

Molecular diagnostic tests to strengthen seed systems

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Natural Resources
Institute

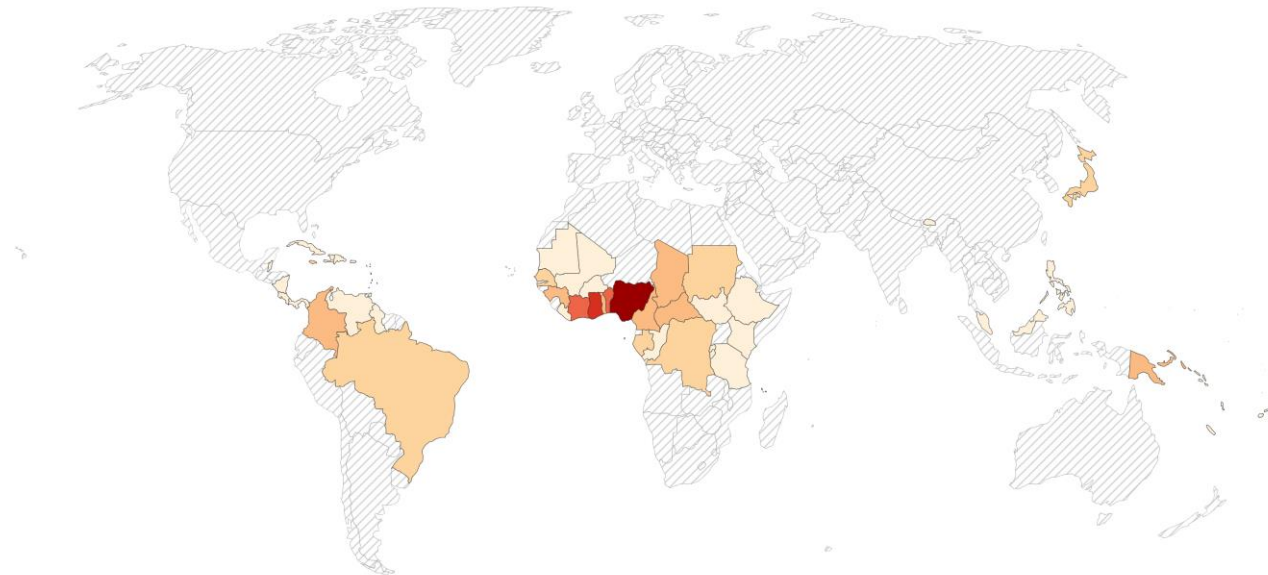
Yam (*Dioscorea* spp.)

- ❖ Major staple food worldwide, particularly for West Africa
- ❖ Important role in food security and for the livelihoods of >60 million people in West Africa

Yams production, 2023

Yam production is measured in tonnes.

Our World
in Data



Data source: Food and Agriculture Organization of the United Nations (2025)

OurWorldinData.org/agricultural-production | CC BY



Diagnostics needed for yam germplasm

- ❖ The **lack of a formal seed system** encourages farmers to use low-quality planting material from their own or neighbouring farms resulting in the **accumulation of diseases in yam germplasm**.
- ❖ **Sanitation methods** are critical for the rapid multiplication of virus-free planting materials but can lead to low virus titres below detection thresholds.
- ❖ **Diagnostics needed** to test sanitised planting material and support the production of high-quality “clean” seed yams.



Taxonomy		
Family	Genus	Species
Alphaflexiviridae	Potexvirus	Dioscorea latent virus (DLV)
		<i>Yam virus X</i> (YVX)
		Yam potexvirus 1
		Yam potexvirus 2
		Yam potexvirus 3
Betaflexiviridae	Carlavirus	<i>Yam latent virus</i> (YLV)
	Unassigned	Yam virus Y (YVY)
Bromoviridae	Cucumovirus	<i>Cucumber mosaic virus</i> (CMV)
Caulimoviridae	Badnavirus	<i>Dioscorea bacilliform ES virus</i> (DBESV) DBV1 ⁺ (Kenyon) or DeBV-A ⁺⁺ (Bousalem) episomal
		DBV2 (Kenyon) ⁺ or DeBV-C ⁺⁺ (Bousalem) unknown
		<i>Dioscorea bacilliform AL virus 2</i> (DBALV2) DBV3 ⁺ (Kenyon) or DeBV-B ⁺⁺ (Bousalem) episomal
		<i>Dioscorea bacilliform SN virus</i> (DBSNV) DBV4 ⁺ (Kenyon) or DsBV ⁺ (Bousalem) episomal
		<i>Dioscorea bacilliform RT virus 3</i> (DBRTV3) DBV5 ⁺ (Kenyon) or DBV-C ⁺⁺ (Bousalem) episomal and endogenous
		DBV6 ⁺ (Kenyon) or DeBV-D ⁺⁺ (Bousalem) unknown
		DBV7 ⁺ (Kenyon) or DeBV-E ⁺⁺ (Bousalem) unknown
		<i>Dioscorea bacilliform AL virus</i> (DBALV) DBV8 ⁺ (Kenyon) or DBV-A(A)/DaBV ⁺⁺ (Bousalem) episomal and endogenous

Taxonomy			
Family	Genus	Species	
Caulimoviridae	Badnavirus	<i>Dioscorea bacilliform TR virus</i> (DBTRV)	
		DBV9 ⁺ (Kenyon) or DBV-B ⁺⁺ (Bousalem) episomal and endogenous	
		DBV10 ⁺ (Kenyon) or DpBV ⁺⁺ (Bousalem) unknown	
		DBV11 ⁺ (Kenyon) or DeBV-F ⁺⁺ (Bousalem) *unknown	
		DBV12 ⁺ (Umber) or DBV-A(B) ⁺⁺ (Bousalem) endogenous and presumably episomal	
		<i>Dioscorea bacilliform RT virus 1</i> (DBRTV1) DBV13 (Bömer) episomal	
		<i>Dioscorea bacilliform RT virus 2</i> (DBRTV2) DBV14 (Bömer) episomal	
		DBV15 (Bömer) presumably episomal	
		Dioscovirus	<i>Dioscorea nummularia associated virus</i> (DNUaV)
		Closteroviridae	Ampelovirus
Velarivirus	<i>Air potato virus 1</i> (AiPoV1)		
Geminiviridae	Begomovirus	Yam yellow spot mosaic virus presumably endogenous	
		EGV1 and EGV2 endogenous	
Caulimoviridae	Macluravirus	<i>Chinese yam necrotic mosaic virus</i> (CYNMV)	
		<i>Yam chlorotic mosaic virus</i> (YCMV)	
		<i>Yam chlorotic necrosis virus</i> (YCNV)	
Caulimoviridae	Potyvirus	<i>Yam mosaic virus</i> (YMV)	
		<i>Yam mild mosaic virus</i> (YMMV)	
		<i>Japanese yam mosaic virus</i> (JYMV)	
		<i>Dioscorea mosaic virus</i> (DMV)	
		Yam potyvirus TGwadE2	
Secoviridae	Fabavirus	<i>Broad bean wilt virus 2</i> (BBWV2)	
	Sadwavirus	<i>Dioscorea mosaic-associated virus</i> (DMaV)	
Tombusviridae	Aureusvirus	<i>Yam spherical virus</i> (YSV)	

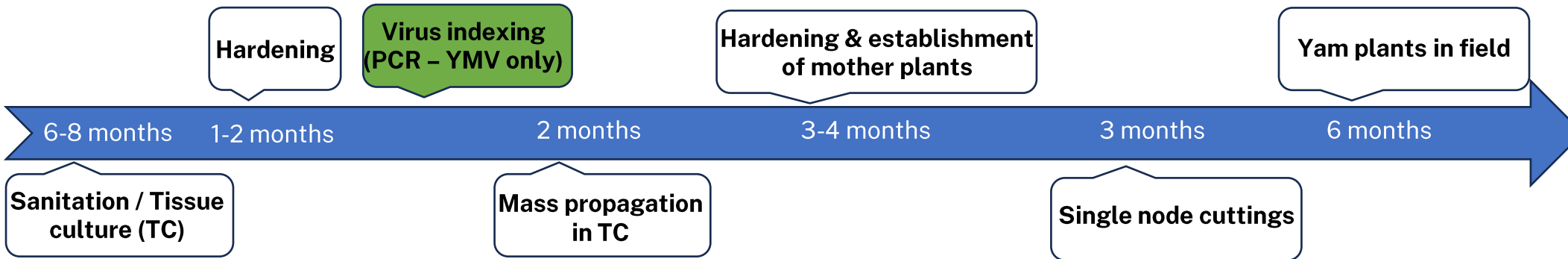
Viruses infecting yam

At least 25 different viruses belonging to 12 genera and eight families

Current seed yam production process

➤ Over 7-8 months wait before PCR indexing!

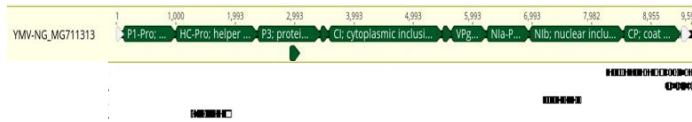
≥20 months later...
Breeder seeds (virus-free)



Optimised MinION workflow for virus detection in yam

Sequencing strategy

Direct RNA sequencing



Yield/estimated bases (Gb)	1.5
Total number reads (M)	2.4

cDNA-PCR sequencing



Yield/estimated bases (Gb)	9.18
Total number reads (M)	23.5

RNA enrichment strategy

RNA Enrichment	Mapped reads (%)	Mean depth	Avg. read length (bp)
Total RNA	0.2–3%	64–110	~900
Poly(A)+	<2%	14–684	~630–890
rRNA-depleted	0.7–14%	226–4398	~470–580
rRNA-depleted + Poly(A)+	0.7–13%	309–2085	~460–475

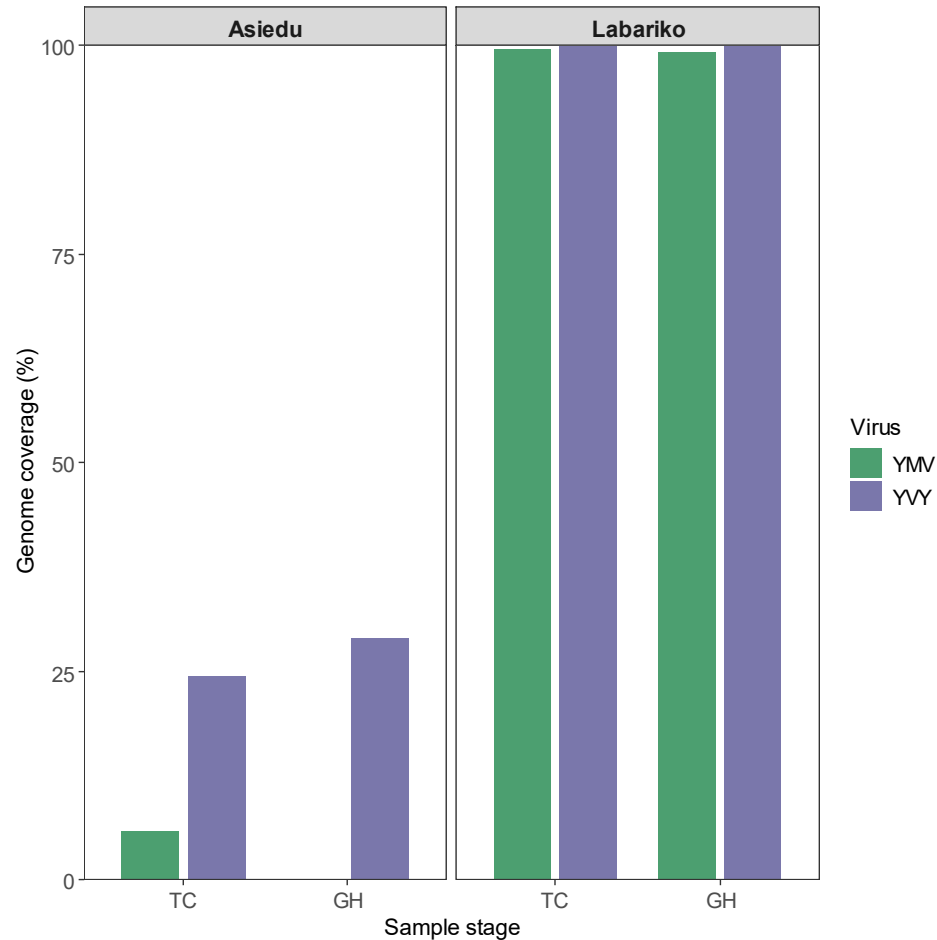
Optimised workflow: Combination of rRNA-depletion + poly(A)+ followed by PCR-cDNA sequencing

MinION protocol reduces virus indexing timelines by ~12 weeks

Tissue culture (TC)
testing after 4 months



Hardening at glasshouse (GH)
testing after 7 months

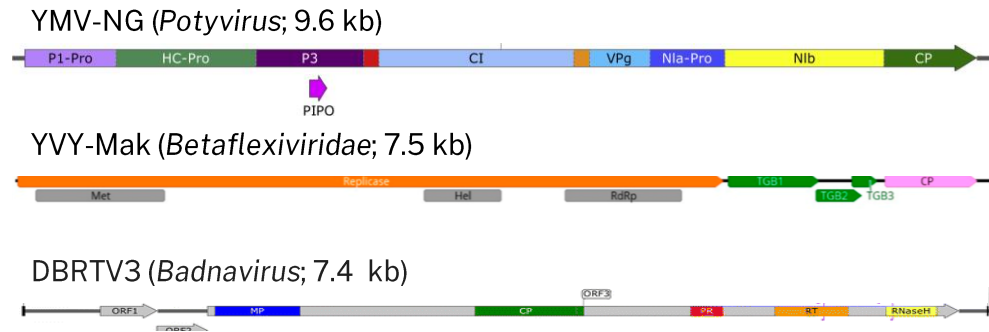


Result	-	+	-	+	+	+	+

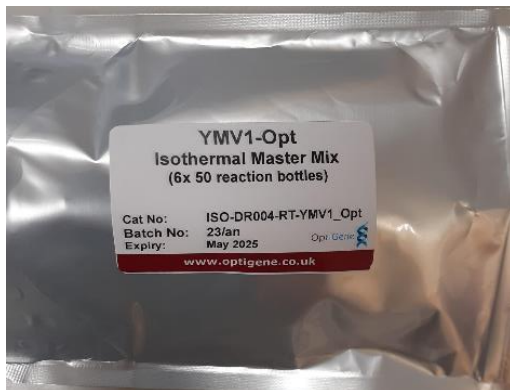
Plant Stage	Total Reads	Reference virus	Mapped reads
Asiedu			
TC	5,082,266	YMV	1
		YVY	22
GH	2,427,095	YMV	0
		YVY	19
Labariko			
TC	3,039,879	YMV	577
		YVY	3,930
GH	1,754,636	YMV	1,278
		YVY	7,747

Opportunities & Challenges of adopting MinION in seed systems

Confirm known viruses and identify new ones



Develop/Improve diagnostic tests



Ready to use YMV LAMP kit



- Cost constraints and strategic integration
- Equipment and infrastructure limitations
- Bioinformatics expertise
- Data storage

Optimised seed yam production workflow

- Saves time (~3-4 months) and resources.

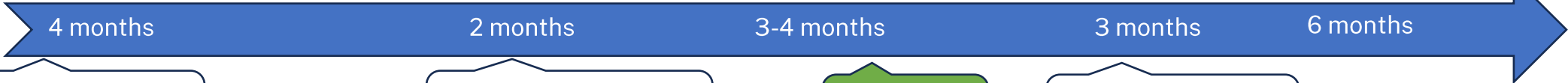
Breeder seeds
(virus-free)



MinION
virus indexing

Hardening & establishment
of mother plants

Yam plants in field



4 months

2 months

3-4 months

3 months

6 months

Sanitation / Tissue
culture (TC)

Mass propagation in TC

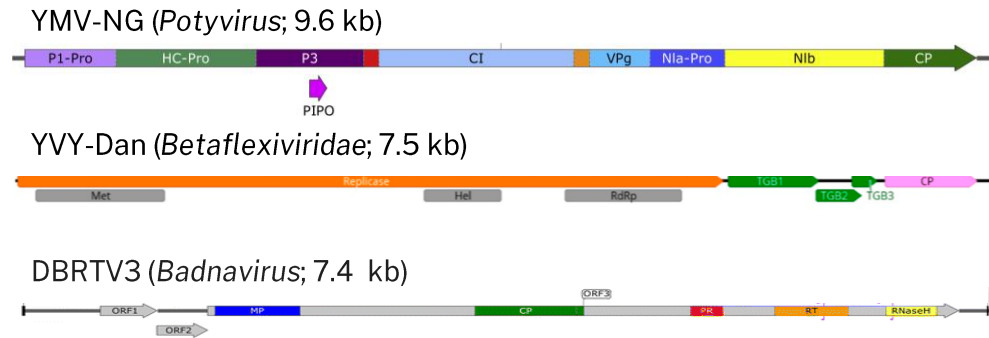
PCR/LAMP
testing

Single node cuttings

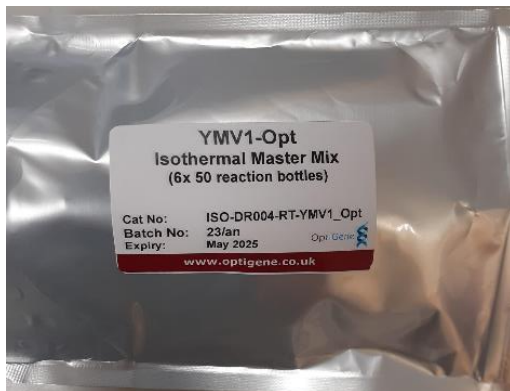


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