Lassa Fever Outbreaks, Transmission Models and Epidemiological Parameters

Pathogen Epidemiology Review Group

MRC Centre for Global Infectious Disease Analysis &
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Jameel Institute, School of Public Health,
Imperial College London

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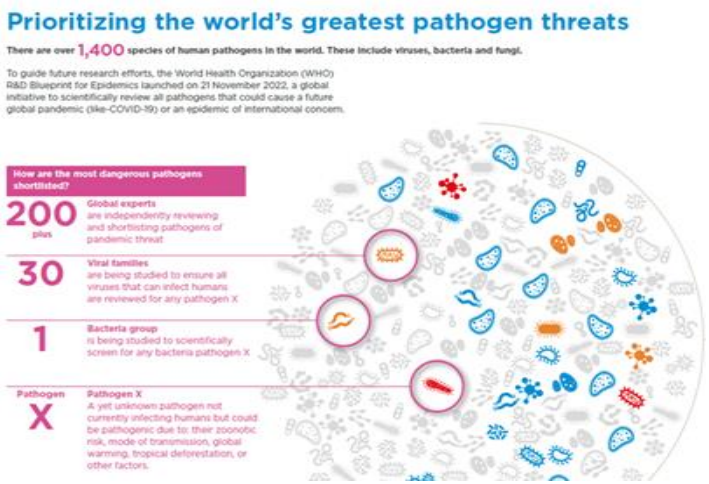
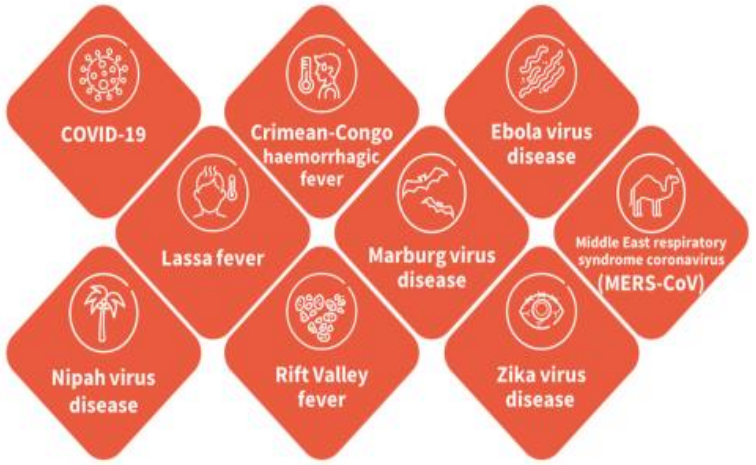
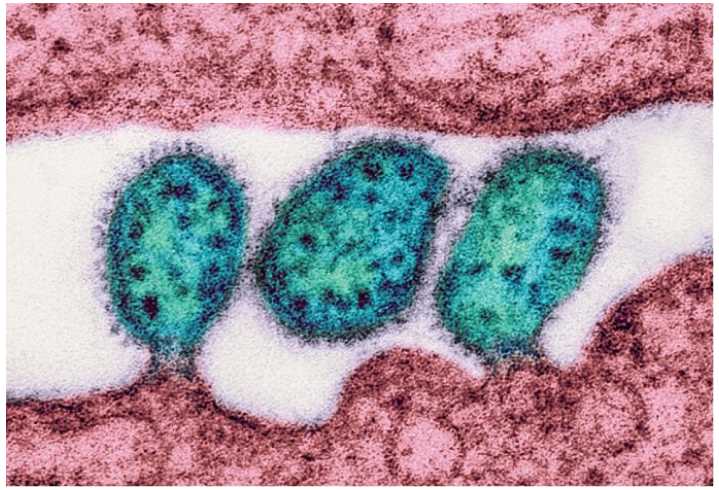
Imperial College London

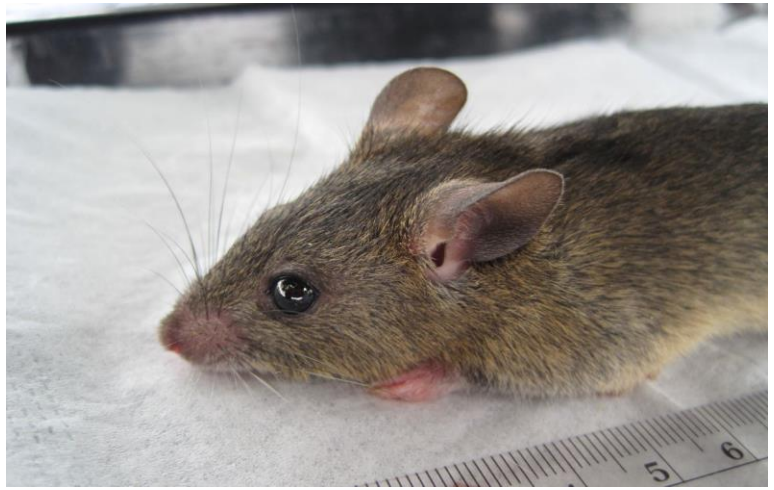
Priority Pathogens Project

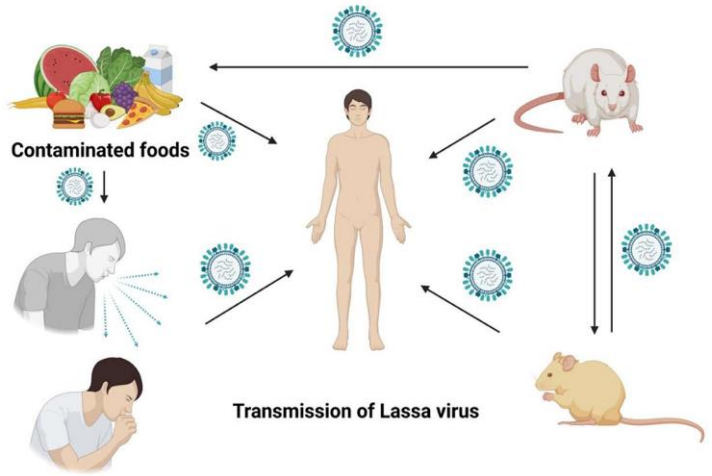




Lassa Mammarenavirus and Haemorrhagic Fever

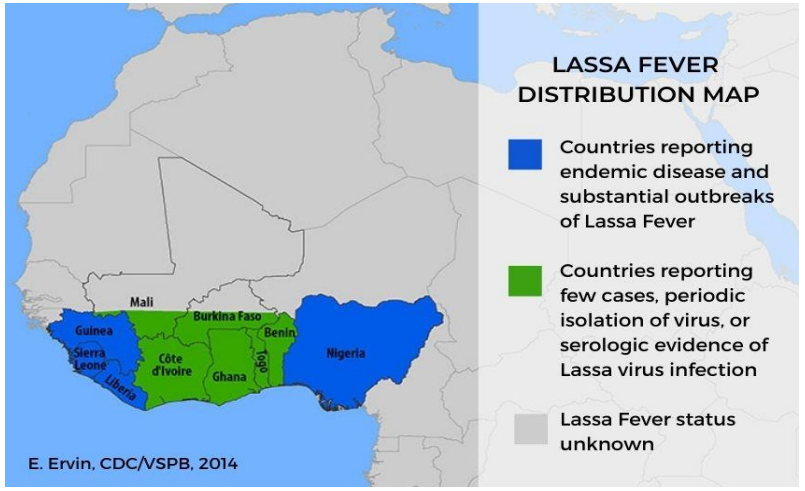






Lassa Fever - Introduction

- Lassa Fever is caused by Lassa Mammarenavirus, an RNA virus in the family *Arenaviridae*
- It is endemic in rodents in West Africa but new reservoirs identified recently
- Frequent spillover to humans via exposure to excretions, human-to-human transmission also
- Reported CFRs range from 20-70%, but high seroprevalence indicates occurrence of asymptomatic/mild infections (estimated at 80%)
- One of the highest-burden priority pathogens:
    - 100-300,000 infections per year
    - 5,000 deaths per year



Lassa Fever - Recent Developments

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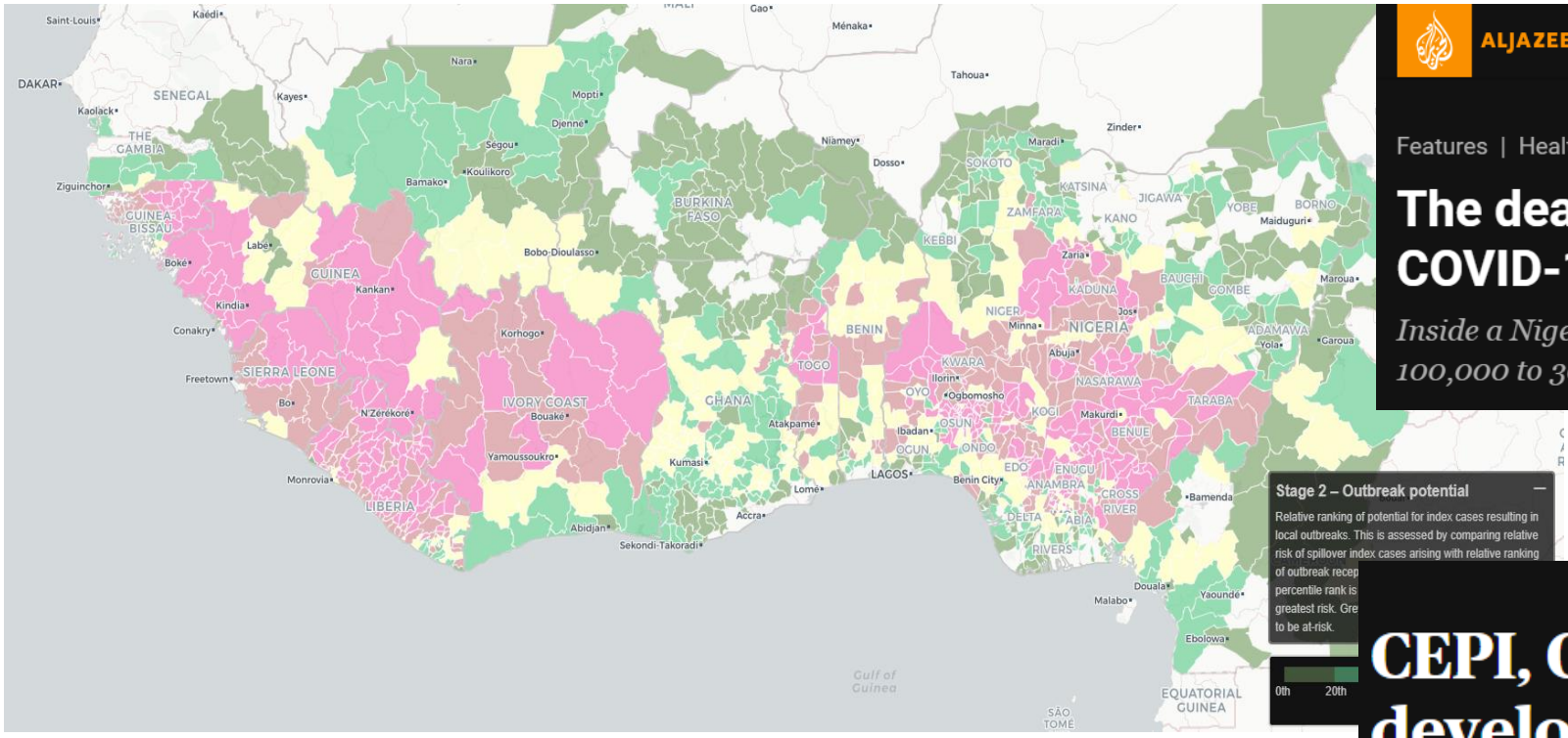

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Features | Health

The deadly virus Nigerians fear more than COVID-19: Lassa fever

Inside a Nigerian hospital ward treating Lassa, a virus that infects 100,000 to 300,000 people in West Africa every year.

CEPI, Oxford launch project to develop arenavirus vaccines

News brief | November 2, 2023

Lisa Schnirring

Topics: Lassa , Misc Emerging Topics , Viral Hemorrhagic Fever

Lassa Fever - Systematic Review

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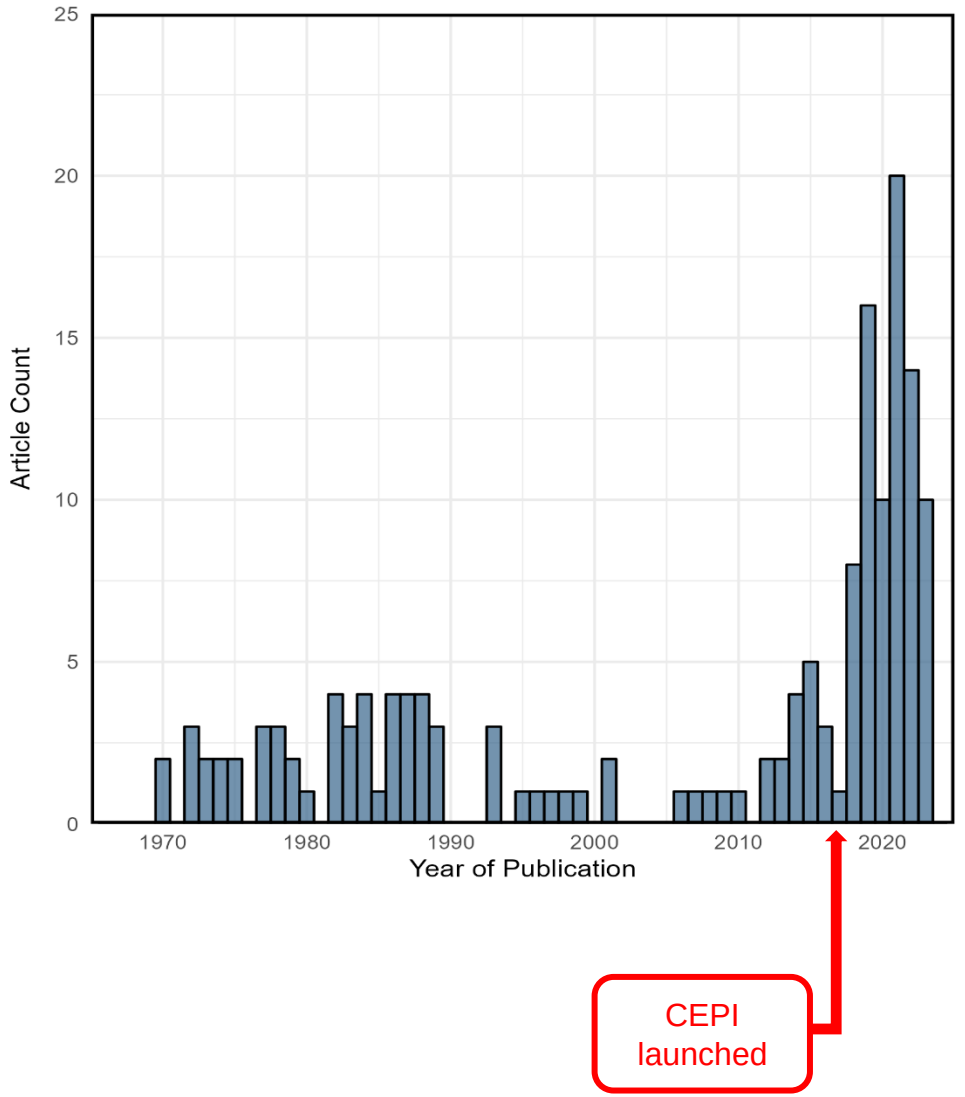
- Systematic literature review of Lassa Fever
  - outbreaks
  - transmission models
  - epidemiological parameters
- Data extracted, curated and included in *epireview* R package (WIP)
- Meta-analysis of parameters of interest



Lassa Fever - Outbreaks & Seroprevalence

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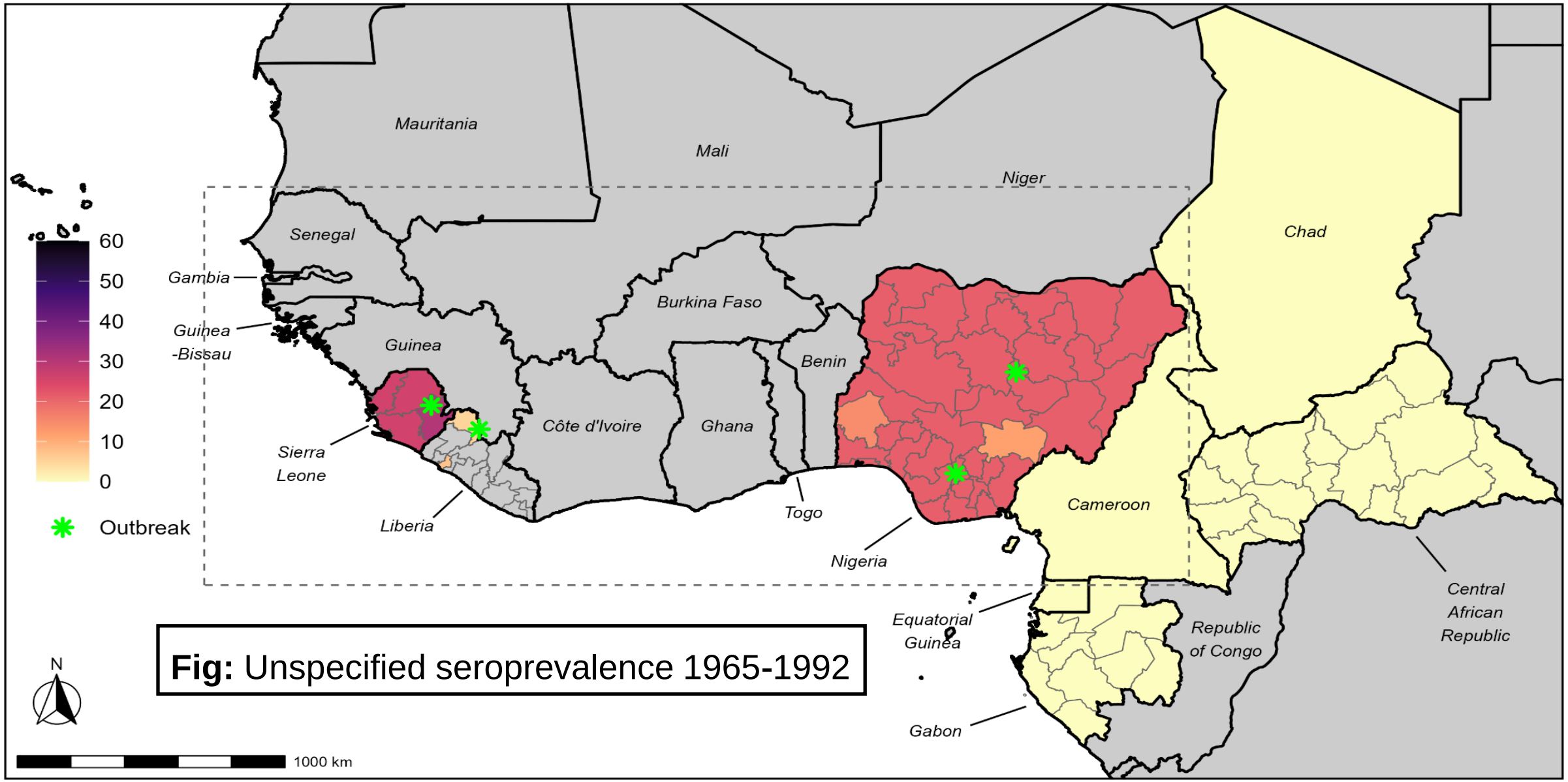

Fig: Unspecified seroprevalence 1965-1992

Lassa Fever - Outbreaks & Seroprevalence

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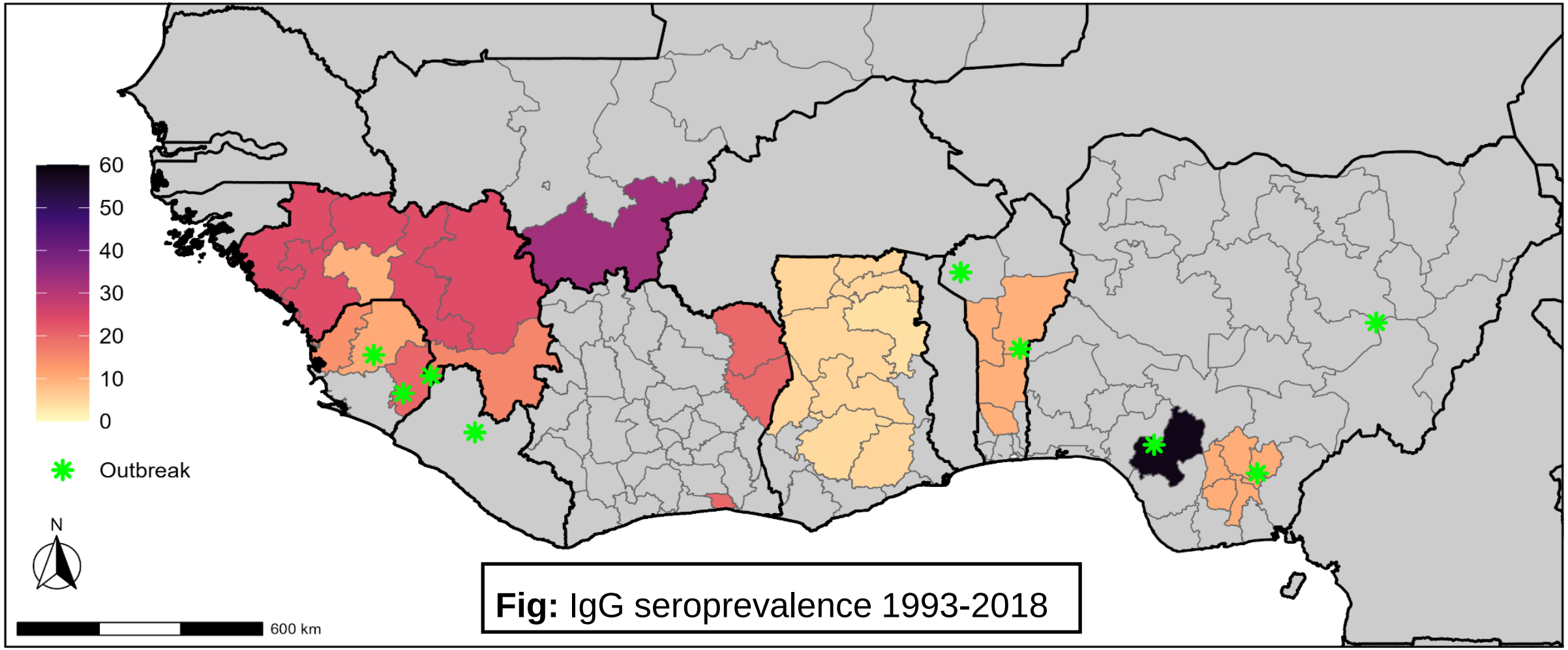

Fig: IgG seroprevalence 1993-2018

Lassa Fever - Lineages

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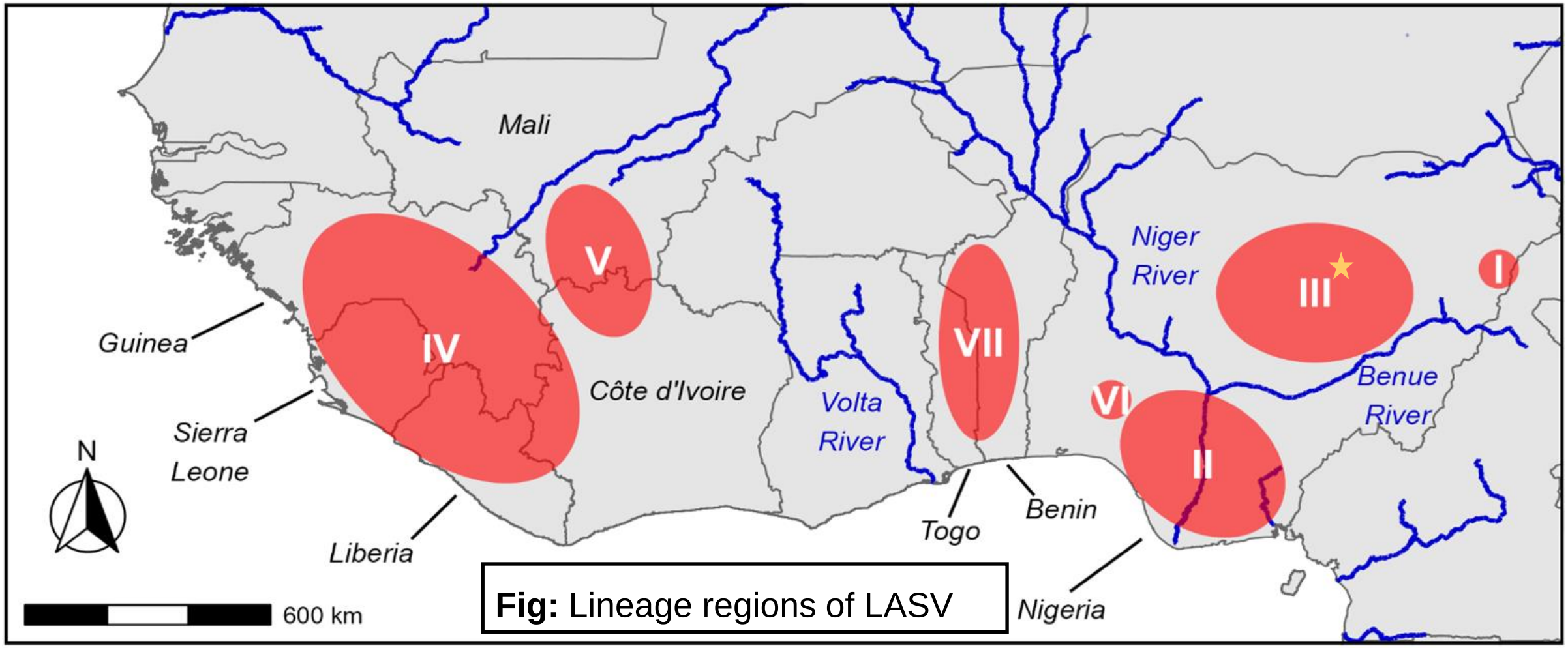

Fig: Lineage regions of LASV

Lassa Fever - Severity

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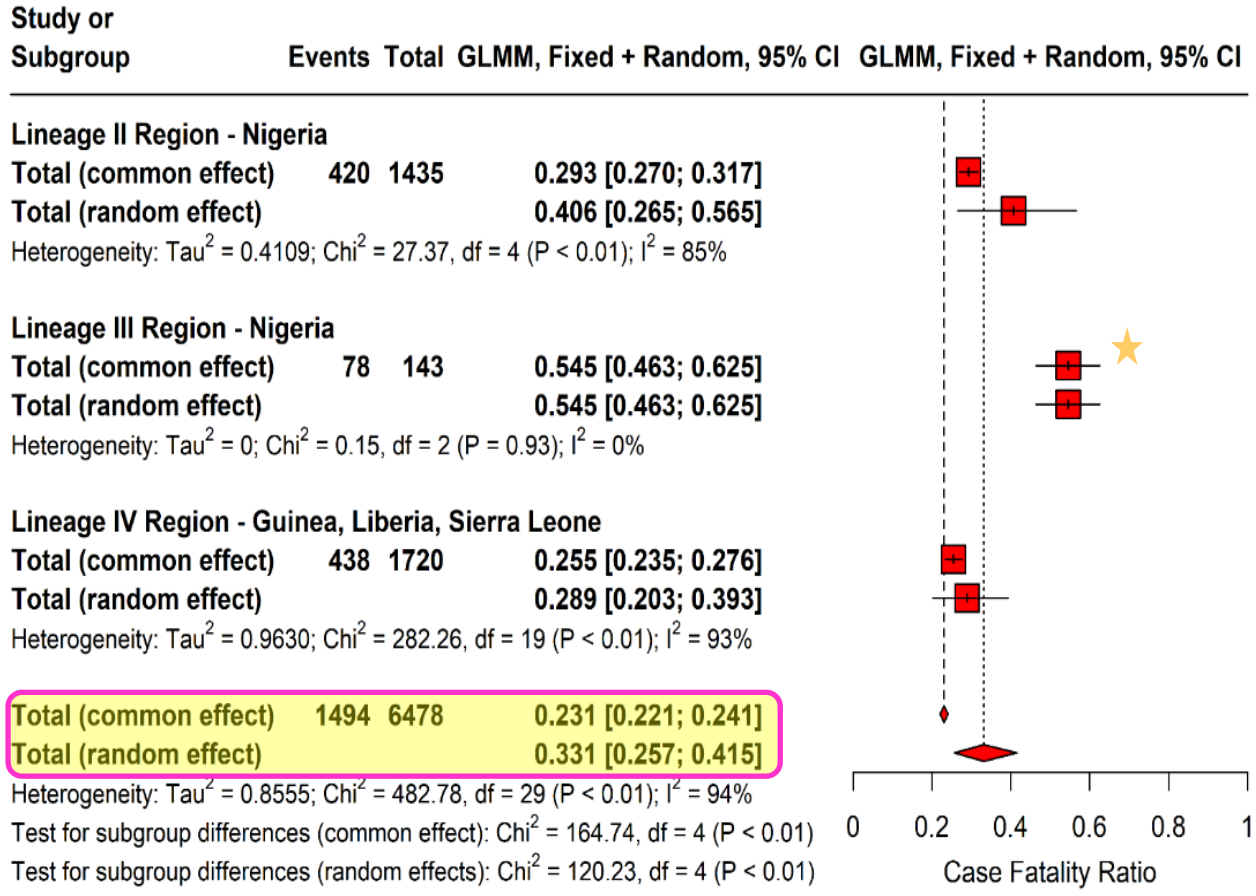
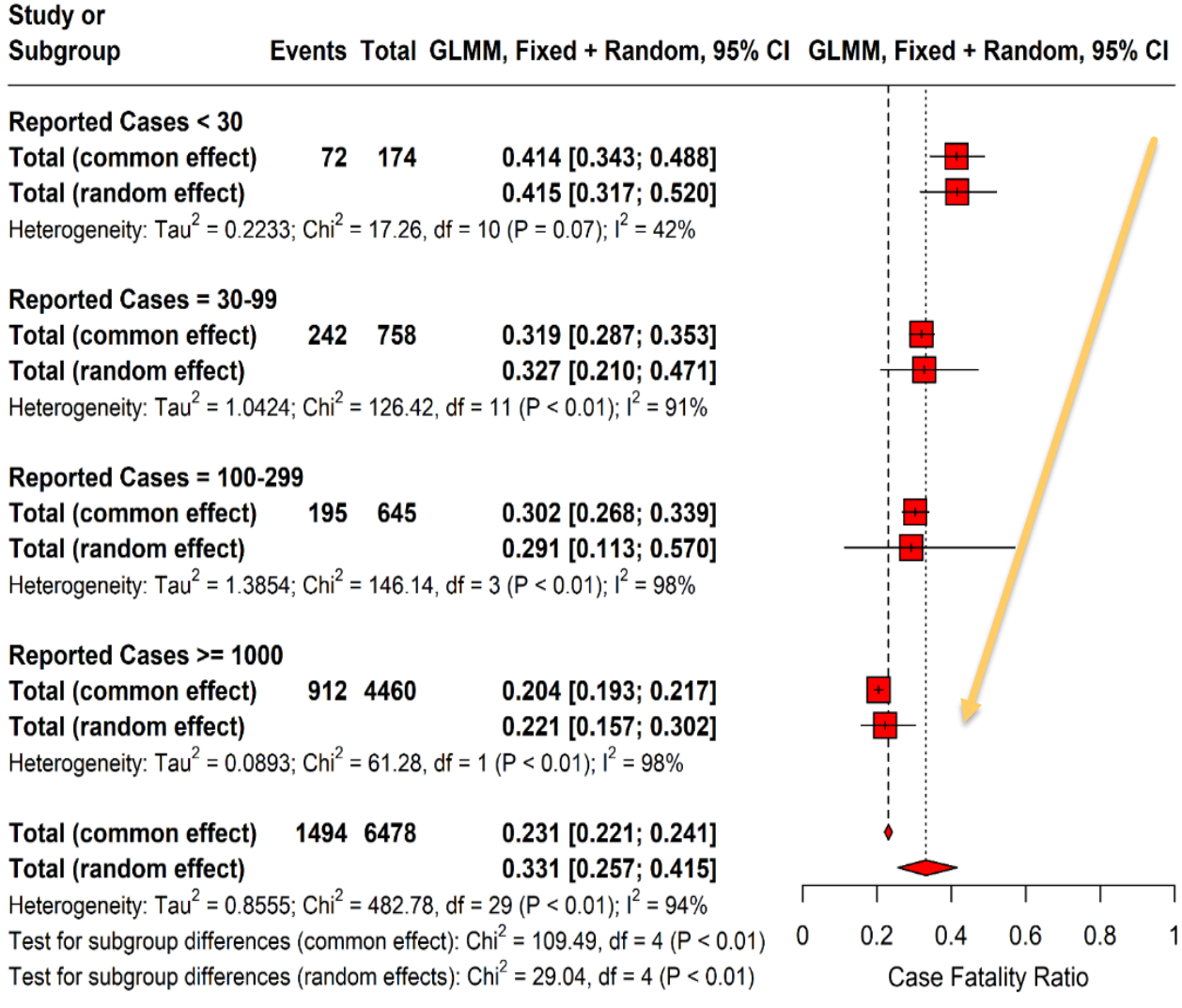
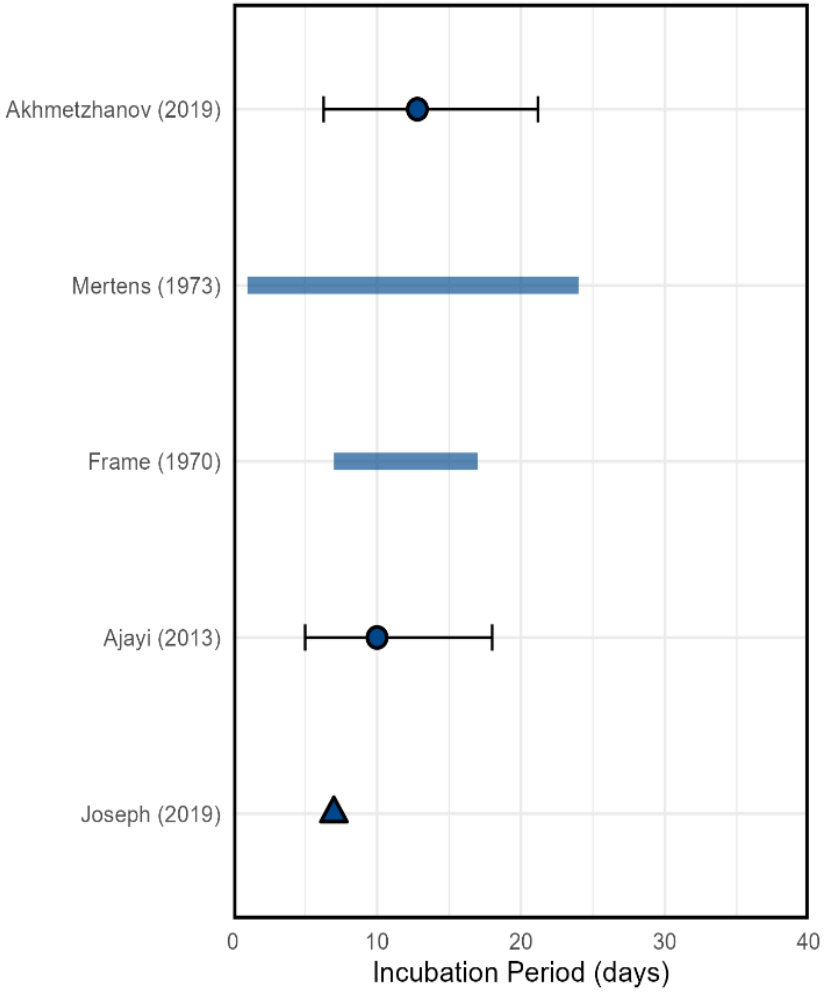
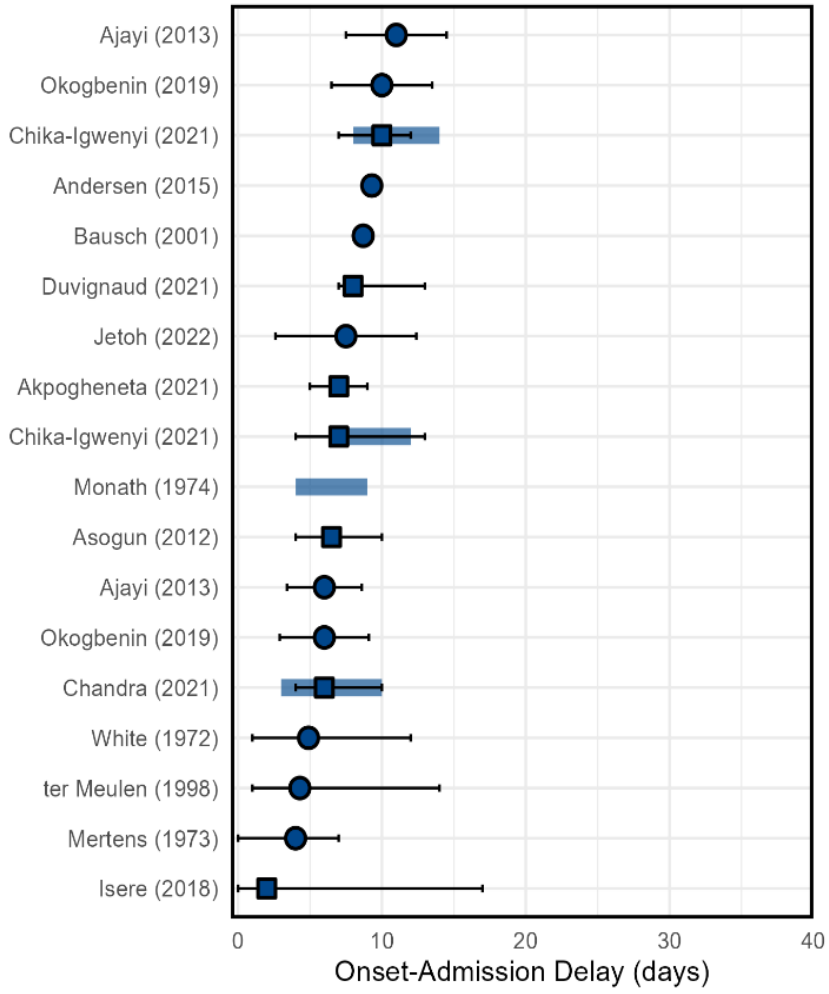
- Meta-analysis of CFRs

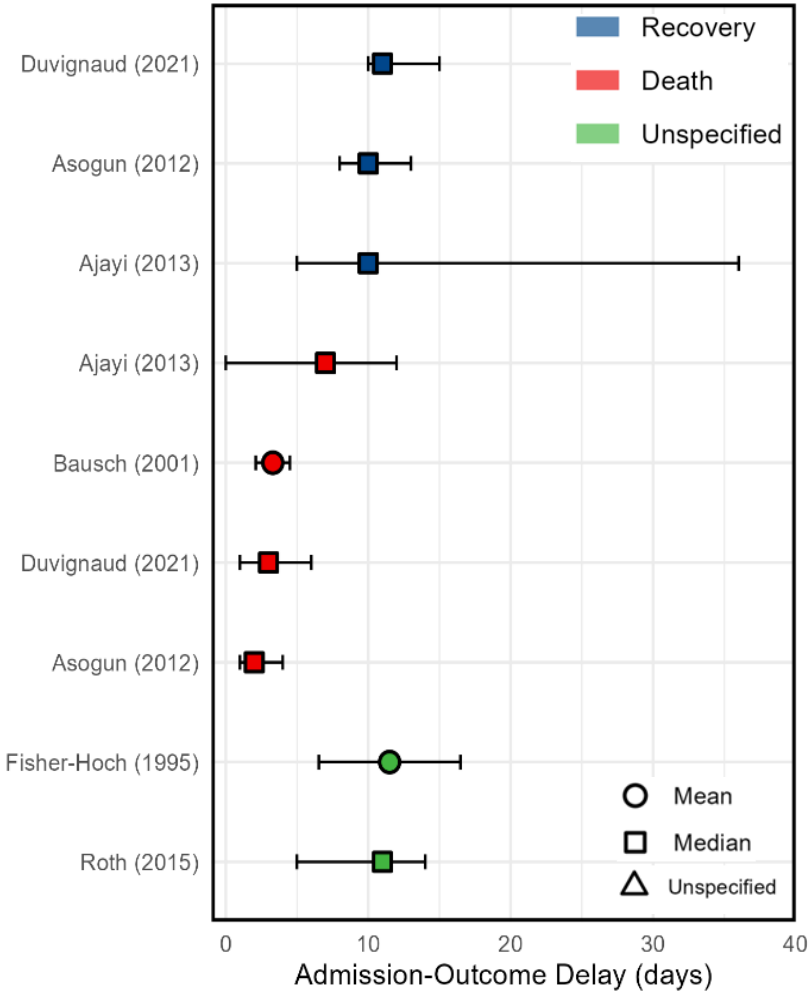




Lassa Fever - Delays







Lassa Fever - Delays

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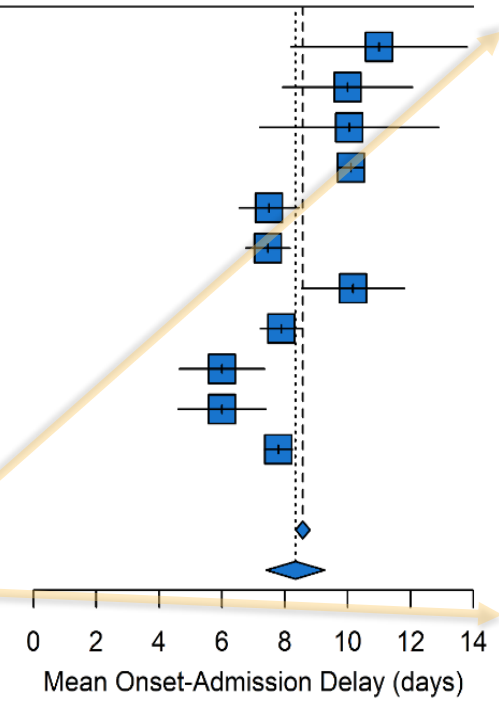
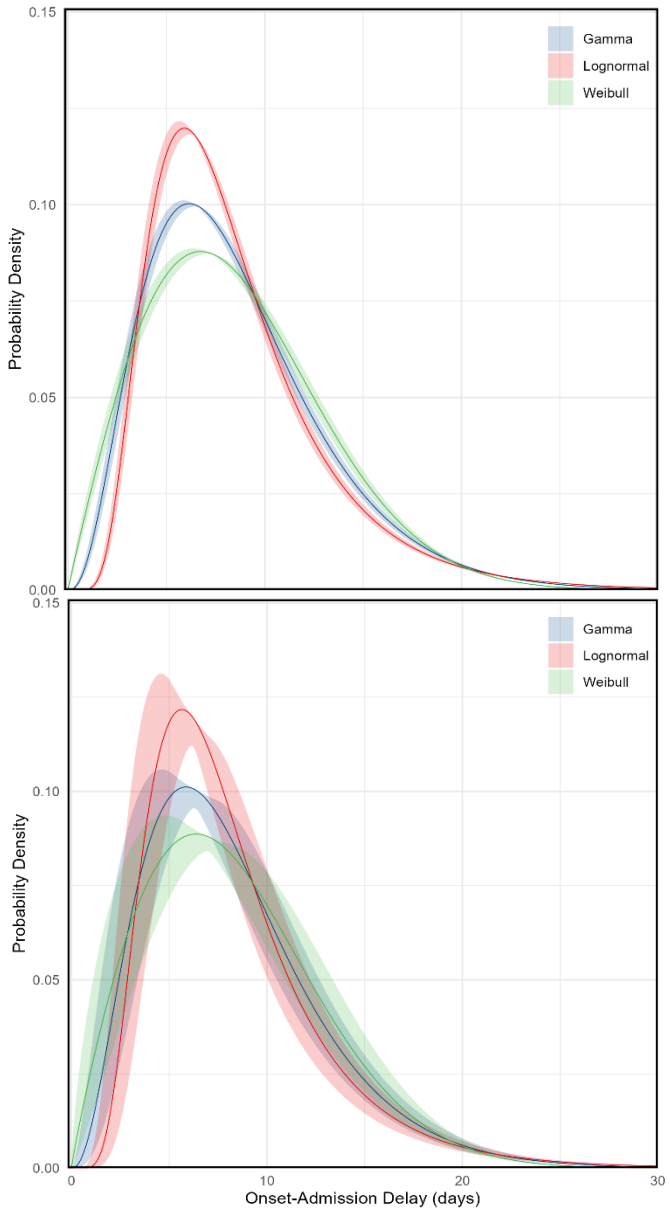
Study	Mean	SD	Total	Weight (common)	Weight (random)	Mean IV, Fixed + Random, 95% CI
Ajayi (2013)	11.00	3.50	6	0.67%	5.65%	11.00 [8.20; 13.80]
Okogbenin (2019)	10.00	3.50	11	1.23%	7.35%	10.00 [7.93; 12.07]
Chika-Igwenyi (2021)	10.05	4.37	9	0.64%	5.53%	10.05 [7.19; 12.91]
Duvignaud (2021)	10.10	4.46	510	35.01%	11.30%	10.10 [9.72; 10.49]
Jetoh (2022)	7.50	4.90	103	5.86%	10.30%	7.50 [6.55; 8.45]
Akpogheneta (2021)	7.46	3.02	71	10.61%	10.82%	7.46 [6.76; 8.17]
Chika-Igwenyi (2021)	10.17	6.81	67	1.97%	8.52%	10.17 [8.54; 11.80]
Asogun (2012)	7.89	4.48	174	11.82%	10.89%	7.89 [7.22; 8.56]
Ajayi (2013)	6.00	2.60	14	2.83%	9.25%	6.00 [4.64; 7.36]
Okogbenin (2019)	6.00	3.10	19	2.70%	9.16%	6.00 [4.61; 7.39]
Chandra (2021)	7.80	4.46	389	26.66%	11.23%	7.80 [7.35; 8.24]
Total (common effect, 95% CI)			**1373**	**100.00%**	**--**	**8.57 [8.34; 8.80]**
Total (random effect, 95% CI)				**--**	**100.00%**	**8.34 [7.41; 9.27]**

Heterogeneity: $Tau^2 = 1.9592$; $Chi^2 = 126.65$, df = 10 ($P < 0.01$); $I^2 = 92\%$





Lassa Fever - Transmission & Evolution

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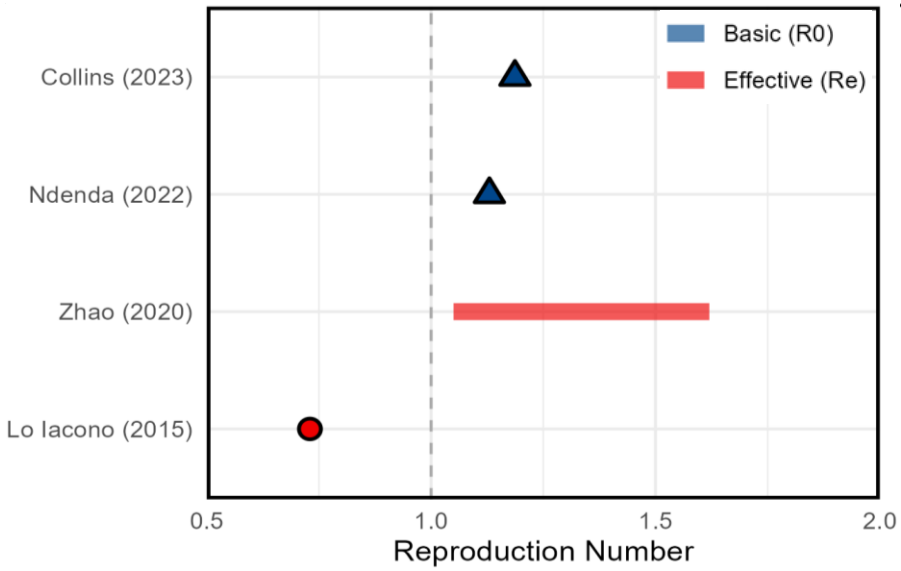
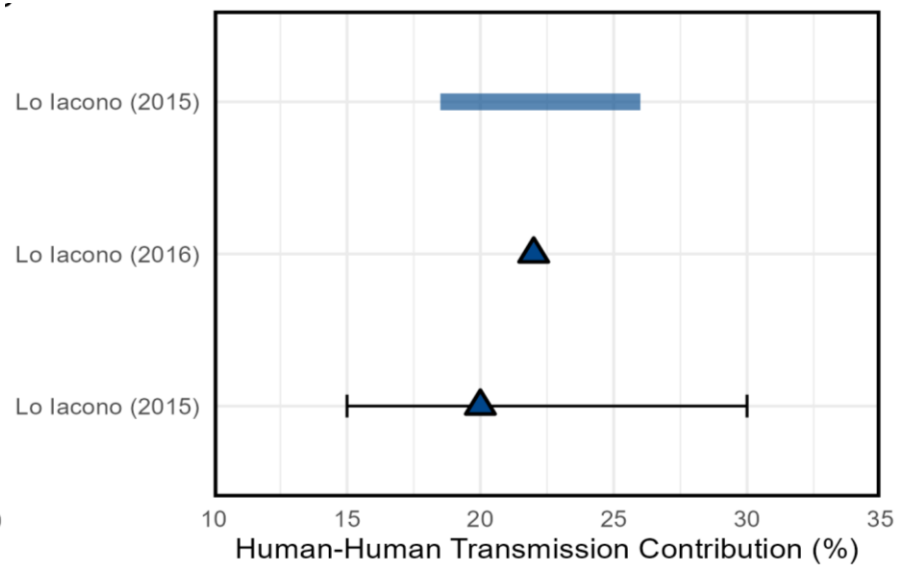
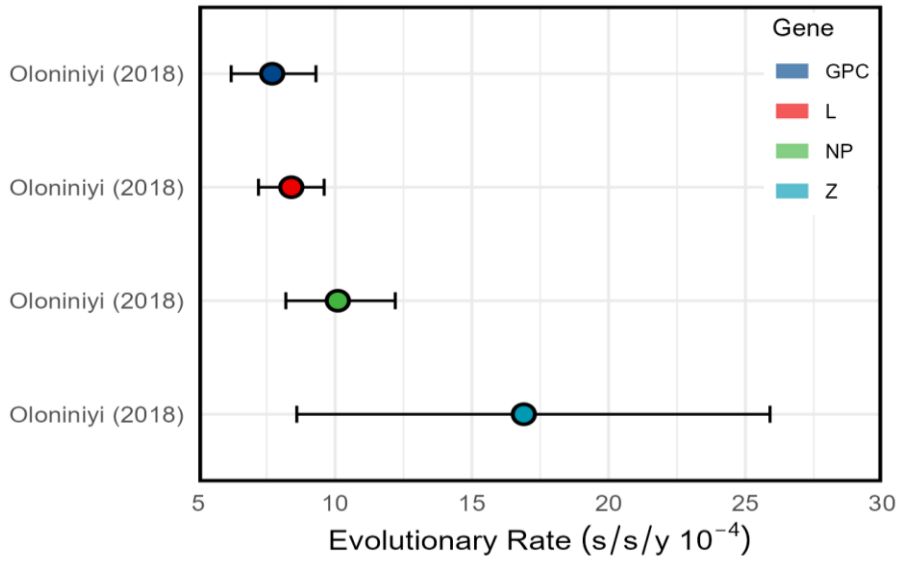
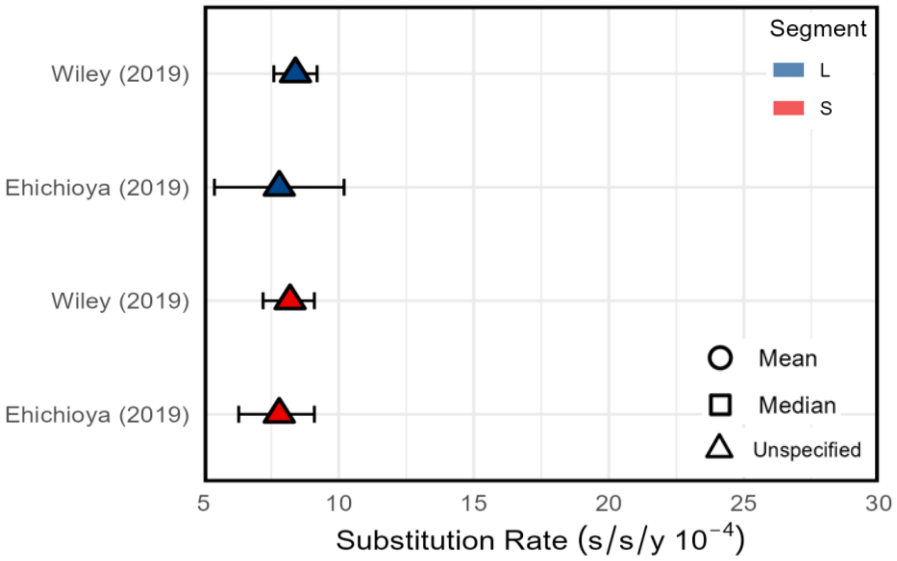
- Transmission difficult to characterise
- Estimates of viral evolution are low
- Fear of new variants
  - Lassa X



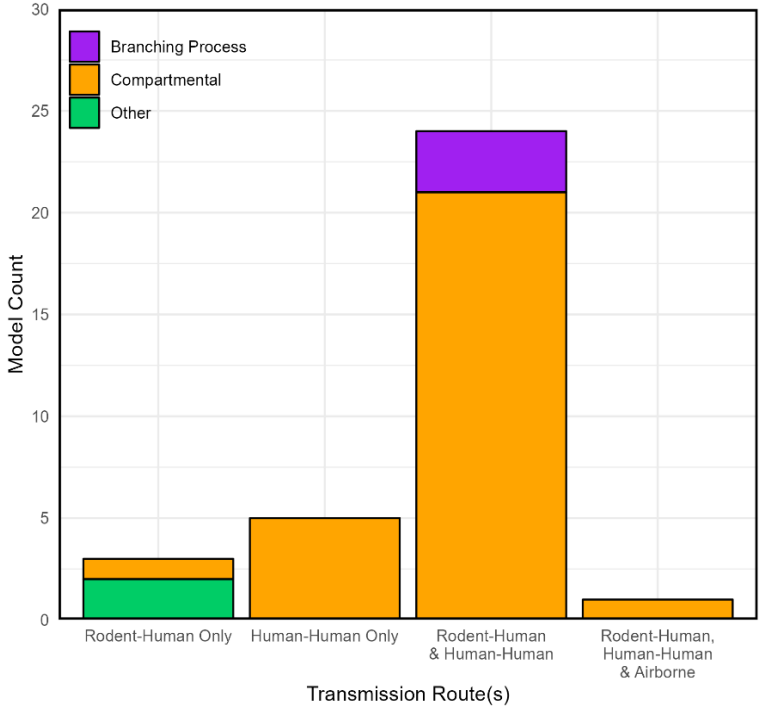


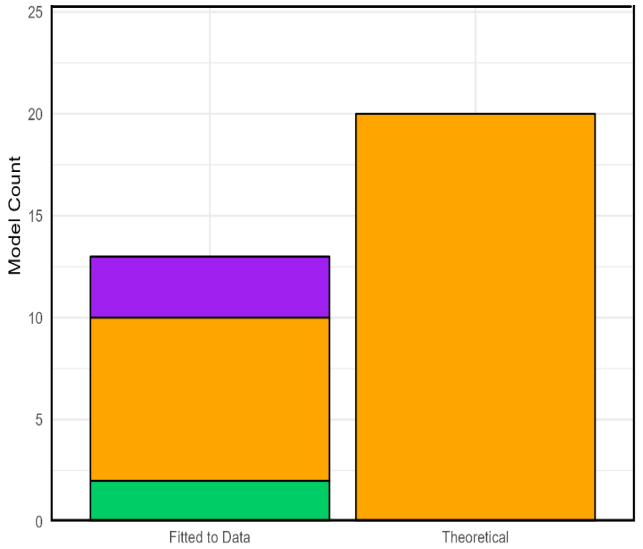




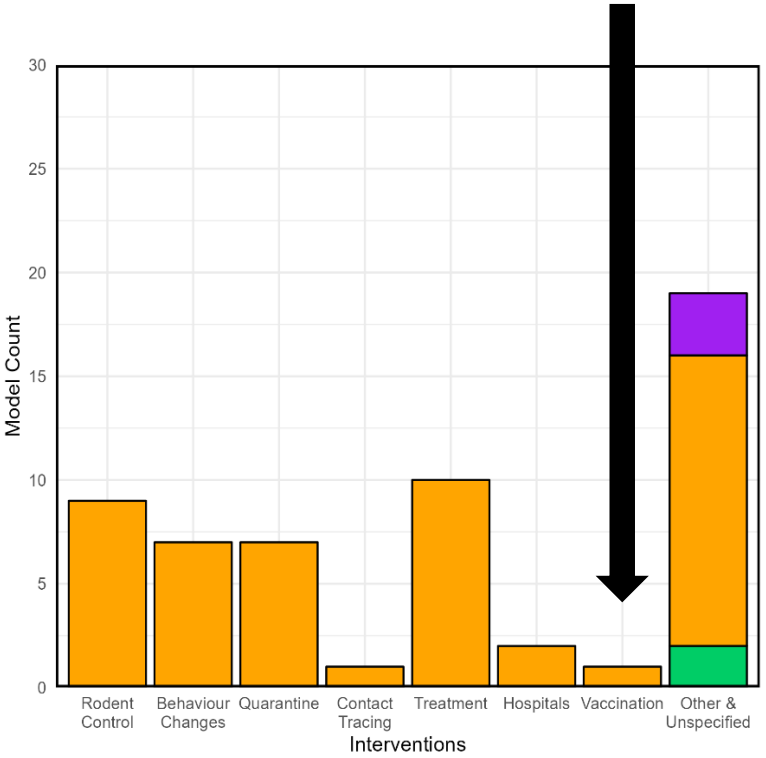
Lassa Fever - Models

- 34 transmission models identified
- Quality is poor ☹





- Limits assessment of impact of interventions
- Only 1 vaccine paper



Lassa Fever - Conclusion & Discussion

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- Comprehensive overview of key epidemiological parameters, mathematical models, and past outbreaks of LASV
- Significant uncertainty as to geographical distribution – seroprevalence is highly spatially heterogenous
- Endemic zone expected to increase due to climate change and land-use change
- CFR estimates in line with previous review and Machupo and Guanarito arenaviruses
- Imperative to better characterise asymptomatic/mild infection and IFRs
- Need for improved mathematical modelling!

Acknowledgements

- https://www.medrxiv.org/content/10.1101/2024.03.23.24304596v1
- https://mrc-ide.github.io/priority-pathogens/articles/pathogen_lassa.html
- https://github.com/mrc-ide/epireview