Lessons learnt from integrating grEPI into WHO's mpox dashboard

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World Health Organization

Background: WHO Mpox Dashboard

- **Launched in Summer 2022** to enable **transparent** and **timely** sharing of outbreak data amid rising global cases

- Built using **R** and **Shiny**

- **Key sections included:**
  - Global trends
  - Case demographics
  - Transmission dynamics
  - Downloadable summary data

- Added a section on **mpox epidemiological parameters** sourced from scientific literature

Mpox Epi Parameters

- **Public Health Agency of Canada (PHAC)** developed a repository of mpox-related literature

- Integrated data from **multiple sources**, including PubMed, Scopus, Europe PMC, and others

- **Extracted key information:** metadata, epi parameter type, reported values, distributions, and uncertainty bounds

- **Regularly updated** to ensure comprehensive and timely coverage

- Used to develop the **initial version** of the mpox epi parameters section

2024-2025 Mpox Outbreak

- **Emergence of new variant (clade Ib)** alongside a surge in cases in DRC and neighboring countries

- **Shifting transmission dynamics** and change in affected populations

- **Dashboard adapted** to focus on highly-affected regions and raise awareness of evolving outbreak trends

- Expanded epi parameter section to:
  - Include **clade information**
  - Specify **study population's country**
  - Incorporate **more recent literature**

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WHO declares mpox virus a public health emergency of international concern
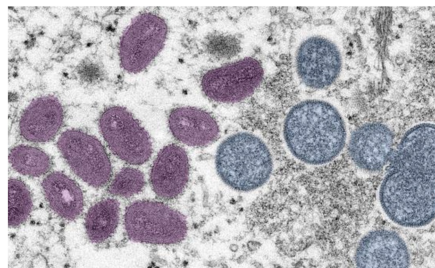
© CDC/Cynthia S. Goldsmith, Russell Regnery | Mpox - formerly monkeypox - is a rare but dangerous infection similar to the now eradicated smallpox virus.

Mpox: countries affected in Africa
from 1 Jan 2022, as of 25 May 2025

Outbreak status
- Active outbreak (cases reported in the last six weeks)
- Control phase (cases reported in the past 90 days)
- Cases reported since 2022, but not in last 90 days
- No mpox reported
- Not applicable
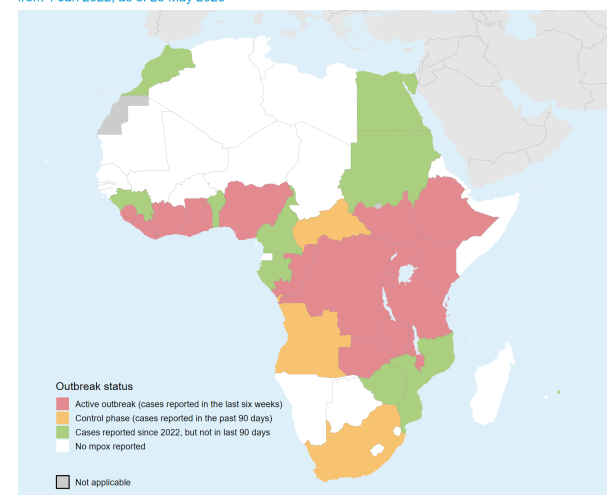
Trends in global mpox cases by WHO region
data as of 30 Apr 2025

Source: WHO

Legend:
- African Region
- Region of the Americas
- Eastern Mediterranean Region
- South-East Asia Region
- European Region
- Western Pacific Region

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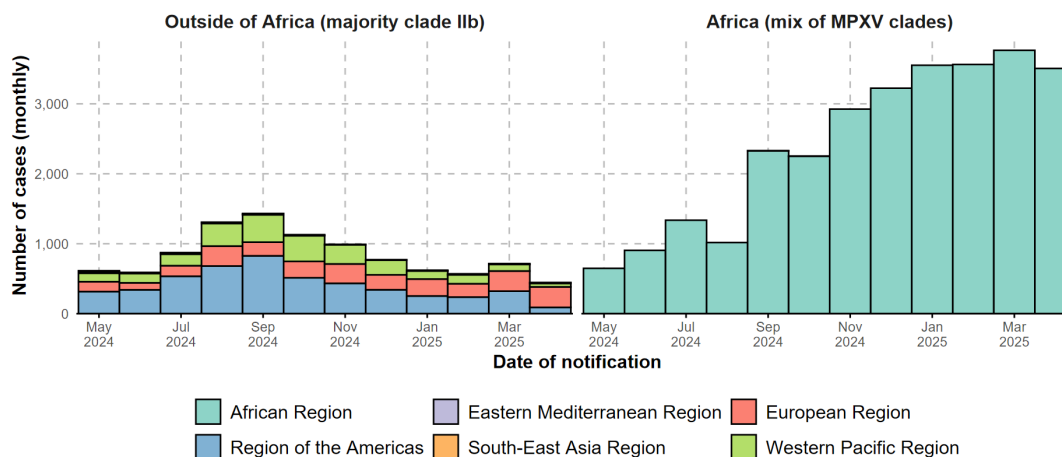
Advantages of grEPI

- **Consolidates data** from **PHAC**, **{epiparameter}** R package, and other public sources into a single harmonized repository

- **Backed by global partners** across academia and public health sector, with growing community of practice

- **Comprehensive** set of available variables

- Remains under **active development**

- **Updated** with emerging evidence

- **Accessible via RESTful API** delivering structured JSON

- **Documentation for using R to access grEPI** mpox epidemiological parameters available here

Additional Mpox parameters to support modelling and analysis
August 2024
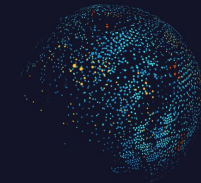
BACKGROUND

The EpiParameter community is a global collaborative working group coordinated by the World Health Organization (WHO), with the aim of establishing an easy-to-use repository of epidemiological parameters accessible by modelers, epidemiologists, subject matter experts and decision makers, to inform mathematical models and other epidemiological analyses and, by extension, public health preparedness and response.

Given the ongoing multi-country Mpox outbreak, a brief extraction of Mpox parameters was undertaken, covering studies already parameterized in the {epiparameter} R package and other publicly available sources. The parameters and data structures provided in this guidance note have been driven and supported by our community partners (see last page of document). This product is one of the key components of the forthcoming Global Repository of Epidemiological Parameters (GREP). The GREP minimum viable product will be made available in early 2025.

Please note that this is an experimental product currently under development.

AVAILABLE PARAMETERS FOR MPOX ANALYSIS

Parameter label	Definition	Example options (based on what is currently in the repository)
PATHOGEN_FK	Selected parameter of interest	Mpox
PARAM_TYPE_FK	Parameter type	Human delay, Reproduction number (Basic R0)
PARAM_SUBTYPE_FK	Parameter sub-type	Incubation period, generation time, All Reproduction number (Basic R0), serial interval
CLADE	Disease clade	I, IIa, IIb
PARAM_UNIT_FK	Parameter units	Days, No units
PARAM_VAL	Value of the selected parameter	
PARAM_BOUND_LOWER (PARAM_BOUND_UPPER)	Lower/upper bound of the parameter estimate	
PARAM_VALUE TYPE	Value category	Mean, Median
POP_SEX_FK	Gender filter	Male, Both
POP_AGE_MIN (POP_AGE_MAX)	Minimum/Maximum age of the study population	Min: 20, 23, 28; Max: 61, 64, 71
POP_COUNTRY	Country the estimate was produced from	Netherlands, United States, Democratic Republic of Congo, United Kingdom
ARTICLE_LABEL	First author and year of the study	
ARTICLE_TITLE	Title of the study	

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Implementation

- Implemented in **R**, rendered with **Quarto**

- API can be accessed using **standard packages**: `httr`, `jsonlite`, `tidyverse`

- **Key steps:**
  1. Connect to WHO Collaboratory xMart API: https://xmart-api-public-uat.who.int/COLLAB/MPOX_PARAMETERS
  2. Identify and extract relevant fields (e.g., type, subtype, uncertainty bounds, population metadata)
  3. Limit to key parameters: *incubation period*, *serial interval*, *generation time*
  4. Infer clade where missing, using genomic surveillance and country/year context
  5. Generate summary tables with {`gt`}, and enable download with {`downloadthis`}

- **Automatically updates** as new evidence is added

ACCESSING PARAMETERS IN R

To access the mpox parameters, first ensure you have installed the required packages:

```r
library(httr)        library(tidyverse)
library(jsonlite)    library(pander)
library(rlist)
```

The core table can then be accessed via the GET() function via the public xmart-api-public-uat.who.int portal:

```r
##--Load tables--##
response1 <- GET("https://xmart-api-public-uat.who.int/COLLAB/MPOX_PARAMETERS")

#FACT_PARAMETERS
json1 <- content(response1, "text")
FACT_PARAMETERS <- data.frame(fromJSON(json1))

#Tidy column names
FACT_PARAMETERS <- FACT_PARAMETERS %>% rename_with(str_sub, start = 7L)
```

An example of a Mpox parameter extraction query has been provided below.

```r
Ex <- subset(FACT_PARAMETERS, PATHOGEN_FK == 'Mpox' &
             PARAM_TYPE_FK == 'Human delay' &
             PARAM_SUBTYPE_FK == 'incubation period' &
             PARAM_UNIT_FK == 'Days')

Result <- data.frame(Ex$ARTICLE_LABEL, Ex$PARAM_VAL, Ex$PARAM_BOUND_LOWER,
Ex$PARAM_BOUND_UPPER, Ex$PARAM_VALUE_TYPE_FK, Ex$POP_COUNTRY)

colnames(Result) <- c("Article label", "Parameter value", "Lower bound", "Upper
bound", "Value type", "Country")

Result
```

Article label	Parameter value	Lower bound	Upper bound	Value type	Country
Miura 2022	8.50	6.60	10.90	Mean	Netherlands
Charniga, 2022	7.60	6.20	9.70	Mean	United States
		...			

Final Product

Contents

6. Epidemiological parameters

This section of the report highlights studies that estimate key mpox epidemiological parameters—**incubation period**, **serial interval**, and **generation time**—to enhance understanding of the outbreak's dynamics.

The WHO Collaboratory Epi Parameters Community maintains a user-friendly repository of epidemiological parameters for modelers, epidemiologists, subject matter experts, and decision-makers to support mathematical modeling, public health preparedness, and response.

The presented studies are sourced from:

1. The {epiparameter} R package, maintained by data.org's Epiverse initiative, which includes periodically reviewed literature and accepts user-submitted parameters via a publicly accessible Google Sheet.

2. A literature screening process conducted by the Public Health Agency of Canada (PHAC), established in 2022, with documented inclusion criteria and methodology in the Methods sheet of their results.

These sources are consolidated in a single repository, accessible via an API (details here). As this is an experimental product under development, feedback is encouraged via Collaboratory@who.int.

The tables below summarize the most relevant estimates for **incubation period**, **serial interval**, and **generation time**, derived from these sources.

Parameters   Bibliography

Incubation Period   Serial Interval   Generation Time

Incubation Period

Reference	Clade	Country	n	Median[1]	Mean[1]	SD[1]	95% CrI / CI[1]	IQR[1]	Range[1]	Distribution
Marziano, 2024	I	Democratic Republic of the Congo	-	-	9.9	-	-	-	-	Weibull
Ponce, 2024[2]	I	Multiple countries	-	-	7.3	-	5 - 10.2	-	-	Gamma
Ponce, 2024[2]	II	Multiple countries	-	-	8.9	-	6.6 - 11.7	-	-	Gamma
Madewell, 2023	IIb[3]	United States	36	-	5.6	-	4.3 - 7.8	-	-	Gamma
Wang, 2022	I	Congo	-	9.5	-	-	-	8 - 12.2	-	-
Tarin-Vicente, 2022	II	Spain	144	7.0	-	-	-	5 - 10	1 - 19	-
Wang, 2022	IIa	United States	-	16.8	-	-	-	11.4 - 23.9	-	-
Angelo, 2022	IIb[3]	Multiple countries	78	8.0	-	-	-	5 - 11	2 - 40	-

Lessons Learnt: Integrating grEPI into WHO Mpox Dashboard

- **Learning curve**
  - Deriving additional fields (e.g., age ranges, uncertainty bounds)
  - Converting data types where necessary

- **Strengths**
  - Comprehensive coverage across multiple pathogens and parameter types
  - Regular updates with new evidence
  - Stable API endpoint performance

- **Challenges**
  - Less intuitive than R packages (`{epiparameter}`, `{epireview}`)
  - Data inconsistencies identified for studies reporting multiple estimates of the same parameter

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Ongoing Development

Collaboratory

1. Refine and expand parameter categories

2. Standardize tools for extracting epidemiological parameters from scientific literature and outbreak data

3. Develop tools to facilitate integration of grEPI into analytical workflows

4. Establish quality assurance processes, enabling traceable community-driven contributions

5. Encourage sustained community engagement through contributor recognition and other incentives

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Interactive Session

Q&A

Thank you