ClonDiag-arrays:
A possible replacement of biological indexing for detecting sweetpotato viruses?

SASHA

Sweetpotato Action for
Security and **Health** in **Africa**

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26 Sept, 2017

Why?

Current procedure

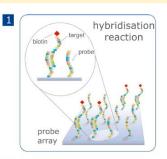# ClonDiag arrays: sensitive detection of multiple viruses
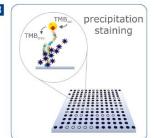
Used for clinical testing bacteria

Multiplex PCR (sensitive) with labled nucleotides → Hybridization to probes on array → ELISA
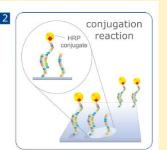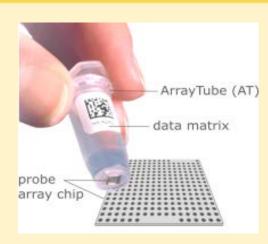
Probes and primers designed by FERA

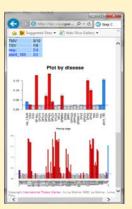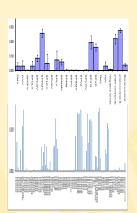# The evolution of a sweetpotato virus array

- 1st iteration: 10 viruses
- 2nd iteration: 14 viruses (tested samples Ghana-Mozambique)
- 3rd iteration: 19 viruses (tested on Pan African virome samples)
- 4th iteration: 19 viruses

Analysis by smartphone

Photo taken with smartphone

Analysis by dedicated software
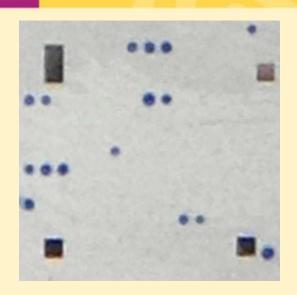
Photo taken with reader

What does it look like?

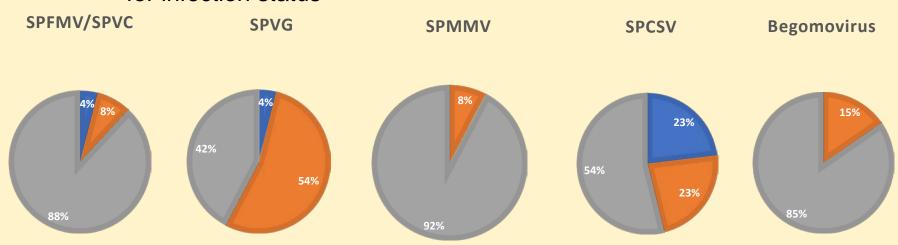# **Validation of the 4th iteration array**

- 25 + 1 samples from greenhouse plants KEPHIS: leaves dried down, ground into powder and 50% sent to CIP-Lima for parallel analysis
- Processed at same time in CIP-Lima and KEPHIS, analyzed at KEPHIS with array reader & in Lima with smartphone
- Results compared

Validation of the 4th iteration array

KEPHIS array reader: 100% consistent with biological indexing for infection status

SPFMV/SPVC	SPVG	SPMMV	SPCSV	Begomovirus

Array reader also detected SPV2, SPC6V, SPLV, SPCV, SPVCV, SPPV

Need to confirm conflict by complementary methods: PCR & NGS

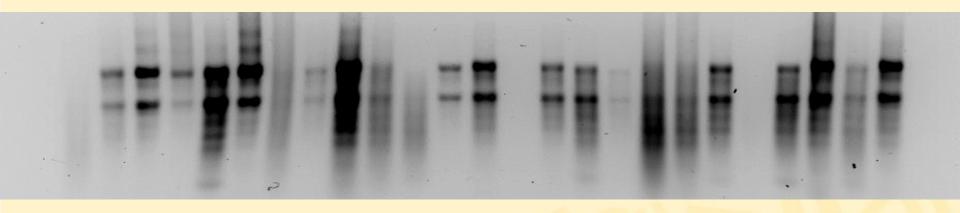# Validation of the 4th iteration array

CIP smartphone app: 96% consistent for infection status

Repeatability same sample same lab: 100%

Sensitivity: loss of some detection between 1/25 and 1/50

Lima RNA quality was not similar between samples:

So, can we replace biological indexing?

- Cost of ClonDiag tube arrays around $ 70 per sample in 2 days, vs $153.71 per sample and 4-6 months for biological indexing
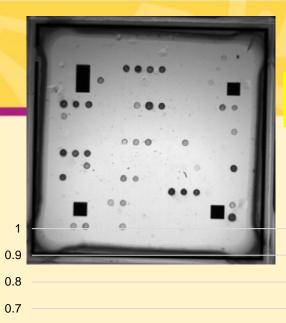
- Could be a good replacement for 1st round indexing

- Test Microfluidic format for running LAMP reactions (Quick-Chip)

- Optimize and validate small RNA sequencing based diagnostics

- Improve speed of virus elimination infected materials by improved tissue culture procedures and antiviral treatments.
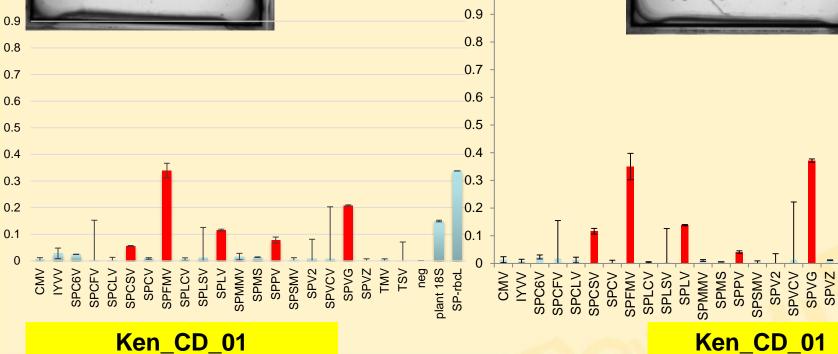
Asante Sana

Repetitive testing

Ken_CD_01
Ran on 12/06/2017

Ken_CD_01
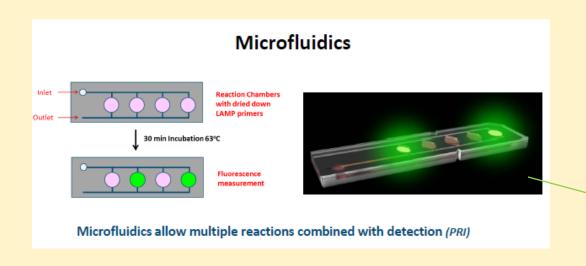Ran on 16/03/2017

In the future: microfluidic LAMP (next generation phytosanitation project)
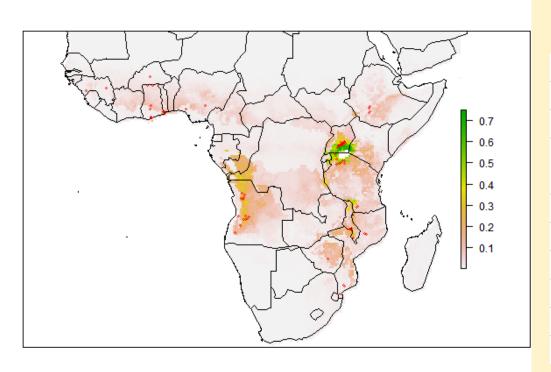
Progress virome analysis

Niche analysis using Maximum Entropy modeling and bioclimatic variables

Example: begomoviruses, top 5 variables can explain 93% of occurrences

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