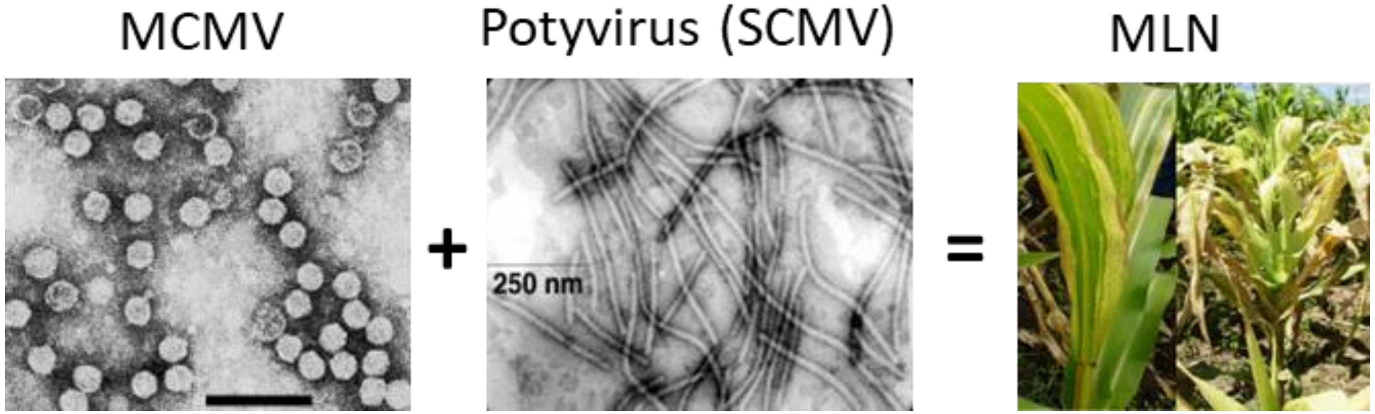


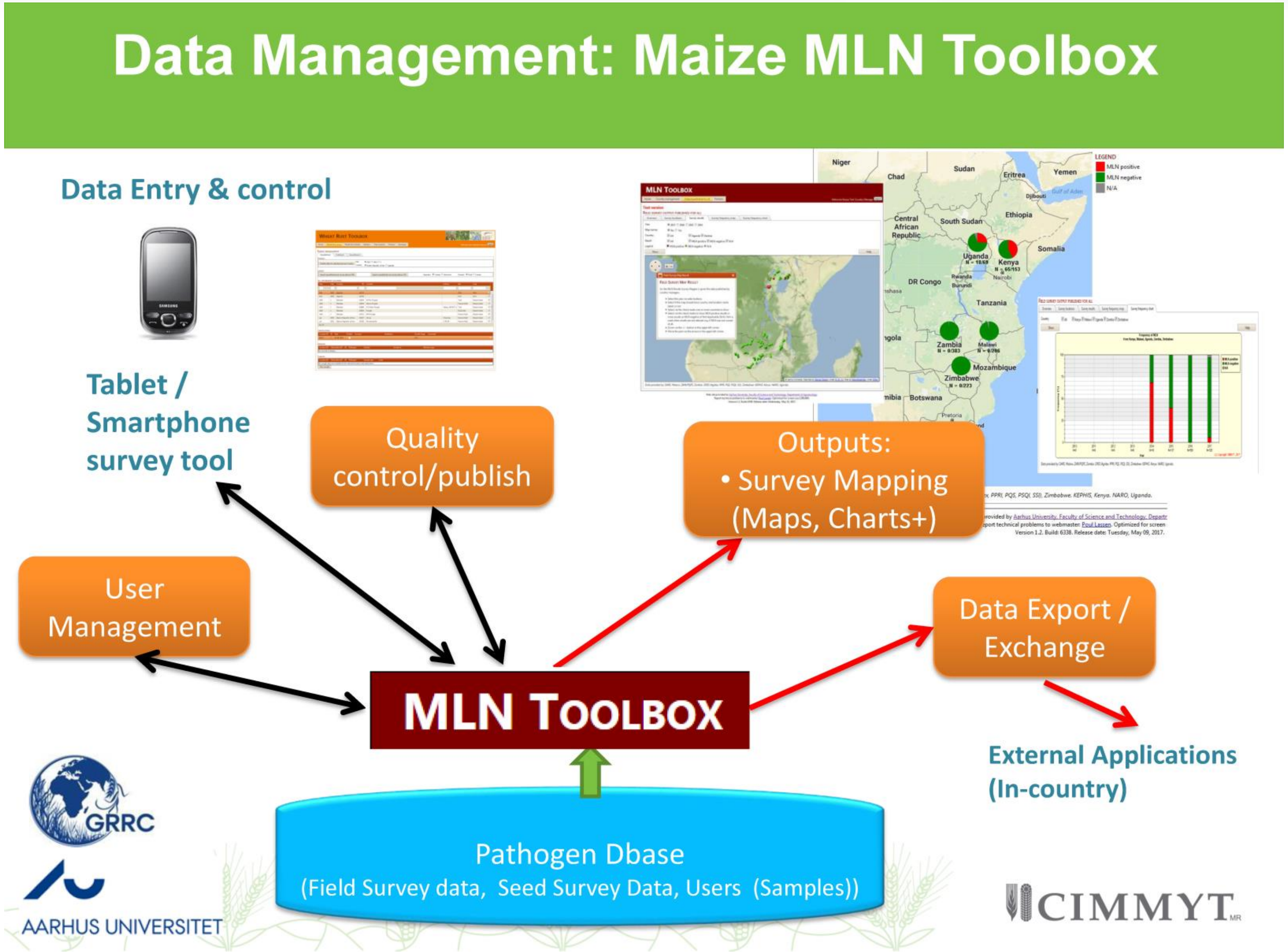


Maize Lethal Necrosis (MLN) in Africa



- MLN first appeared in Kenya in 2011 and was then reported in several countries in Uganda (2012), Tanzania (2012), Rwanda (2013), D.R. Congo (2013) and Ethiopia (2014).
- Losses to maize production in farmers' fields due to MLN in the impacted countries ranged from 25% to 100%.

MLN Diagnostics and Surveillance



- **MLN Diagnostics and Surveillance:** Coordinated by CIMMYT and implemented by NPPOs in five countries in eastern Africa (Ethiopia, Kenya, Uganda, Rwanda, and Tanzania) and three countries in southern Africa (Malawi, Zambia, and Zimbabwe).
- **MLN Toolbox** in partnership with NPPOs and Aarhus University.

Tracking MLN Dynamics over the Years

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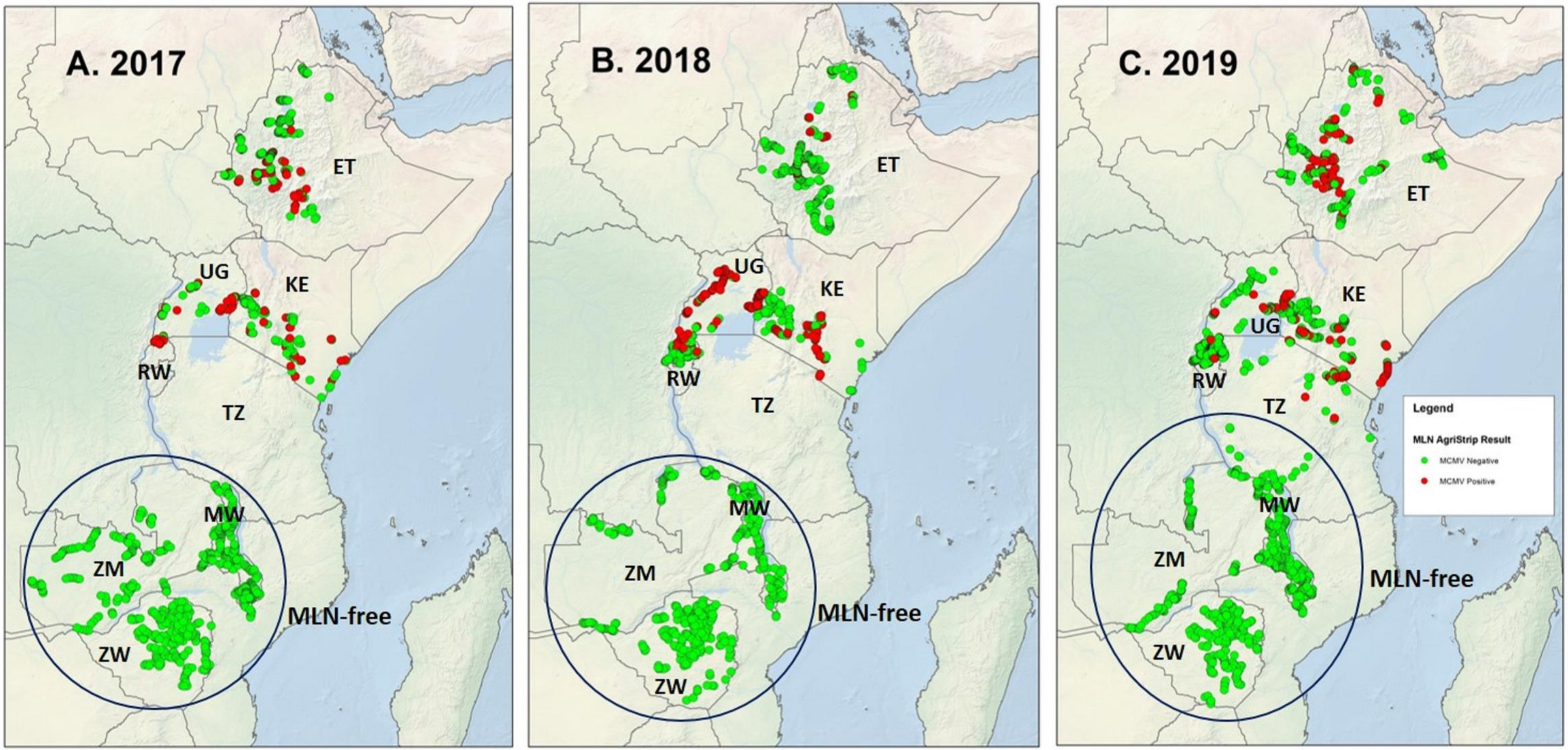
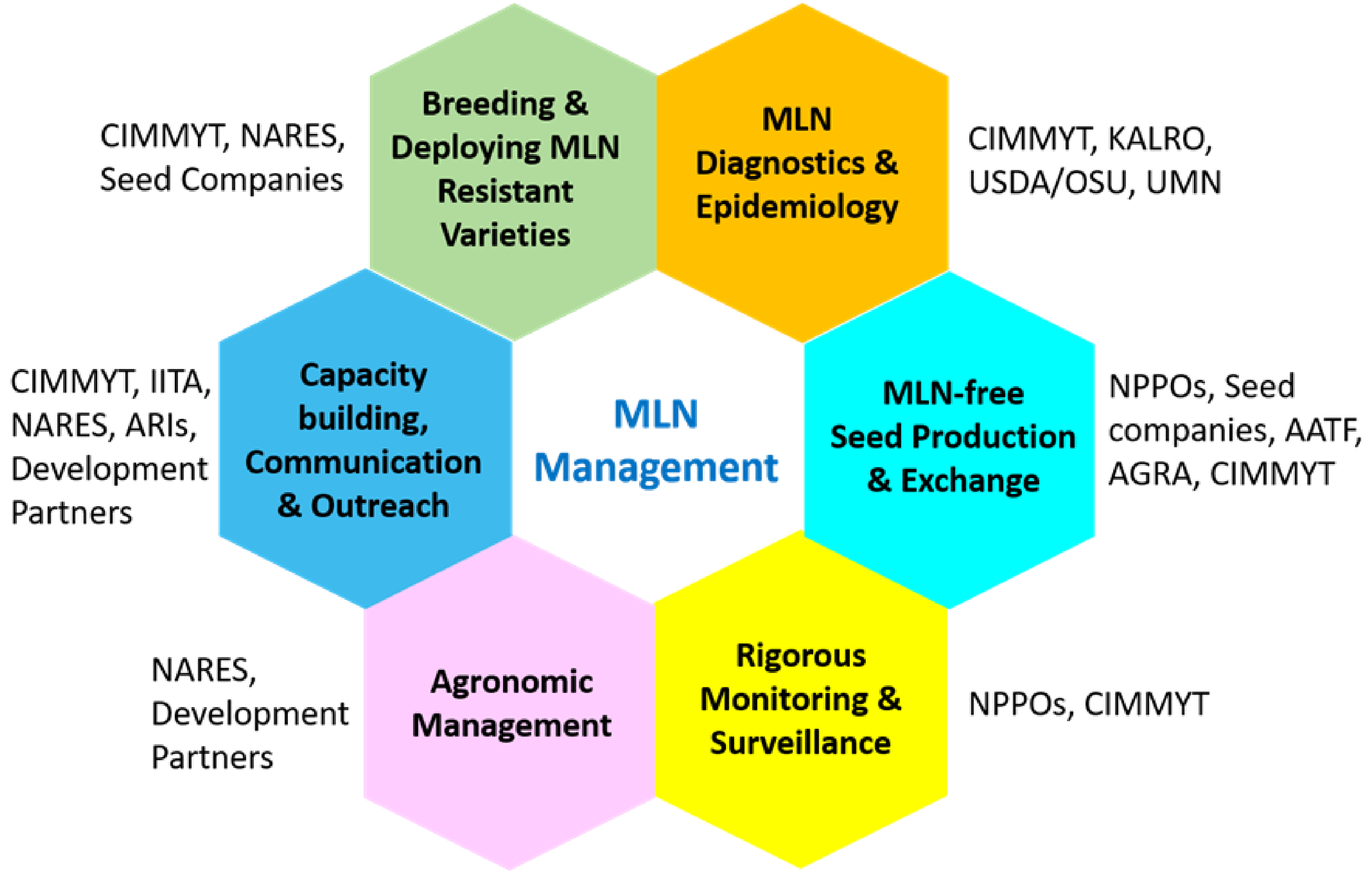
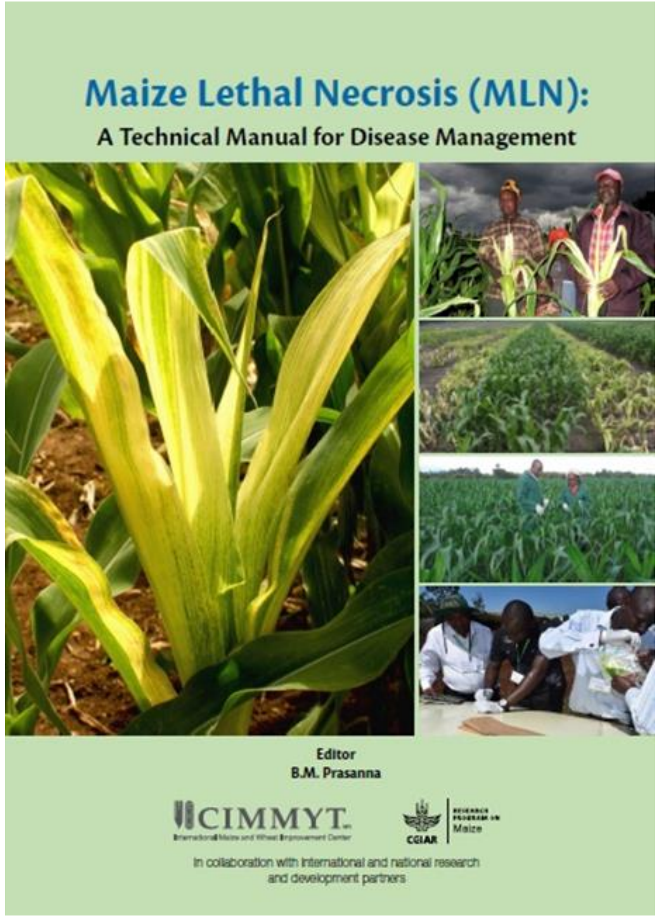


Prasanna et al. (2020): https://doi.org/10.1016/j.virusres.2020.197943

MLN Management in Africa

Success through Integration of Various Components





No scope for complacency as MLN causing viruses are still prevalent in eastern Africa and are not eradicated..

The way forward

Many different databases that are unlinked, sometimes even for same diseases

More data=more power to predict & prepare

Need to make databases interoperable and FAIR (Findable, Accessible, Interoperable and Reusable)

Requires development of Application Program Interface & specifications

CGIAR Germplasm Health Program

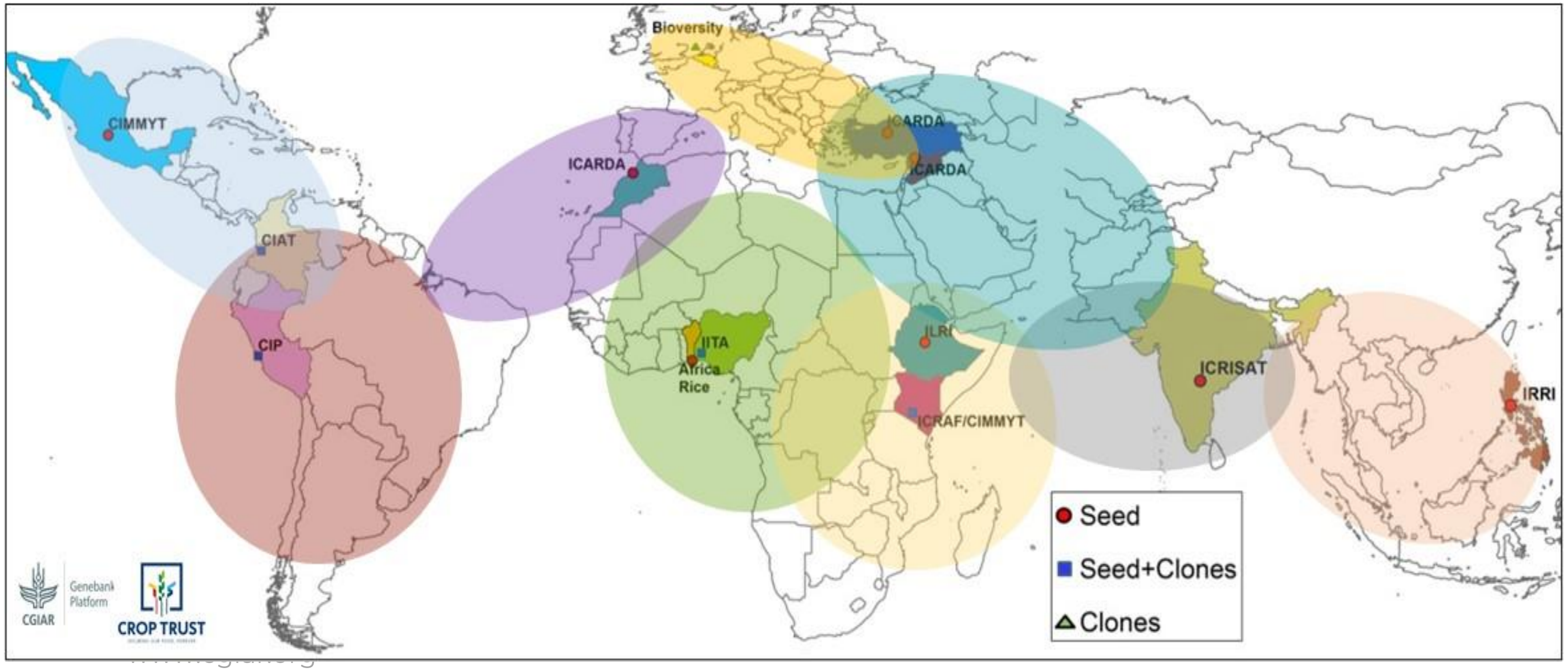
Plant Health Initiative

AU-IAPSC

Genebank Platform

Tools, technologies, strategies and policies for pest-free distribution of plant genetic resources

- Global network committed to ensuring phytosanitary compliance and safe distribution of pest-free germplasm
- Prevention of transboundary spread of pathogens through germplasm



Kumar et al., 2021; Plants *10*(2), 328; https://www.mdpi.com/2223-7747/10/2/328

Thank you!

Plant Health Initiative

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