

# **openFMD**

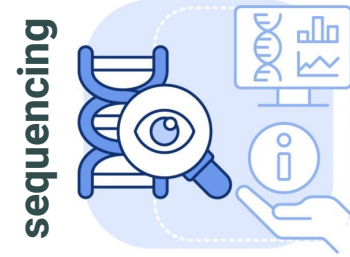
a digital platform to support  
Foot-and-Mouth Disease  
global surveillance

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**Antonello Di Nardo**

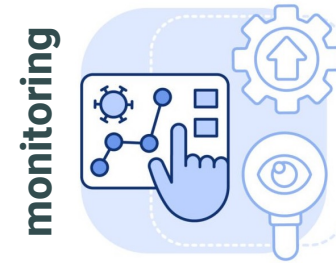
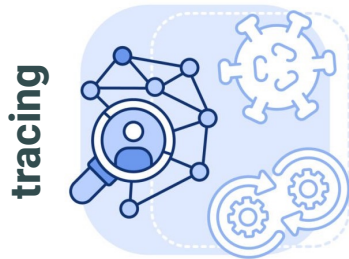
senior molecular epidemiologist

# epidemiological intelligence



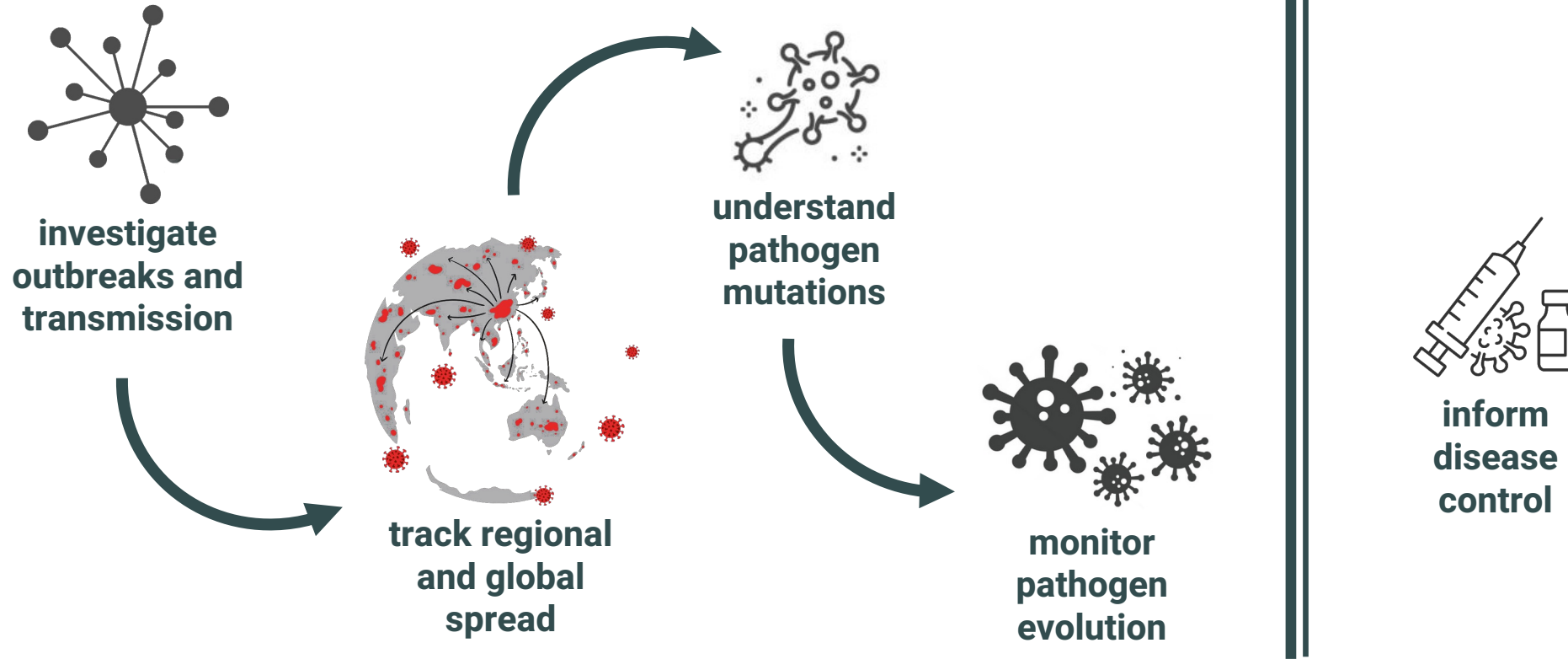
“the cycle of organised and systematic **collection, analysis** and **interpretation** of information from all sources to **detect, verify** and **investigate** potential health risks”

Source: @WHO



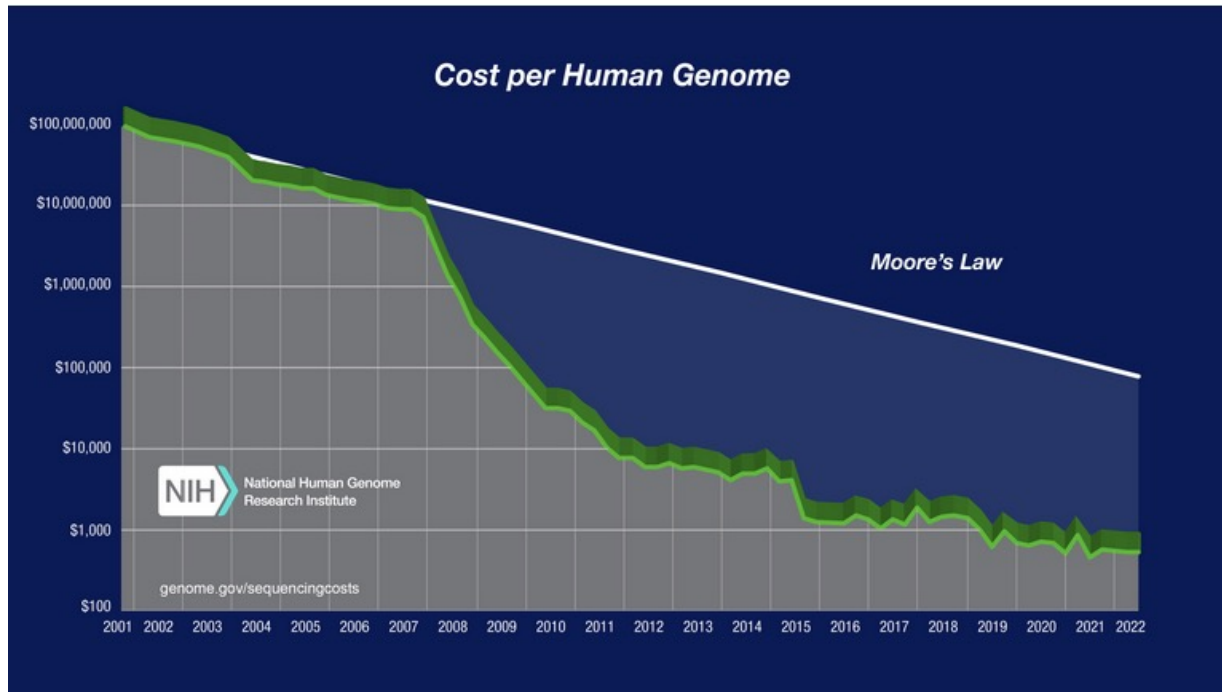
# epidemiological surveillance

surveillance data is **crucial** to get us to **know** about disease threats and trends

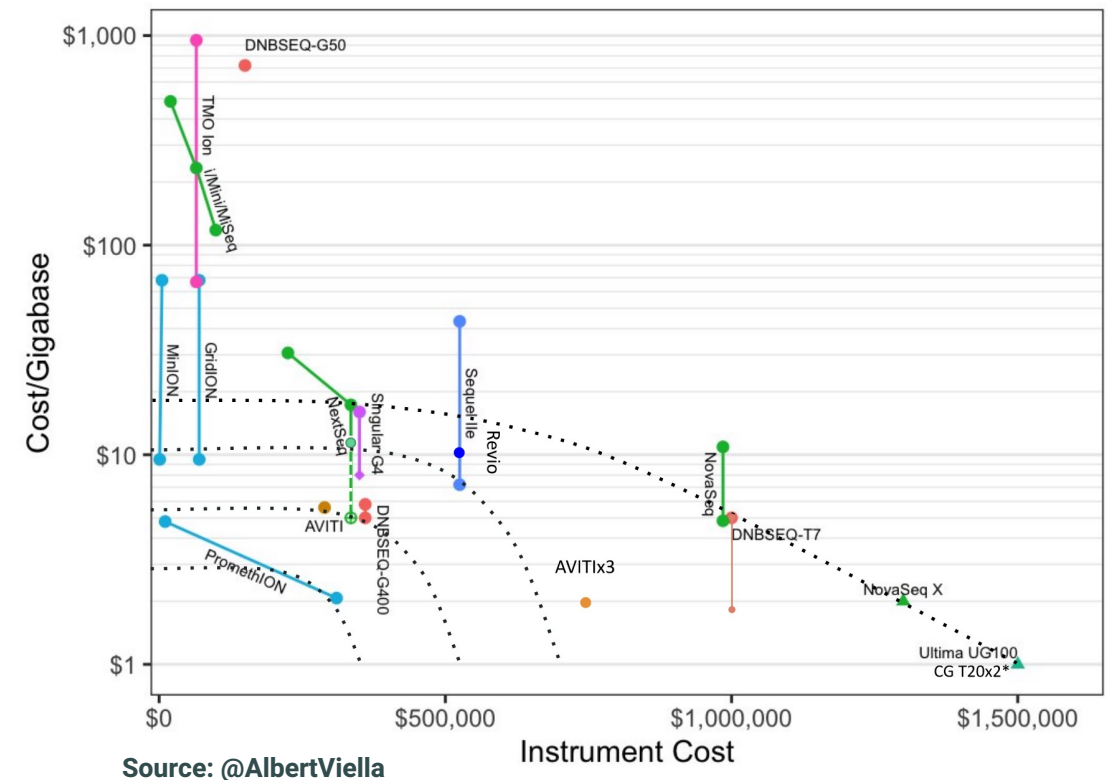


# genomic data

advances in the field of genomics over the past 20 years have led to substantial reductions in the cost of genome sequencing



Source: @NHGRI Genome Sequencing Program



Source: @AlbertViella

# surveillance data

surveillance data is the **raw** material, and because of that it is **critical**

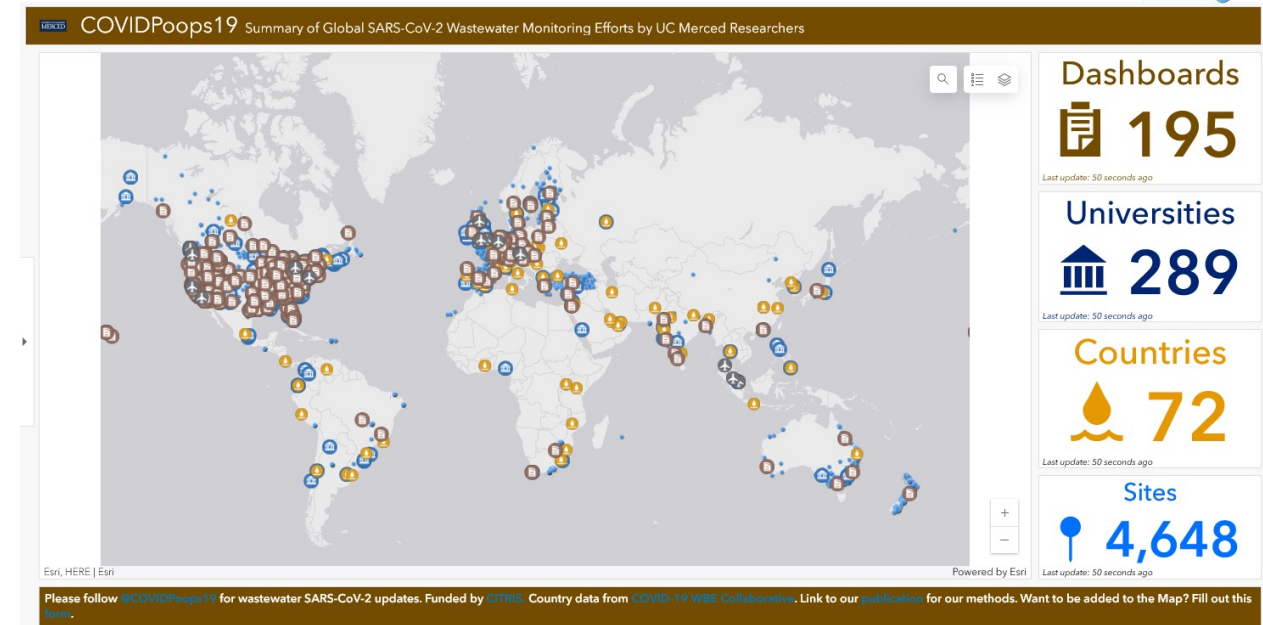
the SARS-CoV-2 pandemic has led to a revolution not only in how we **collect** the data but also in how we **use** it

## scientific publication

- important but not informing real-time response

## revolution in analysis and information

- enabling analysis is key
- building new tools and resources is critical
- sharing and collaboration is essential



Source: @COVIDPoops19

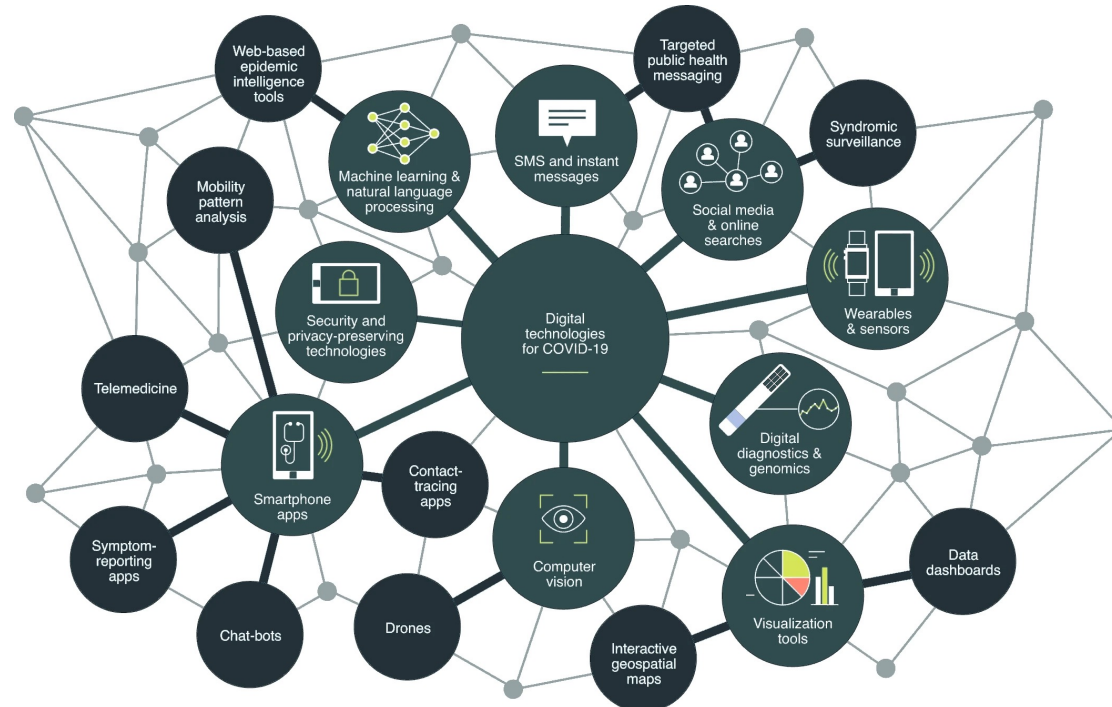
# digital epidemiology and surveillance

How do we empower appropriate surveillance?

Ensuring researchers are given the tools and knowledge they need to understand data

## Enabling research and policy through diverse tools

deployment of agile integrated genomic, clinical, and epidemiologic surveillance systems with seamless interoperability and global interconnectivity



Source: @Budd et al. 2020 *Nat Med*

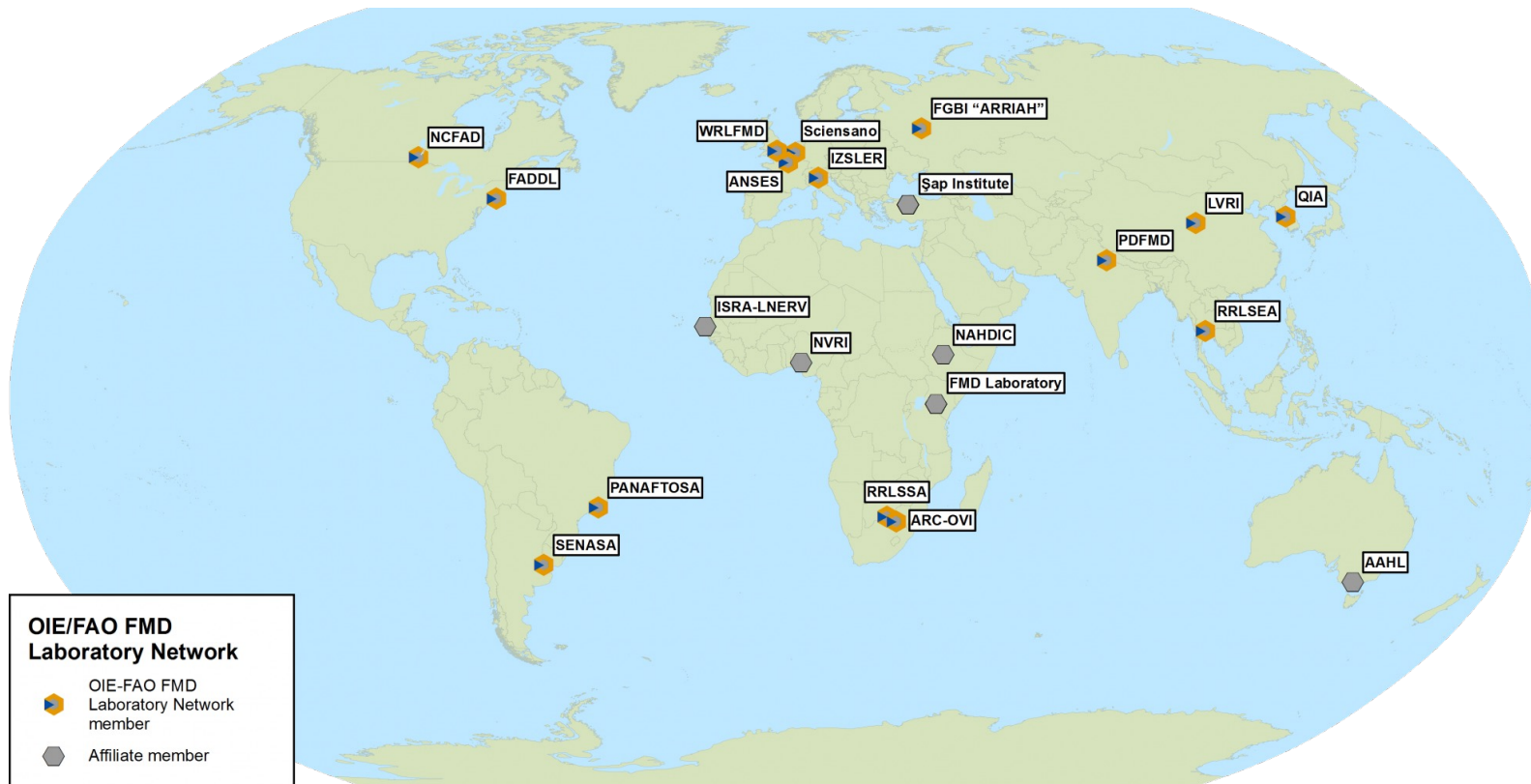
## Make research and knowledge sharing more efficient

wider cross-sectorial collaboration and data sharing between laboratories, health agencies, surveillance databases, and the broader scientific community



# FMD global surveillance

“The genomic surveillance of FMDV contributes to international disease surveillance activities undertaken by the **WOAH/FAO Reference Laboratory Network for FMD**, which are facilitated via links to the FAO and WOAH”



# FMD digital surveillance

“to **help** researchers, national and regional laboratories, governments and international organisations in **planning** and **prioritising** FMD surveillance activities, and to contribute in **reducing** the risk of FMD spread and introduction in disease-free areas”

Provide comprehensive  
information from FMD global  
surveillance

Improve analysis and risk  
assessment of FMDV lineages  
circulating in different parts of  
the world

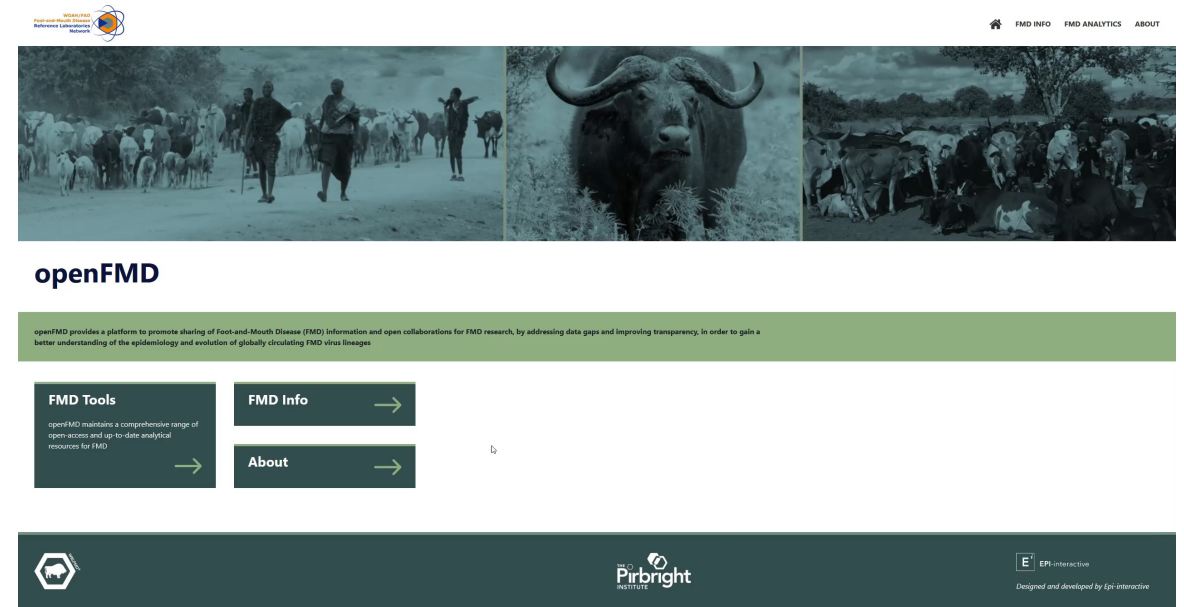
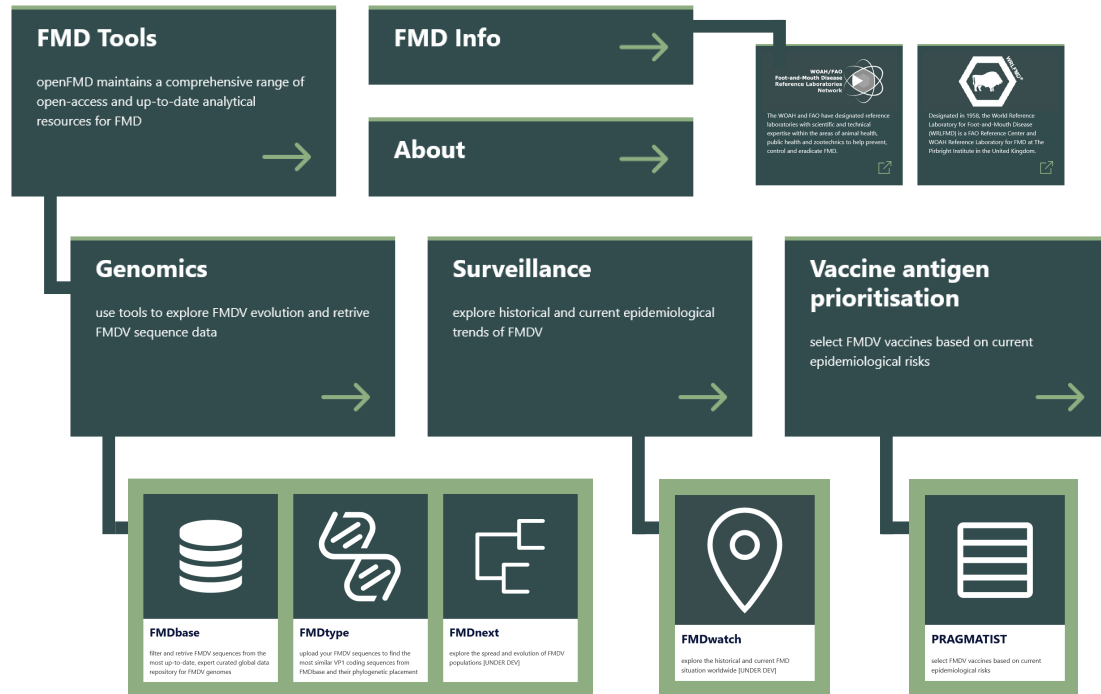
Identify and monitor gaps in FMD  
surveillance and track progress in  
the implementation of the global  
strategy for FMD control

Ensure risk managers have the info  
required to assess and control FMD risk,  
including through selection of the most  
appropriate vaccine strains matched to  
the circulating viruses



# openFMD portal

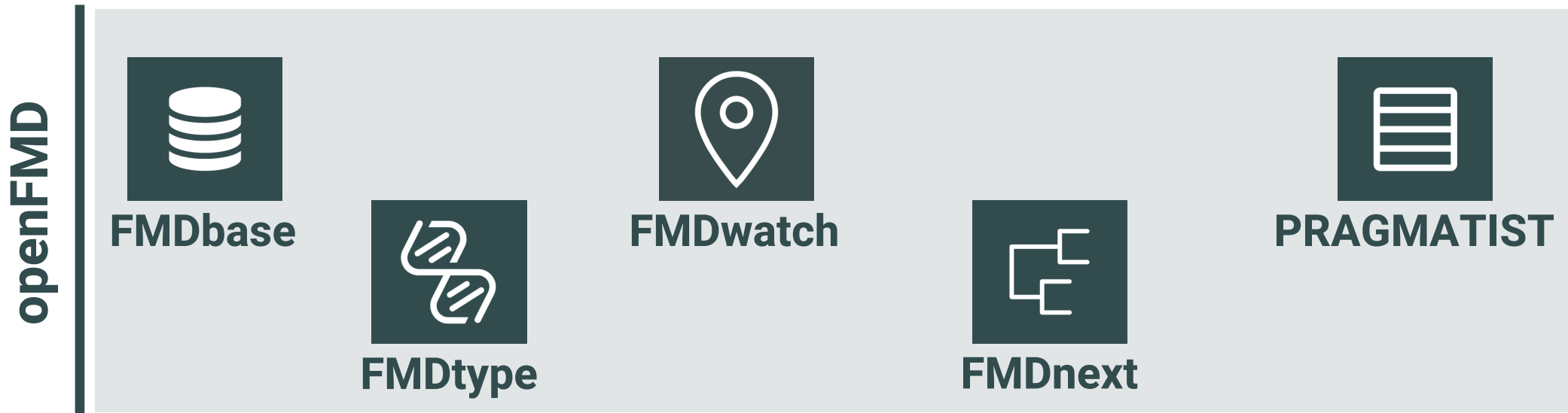
unique access point for all information, data and analytics for FMD



<https://www.openfmd.org/> |

# openFMD analytics

“a portfolio of **interactive analytical tools** developed by the FAO World Reference Laboratory for FMD and the WOA/FAO Reference Laboratory Network for FMD and implemented towards the overarching effort of enhancing the **global epidemiological intelligence** of FMD”





## an expert-curated database of FMDV sequences

- The official repository of FMDV genomic data from the WOAHA/FAO Reference Laboratory Network for FMD
- Fully curated FMDV sequences + associated metadata (n=18177)
  - Public data (n=12622)  
Published material (GenBank submitted)
  - Private data (n=5555)  
Unpublished material (FMD Ref Lab Net data)
- User queries + metadata info
- Download data in either .csv or .fasta format

The screenshot displays the FMDbase web application. On the left, a search sidebar includes filters for Viral lineage, Country, Host, Collection Date (with start and end date pickers), and Genome Region. The main content area shows 'Showing 16 of 18680' results. Above the table are options to 'Export data' in FASTA or CSV format and a 'DOWNLOAD' button. The table lists sequence entries with columns for Viral Lineage, Virus Sample, Country, Host, Collection Date, LEN, and Genome Region. The bottom of the interface shows 'Results per page' set to 16 and 'Page 1 of 1168'.

VIRAL LINEAGE	VIRUS SAMPLE	COUNTRY	HOST	COLLECTION DATE	LEN	GENOME REGION
A	13/febr/1-637	Pakistan			327	1D
A/ASIA/Iran-05	1.2/febr/1-335	Pakistan			325	1D
O	1/Giza/EGY/2014	Egypt		19/02/2014	639	1D-2A
Asia/ASIA	1/YZ/CHA/06	China	Pig	26/06/2006	8201	SUTR- L-1A-1B-1C-1D-2A-2B-2C-3A-3B1-3B2-3B3-3C-3D-3UTR
O	10/Egy/2016	Egypt	Water Buffalo	01/01/2016	992	1D
A/EURO-SA/A12	105325/BOL/98	Bolivia		31/12/1998	588	1D-2A
A/EURO-SA/A12	105329/BOL/98	Bolivia		31/12/1998	315	1D-2A
A/EURO-SA/A12	105330/BOL/98	Bolivia		31/12/1998	606	1D-2A
A/EURO-SA/A24	105331/BOL/98	Bolivia		31/12/1998	586	1D-2A
A/EURO-SA/A24	105357/COL/98	Colombia		31/12/1998	285	1D-2A
A/EURO-SA/A24	106453/PER/99	Peru		31/12/1999	639	1D-2A
A/EURO-SA/A24	106454/PER/99	Peru		31/12/1999	588	1D-2A
A/EURO-SA/A24	106455/PER/99	Peru		31/12/1999	633	1D-2A
O	1068/ Turkmenistan/ USSR/83	USSR		31/12/1983	685	1D-2A
O/ME-SA/ PanAsia-2	11.2	Pakistan	Water Buffalo	31/12/2006	312	1D
Asia/ASIA/ Sindh-08	115-1/4 ISB/Pak 2012	Pakistan	Water Buffalo	31/12/2012	628	1D



## annotating FMDV sequences and generating FMDV genotyping report

- User friendly tool to interrogate user data against the FMDV db in a simple guided fashion
- 'Annotate' user genomic sequences
- Test an 'evolutionary scenario' by including FMDV sequences from the database
- Reconstruct (+download) phylogenetic trees (.nexus file) [limited to 100 tips]
- Generate (+download) ad-hoc genotyping reports in (PDF file)

### FMDtype

Interactive generation of FMDV genotyping reports using nucleotide sequences encoding the FMDV VP1 gene.

1 Upload data

2 Check sequences

3 Tree building options

4 Build tree

#### Upload data



FMDV sequence data are expected to be in FASTA format where the minimum length of each VP1 sequence submitted is ≥ 600 nucleotides (full **U/PMC** notation allowed). This tool limits the computation to up to a maximum of 30 VP1 sequences submitted for each FMDV serotype.

Format: **FASTA** Single sequences


Copy and paste FMDV sequences in **FASTA** format onto this box below (up to a maximum of 30 sequences per FMDV serotype).  
To see how this tool works load an [example](#) of FASTA-formatted sequences.

Paste sequences here

Check sequences →

FMDtype is supported by Eurofins, The FAO World Reference Laboratory for FMD and The Pirbright Institute

 EPI-interactive  
Designed and developed by Epi-interactive



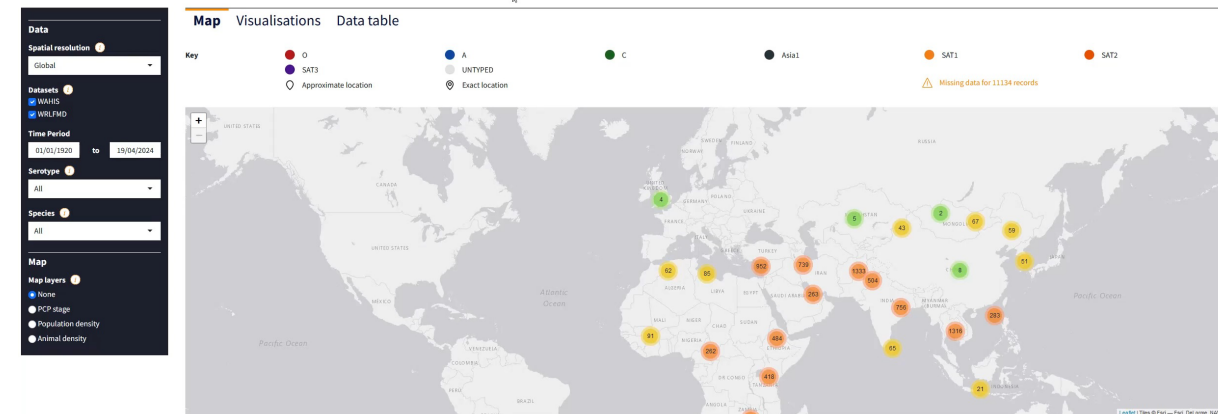


## exploring and visualising FMD surveillance data

- Integrate all sources of FMD surveillance data in a single repository (WRLFMD + FMD Ref Labs + WOAHAHIS)
- Allow to better identify FMD surveillance gaps and option to improve activities related to FMD risk monitoring
- Improve timely analysis and communication of FMDV activities at country/regional levels
- Support evidence-based decision-making processes for FMD control
- [future devs] Help to monitor FMDV antigenic evolution by reporting vaccine-matching data

### FMDwatch

FMD epidemiological intelligence for digital surveillance, exchange and communication of new disease threats.





## evaluation and prioritisation of candidate FMDV strains for inclusion in antigen banks

- Create and test FMD regional/country risk scenarios
- Identify FMD profile risks for different FMDV lineages circulating globally
- Evaluate FMDV vaccine strains coverage and protection
- Identify high-priority vaccine to be included in FMDV antigen banks
- [future devs] Generate (+download) PRAGMATIST reports in (PDF file)

### PRAGMATIST

The Prioritisation of Antigen Management with International Surveillance Tool (PRAGMATIST) is a semi-quantitative FMD vaccine strain selection tool that provides a transparent, evidence-based approach to assist vaccine bank managers to prioritise candidate vaccine strains for inclusion in an antigen bank. The tool combines three relevant parameters from the perspective of an antigen bank manager, namely:

- 1) The relative likelihood of an FMD incursion from different regions of the world (source areas);
- 2) The prevalence of circulating FMD viral strains in these source areas (lineage distribution) and
- 3) The expected protection afforded by different FMD vaccines against these circulating FMD strains (vaccine coverage).

#### Parameter selection

Source areas ●

Lineage distribution ●

Vaccine coverage ●

#### Recommendations

Lineage risk ⓘ Vaccine coverage ⓘ

Serotype

Lineage

Key

● Serotype O

● Serotype A

● Serotype Asia1

● Serotype SAT1

● Serotype SAT2

● Serotype SAT3

● Serotype C

#### SEROTYPE O

FMDV Lineage	Risk Score	Serotype Risk %
O/EA/WA	3233.47	63.91
O/ME-SA/PanAsia2	792.4	15.66

#### SEROTYPE A

FMDV Lineage	Risk Score	Serotype Risk %
A/AFRICA	1169.13	49.68
A/NSA/pan-OS	611.28	25.97

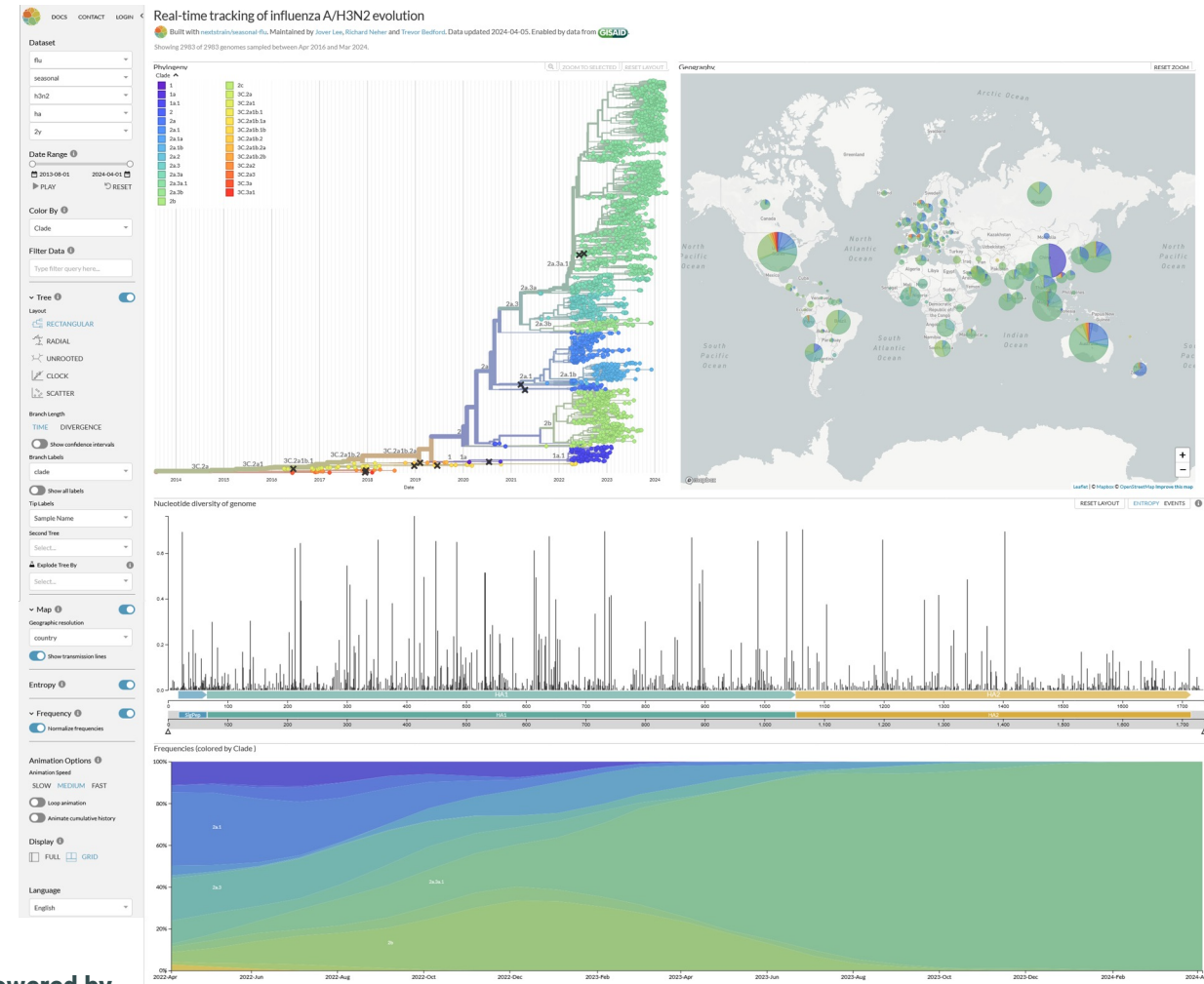
#### SEROTYPE ASIA1

FMDV Lineage	Risk Score	Serotype Risk %
Asia1	208.29	100



## exploring the spread and evolution of FMD viral populations

- Provide a global snapshot of FMDV evolution at serotype level with the analysis of the full repository of FMDV sequences [starting from 1924]
- Assess geographical spread of FMDV lineages at regional level through phylogeographic links
- Monitor FMDV evolution and identify increasing diversity and geographic expansion of new potential threats
- Support evidence-based decision-making processes for FMD control
- [future devs] Predict FMDV antigenic evolution





# openFMD vision



Provide an ecosystem that connect FMD data of different type and from a wide range of sources



Offering the infrastructure and implement policies and practices to equitable sharing and access of FMD data

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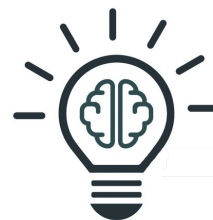


Create a collaborative epidemiological intelligence environment for FMD



Pulling on multiple strengths and works from groups of FMD scientists around the world

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Facilitate the wide availability of analytical tools for FMD



Enabling FMD research communities and animal health institutions to strengthen decision making processes through innovative tools and applications

# acknowledgements

## collaborators

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Liang Yang  
Ben Rhodes



Chandana Tennakoon  
John Hammond  
Morgan Armer  
Tim Haywood



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FMD Reference Laboratory Network

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