International Platform of Registered Systematic Review and Meta-analysis Protocols

INPLASY

Global Identification of Pathogen X, Newly Identified members of Priority Families, Newly Identified Priotity Pathogens Based on Whole Genomes

INPLASY202670012
doi: 10.37766/inplasy2026.7.0012
Received: 6 July 2026
Published: 6 July 2026

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ADMINISTRATIVE INFORMATION

Support - This study was supported by the Prevention and Control of Emerging and Major Infectious Diseases-National Science and Technology Major Project [Grant No. 2025ZD01900100, 2025ZD01900110]; the Major Project of Guangzhou National Laboratory [Grant No. GZNL2024A01025]; and the Specific Research Fund of the Innovation Platform for Academicians of Hainan Island [Grant No. YSPTZX202515].

Review Stage at time of this submission - Data analysis.

Conflicts of interest - None declared.

INPLASY registration number: INPLASY202670012

Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 6 July 2026 and was last updated on 6 July 2026.

INTRODUCTION

Review question / Objective To systematically identify and prioritize animal-origin viruses of emerging concern in the post-pandemic period (Feb 2020–Feb 2025) using the WHO Pathogens Prioritization framework, and to establish a baseline of their phylogenetic relationships, host associations, and geographic distributions for proactive surveillance.

Condition being studied Zoonotic viral diseases of emerging concern, including but not limited to severe acute respiratory syndrome (SARS)-like illnesses, hemorrhagic fevers, encephalitis, and other febrile syndromes caused by animal-origin viruses with potential for human spillover and pandemic transmission.

METHODS

Participant or population Mammals (including bats, rodents, shrews, lagomorphs, pangolins, raccoon dogs, and domestic animals) and arthropod vectors (ticks and mosquitoes) carrying viruses with potential for mammalian/human infection.

Intervention Not applicable — This is a descriptive systematic review of viral discovery and phylogenetic characterization, which does not evaluate any clinical, pharmacological, or public health intervention.

Comparator Not applicable — This descriptive systematic review does not involve comparative interventions or control groups; it focuses on viral discovery, phylogenetic characterization, and geographic distribution mapping.

Study designs to be included Original research articles reporting virome characterization, novel virus discovery, or phylogenetic analysis of animal-origin viruses. Included studies must be based on mammals or arthropod vectors with potential for mammalian/human infection, and must report complete or nearly-complete viral genome sequences (≥90% coverage for non-segmented viruses, or missing no more than one minor segment for segmented viruses). Excluded: reviews, commentaries, case reports, modeling/theoretical studies, and studies restricted to plant or mollusk viruses.

Eligibility criteria Inclusion: (1) Studies on animal-origin virus virome/discovery/phylogeny; (2) Viruses from mammals or arthropods with mammalian infectivity potential; (3) Complete or nearly-complete genomes (>90% coverage or missing ≤1 segment). Exclusion: (1) Non-viral or theoretical/model-only studies; (2) Plant/mollusk/non-mammalian viruses; (3) Unretrievable sequences; (4) Incomplete or unclassifiable sequences.

Information sources PubMed, Web of Science, and NCBI GenBank for sequence retrieval and metadata.

Main outcome(s) (1) Number and taxonomic classification of newly identified animal-origin viruses; (2) Classification under WHO Pathogens Prioritization framework (Pathogen X, newly identified members of priority families, newly identified priority pathogens); (3) Phylogenetic relationships, host associations, and geographic distributions.

Quality assessment / Risk of bias analysis Not formally assessed (descriptive systematic review; no intervention effect estimates). Taxonomic validity verified via BLAST and ICTV criteria.

Strategy of data synthesis Narrative synthesis. Phylogenetic trees reconstructed using MAFFT and IQ-TREE. Host-virus association matrices and Sankey diagrams. Spatial mapping using ArcMap with IUCN and GBIF overlays.

Subgroup analysis By viral family, by host order, by geographic region, and by WHO pathogens prioritization.

Sensitivity analysis Not applicable (no quantitative meta-analysis).

Language restriction China.

Keywords zoonotic viruses; emerging infectious diseases; viral surveillance; pathogen prioritization; WHO R&D Blueprint; animal-origin viruses; wildlife virome; complete genome; phylogeny; host.

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