

Mapping the global diversity and surveillance landscape of medically important bat-borne viruses: a scoping review

George Kiprono Kisoi *et al.*

Corresponding author: George Kiprono Kisoi

Email: kisoikiprono@gmail.com

Available online: <https://www.one-health.panafrican-med-journal.com/content/article/21/11/full/>

Content

Annex 2A: multi-scale validation of zoonotic risk tier distributions

Annex 2B: geographical distribution of high-risk bat-borne viruses by continent

Annex 2C: methodological bias in zoonotic risk classification by detection method

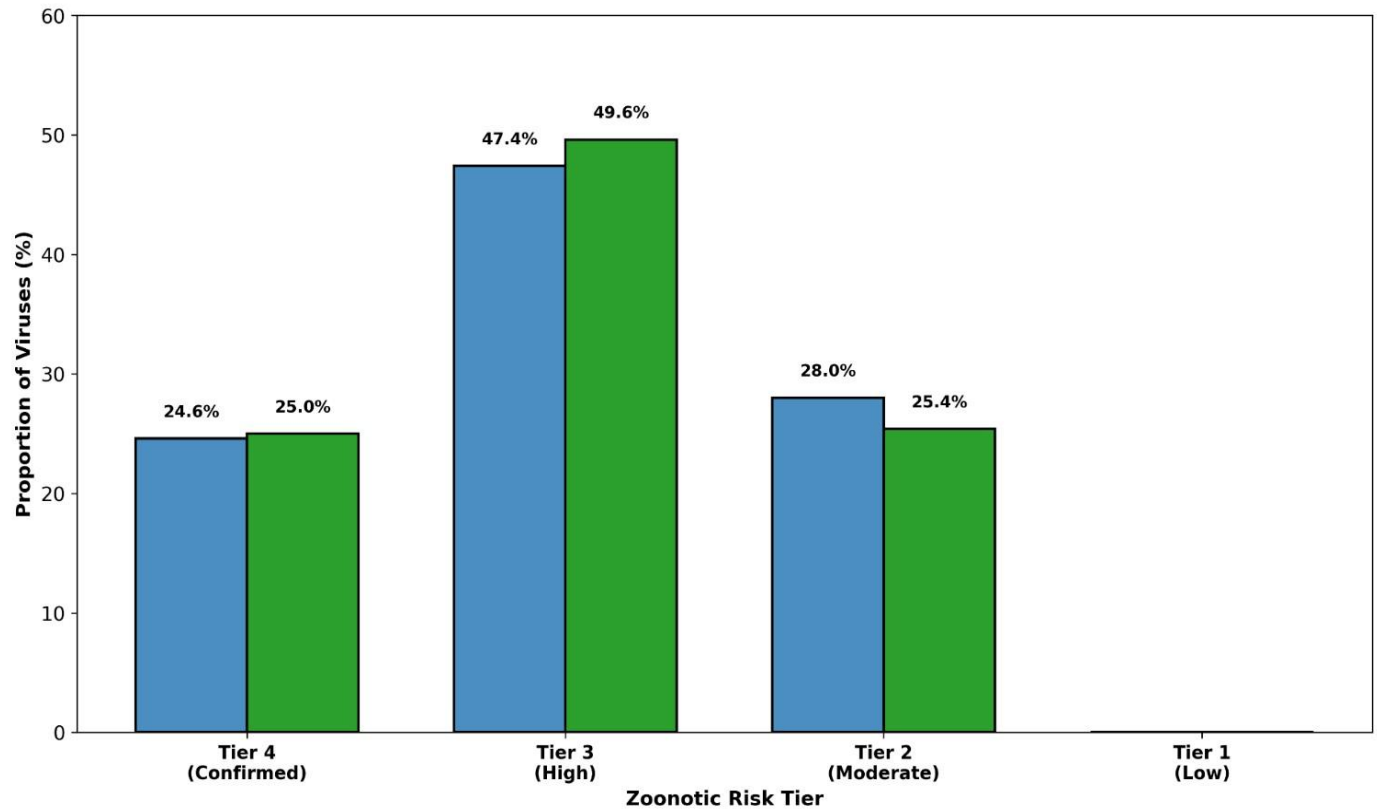
Annex 2D: virus distribution by diet type and geographic region records

Annex 2E: effectiveness of sample types for detecting major bat virus families

Annex 2F: association between bat dietary guilds and viral family diversity

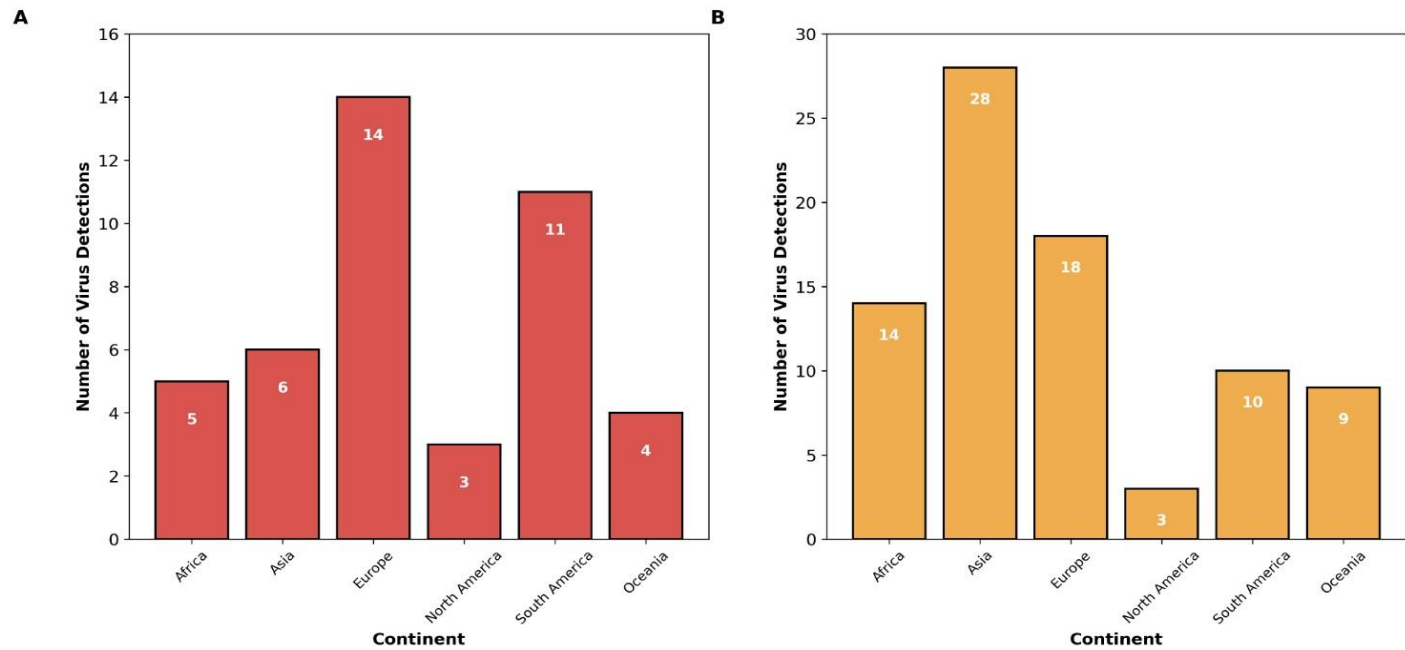
Annex 2G: temporal transition from PCR-based to NGS-based detection methods in bat virus surveillance (2010-2024)

Annex 2A: multi-scale validation of zoonotic risk tier distributions



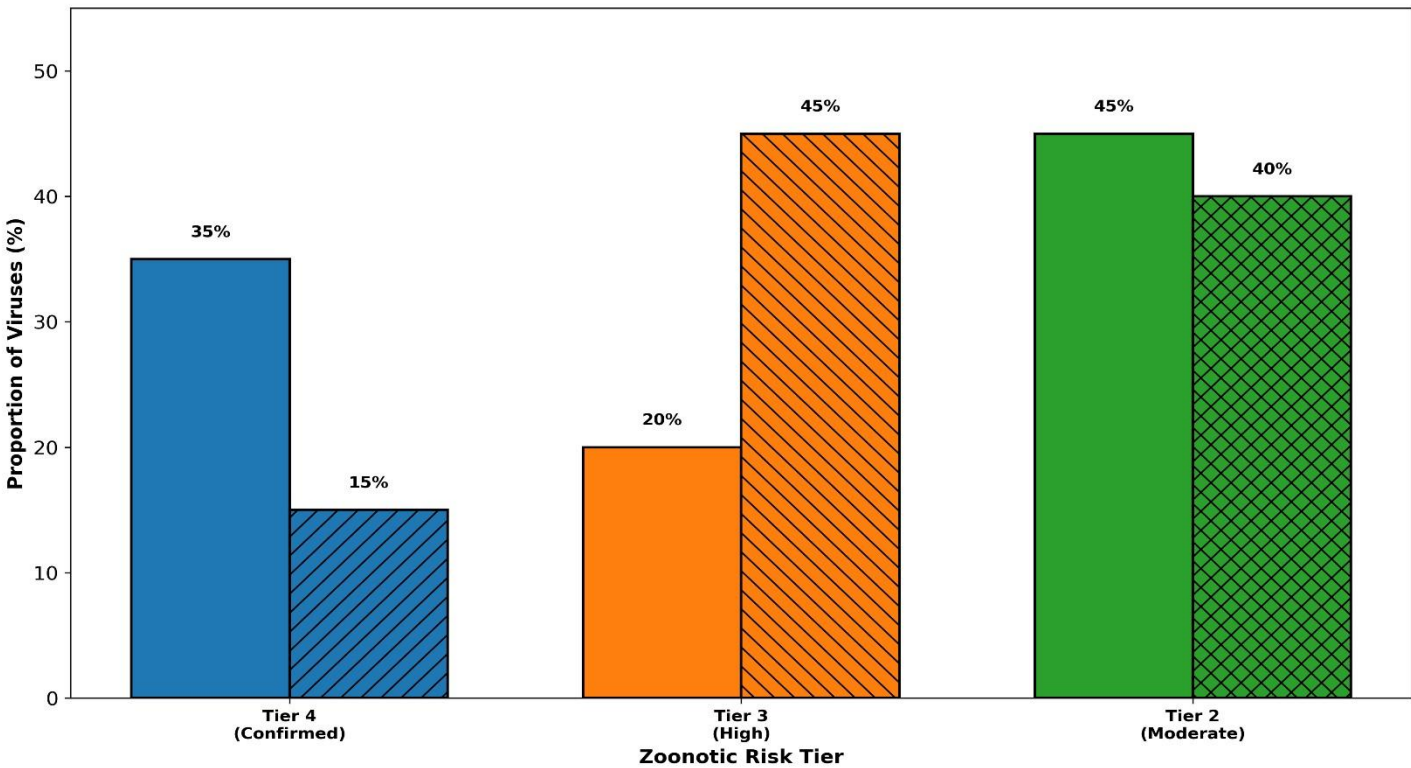
Footnote: the bars show the proportion of viruses in each risk tier (Tier 4, confirmed zoonotic; Tier 3, high potential; Tier 2, moderate potential) in the full dataset (N = 17,134 sequences) and in the curated subset (N = 244 bat-virus associations). Tier 1 (low or no evidence) is not shown.

Annex 2B: geographical distribution of high-risk bat-borne viruses by continent



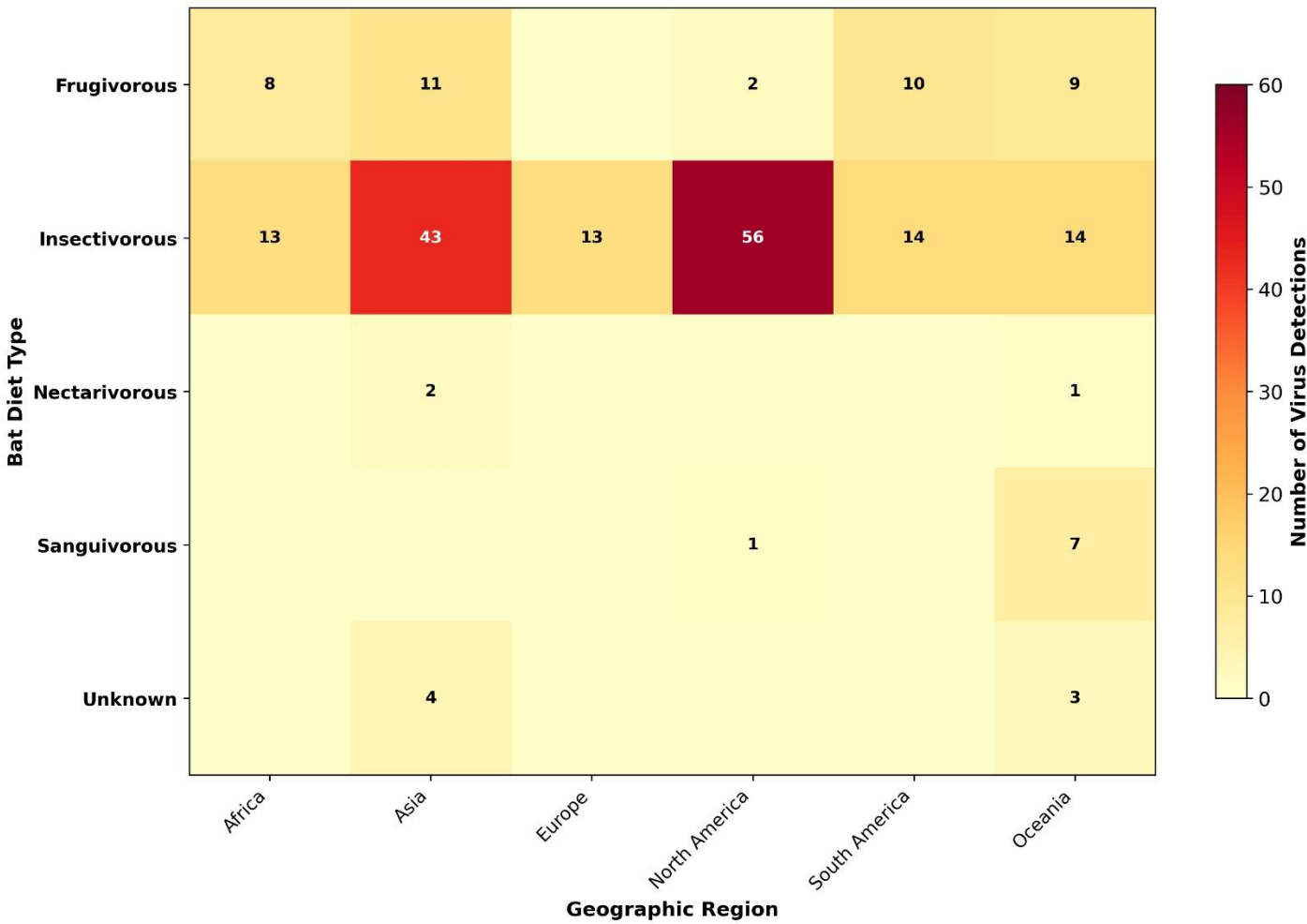
Footnote: (A) Tier 4 viruses (confirmed zoonotic; red bars); (B) Tier 3 viruses (high potential; orange bars). Numbers inside bars indicate virus detections per continent. Data are from the curated dataset (N = 244).

Annex 2C: methodological bias in zoonotic risk classification by detection method



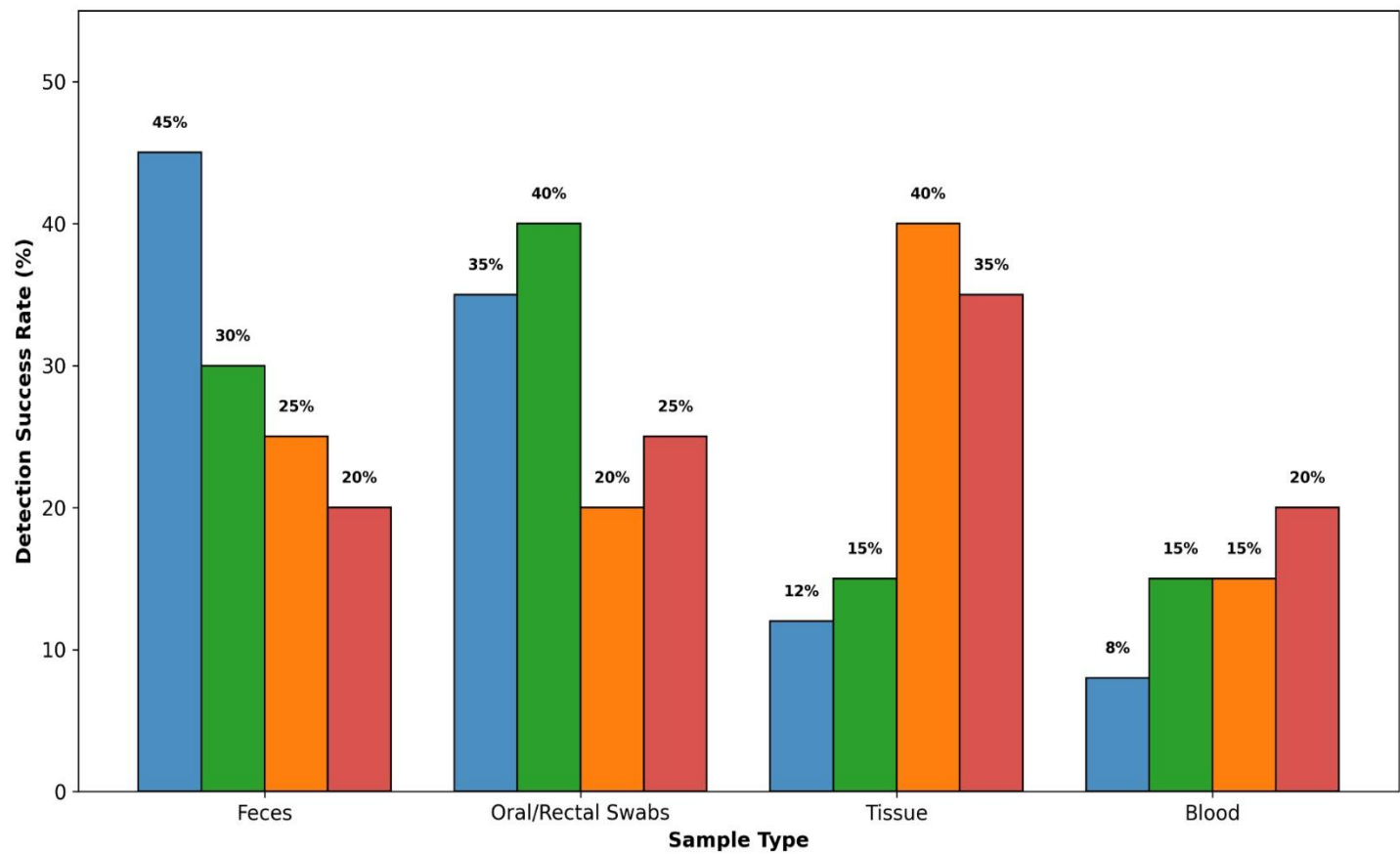
Footnote: hatched bars: NGS/metagenomic methods. Solid bars: PCR-based methods. Abbreviations: NGS = next-generation sequencing; PCR = polymerase chain reaction; Tier 4 = confirmed zoonotic; Tier 3 = high potential; Tier 2 = moderate potential.

Annex 2D: virus distribution by diet type and geographic region records



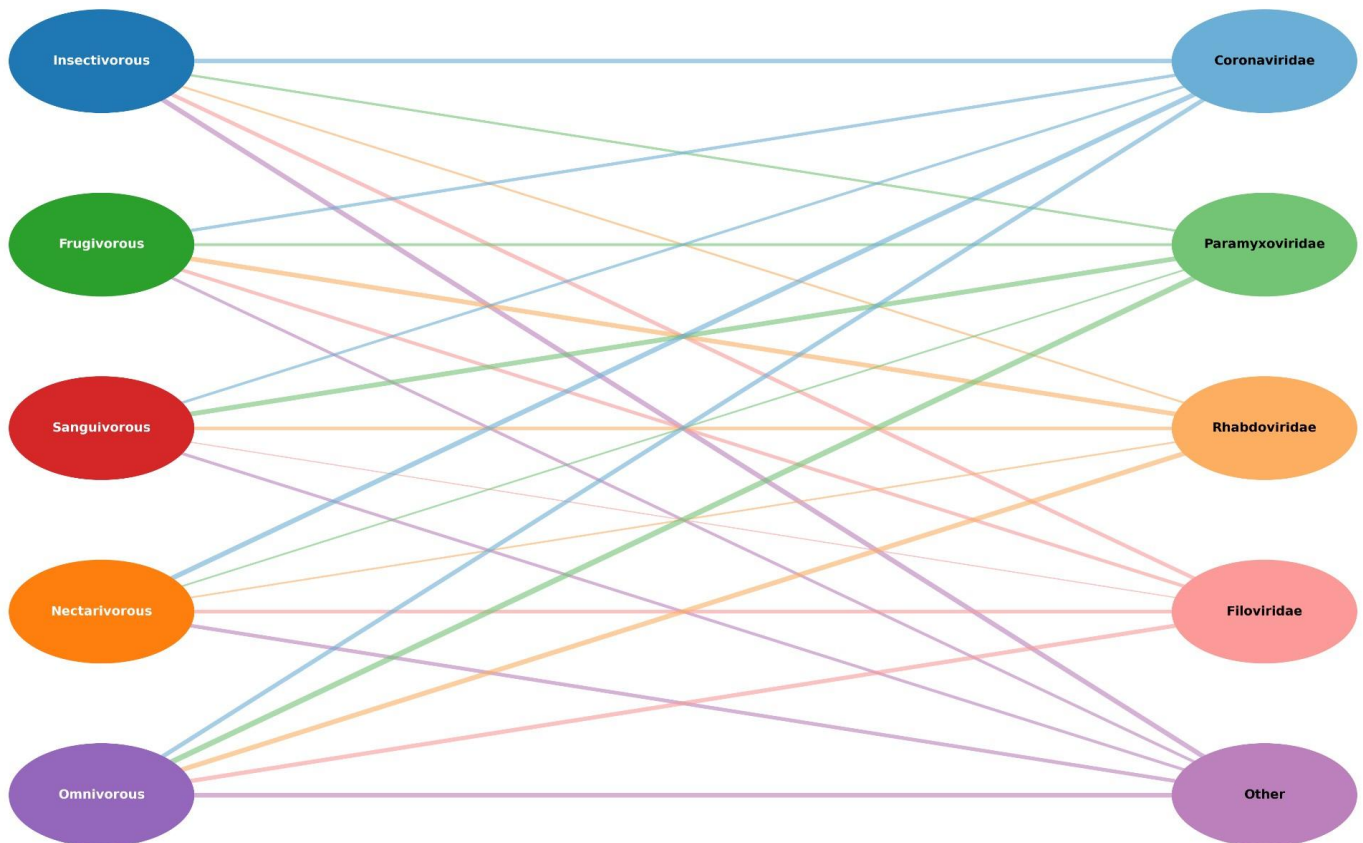
Footnote: color intensity (darker red = more detections) and the numbers inside cells indicate the number of virus detections per diet type and region. Data are from the curated dataset (N = 244).

Annex 2E: effectiveness of sample types for detecting major bat virus families



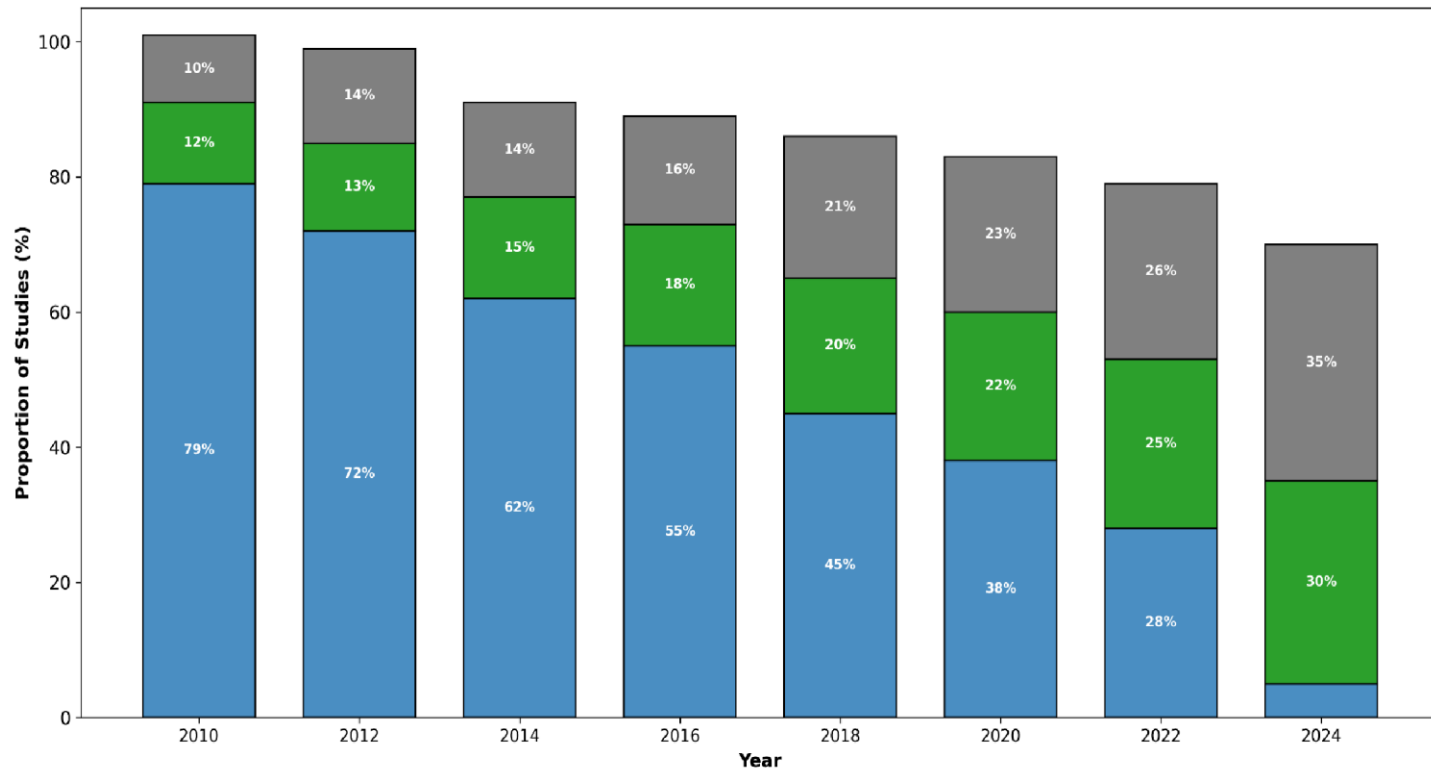
Footnote: detection success rate is the percentage of samples of each type (feces, oral/rectal swabs, tissue, blood) reported as positive for each virus family (*Coronaviridae*, *Paramyxoviridae*, *Rhabdoviridae*, *Filoviridae*) among the included studies; numbers above bars show this percentage. It reflects reported detection outcomes rather than validated diagnostic sensitivity or specificity and may be confounded by differences in testing effort or assay type across studies.

Annex 2F: association between bat dietary guilds and viral family diversity



Footnote: circle colors represent virus families: blue, *Coronaviridae*; green, *Paramyxoviridae*; orange, *Rhabdoviridae*; red, *Filoviridae*; purple, other virus families. Line thickness indicates the strength of association, and numbers adjacent to lines are association percentages (e.g., insectivorous (*Coronaviridae*), 69.6%).

Annex 2G: temporal transition from PCR-based to NGS-based detection methods in bat virus surveillance (2010-2024)



Footnote: stacked bars show the percentage of studies per year using PCR-based methods (blue; targeted detection requiring prior sequence knowledge), NGS/metagenomics (green; untargeted sequencing of all genetic material), or other methods (gray; e.g., serology, virus isolation). NGS: next-generation sequencing.