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R&DBlueprint

Powering research
to prevent epidemics

PATHOGENS PRIORITIZATION

A SCIENTIFIC FRAMEWORK
FOR EPIDEMIC AND PANDEMIC
RESEARCH PREPAREDNESS

HEALTH
EMERGENCIES
programme

JUNE 2024

TABLE OF CONTENTS

| | |
|---|-----------|
| EXECUTIVE SUMMARY | 4 |
| Identifying priorities using the Pathogen Family approach | 10 |
| Independent Family Expert Groups (FEGs) examined the evidence and reviewed individual Families and pathogens, and the scientific knowledge gaps that need to be addressed | 10 |
| Family Expert Groups (FEGs) methodology | 10 |
| The Prioritization Advisory Committee (PAC) took a broad view across all Families and pathogens and outlined priority research to accelerate the development and evaluation challenges of medical countermeasures | 14 |
| R for RESEARCH for all Families | 17 |
| Proactive pathogen discovery & Surveillance | 19 |
| Targeted basic research | 20 |
| Translational research and product development | 20 |
| Establishing robust clinical trial capabilities and deployment strategies | 20 |
| Collaborative research | 20 |
| D for DEVELOPMENT of MCMs against known threats | 21 |
| D+ for DEVELOPMENT of MCMs for Prototype Pathogens | 24 |
| R&D - PREPARING FOR THE INEVITABLE | 27 |
| A GLOBAL AND A REGIONAL PERSPECTIVE | 29 |

| | |
|---|-----------|
| African Region | 31 |
| Region of the Americas | 32 |
| Eastern Mediterranean Region | 33 |
| European Region | 34 |
| South-East Asia Region | 35 |
| Western Pacific Region | 36 |
| KEY COLLABORATIVE GLOBAL RESEARCH ACTIONS ACROSS FAMILIES AND PATHOGENS | 37 |
| Collaboration, collaboration, collaboration... | 37 |
| Collaborative Open Research Consortium (CORC) for each Priority Pathogen Family | 37 |
| A navigator's approach to guide research efforts | 38 |
| Preparing for the inevitable | 38 |
| Accelerating evaluation and deployment of MCMs in the context of epidemics and pandemics | 41 |
| ANNEX 1. SCIENTISTS WHO EVALUATED THE EVIDENCE RELATED TO 28 VIRAL FAMILIES AND ONE CORE GROUP OF BACTERIA, ENCOMPASSING 1,652 PATHOGENS | 44 |
| ANNEX 2. PRIORITIZATION ADVISORY COMMITTEE (PAC) | 51 |
| ANNEX 3. SUMMARY OF EPIDEMIOLOGICAL INFORMATION ON PROPOSED PRIORITY PATHOGENS | 58 |
| ANNEX 4. CURRENT LANDSCAPE OF CANDIDATE VACCINES AND THERAPEUTICS FOR PROPOSED PRIORITY PATHOGENS | 60 |

EXECUTIVE SUMMARY

The WHO R&D Blueprint for Epidemics has a primary goal to accelerate the development of medical countermeasures (MCMs). Since 2015, its primary goal is to make these countermeasures available for diseases with epidemic and pandemic potential, thereby contributing to the prevention of Public Health Emergencies of International Concern (PHEICs) and saving lives during outbreaks. The WHO R&D Blueprint for Epidemics functions as a global platform for research and development collaboration, stressing the significance of international cooperation in expediting the research and development of medical countermeasures (MCMs) to respond to epidemics and pandemics. At the core of its efforts lies the concept of 'pathogen prioritization'. This document outlines the findings of a global pathogen prioritization process involving over 200 scientists from more than 50 countries who evaluated the evidence related to 28 Viral Families and one core group of Bacteria, encompassing 1,652 pathogens. This process emphasized the imperative nature of collaborative efforts to attain global resilience against epidemics and pandemics.

The approach used advocates for a scientific framework to enhance preparedness for forthcoming outbreaks, Public Health Emergencies of International Concern (PHEICs), and pandemics by focusing on research of Viral and Bacterial Families, rather than isolated pathogens deemed to present global risks.

It also emphasizes the critical necessity for investments in research, development, and innovation on an international scale, underscoring the need to uphold fundamental principles. Within this context of numerous collaborative initiatives striving to support MCM R&D during epidemics and pandemics, regarding a collaborative effort to ensure

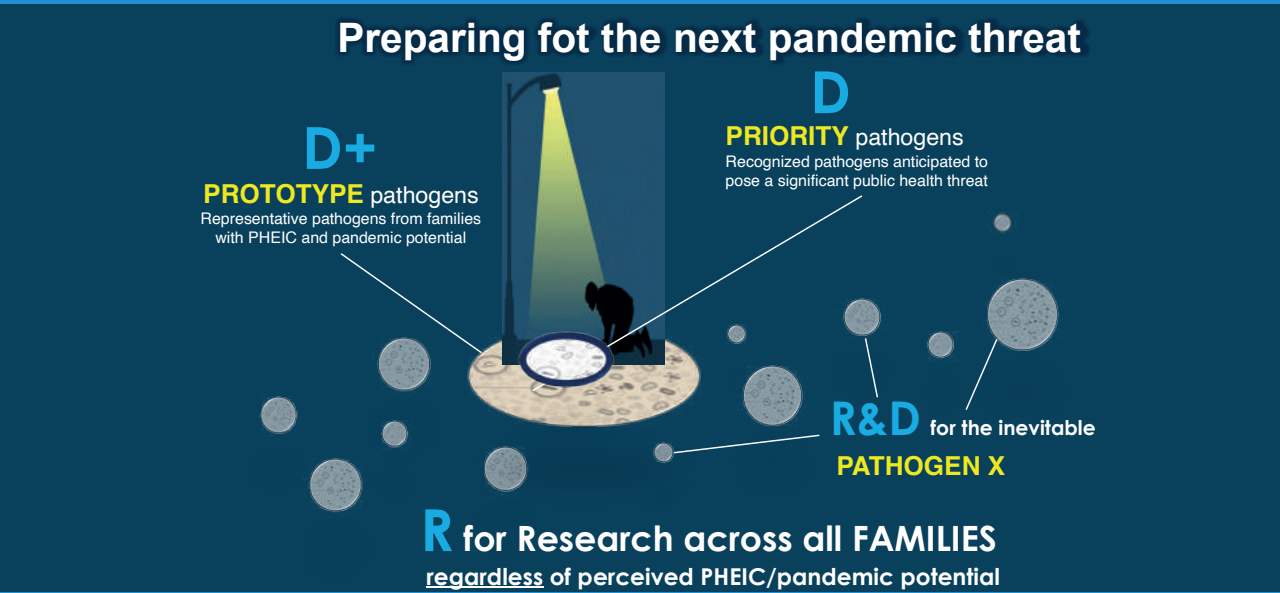
access to MCMs during pandemics, some have emphasized the importance of speed and sometimes cost in responding to future pandemics. It is equally important in considering the entire value chain to take a broader view that recognizes the primary importance of quality, equity in access, and trust in the product's safety and efficacy. Preparations and implementation of pandemic response thus should be country-centered, transparent, and collaborative.

By prioritizing research on entire pathogen Families as opposed to a handful of individual pathogens, this strategy bolsters the capability to respond efficiently to unforeseen variants, emerging pathogens, zoonotic transmissions, and unknown threats such as 'Pathogen X.' It also emphasizes the need for prompt identification and characterization of emerging threats, the streamlining of global R&D efforts, via collaborative and efficient research roadmaps and the integration of research into outbreak and pandemic response. The widespread geographic distribution of the viral and bacterial families and pathogens identified in this report, with several known to circulate across diverse nations and regions globally, underscores the pivotal role of global initiatives in linking national and regional research actions. Significantly, the strategy advocates for decentralized collaborative approaches and supporting research efforts in areas critical for pandemic research preparedness. This comprehensive approach aims to foster international collaboration by establishing a global framework for researchers, developers, policymakers, funders, manufacturers, and institutions, fostering a collaborative space to advance research across all Viral and Bacterial Families, as well as R&D for Priority and Prototype pathogens.

BOX 1 The streetlight effect

The metaphor of looking for lost keys under a streetlamp – often referred to as the 'streetlight effect' – is a powerful illustration of the ongoing challenges and biases in identifying the pathogen that will cause the next pandemic. This metaphor highlights how researchers and public health

officials might focus their efforts on illuminated areas where it is easiest to search, rather than where the actual answers might lie. This proposed Family approach to identifying the next pandemic pathogen emphasizes the importance of broadening our perspective strategically.



Imagine scientists and public health officials as individuals searching for the "lost keys" (the next pandemic pathogen). The area illuminated by the "streetlight" represents the Priority Pathogens, well-studied pathogens with readily accessible data that indicate their risk of causing a PHEIC or a pandemic. We can expand the lighted area a bit by researching the Prototype Pathogens and using them as pathfinders within Families to expand our knowledge and understanding. Neglecting the "Dark Areas" is not advisable given the uncertainty about which pathogen will indeed cause the next PHEIC or pandemic. The "Dark Areas" in this metaphor include many regions, particularly in resource-scarce settings with high biodiversity, which are still under-monitored and under-studied. These areas might harbour novel pathogens, but the lack of infrastructure and resources makes it difficult to conduct comprehensive research. The focus on known pathogens can lead to a neglect of emerging or re-emerging pathogens that have not yet caused significant outbreaks but have the potential to do so.

Therefore, the proposed approach of supporting research in all families, regardless of their pandemic potential, helps mitigate the risk of missing potential pandemic pathogens that might be lurking in the "dark areas" beyond the immediate reach of current surveillance systems and research efforts.

The Prioritization meeting held on 9-10 May 2024 engaged all collaborators in the Pathogen Prioritization process to further develop a strategy that advocates for research spanning various pathogen families based on our existing understanding of their pandemic potential. This strategy also emphasizes research and development efforts aimed at readiness for both anticipated and unanticipated threats by focusing on entire families, Prototype Pathogens, and Priority Pathogens.

The continuous revision of this strategy will facilitate the ongoing assessment of risks associated with emerging infectious diseases and advancements in scientific research.

The global health landscape is subject to constant evolution, with the potential emergence of new pathogens and evolution in the threat levels posed by existing ones. These developments play a crucial role in shaping strategies to tackle emerging challenges. The strategy adopted demonstrates a proactive stance towards addressing emerging infectious diseases, as well as improving global research and development preparedness and response capabilities.

Table 1 compares the results of previous R&D Blueprint for Epidemics Priority Pathogen lists in 2017 and 2018 with the results from 2024. Following the finalization of the list of Families, Priority pathogens, and Prototype Pathogens, the combinations were arranged by family and alphabetical order.

Importantly, the outputs in 2024 incorporate for the first time the concept of the Family approach and the addition of the Prototype Pathogen. Some of the “new” Priority Pathogens incorporated in the 2024 outputs were noted in 2017 and or 2018 as pathogens of concern or as outside the remit of the WHO R&D Blueprint for Epidemics^{1,2}.

Lastly, besides the pathogens listed in 2018, the WHO R&D Blueprint for Epidemics has supported R&D efforts for Plague, SARS CoV2 and Monkeypox following the declaration of outbreaks, PHEICs, or pandemics and considering the lack of suitable MCMs.

Nota Bene

As scientific understanding deepens, viruses are renamed, or currently classified as members of one family may be moved or adopted into another family, or be put into a completely new family of their own. In this document, an effort was made to refer to the most recent recommendations of the International Committee on Taxonomy of Viruses (ICTV)³. However, to facilitate the readers’ review, we have created a “translation table” (Table 14) that provides the MSL39 Viral Species name and reference to the previous, perhaps more familiar, names of the various viruses.

¹ <https://www.who.int/publications/m/item/an-r-d-blueprint-for-action-to-prevent-epidemics---update-2017>

² <https://www.who.int/activities/prioritizing-diseases-for-research-and-development-in-emergency-contexts>

³ <https://ictv.global/>

Table 1. Families and Pathogens that were prioritized in the 2024 update, as compared with the 2017 and 2018 prioritization processes⁴.

| | 2017 | 2018 | 2024 | | |
|----------------|--|--|------------|---|---|
| Family | Priority Pathogens | Priority Pathogens | PHEIC risk | Priority Pathogens | Prototype Pathogens |
| Adenoviridae | | | Low-Medium | | Recombinant Mastadenovirus |
| Adenoviridae | | | Low-Medium | | Mastadenovirus blackbeardi serotype 14 |
| Anelloviridae | | | Low | | |
| Arenaviridae | Arenaviral hemorrhagic fevers including Lassa Fever | Lassa Fever virus | High | Mammarenavirus lassaense | Mammarenavirus lassaense |
| Arenaviridae | | | High | | Mammarenavirus juninense |
| Arenaviridae | | | High | | Mammarenavirus lujoense |
| Astroviridae | | | Low | | Mamastrovirus virginiaense |
| Bacteria | | | High | <i>Vibrio cholerae</i> serogroup 0139 | |
| Bacteria | | | High | <i>Yersinia Pestis</i> | |
| Bacteria | | | High | <i>Shigella dysenteriae</i> serotype 1 | |
| Bacteria | | | High | <i>Salmonella enterica</i> non typhoidal serovars | |
| Bacteria | | | High | <i>Klebsiella pneumoniae</i> | |
| Bornaviridae | | | Low | | Orthobornavirus bornaense |
| Coronaviridae | Middle East Respiratory Syndrome Coronavirus | Middle East Respiratory Syndrome Coronavirus | High | Subgenus Merbecovirus | Subgenus Merbecovirus |
| Coronaviridae | Other highly pathogenic coronaviral diseases such as Severe Acute Respiratory Syndrome | Severe Acute Respiratory Syndrome | High | Subgenus Sarbecovirus | Subgenus Sarbecovirus |
| Filoviridae | Filoviral diseases Ebola | Ebola virus disease | High | Orthoebolavirus zairense | Orthoebolavirus zairense |
| Filoviridae | Filoviral diseases Marburg | Marburg virus disease | High | Orthomarburgvirus marburgense | |
| Filoviridae | | | High | Orthoebolavirus sudanense | |
| Flaviviridae | Zika virus | Zika virus | High | Orthoflavivirus zikaense | Orthoflavivirus zikaense |
| Flaviviridae | | | High | Orthoflavivirus denguei | Orthoflavivirus denguei |
| Flaviviridae | | | High | Orthoflavivirus flavi | |
| Flaviviridae | | | High | | Orthoflavivirus encephalitidis |
| Flaviviridae | | | High | | Orthoflavivirus nilense |
| Hantaviridae | | | High | Orthohantavirus sinnombreense | Orthohantavirus sinnombreense |
| Hantaviridae | | | High | Orthohantavirus hantanense | |
| Hepadnaviridae | | | Low | | Orthohepadnavirus hominoidei genotype C |

| | 2017 | 2018 | 2024 | | |
|------------------|---|----------------------------------|------------|------------------------------------|------------------------------------|
| Family | Priority Pathogens | Priority Pathogens | PHEIC risk | Priority Pathogens | Prototype Pathogens |
| Hepeviridae | | | Low | | Paslahepevirus balayani genotype 3 |
| Herpesviridae | | | Low | | |
| Nairoviridae | Crimean Congo Haemorrhagic Fever | Crimean Congo Haemorrhagic Fever | High | Orthonairovirus haemorrhagiae | Orthonairovirus haemorrhagiae |
| Orthomyxoviridae | | | High | Alphainfluenzavirus Influenzae H1 | Alphainfluenzavirus Influenzae H1 |
| Orthomyxoviridae | | | High | Alphainfluenzavirus Influenzae H2 | |
| Orthomyxoviridae | | | High | Alphainfluenzavirus Influenzae H3 | |
| Orthomyxoviridae | | | High | Alphainfluenzavirus Influenzae H5 | Alphainfluenzavirus Influenzae H5 |
| Orthomyxoviridae | | | High | Alphainfluenzavirus Influenzae H6 | |
| Orthomyxoviridae | | | High | Alphainfluenzavirus Influenzae H7 | |
| Orthomyxoviridae | | | High | Alphainfluenzavirus Influenzae H10 | |
| Papillomaviridae | | | Low | | |
| Paramyxoviridae | Nipah and related henipaviral diseases | Nipah and henipaviral diseases | High | Henipavirus nipahense | Henipavirus nipahense |
| Parvoviridae | | | Low | | Protoparvovirus carnivoran |
| Peribunyaviridae | | | Low | | Orthobunyavirus oropoucheense |
| Phenuiviridae | Severe Fever with Thrombocytopenia Syndrome | | High | Bandavirus dabiense | Bandavirus dabiense |
| Phenuiviridae | Rift Valley Fever | Rift Valley Fever | High | | Phlebovirus riftense |
| Picobirnaviridae | | | Low | | Orthopicobirnavirus hominis |
| Picornaviridae | | | Medium | Enterovirus coxsackiepol | |
| Picornaviridae | | | Medium | | Enterovirus alphacoxsackie 71 |
| Picornaviridae | | | Medium | | Enterovirus deconjecti 68 |
| Pneumoviridae | | | Low-Medium | | Metapneumovirus hominis |
| Polyomaviridae | | | Low | | |
| Poxviridae | | | High | Orthopoxvirus variola | |
| Poxviridae | | | High | | Orthopoxvirus vaccinia |
| Poxviridae | | | High | Orthopoxvirus monkeypox | Orthopoxvirus monkeypox |
| Retroviridae | | | Medium | Lentivirus humimdef1 | Lentivirus humimdef1 |
| Rhabdoviridae | | | Low | | Genus Vesiculovirus |
| Sedoreoviridae | | | Low | | Genus Rotavirus |
| Spinareoviridae | | | Low | | Orthoreovirus mammalis |
| Togaviridae | | | High | Alphavirus chikungunya | Alphavirus chikungunya |
| Togaviridae | | | High | Alphavirus venezuelan | Alphavirus venezuelan |
| Pathogen X | Pathogen X | Pathogen X | | Pathogen X | |

⁴ <https://www.who.int/activities/prioritizing-diseases-for-research-and-development-in-emergency-contexts>

Identifying priorities using the Pathogen Family approach

Independent Family Expert Groups (FEGs) examined the evidence and reviewed individual Families and pathogens, and the scientific knowledge gaps that need to be addressed

Starting in late 2022, over 200 scientists from 54 countries evaluated the evidence related to 28 Viral Families and one core group of Bacteria, encompassing 1,652 pathogens (Annex 1). The overall aim of FEGs was to assemble and debate the current knowledge that would provide the foundation for the Families and Pathogens selection and prioritization.

Family Expert Groups (FEGs) methodology.

Thousands of known viruses and bacteria can infect humans, but only a relatively small number have caused pandemics or large-scale epidemics in history. Much of the information required for decision-making on many pathogens is either unavailable, not documented in the literature, or not conducive to systematic review. The specific number of pathogens to consider can change over time as our comprehension of infectious diseases expands and as new pathogens emerge or known ones evolve.

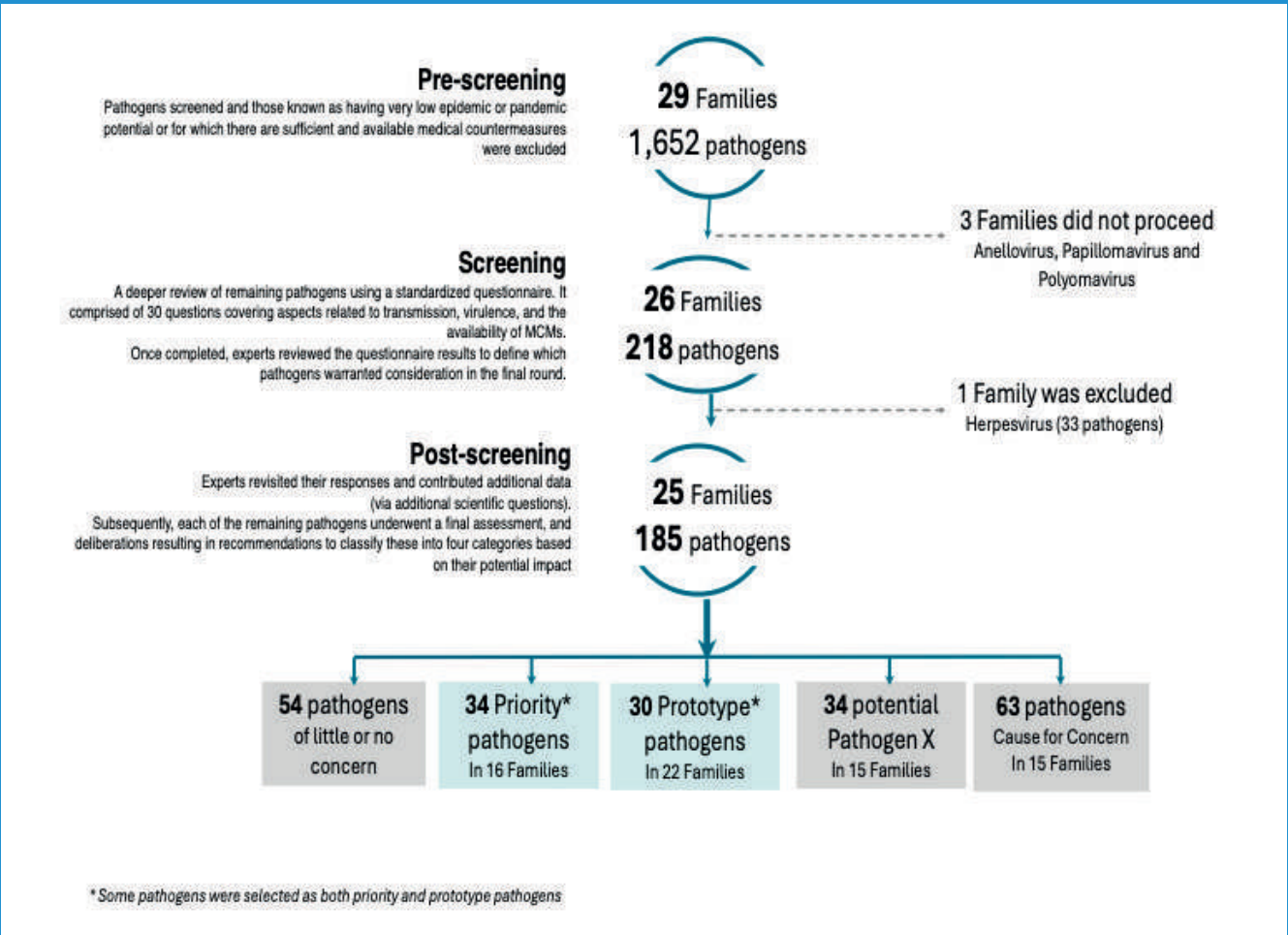
Family Expert Groups (FEGs) were established for 28 viral families and one for bacteria. The expectation was that there would be enough common ground within each FEG to allow consensus to emerge and to provide a basis for defining the risks associated with the various pathogens in each family and for selecting priority pathogens, prototype pathogens, and potential Pathogen X.

The aim was to foster a consensus

development process that was transparent and well-documented. The recognized Delphi method was used, starting with participants giving independent answers to a series of questions, and then receiving anonymized feedback in the form of frequency distributions of pre-coded answers and free-text comments from the rest of the group. Our process followed this by at least one meeting (often two or more) to discuss and conclude on consensus recommendations. This process has the advantage of providing within each FEG: a) some limits on the influence of groupthink and context for dominating views; b) an indication of how many experts felt the available knowledge made them able to answer each question; and c) an indication of the extent of consensus.

Potential chairpersons for each group were contacted by the WHO Secretariat, from a pool of global experts for each family. Each chairperson was invited to contribute to identifying the expertise needed for each FEG. Potential experts that matched those knowledge needs were approached by the WHO Secretariat, based primarily on their scientific expertise, but also aiming to achieve overall balance in terms of gender and representativeness of all world regions. To facilitate the latter, the meetings of the FEGs were all conducted online. Experts signed Declarations of Conflict of Interest and Confidentiality Disclosure Agreements as per WHO guidelines.

Figure 1. Overview of the prioritization process within each of the FEGs



A review of the International Committee on Taxonomy of Viruses list⁵ (2022) helped create an initial comprehensive list of viral families containing pathogens that can infect humans and have the potential to cause outbreaks.

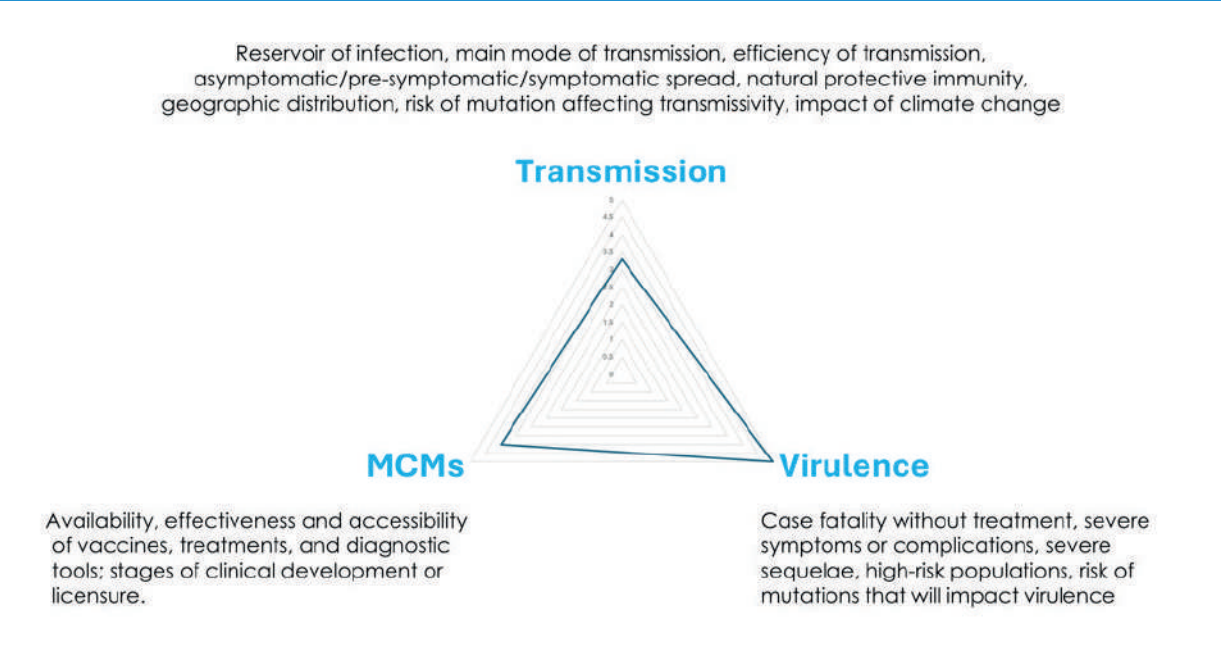
At their first meeting experts within each FEG, experts reviewed the initial list of pathogens in their family and eliminated those considered (based on current knowledge) to have very low or no epidemic or pandemic potential. They noted the reasons for their elimination. The bacterial FEG also compiled a list of bacterial pathogens considered to have PHEIC or pandemic potential (Figure 1).

After this step, each member of every FEG independently completed an online questionnaire for each pathogen on the agreed list. The questionnaire was tested with the assistance of a dozen global experts, and the final version incorporated the feedback received.

The first section of the questionnaire included technical questions that assessed current knowledge (Figure 2).

⁵ International Committee on Taxonomy of Viruses: ICTV <https://ictv.global/>

Figure 2. Evidence elements considered to assess a pathogen’s potential to cause a PHEIC or pandemic



The second section necessitated expert adjudication, soliciting comprehensive evaluations to determine whether each pathogen warranted inclusion in either of two categories: (i) if there existed substantial evidence indicating its high transmissibility and virulence, capable of triggering a PHEIC or a pandemic if left unchecked, and (ii) if available evidence was inadequate to support classification under (i), but sufficient to raise concerns and potentially qualify as Pathogen X (refer to operational definition provided below).

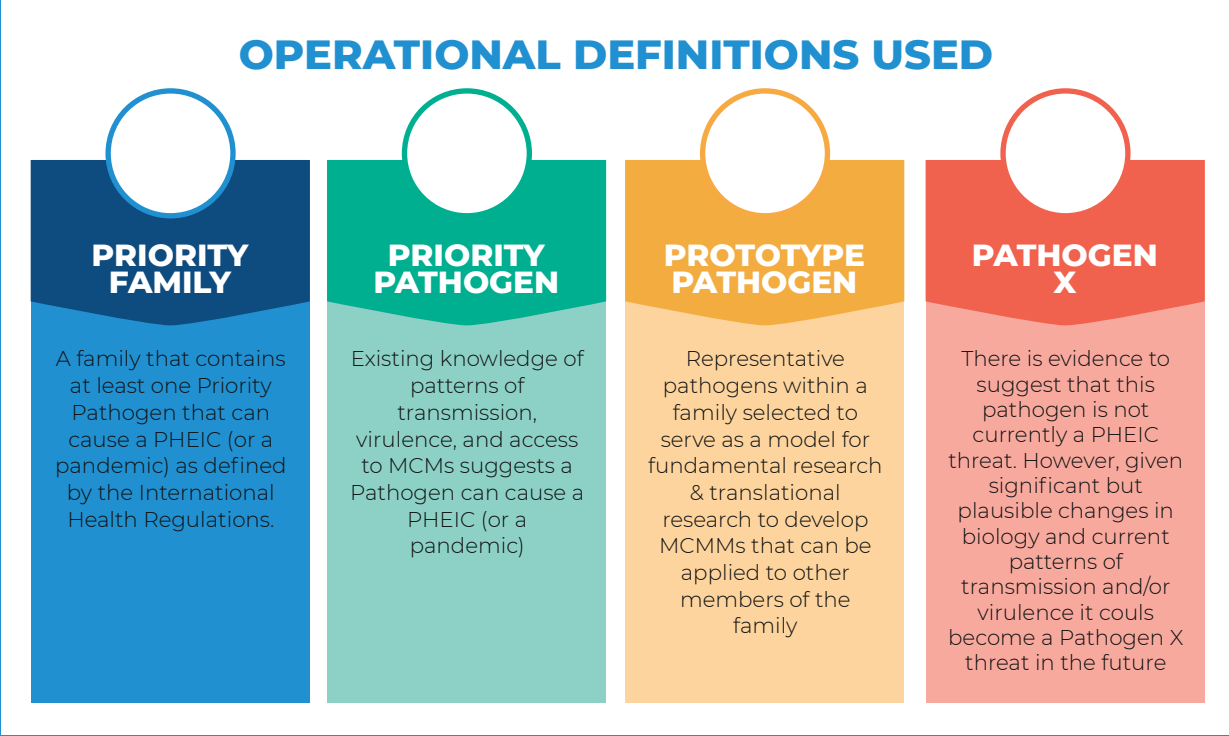
In each Functional Expert Group (FEG), participants received individual anonymized feedback on their group outcomes. Subsequently, a deliberation session was held, allowing members the option to amend their initial responses. Upon the conclusion of this revision phase, the WHO Secretariat reviewed each survey for comprehensiveness and to document any open-ended remarks. The surveys were then finalized to prevent any further modifications. In certain groups, there was an additional

opportunity for deliberation on the potential exclusion of certain pathogens that were determined to pose no significant threats upon further evaluation. Following this, participants in each FEG completed a post-screening survey for each remaining pathogen, which encompassed supplementary inquiries and an expanded evaluation segment.

Each participant was requested to furnish a risk assessment for each pathogen, taking into account the probability of triggering a PHEIC or a pandemic, by evaluating its transmission capabilities, virulence, and the accessibility of MCMs. A rating ranging from 1 to 5 (indicating very low to very high risk) or "insufficient data" to render a judgment was employed.

Subsequently, members of the FEG were inquired about their inclination to endorse each pathogen for any of the listed below (see Figure 3), utilizing the provided definitions aimed at enhancing uniformity within and across FEGs.

Figure 3. Operational definitions used⁶



In addition, some pathogens were designated as Cause for Concern. These pathogens are characterized by limited existing knowledge of transmission, virulence, and MCMs, which prevents them from being categorized elsewhere. However, current understanding gives cause for concern, nonetheless.

During the FEGs’ final meetings, reports prepared by the WHO Secretariat on the responses to the questionnaires and used to debate the risk assessments, and the listings by individual group members were discussed. Each FEG provided recommendations regarding which pathogens should be categorized.

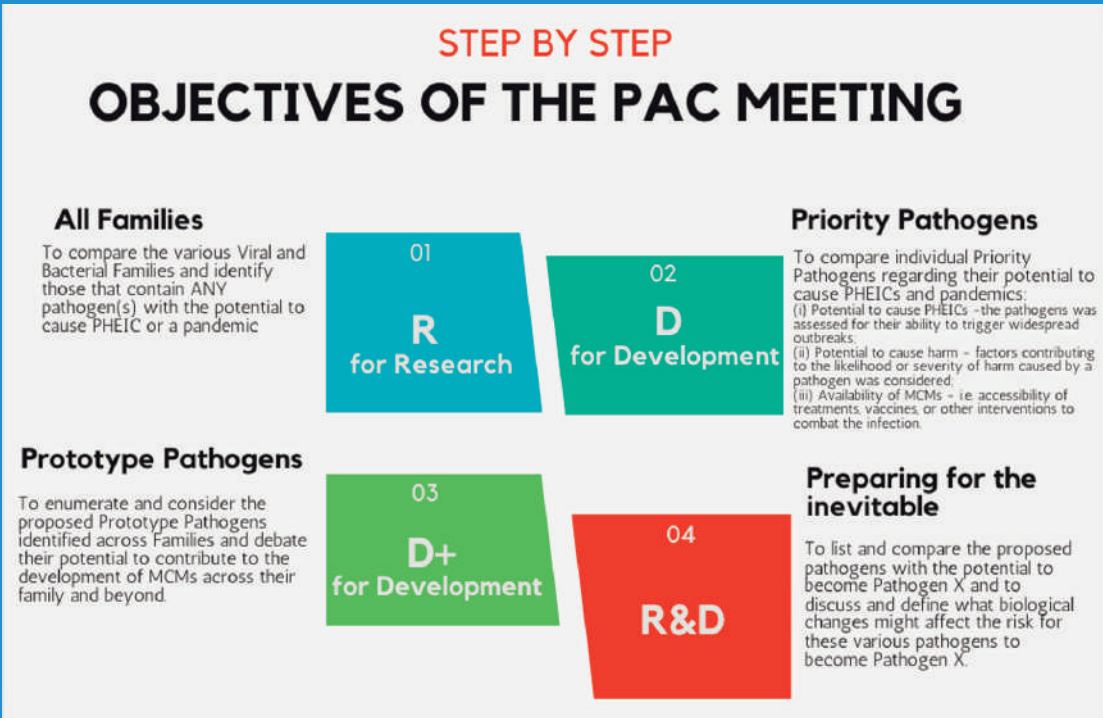
These recommendations laid the groundwork for the final discussions of the overarching Prioritization Advisory Committee (PAC) when all FEGs were joined by additional experts to conclude the results of the prioritization process.

⁶ PHEIC as defined in the International Health Regulations. <https://www.who.int/news-room/questions-and-answers/item/emergencies-international-health-regulations-and-emergency-committees#>

The Prioritization Advisory Committee (PAC) took a broad view across all Families and pathogens and outlined priority research to accelerate the development and evaluation challenges of medical countermeasures

The meeting of the PAC in 2024 served as the culmination of the process initiated in late 2022. It provided an opportunity to share the outcomes across various viral and bacterial families and finalize the prioritization process (Figure 4).

Figure 4. Objectives of the PAC deliberations



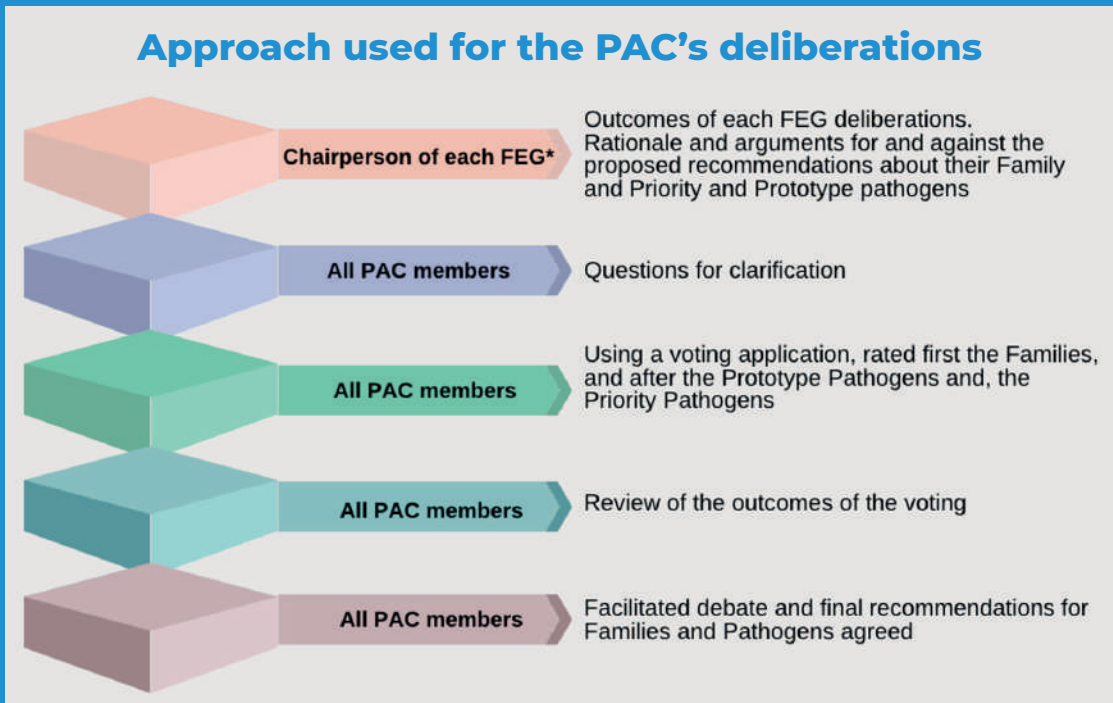
On day 1, the meeting welcomed a diverse group of participants, including the Chairpersons of each of the FEG (or their delegates) and additional experts in research and development and public health. Observers included representatives from R&D funders, experts, and emergency response focal points from WHO's regional and global levels.

Deliberations were structured using strategic presentations from invited experts. The rationale behind adopting a family approach and the importance of fundamental research across all families set the stage. Guest speakers showcased notable advancements, tools, and innovative approaches in basic research during keynote presentations, covering early R&D and R&D, to clinical research.

Day 1 also included the review of the outcomes of initial prioritization across the 29 families and the 185 pathogens from the post-screening round (Figure 1). The ISARIC (International Severe Acute Respiratory and Emerging Infection Consortium) team independently analyzed the responses from each FEG member across the different families and presented a summary of preliminary results (<https://blueprint-who-isaric-x36.replit.app/> using the following password: WhO_Blu3PrInT!).

The ISARIC analysis of the FEG members' responses to questionnaires and outcomes also uncovered a small list of pathogens with similar scores from the experts' answers in the categories of Family risk and Priority Pathogens but which were not included in the FEGs recommendations. Those pathogens were considered again on Day 2.

Figure 5. The approach used for the deliberations of the PAC



It was planned that the final recommendations would be informed by the recommendations of each individual FEG but adjusted once a final review of all families by the PAC members takes place.

On Day 2, deliberations delved deeper into the review process. The Prioritization Advisory Committee discussions were led by the FEGs Chairpersons (Figure 5).

Despite facing challenges such as evidence gaps in surveillance, serology, transmission, virulence, and zoonotic infections, the consistency of the results across the various FEGs underscored the validity of the methodology. Addressing these knowledge gaps is crucial for

advancing the development of MCMs and delineating actions required for each family regarding basic research, surveillance, diagnostics, vaccine development, and antivirals.

PAC members welcomed the regional analyses and emphasized the varying relevance of identifying important families and Priority Pathogens across different Regions. Contextualizing research efforts in each Region promotes equity and fosters multidisciplinary collaborations, particularly in "at-risk" countries. This collaborative approach is the swift integration of research into future epidemic responses, supported by global networks of designated researchers.

PAC members were asked to consider strategic research priorities that have broad applicability across diverse regions, as well as to outline those that are critical for specific regions. Furthermore, experts utilized the identified knowledge gaps to create a comprehensive list of research priorities aimed at addressing broader public health concerns and advancing the development of MCMs.

Figure 6 illustrates the criteria used to guide the deliberations of the PAC members while preparing the final list of Families, and Priority and Prototype pathogens. The deliberations also considered what biological changes can trigger a pathogen to become Pathogen X.

R for RESEARCH for all Families

The priority of families was evaluated with consideration given to the pathogens they encompass. Figure presented below depicts the viral and bacterial families that were analyzed, along with the results of deliberations by the PAC members. Overall, the PAC members reviewed and discussed evidence from eight DNA virus families, nineteen RNA virus families, and five bacterial families.

Families were classified based on their capacity to harbour priority pathogens capable of causing a PHEIC or a pandemic. Of significance, four families were previously categorized as low risk by their respective FEG (Anelloviridae, Papillomaviridae, Polyomaviridae, and Herpesviridae), and they were reaffirmed as low risk during the PAC deliberations.

Figure 6. Prioritization categories, definitions, and levels

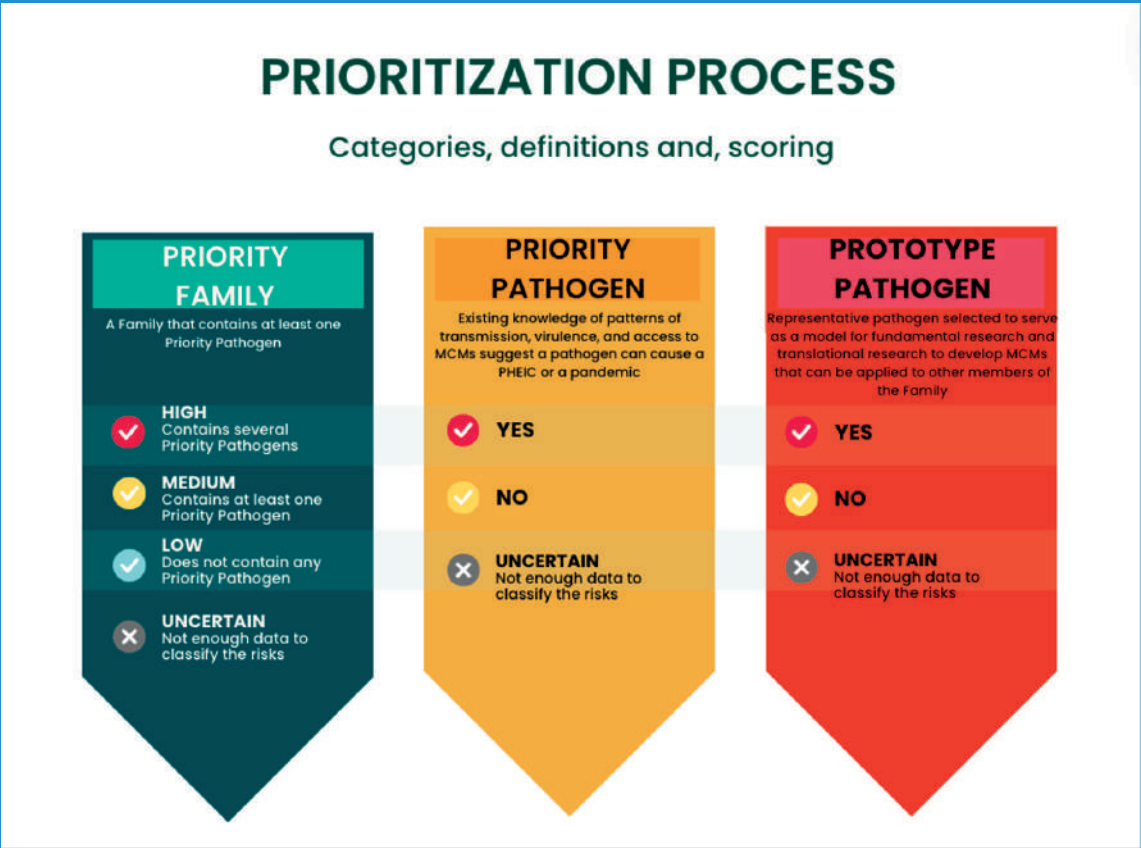


Figure 7. Families considered by the PAC and overview of the outcomes of the risk of PHEIC assessment

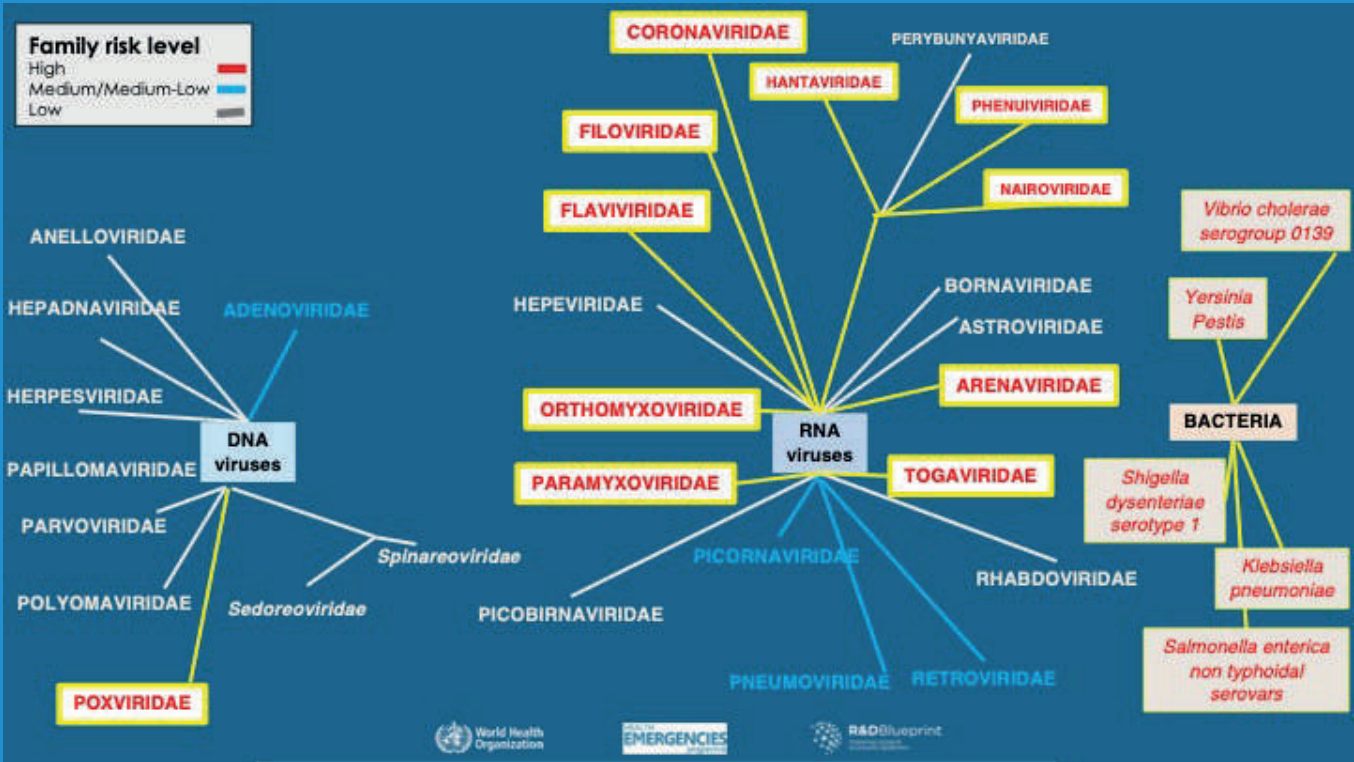


Table 2 presents a summary of the conclusions concerning the PHEIC risks associated with pathogens in specific families. It also outlines the concerns raised by members of the PAC during discussions on the risks posed by pathogens in different families.

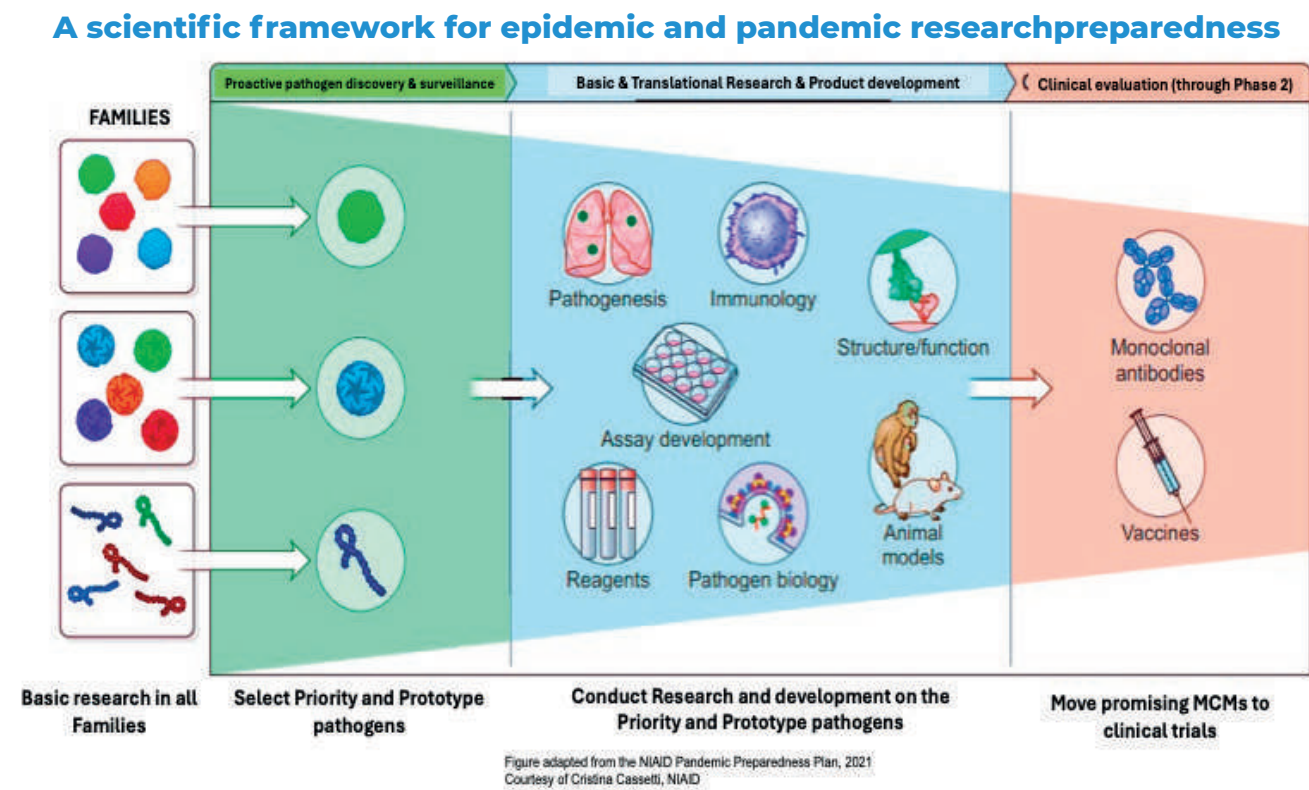
It is crucial to emphasize the need for regular examination of evidence to evaluate whether families previously deemed of minimal or no risk (due to the absence of known human-infecting pathogens) could serve as a potential reservoir for pathogen X (as discussed in the PAC meeting, including arteriviridae, Deltaarterivirus hemfev, etc.).

Table 2. Outcomes of the PAC considerations on the risks of various Families

| Family | PHEIC risk | PHEIC or pandemic risk notes on pathogens in each Family |
|------------------|---------------|---|
| Adenoviridae | Low to Medium | Respiratory transmission for some viruses suggests greater than low risk, but no priority pathogen was selected. Adenovirus can cause outbreaks in military recruits, and other settings. Capability for recombination can increase tropism/host range. |
| Anelloviridae | Low | No known human or mammalian disease. Considered to be low pathogenic or pandemic potential. |
| Arenaviridae | High | Some viruses have documented high pathogenicity and transmissibility via rodent vectors, some human-human transmission. |
| Astroviridae | Low | All viruses have low risk of transmission and relatively low virulence (though some possible risk to immunocompromised). |
| Bacteria | High | Highly pathogenic bacteria with high level enteric or respiratory spread have caused and will cause severe outbreaks. |
| Bornaviridae | Low | High genetic stability, fatal encephalitis, no evidence of human-to-human transmission. |
| Coronaviridae | High | Includes viruses with known risk to cause of pandemics, with multiple pandemic threats in family. |
| Filoviridae | High | Includes viruses which are highly pathogenic, history of devastating regional outbreaks. |
| Flaviviridae | High | Include multiple insect-vector-borne pathogenic and virulent viruses. |
| Hantaviridae | High | Includes multiple viruses with high virulence. |
| Hepadnaviridae | Low | Existing vaccine protects against current Orthohepadnavirus hominoid strains. |
| Hepeviridae | Low | Virulence and pathogenicity for included viruses generally considered low but some viruses have large numbers of animal reservoirs. |
| Herpesviridae | Low | Herpesviridae has a low PHEIC or pandemic potential, though they cause very important diseases, latent infections and long-term consequences. |
| Nairoviridae | High | Several viruses with high virulence & broad geographic distribution. |
| Orthomyxoviridae | High | New alphainfluenza influenzae strains can evolve quickly and pose high PHEIC and pandemic risk. |
| Papillomaviridae | Low | Includes viruses with low PHEIC and pandemic risk (transmission by direct contact). Risks tend to be species-specific and MCMs are available. |
| Paramyxoviridae | High | Includes an important priority pathogen. |
| Parvoviridae | Low | Includes pathogenic members, some with evidence of species jumps, but low risk for human pandemics and PHEICs. |
| Peribunyaviridae | Low | Include viruses with lower virulence than other families in the class Bunyaviricetes. |
| Phenuiviridae | High | Includes multiple pathogens with high virulence. |
| Picobirnaviridae | Low | Pathogenicity in mammals including humans is unclear. |
| Picornaviridae | Medium | Includes an important priority pathogen (though vaccine-controllable). |
| Pneumoviridae | Low to Medium | Respiratory transmission of some viruses suggests higher than low priority, existing orthopneumovirus hominis vaccine. |
| Polyomaviridae | Low | No pandemic or PHEIC risk identified. |
| Poxviridae | High | Orthopoxvirus monkeypox caused previous PHEIC. |
| Retroviridae | Medium | Lentivirus humimdef1 caused global pandemic. Delayed but devastating symptoms, ability to jump species contribute to threat. Antivirals are effective. There is no vaccine. |
| Rhabdoviridae | Low | Includes viruses with high pathogenicity but relatively low transmissibility. |
| Sedoreoviridae | Low | High global immunity to genus rotavirus makes it an unlikely PHEIC or pandemic pathogen. |
| Spinareoviridae | Low | Spinareoviruses have a broad host range, infecting animals, fungi and plants, but have low pandemic potential. |
| Togaviridae | High | Includes several viruses that cause severe disease and with PHEIC and pandemic concern. Overall seropositivity rates not known. |

The deliberations also identified key research actions that should be supported across all Families considered⁷.

Figure 8. Overview of priority research actions



Proactive Pathogen Discovery & Surveillance

Efforts should be directed toward improving the detection, monitoring, and response to infectious disease outbreaks through the utilization of various data streams and advanced technologies.

It is essential to promptly detect and characterize new pathogens that have the potential to cause pandemics. Adopting a One Health approach, which acknowledges the interconnection of human, animal, and environmental health in surveillance and response endeavors, holds significant importance. The significance and utility of monitoring migrating birds and wastewater were

acknowledged. Particularly, monitoring activities at interfaces between humans and animals (e.g., slaughterhouses, etc.) entail enhancing genomic sequencing capacities, creating comprehensive diagnostic tools, and strengthening worldwide surveillance systems for emerging infectious diseases.

Efforts aimed at broadening viral surveillance and pathogen discovery networks are multifaceted, encompassing the incorporation of advanced genomic technologies, digital disease detection tools, and sophisticated risk modeling approaches. This encompasses the surveillance of zoonotic diseases and antimicrobial resistance.

⁷ A scientific framework for epidemic and pandemic research preparedness. https://cdn.who.int/media/docs/default-source/consultation-rdb/who-report-scientific-approach-pandemic-preparedness.pdf?sfvrsn=1f209cb3_4

Targeted basic research

It is essential to investigate the basic biology, transmission, and pathogenesis of high-risk viral families, prioritizing priority and prototype pathogens. Additional important requirements involve the creation of suitable animal models, validated assays, reference materials, and adjuvants to expedite the development and assessment of countermeasures. The comprehension of viral structures, infection mechanisms, immune responses, and host interactions is crucial in informing the development of medical interventions.

Translational research and product development

It is essential to narrow the gap between fundamental scientific discoveries and their practical applications in the field of public health. Efforts should include a focus on developing broad-spectrum antiviral drugs that can be readily deployed during an outbreak. Additionally, the creation of vaccines using a prototype pathogen approach entails developing MCMs for representative viruses within a viral family. Such research could facilitate the development of MCMs with a broader spectrum, capable of addressing multiple pathogens or evolving pathogens.

Furthermore, there is a necessity for further research on host-directed antivirals that target human proteins vital for the viral life cycle, which can potentially provide broad-spectrum activity against multiple viruses; evaluate diverse vaccine platforms to ensure rapid adaptability to new pathogens; rapid development and deployment of monoclonal antibodies for immediate response to emerging pathogens; and point-of-care diagnostics.

Establishing robust clinical trial capabilities and deployment strategies

The prompt initiation of clinical trials is essential for the prompt evaluation and distribution of new medical countermeasures during an outbreak. This involves simplifying trial design and establishing public confidence in the evidence generated. Efforts to streamline trial design, such as the creation of CORE clinical trial designs capable of swift adaptation to evaluate novel treatments and vaccines in the event of an outbreak, are crucial. Simplified regulatory processes could facilitate the rapid authorization of new vaccines, treatments, and diagnostic tools in times of pandemics. This involves the advance approval of CORE protocols and the promotion of cooperation between international ethics committees and regulatory bodies.

Collaborative research

In employing a multifaceted research strategy is crucial to ensure equitable global access and sustain adequate manufacturing capacity. It is essential to emphasize the significance of global networks and capacity enhancement through collaborative efforts. Collaborative research that encompasses pathogen discovery, basic and translational research, product development, clinical assessment, and worldwide coordination is imperative to bolster preparedness for Pathogen X and potential future pandemics. Additionally, the establishment of networks of networks and the sharing of data play pivotal roles in this context.

D for DEVELOPMENT of MCMs against known threats

The risk of Priority Pathogens causing a PHEIC was determined by considering available information on transmission patterns, virulence, and availability of countermeasures, indicating the potential threat.

In the initial prioritization process, no priority pathogens were identified for four viral families, all of which belong to DNA viruses: Anelloviridae, Herpesviridae, Polyomaviridae, and Papillomaviridae.

Priority pathogens with a high potential to cause a PHEIC necessitate immediate research and development interventions (refer to Table 3). The majority of the newly identified Priority Pathogens align with those identified in previous pathogen prioritization reports issued by the WHO R&D Blueprint for Epidemics.

Table 4 presents a summary of the conclusions concerning the PHEIC risks associated with the chosen Priority Pathogens and the concerns raised by PAC members during discussions on the risks posed by pathogens within different Families. Annexes 2 and 3 offer a comprehensive outline of the principal epidemiological features of the selected Priority Pathogens and the potential vaccines and therapies currently in progress.

Among the selected Priority Pathogens some exhibit a global distribution, being present in all six WHO Regions, while others are concentrated in specific regions, often associated with the presence of an animal reservoir, transmitting vector, or substandard living conditions.

Pathogens with worldwide distribution encompass viruses (such as Subgenus Sarbecovirus, Alphainfluenzavirus influenzae, Lentivirus humimdefl, and Orthoflavivirus denguei) and bacteria (such as *Salmonella enterica invasive non-typhoidal serovars* and *Klebsiella pneumoniae*).

Moreover, several prototype pathogens belonging to lower-risk viral families are present in all six regions, such as Metapneumovirus hominis and Rotavirus. Further information can be found in the section titled Global and Regional Perspective.

Table 3. Selected Priority pathogens by family and known geographic distribution

| Family | Priority Pathogen | AFR | AMR | EMR | EUR | SEAR | WPR |
|------------------|--|-----|-----|-----|-----|------|-----|
| Adenoviridae | No Priority pathogen proposed | | | | | | |
| Anelloviridae | No Priority pathogen proposed | | | | | | |
| Arenaviridae | Mammarenavirus lassaense | X | | | | | |
| Astroviridae | No Priority pathogen proposed | | | | | | |
| Bacteria | Vibrio cholera (O139) | X | | X | | X | X |
| Bacteria | Yersinia pestis | X | X | | | | |
| Bacteria | Shigella dysenteriae serotype 1 | X | | X | | X | |
| Bacteria | Salmonella enterica non typhoidal serovars | X | X | X | X | X | X |
| Bacteria | Klebsiella pneumoniae | X | X | X | X | X | X |
| Bornaviridae | No Priority pathogen proposed | | | | | | |
| Coronaviridae | Subgenus Merbecovirus | | | X | | | |
| Coronaviridae | Subgenus Sarbecovirus | X | X | X | X | X | X |
| Filoviridae | Orthoebolavirus zairense | X | | | | | |
| Filoviridae | Orthoebolavirus sudanens | X | | X | | | |
| Filoviridae | Orthomarburgvirus marburgense | X | | | | | |
| Flaviviridae | Orthoflavivirus flavi | X | X | | | | |
| Flaviviridae | Orthoflavivirus denguei | X | X | X | X | X | X |
| Flaviviridae | Orthoflavivirus zikaense | X | X | | | X | X |
| Hantaviridae | Orthohantavirus hantanense | | | | X | | X |
| Hantaviridae | Orthohantavirus sinnombreense | | X | | | | |
| Hepadnaviridae | No Priority pathogen proposed | | | | | | |
| Hepeviridae | No Priority pathogen proposed | | | | | | |
| Herpesviridae | No Priority pathogen proposed | | | | | | |
| Nairoviridae | Orthonairovirus haemorrhagiae | X | | X | X | | X |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H1, H2, H3, H5, H6, H7, H10 | X | X | X | X | X | X |
| Papillomaviridae | No Priority pathogen proposed | | | | | | |
| Paramyxoviridae | Henipavirus nipahense | | | | | X | X |
| Parvoviridae | No Priority pathogen proposed | | | | | | |
| Peribunyaviridae | No Priority pathogen proposed | | | | | | |
| Phenuiviridae | Bandavirus dabiense | | | | | X | X |
| Picobinaviridae | No Priority pathogen proposed | | | | | | |
| Picornaviridae | Enterovirus coxsackiepol | X | | X | | X | |
| Pneumoviridae | No Priority pathogen proposed | | | | | | |
| Polyomaviridae | No Priority pathogen proposed | | | | | | |
| Poxviridae | Orthopoxvirus variola | | | | | | |
| Poxviridae | Orthopoxvirus monkeypox | X | X | X | X | X | X |
| Retroviridae | Lentivirus humimdefl | X | X | X | X | X | X |
| Rhabdoviridae | No Priority pathogen proposed | | | | | | |
| Sedoreoviridae | No Priority pathogen proposed | | | | | | |
| Spinareoviridae | No Priority pathogen proposed | | | | | | |
| Togaviridae | Alphavirus chikungunya | X | X | | | X | X |
| Togaviridae | Alphavirus venezuelan | | X | | | | |

Table 4. Selected Priority Pathogens by Family and PAC notes during deliberations

| Family | PHEIC risk | Priority Pathogen(s) | Priority Pathogen notes |
|------------------|---------------|---|--|
| Adenoviridae | Low to Medium | No Priority pathogen proposed | |
| Anelloviridae | Low | No Priority pathogen proposed | |
| Arenaviridae | High | Mammarenavirus lassaense | Currently causes annual outbreaks in West Africa, highest disease burden with broad range of natural reservoir. |
| Astroviridae | Low | No Priority pathogen proposed | |
| Bacteria | High | <i>Vibrio cholera</i> (O139) | Enteric, concern for new O serogroup (Pandemic risk). |
| Bacteria | High | <i>Yersinia pestis</i> | Respiratory (Pandemic risk). |
| Bacteria | High | <i>Shigella dysenteriae</i> serotype 1 | Enteric, Shiga toxin, concern for other serotypes (Pandemic risk). |
| Bacteria | High | <i>Salmonella enterica</i> invasive non typhoidal | Enteric (PHEIC risk). |
| Bacteria | High | <i>Klebsiella pneumoniae</i> | MDR is an emerging issue globally, can cause PHEIC. |
| Bornaviridae | Low | No Priority pathogen proposed | |
| Coronaviridae | High | Subgenus Sarbecovirus | Beta Subgenus sarbecoviruses considered greatest risk within family. |
| Coronaviridae | High | Subgenus Merbecovirus | A subgenus of viruses in the genus Betacoronavirus, including the human pathogen Middle East respiratory syndrome-related coronavirus (MERS-CoV). |
| Filoviridae | High | Orthoebolavirus zairense | No cross-protection among these viruses. |
| Filoviridae | High | Orthoebolavirus sudanense | Licensed vaccines available for Orthoebolavirus zairense. |
| Filoviridae | High | Orthomarburgvirus marburgense | A highly virulent disease that causes haemorrhagic fever, with a fatality ratio of up to 88%. |
| Flaviviridae | High | Orthoflavivirus flavi | Yellow Fever Vaccine available but shortages frequent. |
| Flaviviridae | High | Orthoflavivirus denguei | Dengue: severe disease due to antibody-dependant enhancement ADE. |
| Flaviviridae | High | Orthoflavivirus zikaense | Previous PHEIC with congenital disease. |
| Hantaviridae | High | Orthohantavirus hantanense | Spread from rodents to humans, old and new world Hantavirus has become endemic in many continents, with sporadic cases of person-to-person transmission. |
| Hantaviridae | High | Orthohantavirus sinnombreense | It is unclear how climate change and demographic shifts, such as the continued migration of people from rural to urban settings, will impact both rodent populations and the potential for transmission to people. |
| Hepadnaviridae | Low | No Priority pathogen proposed | |
| Hepeviridae | Low | No Priority pathogen proposed | |
| Herpesviridae | Low | No Priority pathogen proposed | |
| Nairoviridae | High | Orthonairovirus haemorrhagiae | Most widespread haemorrhagic fever virus in the world. |
| Orthomyxoviridae | High | Alphainfluenzavirus influenzae (H1N1) | Ability to reassort places all new types as high risk. |
| Orthomyxoviridae | High | Alphainfluenzavirus influenzae (H2Nx) | All proposed priority pathogens also have high virulence. |
| Orthomyxoviridae | High | Alphainfluenzavirus influenzae (H3N2) | All proposed priority pathogens also have high virulence. |
| Orthomyxoviridae | High | Alphainfluenzavirus influenzae (H5Nx) | All proposed priority pathogens also have high virulence. |
| Orthomyxoviridae | High | Alphainfluenzavirus influenzae (H6Nx) | All proposed priority pathogens also have high virulence. |
| Orthomyxoviridae | High | Alphainfluenzavirus influenzae (H7Nx) | All proposed priority pathogens also have high virulence. |
| Orthomyxoviridae | High | Alphainfluenzavirus influenzae (H10Nx) | All proposed priority pathogens also have high virulence. |
| Paramyxoviridae | High | Henipavirus nipahense | Mid-high transmissivity in animals, high virulence, no MCMs. |
| Parvoviridae | | No Priority Pathogen proposed | |
| Peribunyaviridae | Low | No Priority pathogen proposed | |
| Phenuiviridae | High | Bandavirus dabiense | High lethality and known person to person spread. |
| Picobinaviridae | Low | No Priority pathogen proposed | |
| Picornaviridae | Medium | Enterovirus coxsackiepol | Despite vaccines, polio presents continuing PHEIC threat. |
| Pneumoviridae | Low to Medium | No Priority pathogen proposed | |
| Polyomaviridae | Low | No Priority pathogen proposed | |
| Poxviridae | High | Orthopoxvirus variola | As immunity wanes, orthopoxvirus variola has potential to cause pandemic if released. |
| Poxviridae | High | Orthopoxvirus monkeypox | Orthopoxvirus monkeypox has caused PHEIC. |
| Retroviridae | Medium | Lentivirus humimdefl | No vaccine available yet. |
| Rhabdoviridae | | No Priority Pathogen proposed | |
| Sedoreoviridae | Low | No Priority pathogen proposed | |
| Spinareoviridae | Low | No Priority pathogen proposed | |
| Togaviridae | High | Alphavirus chikungunya | Aerosol transmission and encephalitis. |
| Togaviridae | High | Alphavirus venezuelan | Enteric, concern for new O serogroup (Pandemic risk). |

D+ for DEVELOPMENT of MCMs for Prototype Pathogens

If a Family was considered to contain pathogens with attributes that suggest the likelihood (even remote) of causing a PHEIC, Prototype Pathogens were identified. Prototype pathogens were not recommended for bacteria, because of the uniqueness of each priority pathogen (Table 5).

Selecting Prototype Pathogens is challenging due to the breadth and diversity of some viral Families (Table 6). Prototype Pathogens were selected primarily for their potential ability to serve as a guide for generating generalizable evidence and filling knowledge gaps that will facilitate the development of MCMs for other pathogens in the same family or functional group (which may include existing vaccines or countermeasures).

Considerations for Prototype Pathogen selection varied across the FEGs and included their importance as human pathogens, current knowledge of replication and pathogenesis, the existence of animal reservoirs causing cross-species infections, the shared structural and functional properties, the existing research knowledge, for example, the availability of animal models that recapitulate human disease, and the status of countermeasure development.

Where the weight of these considerations was similar among potential Prototype Pathogens, the PAC also considered additional factors: burden and type of disease, existing collaborations, and reagents are likely to speed up work on one pathogen or another.

Additional considerations included the geographic distribution of the pathogen and its perceived local and regional relevance (e.g., old world vs new world), differences in pathogenesis (e.g., insect vectors, intermediate hosts), and biocontainment levels (e.g., Orthopoxvirus vaccinia selected along with Orthopoxvirus monkeypox).

Therefore, multiple prototype pathogens were recommended for some virus families. The main reason for selecting multiple pathogens was the diversity of viruses within the group, such that the study of a single pathogen might not be sufficient to facilitate the development of countermeasures that could be useful for the entire group. For example, in the flavivirus family, additional prototype pathogens were recommended due to differences in vector and viral transmission mechanisms. Such additional representative family members were sometimes instead classified as “viruses of concern”, as in the parvovirus family.

Table 5. Selected Prototype Pathogens by family and known geographic distribution

| Family | Perceived Risk | Prototype Pathogen | AFR | AMR | EMR | EUR | SEAR | WPR |
|------------------|----------------|---|-----|-----|-----|-----|------|-----|
| Adenoviridae | Low-Medium | Mastadenovirus blackbeardi serotype 14 | | X | | | | X |
| Adenoviridae | Low-Medium | Recombinant mastadenovirus | X | X | X | X | X | X |
| Anelloviridae | Low | No Prototype pathogen proposed | | | | | | |
| Arenaviridae | High | Mammarenavirus juninense | | X | | | | |
| Arenaviridae | High | Mammarenavirus lasaense | X | | | | | |
| Arenaviridae | High | Mammarenavirus lujoense | X | | | | | |
| Astroviridae | Low | Mamastrovirus virginiaense | X | X | X | X | X | X |
| Bacteria | High | No Prototype pathogen proposed | | | | | | |
| Bornaviridae | Low | Orthobornavirus bornaense | | | | X | | |
| Coronaviridae | High | Subgenus Merbecovirus | | | X | | | |
| Coronaviridae | High | Subgenus Sarbecovirus | X | X | X | X | X | X |
| Filoviridae | High | Orthoebolavirus zairense | X | | | | | |
| Flaviviridae | High | Orthoflavivirus denguei | X | X | X | X | X | X |
| Flaviviridae | High | Orthoflavivirus encephalitis | | | | X | | X |
| Flaviviridae | High | Orthoflavivirus nilense | X | X | X | X | X | X |
| Flaviviridae | High | Orthoflavivirus zikaense | X | X | | | X | X |
| Hantaviridae | High | Orthohantavirus sinnombreense | | X | | | | |
| Hepadnaviridae | Low | Orthohepadnavirus hominoidei genotype C | | | | | X | |
| Hepeviridae | Low | Paslahepevirus balayani genotype HEV-3 | X | X | X | X | X | X |
| Herpesviridae | Low | No Prototype pathogen proposed | | | | | | |
| Nairoviridae | High | Orthonairovirus haemorrhagiae | X | | X | X | | X |
| Orthomyxoviridae | High | Alphainfluenzavirus influenzae (H1N1) | X | X | X | X | X | X |
| Orthomyxoviridae | High | Alphainfluenzavirus influenzae (H5Nx) | X | X | X | X | X | X |
| Papillomaviridae | Low | No Prototype pathogen proposed | | | | | | |
| Paramyxoviridae | High | Henipavirus nipahense | | | | | X | X |
| Parvoviridae | Low | Protoparvovirus carnivoran | X | X | X | X | X | X |
| Peribunyaviridae | Low | Orthobunyavirus oropoucheense | | X | | | | |
| Phenuiviridae | High | Bandavirus dabiense | | | | | X | X |
| Phenuiviridae | High | Phlebovirus riftense | X | | | | | |
| Picobimaviridae | Low | Orthopicobimavirus hominis | X | X | X | X | X | X |
| Picornaviridae | Medium | Enterovirus alphacoxsackie 71 | X | X | X | X | X | X |
| Picornaviridae | Medium | Enterovirus deconjecti 68 | X | X | X | X | X | X |
| Pneumoviridae | Low-Medium | Metapneumovirus hominis | X | X | X | X | X | X |
| Polyomaviridae | Low | No Prototype pathogen proposed | | | | | | |
| Poxviridae | High | Orthopoxvirus monkeypox | X | X | X | X | X | X |
| Poxviridae | High | Orthopoxvirus vaccinia | | X | X | | X | |
| Retroviridae | Medium | Lentivirus humimdefl | X | X | X | X | X | X |
| Rhabdoviridae | Low | Genus Vesiculovirus | X | X | X | X | X | X |
| Sedoreoviridae | Low | Genus Rotavirus | X | X | X | X | X | X |
| Spinareoviridae | Low | Orthoreovirus mammalis | X | X | X | X | X | X |
| Togaviridae | High | Alphavirus chikungunya | X | X | | | X | X |
| Togaviridae | High | Alphavirus venezuelan | | X | | | | |

Table 6. Selected Prototype Pathogens by family and PAC notes during deliberations

Concentrating research efforts on Prototype Pathogens within each virus family is expected to increase synergies and opportunities for collaboration, more efficiently leading to knowledge that can be applied to other pathogens within the same family. Ideally, the development of a vaccine or countermeasure for the recommended prototype pathogens will yield sufficient knowledge to facilitate the development of parallel countermeasures against related viruses.

For antivirals, inhibitors of viral enzymes that are similar within the family may be effective against multiple family members. For vaccines, this knowledge may facilitate understanding of viral antigens likely to induce protective immunity or likely correlates of protection.

| Family | Prototype Pathogens | Prototype pathogen notes |
|------------------|---|---|
| Adenoviridae | Recombinant adenovirus | Recombinant adeno needs more definition. No MCMs available. Recombination should also be studied. |
| Adenoviridae | Mastadenovirus blackbeardi serotype 14 | No MCMs available. Recombination should also be studied. |
| Anelloviridae | No Prototype Pathogens proposed | |
| Arenaviridae | Mammarenavirus juninense | Old world, several MCMs under development. |
| Arenaviridae | Mammarenavirus lassause | New world, treatments available. |
| Arenaviridae | Mammarenavirus lujoense | 80% mortality, in single known outbreak. |
| Astroviridae | Mamastrovirus virginiaense | Human origin, association with encephalitis, able to propagate in cell culture. |
| Bacteria | No Prototype Pathogens proposed | Prototypes aren't as meaningful for bacteria. |
| Bornaviridae | Orthobornavirus bornaense | Spill-over from animal reservoir; fatal encephalitis in humans. |
| Coronaviridae | Subgenus Merbecovirus | Surveillance should consider animal reservoirs. |
| Coronaviridae | Subgenus Sarbecovirus | Surveillance should consider animal reservoirs. |
| Filoviridae | Orthoebolavirus zairense | Concern re different strains and variants of Ebola as a potential threat. Ebola can yield information relevant to MCMs for other viruses. |
| Flaviviridae | Orthoflavivirus denguei | Flavivirus prototypes chosen to represent different vectors and intermediate hosts - transmitted by Aedes aegypti |
| Flaviviridae | Orthoflavivirus zikaense | Flavivirus prototypes chosen to represent different vectors and intermediate hosts - transmitted by Aedes mosquitoes |
| Flaviviridae | Orthoflavivirus nilense | Flavivirus prototypes chosen to represent different vectors and intermediate hosts - |
| Flaviviridae | Orthoflavivirus encephalitidis | Flavivirus prototypes chosen to represent different vectors and intermediate hosts - tick- |
| Hantaviridae | Orthohantavirus sinnombreense | Higher lethality with less evidence of person-person spread. |
| Hepadnaviridae | Orthohepadnavirus hominoidei genotype C | Genotype C has higher mortality, higher mutation rate with reported false negative HBsAg test result and reported lower treatment response. |
| Hepeviridae | Paslahepevirus balayani genotype HEV-3 | Human infections with a large number of animal reservoirs, wide geographic distribution. Foodborne transmission (FAO/WHO considered Paslahepevirus balayani one of the top 3 foodborne viral pathogens). Can cause chronic hepatitis, neurological complications. |
| Herpesviridae | No Prototype Pathogens proposed | |
| Nairoviridae | Orthonaivirus haemorrhagiae | Outbreaks occur infrequently, typically infect only very few individuals, and most cases are asymptomatic or mild (e.g. headache, myalgia, joint pain, fever and nausea with vomiting). However, the disease may present with a sudden onset and rapid deterioration to severe haemorrhage, organ shutdown and death (lethality 5-80%). |
| Orthomyxoviridae | Alphainfluenzavirus influenzae (H1N1). | Human alphainfluenzavirus influenzae. |
| Orthomyxoviridae | Alphainfluenzavirus influenzae (H5Nx). | Avian alphainfluenzavirus influenzae. |
| Papillomaviridae | No Prototype Pathogens proposed | |
| Paramyxoviridae | Henipavirus nipahense | Pathogenic in humans without effective MCMs. |
| Parvoviridae | Protoparvovirus camivoran | Demonstrated ability to jump species and cause severe animal disease. Animal vaccine exists. |
| Peribunyaviridae | Orthobunyavirus oropoucheense | Normally not fatal. |
| Phenuiviridae | Bandavirus dabieense | Causes Severe Fever with Thrombocytopenia Syndrome. |
| Phenuiviridae | Phlebovirus riftense | Rodent screening plus seroepidemiology in people at risk. |
| Picobirnaviridae | Human picobirnavirus | No known human disease, likely enteric transmission. |
| Picomaviridae | Enterovirus deconjecti 68 | Causes outbreaks. |
| Picomaviridae | Enterovirus alphacoxsackie 71 | Respiratory transmission and causes paralysis (vaccine available in Asia). |
| Pneumoviridae | Metapneumovirus hominis | Currently causes important outbreaks in children and adults. RSV evolved from avian metapneumovirus. Key need: antivirals. |
| Polyomaviridae | No Prototype Pathogens proposed | |
| Poxviridae | Orthopoxvirus monkeypox | Orthopox monkeypox needed to study pathogenesis. Impossible to work with variola except in special settings. |
| Poxviridae | Orthopoxvirus vaccinia | Vaccinia provides BSL2 alternative that is cross-protective and likely susceptible to same antivirals. |
| Retroviridae | Lentivirus humimdefl | Most important human retroviral pathogen, with widespread research programs. Research has already shown benefits for understanding of other viruses. |
| Rhabdoviridae | Genus Vesiculovirus | Important as vaccine vector and as potential prototype for future vaccines. |
| Sedoreoviridae | Genus Rotavirus | Genus rotavirus vaccines less effective in LMICs. |
| Spinareoviridae | Orthoreovirus mammalis | Have long been considered non-pathogenic, although mild respiratory and enteric diseases have occasionally been reported in young animals and children. Recent data have shown that MRVs can cause severe disease. |
| Togaviridae | Alphavirus chikungunya | Vaccine prototype. |
| Togaviridae | Alphavirus venezuelan | Vaccine prototype. |

R&D - PREPARING FOR THE INEVITABLE

Pathogen X is a term used to denote an unidentified or unspecified pathogen. Unknown pathogens with the potential to induce a PHEIC or pandemics in the future.

It is challenging to predict the specific pathogen that may lead to the next PHEIC or pandemic. While numerous viruses and bacteria capable of infecting humans exist, only a limited subset has historically been responsible for pandemics or widespread epidemics.

Hence, researchers utilize the term to refer to potential infectious pathogens without singling out a specific one. This term symbolizes a theoretical pathogen that could result in significant outbreaks, PHEICs, or pandemics. Pathogen X is envisioned as an unidentified future hazard that could originate from recognized viruses within each viral family or potentially from viruses that are currently unidentified.

The concept of Pathogen X underscores the importance of readiness for an unidentified disease-causing pathogen with the potential to cause a pandemic. Regardless of the preparations undertaken, it is improbable to have a readily available effective vaccine or treatment for a particular pandemic pathogen strain at the onset of the next pandemic.

Hence, the challenge in pandemic preparedness lies in acquiring the essential knowledge to promptly disseminate globally high-quality, cost-effective, and reliable countermeasures.

Utilizing the aforementioned definition, potential Pathogens X was selected for each pathogen family (excluding bacteria) as outlined in Table 7. This selection of potential Pathogen X from each family serves as a resource tool for strategizing necessary research and efforts needed to enhance the understanding developed within the family, thereby effectively addressing spectrum diversity potential threats. arise.

Pre-pandemic readiness should prioritize the advancement of discovery, basic, and translational research. It is essential to underscore the importance of employing generalizable strategies. This will ensure that in the event of identifying Pathogen X, expedited product development and clinical trials can be promptly initiated.

Furthermore, the experts discussed the potential alterations in the pathogen's biology, climate, and that could enable any pathogen to evolve into the next Pathogen X. Of particular significance was the discussion on strategies for monitoring these changes.

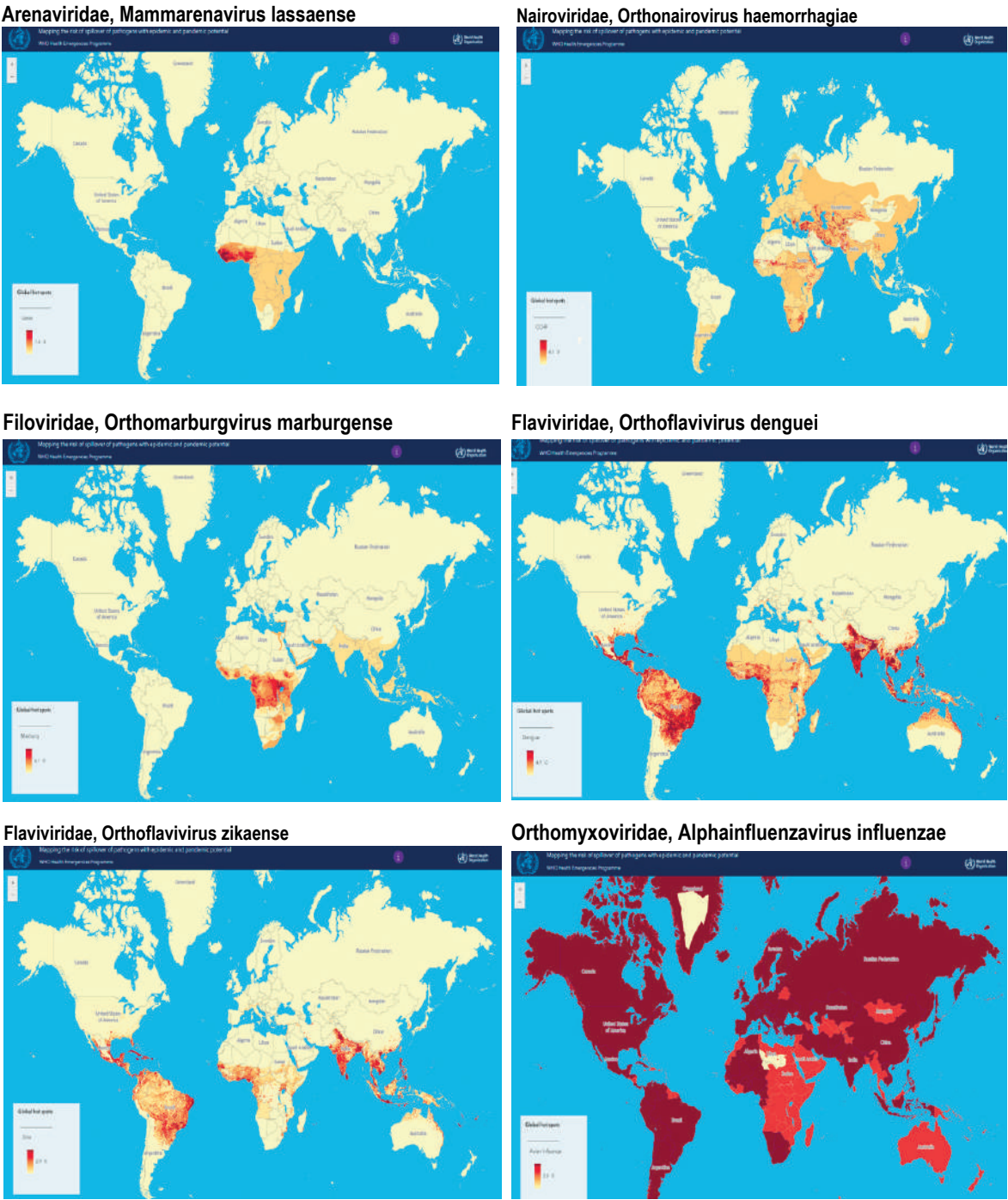
Table 7. Some of the proposed Pathogen X and other Pathogens of Concern per Family

| Viral Family | Pathogen X | Other Pathogens of Concern |
|------------------|---|--|
| Adenoviridae | Mastadenovirus blackbeardi 21 | 10 Mastadenovirus species |
| Adenoviridae | Mastadenovirus blackbeardi 55 | |
| Adenoviridae | Mastadenovirus blackbeardi 7 | |
| Adenoviridae | Mastadenovirus exoticum | |
| Arenaviridae | Mammarenavirus chapareense | Mammarenavirus cardamones |
| Arenaviridae | Mammarenavirus choriomeningitis | Mammarenavirus guanaritoense |
| Arenaviridae | Mammarenavirus lujoense | |
| Arenaviridae | Mammarenavirus machupoense | |
| Astroviridae | | Mamastrovirus mustelae |
| Astroviridae | | Mamastrovirus ovis |
| Astroviridae | | Mamastrovirus porcine |
| Astroviridae | | Mamastrovirus virginiae |
| Bornaviridae | | Orthobornavirus bornaense |
| Bornaviridae | | Orthobornavirus sciuri |
| Coronaviridae | Alphacoronavirus suis (CCoV-HuPn-2018) | Betacoronavirus gruedinensis (PHEV) |
| Coronaviridae | Alphacoronavirus porci | Recombinant alphacoronavirus |
| Coronaviridae | | Group 2d betacoronaviruses |
| Coronaviridae | | Alphacoronavirus amsterdamense |
| Coronaviridae | | Subgenus Embecovirus |
| Coronaviridae | | Deltacoronavirus (PDCoV) |
| Filoviridae | Orthoebolavirus bombaliense | Thamnovirus thamnaconi |
| Filoviridae | Orthoebolavirus X | Cuevavirus lloviuense |
| Filoviridae | Orthoebolavirus restonense | Dianlovirus menglaense |
| Filoviridae | | Striavirus antennarii |
| Flaviviridae | Orthoflavivirus japonicum | Orthoflavivirus ilheusense |
| Flaviviridae | Orthoflavivirus encephalitis | Orthoflavivirus usutuense |
| Flaviviridae | Orthoflavivirus nilense | Orthoflavivirus wesselsbronense |
| Flaviviridae | | Jingmenvirus |
| Flaviviridae | | Orthoflavivirus rocio |
| Flaviviridae | | Orthoflavivirus spondweni |
| Hepadnaviridae | Orthohepadnavirus felisdomestici | Orthohepadnavirus pomi |
| Hepadnaviridae | Recombinant Orthohepadnavirus | |
| Hepeviridae | | Paslahepevirus balayani (genotype 1) |
| Hepeviridae | | Paslahepevirus balayani (genotype 2) |
| Hepeviridae | | Paslahepevirus balayani (genotype 3) |
| Hepeviridae | | Paslahepevirus balayani (genotype 4) |
| Orthomyxoviridae | Alphainfluenzavirus influenzae (H9N2) | |
| Orthomyxoviridae | Betainfluenzavirus influenzae | |
| Paramyxoviridae | Henipavirus hendraense | Orthorubulavirus mapueraense |
| Paramyxoviridae | | Pararubulavirus menangleense |
| Paramyxoviridae | | Pararubulavirus sosugaense |
| Paramyxoviridae | | Parahenipavirus genus |
| Parvoviridae | Protoparvovirus carnivoran | Amdoparvovirus carnivoran |
| Parvoviridae | | Erythroparvovirus primate |
| Phenuiviridae | Phlebovirus riftense | Phlebovirus napoliense, Phlebovirus siciliaense, Phlebovirus toscanaense |
| Picobimaviridae | | Orthopicobimavirus hominis |
| Picomaviridae | Enterovirus deconjecti 68 | Enterovirus-X |
| Picomaviridae | Enterovirus alphacoxsackie 71 | |
| Pneumoviridae | | Metapneumovirus avis |
| Pneumoviridae | | Metapneumovirus hominis |
| Pneumoviridae | | Novel emerging pneumovirus |
| Poxviridae | Orthopoxvirus cowpox | Orthopoxvirus alaskapox |
| Poxviridae | | Orthopoxvirus vaccinia |
| Reovirales | | Orthoreovirus mammalis |
| Retroviridae | Gammaretrovirus gibleu-like viruses in koalas, bats and rodents | Lentivirus humimdef2 |
| Retroviridae | Lentivirus simimdef | Deltaretrovirus priTlym3 |
| Rhabdoviridae | | Genus Ledantivirus |
| Rhabdoviridae | | Genus Tibrovirus |
| Rhabdoviridae | | Genus Vesiculovirus |
| Togaviridae | Alphavirus eastern | Alphavirus onyong |
| Togaviridae | Alphavirus madariaga | |
| Togaviridae | Alphavirus mayaro | |
| Togaviridae | Alphavirus rossriver | |

A GLOBAL AND A REGIONAL PERSPECTIVE

Priorities may differ if a regional perspective is adopted, as many pathogens are limited to, or more of a problem in, particular geographic regions. To stimulate research in each region it is particularly important to have a locally relevant prototype pathogen. For many families, a single prototype pathogen was considered sufficient to cover the entire family. However, for other families, it was considered necessary to select multiple prototype pathogens, if, for example, potential prototype pathogens were confined to certain regions or were transmitted by different vectors.

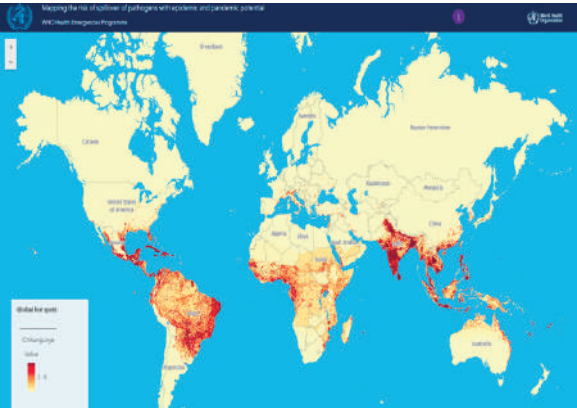
Figure 9. Geographic distribution of selected Priority Pathogens



Paramyxoviridae, Henipavirus nipahense



Poxviridae, Orthopoxvirus Variola



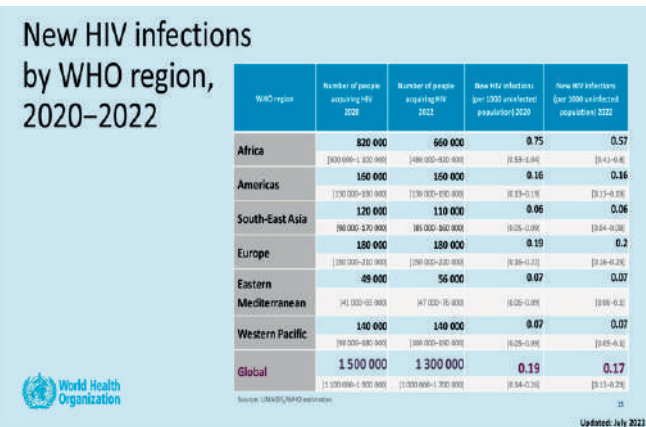
Poxviridae, Orthopoxvirus monkeypox



Togaviridae, Alphavirus chikungunya



Retroviridae, Lentivirus humimdef1



African Region

Particular priorities in the African Region include the Filoviruses (Orthoebolavirus zairense, sudanense, and marburgense), Orthopoxvirus monkeypox, and Mammarenavirus lassaense. Others include all three priority Orthoflaviviruses (denguei, encephalitidis, and zikaense), and Alphavirus chikungunya. Of the global pathogens, Lentivirus humimdef1, has particular significance. All five bacterial priority pathogens are also significant in this Region (Vibrio cholerae O139, Yersinia pestis, Shigella dysenteriae serotype 1, Salmonella enterica (invasive non-typhoidal), Klebsiella pneumoniae). The following Prototype Pathogens are specific to the African Region: Mammarenavirus lujose and the Phlebovirus riftense.

Table 8. Selected Priority Pathogens with circulation in the WHO African Region

| Family | PHEIC risk | Priority Pathogens | Prototype Pathogens |
|------------------|------------|--|------------------------------------|
| Arenaviridae | High | Mammarenavirus lassaense | Mammarenavirus lassaense |
| Arenaviridae | High | | Mammarenavirus lujose |
| Bacteria | High | Klebsiella pneumoniae | |
| Bacteria | High | Salmonella enterica non typhoidal serovars | |
| Bacteria | High | Shigella dysenteriae serotype 1 | |
| Bacteria | High | Vibrio cholerae serogroup 0139 | |
| Bacteria | High | Yersinia Pestis | |
| Coronaviridae | High | Subgenus Sarbecovirus | Subgenus Sarbecovirus |
| Filoviridae | High | Orthoebolavirus sudanense | |
| Filoviridae | High | Orthoebolavirus zairense | Orthoebolavirus zairense |
| Filoviridae | High | Orthomarburgvirus marburgense | |
| Flaviviridae | High | Orthoflavivirus denguei | Orthoflavivirus denguei |
| Flaviviridae | High | Orthoflavivirus flavi | |
| Flaviviridae | High | Orthoflavivirus zikaense | Orthoflavivirus zikaense |
| Flaviviridae | High | | Orthoflavivirus nilense |
| Hantaviridae | High | | |
| Nairoviridae | High | Orthonairovirus haemorrhagiae | Orthonairovirus haemorrhagiae |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H1 | Alphainfluenzavirus Influenzae H1 |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H2 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H3 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H5 | Alphainfluenzavirus Influenzae H5 |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H6 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H7 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H10 | |
| Paramyxoviridae | High | | |
| Phenuiviridae | High | | Phlebovirus riftense |
| Poxviridae | High | Orthopoxvirus monkeypox | Orthopoxvirus monkeypox |
| Togaviridae | High | Alphavirus chikungunya | Alphavirus chikungunya |
| Picornaviridae | Medium | Enterovirus coxsackiepol | |
| Picornaviridae | Medium | | Enterovirus alphacoxsackie 71 |
| Picornaviridae | Medium | | Enterovirus deconjecti 68 |
| Retroviridae | Medium | Lentivirus humimdef1 | Lentivirus humimdef1 |
| Adenoviridae | Low-Medium | | Recombinant mastadenovirus |
| Pneumoviridae | Low-Medium | | Metapneumovirus hominis |
| Anelloviridae | Low | | |
| Astroviridae | Low | | Mamastrovirus virginiaense |
| Bornaviridae | Low | | |
| Hepadnaviridae | Low | | |
| Hepeviridae | Low | | Paslahepevirus balayani genotype 3 |
| Herpesviridae | Low | | |
| Papillomaviridae | Low | | |
| Parvoviridae | Low | | Protoparvovirus carnivoran |
| Peribunyaviridae | Low | | |
| Picobirnaviridae | Low | | Orthopicobimavirus hominis |
| Polyomaviridae | Low | | |
| Rhabdoviridae | Low | | Genus Vesiculovirus |
| Sedoreoviridae | Low | | Genus Rotavirus |
| Spinareoviridae | Low | | Orthoreovirus mammalis |

Region of the Americas

The priority pathogens specific to the Region of the Americas are Orthohantavirus sinnombreense, and Alphavirus venezuelan. All three priority Orthoflaviviruses (denguei, encephalitidis, and zikaense) are endemic in the Region. The prototype viruses specific to the Region of the Americas are: Mammarenavirus juninense and Orthobunyavirus oropoucheense.

Table 9. Selected Priority Pathogens with circulation in the WHO Americas Region

| Family | PHEIC risk | Priority Pathogens | Prototype Pathogens |
|------------------|------------|--|--|
| Arenaviridae | High | | Mammarenavirus juninense |
| Bacteria | High | Klebsiella pneumoniae | |
| Bacteria | High | Salmonella enterica non typhoidal serovars | |
| Bacteria | High | Yersinia Pestis | |
| Coronaviridae | High | Subgenus Sarbecovirus | Subgenus Sarbecovirus |
| Filoviridae | High | | |
| Flaviviridae | High | Orthoflavivirus denguei | Orthoflavivirus denguei |
| Flaviviridae | High | Orthoflavivirus flavi | |
| Flaviviridae | High | Orthoflavivirus zikaense | Orthoflavivirus zikaense |
| Flaviviridae | High | | Orthoflavivirus encephalitidis |
| Flaviviridae | High | | Orthoflavivirus nilense |
| Hantaviridae | High | Orthohantavirus sinnombreense | Orthohantavirus sinnombreense |
| Nairoviridae | High | | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H1 | Alphainfluenzavirus Influenzae H1 |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H2 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H3 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H5 | Alphainfluenzavirus Influenzae H5 |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H6 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H7 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H10 | |
| Paramyxoviridae | High | | |
| Phenuiviridae | High | | |
| Poxviridae | High | Orthopoxvirus monkeypox | Orthopoxvirus monkeypox |
| Poxviridae | High | | Orthopoxvirus vaccinia |
| Togaviridae | High | Alphavirus chikungunya | Alphavirus chikungunya |
| Togaviridae | High | Alphavirus venezuelan | Alphavirus venezuelan |
| Picornaviridae | Medium | | Enterovirus alphacoxsackie 71 |
| Picornaviridae | Medium | | Enterovirus deconjecti 68 |
| Retroviridae | Medium | Lentivirus humimdefl | Lentivirus humimdefl |
| Adenoviridae | Low-Medium | | Mastadenovirus blackbeardi serotype 14 |
| Adenoviridae | Low-Medium | | Recombinant mastadenovirus |
| Pneumoviridae | Low-Medium | | Metapneumovirus hominis |
| Anelloviridae | Low | | |
| Astroviridae | Low | | Mamastrovirus virginiaense |
| Bornaviridae | Low | | |
| Hepadnaviridae | Low | | |
| Hepeviridae | Low | | Paslahepevirus balayani genotype 3 |
| Herpesviridae | Low | | |
| Papillomaviridae | Low | | |
| Parvoviridae | Low | | Protoparvovirus camivoran |
| Peribunyaviridae | Low | | Orthobunyavirus oropoucheense |
| Picobirnaviridae | Low | | Orthopicobirnavirus hominis |
| Polyomaviridae | Low | | |
| Rhabdoviridae | Low | | Genus Vesiculovirus |
| Sedoreoviridae | Low | | Genus Rotavirus |
| Spinareoviridae | Low | | Orthoreovirus mammalis |

Eastern Mediterranean Region

Subgenus merbecoviruses and enterovirus coxsackiepol are particular priorities in the Eastern Mediterranean Region. Bacterial pathogens are also significant including Vibrio cholera O139 and Shigella dysenteriae serotype 1.

Table 10. Selected Priority Pathogens with circulation in the WHO Eastern Mediterranean Region

| Family | PHEIC risk | Priority Pathogens | Prototype Pathogens |
|------------------|------------|--|------------------------------------|
| Arenaviridae | High | | |
| Bacteria | High | Klebsiella pneumoniae | |
| Bacteria | High | Salmonella enterica non typhoidal serovars | |
| Bacteria | High | Shigella dysenteriae serotype 1 | |
| Bacteria | High | Vibrio cholerae serogroup 0139 | |
| Coronaviridae | High | Subgenus Merbecovirus | Subgenus Merbecovirus |
| Coronaviridae | High | Subgenus Sarbecovirus | Subgenus Sarbecovirus |
| Filoviridae | High | Orthoebolavirus sudanense | |
| Flaviviridae | High | Orthoflavivirus denguei | Orthoflavivirus denguei |
| Flaviviridae | High | | Orthoflavivirus nilense |
| Hantaviridae | High | | |
| Nairoviridae | High | Orthonairovirus haemorrhagiae | Orthonairovirus haemorrhagiae |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H1 | Alphainfluenzavirus Influenzae H1 |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H2 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H3 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H5 | Alphainfluenzavirus Influenzae H5 |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H6 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H7 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H10 | |
| Paramyxoviridae | High | | |
| Phenuiviridae | High | | |
| Poxviridae | High | Orthopoxvirus monkeypox | Orthopoxvirus monkeypox |
| Poxviridae | High | | Orthopoxvirus vaccinia |
| Togaviridae | High | | |
| Picornaviridae | Medium | Enterovirus coxsackiepol | |
| Picornaviridae | Medium | | Enterovirus alphacoxsackie 71 |
| Picornaviridae | Medium | | Enterovirus deconjecti 68 |
| Retroviridae | Medium | Lentivirus humimdefl | Lentivirus humimdefl |
| Adenoviridae | Low-Medium | | Recombinant mastadenovirus |
| Pneumoviridae | Low-Medium | | Metapneumovirus hominis |
| Anelloviridae | Low | | |
| Astroviridae | Low | | Mamastrovirus virginiaense |
| Bornaviridae | Low | | |
| Hepadnaviridae | Low | | |
| Hepeviridae | Low | | Paslahepevirus balayani genotype 3 |
| Herpesviridae | Low | | |
| Papillomaviridae | Low | | |
| Parvoviridae | Low | | Protoparvovirus camivoran |
| Peribunyaviridae | Low | | |
| Picobirnaviridae | Low | | Orthopicobirnavirus hominis |
| Polyomaviridae | Low | | |
| Rhabdoviridae | Low | | Genus Vesiculovirus |
| Sedoreoviridae | Low | | Genus Rotavirus |
| Spinareoviridae | Low | | Orthoreovirus mammalis |

European Region

In addition to the priority pathogens with global distribution, Orthonairovirus haemorrhagiae occurs in the European Region. The prototypes Orthoflavivirus encephalitis and Orthobornavirus bornaense are mostly found in the European Region.

Table 11. Selected Priority Pathogens with circulation in the WHO European Region

| Family | PHEIC risk | Priority Pathogens | Prototype Pathogens |
|------------------|------------|---|------------------------------------|
| Arenaviridae | High | | |
| Bacteria | High | <i>Klebsiella pneumoniae</i> | |
| Bacteria | High | <i>Salmonella enterica non typhoidal serovars</i> | |
| Coronaviridae | High | Subgenus Sarbecovirus | Subgenus Sarbecovirus |
| Filoviridae | High | | |
| Flaviviridae | High | Orthoflavivirus denguei | Orthoflavivirus denguei |
| Flaviviridae | High | | Orthoflavivirus encephalitis |
| Flaviviridae | High | | Orthoflavivirus nilense |
| Hantaviridae | High | Orthohantavirus hantanense | |
| Nairoviridae | High | Orthonairovirus haemorrhagiae | Orthonairovirus haemorrhagiae |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H1 | Alphainfluenzavirus Influenzae H1 |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H2 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H3 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H5 | Alphainfluenzavirus Influenzae H5 |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H6 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H7 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H10 | |
| Paramyxoviridae | High | | |
| Phenuiviridae | High | | |
| Poxviridae | High | Orthopoxvirus monkeypox | Orthopoxvirus monkeypox |
| Togaviridae | High | | |
| Picornaviridae | Medium | | Enterovirus alphacoxsackie 71 |
| Picornaviridae | Medium | | Enterovirus deconjecti 68 |
| Retroviridae | Medium | Lentivirus humimdefl | Lentivirus humimdefl |
| Adenoviridae | Low-Medium | | Recombinant mastadenovirus |
| Pneumoviridae | Low-Medium | | Metapneumovirus hominis |
| Anelloviridae | Low | | |
| Astroviridae | Low | | Mamastrovirus virginiaense |
| Bornaviridae | Low | | Orthobornavirus bornaense |
| Hepadnaviridae | Low | | |
| Hepeviridae | Low | | Paslahepevirus balayani genotype 3 |
| Herpesviridae | Low | | |
| Papillomaviridae | Low | | |
| Parvoviridae | Low | | Protoparvovirus camivoran |
| Peribunyaviridae | Low | | |
| Picobirnaviridae | Low | | Orthopicobirnavirus hominis |
| Polyomaviridae | Low | | |
| Rhabdoviridae | Low | | Genus Vesiculovirus |
| Sedoreoviridae | Low | | Genus Rotavirus |
| Spinareoviridae | Low | | Orthoreovirus mammalis |

South-East Asia Region

Bacterial pathogens are priorities in the South-East Asia Region including *Vibrio cholera* O139 and *Shigella dysenteriae* serotype 1. The priority pathogens Henipavirus nipahense and Bandavirus dabiense are endemic in the South-East Asia Region, as are the mosquito-borne Orthoflavivirus denguei and zikaense, and Alphavirus chikungunya. The prototype pathogen Orthohepadnavirus hominoidei genotype C is most common in the South-East Asia Region.

Table 12. Selected Priority Pathogens with circulation in the WHO South East Asia Region

| Family | PHEIC risk | Priority Pathogens | Prototype Pathogens |
|------------------|------------|---|---|
| Arenaviridae | High | | |
| Bacteria | High | <i>Klebsiella pneumoniae</i> | |
| Bacteria | High | <i>Salmonella enterica non typhoidal serovars</i> | |
| Bacteria | High | <i>Shigella dysenteriae</i> serotype 1 | |
| Bacteria | High | <i>Vibrio cholerae</i> serogroup 0139 | |
| Coronaviridae | High | Subgenus Sarbecovirus | Subgenus Sarbecovirus |
| Filoviridae | High | | |
| Flaviviridae | High | Orthoflavivirus denguei | Orthoflavivirus denguei |
| Flaviviridae | High | Orthoflavivirus zikaense | Orthoflavivirus zikaense |
| Flaviviridae | High | | Orthoflavivirus nilense |
| Hantaviridae | High | | |
| Nairoviridae | High | | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H1 | Alphainfluenzavirus Influenzae H1 |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H2 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H3 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H5 | Alphainfluenzavirus Influenzae H5 |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H6 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H7 | |
| Orthomyxoviridae | High | Alphainfluenzavirus Influenzae H10 | |
| Paramyxoviridae | High | Henipavirus nipahense | Henipavirus nipahense |
| Phenuiviridae | High | Bandavirus dabiense | Bandavirus dabiense |
| Poxviridae | High | Orthopoxvirus monkeypox | Orthopoxvirus monkeypox |
| Poxviridae | High | | Orthopoxvirus vaccinia |
| Togaviridae | High | Alphavirus chikungunya | Alphavirus chikungunya |
| Picornaviridae | Medium | Enterovirus coxsackiepol | |
| Picornaviridae | Medium | | Enterovirus alphacoxsackie 71 |
| Picornaviridae | Medium | | Enterovirus deconjecti 68 |
| Retroviridae | Medium | Lentivirus humimdefl | Lentivirus humimdefl |
| Adenoviridae | Low-Medium | | Recombinant mastadenovirus |
| Pneumoviridae | Low-Medium | | Metapneumovirus hominis |
| Anelloviridae | Low | | |
| Astroviridae | Low | | Mamastrovirus virginiaense |
| Bornaviridae | Low | | |
| Hepadnaviridae | Low | | Orthohepadnavirus hominoidei genotype C |
| Hepeviridae | Low | | Paslahepevirus balayani genotype 3 |
| Herpesviridae | Low | | |
| Papillomaviridae | Low | | |
| Parvoviridae | Low | | Protoparvovirus camivoran |
| Peribunyaviridae | Low | | |
| Picobirnaviridae | Low | | Orthopicobirnavirus hominis |
| Polyomaviridae | Low | | |
| Rhabdoviridae | Low | | Genus Vesiculovirus |
| Sedoreoviridae | Low | | Genus Rotavirus |
| Spinareoviridae | Low | | Orthoreovirus mammalis |

Western Pacific Region

Influenza and Subgenus sarbecoviruses are a high priority in the Western Pacific region. The priority pathogens henipavirus nipahense, Orthohantavirus hantanense and Bandavirus dabieense are endemic in the Western Pacific Region, as are the mosquito-borne Orthoflavivirus denguei and Alphavirus chikungunya.

Table 13. Selected Priority Pathogens with circulation in the WHO Western Pacific Region

| Family | Family Risk | Priority Pathogens | Prototype Pathogens |
|---|-------------|--|--|
| Arenaviridae | High | | |
| Bacteria | High | <i>Vibrio cholera</i> (O139) <i>Salmonella enterica</i> non typhoidal serovars <i>Klebsiella pneumoniae</i> | |
| Bunyavirales Nairoviridae | High | Orthonairovirus haemorrhagiae | Orthonairovirus haemorrhagiae |
| Bunyavirales Bunyavirales Hantaviridae | High | Orthohantavirus hantanense | |
| Bunyavirales Phenuiviridae | High | Bandavirus dabieense | Bandavirus dabieense |
| Coronaviridae | High | Subgenus Sarbecoviruses | Subgenus Sarbecoviruses |
| Filoviridae | High | | |
| Flaviviridae | High | Orthoflavivirus denguei Orthoflavivirus zikaense | Orthoflavivirus denguei Orthoflavivirus zikaense Orthoflavivirus nilense encephalitis |
| Orthomyxoviridae | High | Alphainfluenzavirus influenzae (H1N1), Alphainfluenzavirus influenzae (H2Nx), Alphainfluenzavirus influenzae (H3N2), Alphainfluenzavirus influenzae (H5Nx), Alphainfluenzavirus influenzae (H6Nx), Alphainfluenzavirus influenzae (H7Nx), Alphainfluenzavirus influenzae (H10Nx) | Alphainfluenzavirus influenzae (H1N1), Alphainfluenzavirus influenzae (H5Nx), |
| Paramyxoviridae | High | Henipavirus nipahense Orthopoxvirus vaccinia | Henipavirus nipahense Orthopoxvirus vaccinia |
| Poxviridae | High | Orthopoxvirus monkeypox | Orthopoxvirus monkeypoxOrthopoxvirus vaccinia |
| Tagaviridae | High | Alphavirus chikungunya | Alphavirus chikungunya |
| Picornaviridae | Medium | Human polioviruses | Enterovirus D68, (EV-D68) Enterovirus A71 (EV-A71) |
| Retroviridae | Medium | Human immunodeficiency virus 1 (HIV-1) | Human immunodeficiency virus 1 (HIV-1) |
| Adenoviridae | Low-Medium | | Human mastadenovirus B |
| Pneumoviridae | Low-Medium | | Metapneumovirus hominis |
| Astroviridae | Low | | Mamastrovirus 9 (GII.B-human) |
| Bornaviridae | Low | | |
| Bunyavirales Peribunyavirus | Low | | |
| Hepadnaviridae | Low | | |
| Hepeviridae | Low | | Paslahepevirus balayani, genotype 3 |
| Parvoviridae | Low | | Carnivore protoparvoviruses (CPV) |
| Picobimaviridae | Low | | Human picobimavirus |
| Reovirales Spinareoviridae Sedoreoviridae | Low | | Orthoreovirus mammalis Genus Rotavirus |
| Rhabdoviridae | Low | | Genus Vesiculovirus |

KEY GLOBAL COLLABORATIVE RESEARCH ACROSS FAMILIES AND PATHOGENS

The WHO's scientific framework for pandemic preparedness emphasizes a comprehensive approach to research and development⁸. By focusing on entire pathogen families and Priority and Prototype pathogens, the strategy aims to create generalizable knowledge and tools that can be rapidly adapted to emerging threats. This framework underscores the importance of global collaboration, sustained support, and equitable access. Implementing these key research actions will significantly enhance the world's ability to detect, prevent, and respond to potential pandemic threats. Coordinating and accelerating global research must promote universal values. Regarding a collaborative effort to ensure access to MCMs during pandemics, some have emphasized the importance of speed and sometimes cost in responding to future pandemics. It is equally important to take a broader view that recognizes the primary importance of quality, equity in access, and trust in the products' safety and efficacy. As a community, we need to explore the different scientific challenges openly and broadly.

Collaboration, collaboration, collaboration...

Collaborative Open Research Consortium (CORC) for each Priority Pathogen Family

A key action for improving global research collaboration and, advance research preparedness and response to epidemics and pandemics include establishing a CORC for each Family. Each CORC is

supported by one or more WHO Collaborative Centers, using an agreed approach and common goals.

Decentralized Approach: the CORCs, distributed globally, will be implemented using a decentralized structure that promotes equitable participation from researchers in high-, middle-, and low-income countries, particularly those from locations where pathogens are known to circulate.

The aims of the CORCs

This Consortia approach aims to leverage scientific advancements and global collaboration to ensure rapid, equitable, and effective research and development. The CORC initiative aims to establish a network of international research consortia focused on priority Families, Priority pathogens and Prototype pathogens. This concept builds on the WHO's scientific framework for pandemic research preparedness and leverages global scientific expertise to enhance our collective ability to detect, prevent, and respond to emerging pathogen threats⁹.

A concerted parallel effort to advance research in all priority Families

CORCs aim to promote collaborative approaches to: (i) assess and characterize the diversity of pathogens in each Family, their evolution and potential for zoonotic spill-over events; (ii) promote targeted basic research, and (iii) support the R&D of MCMs. Each CORC will operate in parallel with the others to accelerate the

⁸ <https://www.who.int/news-room/events/detail/2024/01/09/default-calendar/a-scientific-framework-for-epidemic-and-pandemic-research-preparedness>

⁹ <https://journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1010805>

development of MCMs, while establishing sustainable processes aiming to improve research preparedness and response.

A navigator's approach to guide research efforts

The navigator's approach In the context of R&D for pandemic preparedness this approach entails knowing the destination (equitable access to effective MCMs for epidemic and pandemic response) and the best route to get there (collaborative Research and R&D approaches).

The focus of this objective is on developing comprehensive Roadmaps and TPPs while building the necessary infrastructure for sustained global cooperation in research and development.

Global R&D and Innovation Roadmaps for each Family. These Roadmaps identify the knowledge gaps and research priorities in all areas of pandemic preparedness research, including enabling research. These Roadmaps function as strategic blueprints, regularly updated, guiding crucial research initiatives focused on each identified priority Viral or Bacterial Family. They draw on expertise from scientists and experts across the world. These roadmaps are debated openly and benefit from inputs from various stakeholders.

WHO priority Family-specific Target Product Profile (TPPs) for MCMs. For all Priority Pathogens Families, these TPPs will help to guide research directed toward the development of one or more prototype vaccines, therapeutics and diagnostics. These TPPs will emphasize research needs that may be generalizable both within and outside of a given Family. These Family-specific TPPs are to be distinguished from TPPs that are developed for specific products intended

to address individual pathogens. The Family TPPs provide the vital public health specifications and attributes necessary in formulating vaccines, treatments, or diagnostic tests with a generalizability approach in mind.

Preparing for the inevitable.

By prioritizing research on entire Families as opposed to a handful of individual Priority Pathogens, this strategy bolsters the capability to respond efficiently to unforeseen variants, emerging pathogens, zoonotic transmissions, and unknown threats such as 'Pathogen X.'

It also emphasizes the need for prompt identification and characterization of emerging threats, the streamlining of global R&D efforts, via collaborative and efficient research Roadmaps and the integration of research into outbreak and pandemic response.

Depending on what Pathogen X turns out to be, there may be gaps in the pre-pandemic research, and activities outlined in this document aim to promptly fill these knowledge gaps.

The lessons drawn from the COVID-19 pandemic underscore the importance of continued investment in basic, clinical, and implementation research, technology development, and engineering innovation. A brief summary is presented below.

Pathogen Discovery and Surveillance

Basic research into infectious disease is the foundation of design for applied research. Even when MCMs exist, the relevance of these MCMs needs to be assured in the event of natural evolution in the face of selective pressure. Whilst laboratory isolates are invaluable to MCMs development, being able to reach into

at-risk populations to obtain meaningful surveillance information is essential for an applied research programme.

International networking will be essential to ensure at-risk populations have assurance that developing MCMs remain relevant to the contemporary risk. This objective will require in-country collaboration to monitor both in humans and potential zoonotic or other reservoirs of infectious agents. Coordinated and collaborative viral monitoring in hotspot regions is a priority. Initiatives aiming to enhance genomic sequencing, bioinformatics, and data sharing to rapidly identify and characterize in real-time novel pathogen threats globally.

Targeted basic research

The genetic and molecular composition of an infectious disease agent provides invaluable data to inform and design MCMs. Without basic research, MCMs design is at risk of becoming outdated and at worse, redundant in the face of natural evolution. Sharing the outcome and potential rewards of such basic research will be essential in ensuring that meaningful collaborations are formed and endure even in the event of an epidemic or a new pandemic. Sharing resources will also be essential to the downstream applied research.

Critical needs include improved understanding of pathogen microbiology (i.e., virology and bacteriology), pathogenesis (e.g., virulence, pathogen-host interactions) and immunology (including protective immune responses against different types of pathogens). Improved high-throughput tools to apply cutting-edge science to pandemic research will increase its impact. Understanding the roles of different arms of the immune system in protection, and how to induce immune

responses with particular specificities and memory phenotypes, has the potential to lead to more effective pandemic vaccines. Rapid detection and isolation of human monoclonal antibodies is at the nexus of reagents needed for developing vaccines and diagnostics and the development of potential therapeutic MCMs.

Translational Research and Product Development

Equitable access to knowledge of discoveries, research methods and manufacturing methods is important to address local problems before they become global.

For example, developing of reagents and tools and MCMs development (vaccines, therapeutics, and diagnostics) using cutting-edge technologies like AI, structural biology, and high-throughput screening. Further research is expected to improve predictions of how genetic sequences lead to pathogenicity and antigenicity (termed “functional viromics”). These methods combined with high throughput synthetic biology will enable rapid execution of design-build-validate cycles to aid in designing antigens that will induce the desired immune responses.

Equitable access to knowledge of discoveries, research methods and manufacturing is critical to address local problems before they become global. Animal models enable the study of viral pathogenesis and vaccines in live organisms containing the full range of cell and organ types, including the diverse elements of the immune system.

Target Product Profiles and Vaccine Development

To maximize pandemic preparedness, it will be important to emphasize

generalizability and high-priority pathogen Families and prototypes in infrastructure development. An example of considerations to bear in mind is presented here.

For all priority Families, a WHO pathogen family-specific target product profile (TPP) will help to guide research directed toward the development of one or more prototype vaccines, therapeutics and diagnostics. These TPPs will emphasize research needs that may be generalizable both within and outside of a pathogen Family. These Family-based TPPs are to be distinguished from TPPs that are developed for products intended to address individual pathogens. The Family TPPs provide the vital specifications and attributes necessary in formulating vaccines, treatments, or diagnostic tests with a generalizability approach in mind.

Monitor the pipeline of candidate MCMs and prioritize for evaluation during outbreaks

- A critical activity in delivering effective medical countermeasures is the dissemination of the best available knowledge and evidence on the clinical development pipeline of candidate vaccines and treatments.
- This is achieved by meticulously tracking the progress of promising candidate products throughout the clinical research pipeline.

Product development and production

Further work on vaccine platforms, and in particular, identification of vaccine platforms that induce the types of immune responses likely to be important for members of an individual pathogen Family, could help to maximize protective responses. To maximize pandemic preparedness, to the extent possible, it will be important to emphasize generalizability and high-priority pathogen Families and prototypes in

infrastructure development.

Finding mechanisms to make small-market MCMs economically feasible and sustainable would be a more productive way to have vaccines readily available for future potential pandemic threats. GMP material is needed to perform clinical studies during epidemics, and it is considered important to fund and study candidate MCMs for Families with pandemic potential, even if short-term public health needs are less clear.

The ultimate goal (and pre-pandemic stopping point) of vaccine development for each pathogen Family will need to be individually considered. For example, if regulators indicated that phase 1 or phase 2 data for a prototype vaccine could support going directly into phase 3 with a pandemic vaccine, this could be an argument for obtaining phase 1 or phase 2 data before the next pandemic. Decisions about performing phase 3 studies would likely depend on independent reviews, regulatory science, and various regulatory pathways.

Independent expert evaluation of various candidate MCMs will contribute to achieving this. Unless there is substantial progress on broadly protective vaccines (though it's unlikely that an effective vaccine will be on the shelf when a pandemic occurs), stockpiling of candidate vaccines is unlikely to be highly successful or cost-effective.

Similar efforts and deliberations are important and will be promoted for Therapeutics and Diagnostics.

Through collaboration with at-risk countries, there is a need to help build the infrastructure to enable production and development of MCMs in at-risk locations, as appropriate.

Clinical Trial Infrastructure and Research Deployment Capacity

Outbreaks often occur in areas where these do not exist, thus efforts aiming to facilitate the development of research capability are needed. Those efforts must include technology sharing and transfer and, access to funding sources to bring those resources to at-risk locations¹⁰. Building infrastructure for simple clinical trials integrated into outbreak response and ensuring efficient research deployment of MCMs¹¹.

WHO independent Expert Groups provide advice on which candidate MCMs should be given priority for evaluation in the context of an outbreak.

Harmonization of research protocols and tools are being made to standardize viral assays, animal models, reagents, and CORE protocols for clinical evaluation across Families¹² to streamline research during epidemics and pandemics. This proactive approach facilitates the agreement on clinical trial designs and the selection of investigational products and candidates to prioritize in clinical trials during an outbreak.

In the context of epidemics and pandemics, the WHO R&D Blueprint for Epidemics and other stakeholders collaboratively co-Sponsors clinical trials integrated into the outbreak response for MCMs with Ministries of Health.

Valid and rigorous observational effectiveness studies are needed, especially during an epidemic or outbreak, to advance evidence-based programmatic and policy decisions¹³.

¹⁰ [chrome-extension://efaidnbmnnnibpcajpcgiclfefindmkaj/https://www.who.int/docs/default-source/blue-print/working-group-for-vaccine-evaluation-\(4th-consultation\)/api-guidelines-online-consultation.pdf](https://www.who.int/docs/default-source/blue-print/working-group-for-vaccine-evaluation-(4th-consultation)/api-guidelines-online-consultation.pdf)

¹¹ [chrome-extension://efaidnbmnnnibpcajpcgiclfefindmkaj/https://www.who.int/docs/default-source/blue-print/working-group-for-vaccine-evaluation-\(4th-consultation\)/api-guidelines-online-consultation.pdf](https://www.who.int/docs/default-source/blue-print/working-group-for-vaccine-evaluation-(4th-consultation)/api-guidelines-online-consultation.pdf)

Accelerating evaluation and deployment of MCMs in the context of epidemics and pandemics

In the context of outbreaks, the aim is to provide a blueprint that contributes to the rapid start of simple trials integrated into initial outbreak response (randomized trials or randomization during deployment). It also incorporates elements to facilitate the rapid deployment of candidate MCMs (as expanded access/compassionate use) if evidence is available/ is emerging that they are efficacious and safe.

The availability of candidate MCMs is one of the essential steps to evaluate candidate MCMs and generate data required for regulatory review, eventual licensure, and policy recommendation, considering the limited time-span to evaluate field efficacy during outbreaks caused by infrequent and unpredictable diseases outbreaks.

In addition, greater global coordination and a new mechanism for the supply, financing, and maintenance of candidate vaccines in preparation for future outbreaks of priority pathogens is needed.

Through these efforts candidate MCMs will be promptly evaluated according to innovative simple protocols, which meet the highest scientific and ethical standards, and which generate results to inform regulatory assessment and policy decisions, while ensuring that national and individual interests are respected. Such simple protocols can be integrated in the outbreak response. In addition, the collaborative approach pursued puts the Ministries of Health at the core of all research efforts during outbreaks.

¹² <https://www.science.org/doi/10.1126/scitranslmed.aat0360>

¹³ <https://www.who.int/news-room/events/detail/2023/09/14/default-calendar/improving-vaccine-effectiveness-studies--a-vital-step-before-the-next-pandemic>

Table 14. “Translation table” MSL39 Viral Species name and previous, perhaps more familiar, names of the various viruses.

| Family | Previous Name | MSL39 Viral Species Name |
|---------------|--|--|
| Adenoviridae | Adenovirus B | Mastadenovirus blackbeardi |
| Adenoviridae | Human mastadenovirus E | Mastadenovirus exoticum |
| Arenaviridae | Cardamones variant Wenzhou virus (CVWV) | Mammarenavirus cardamones |
| Arenaviridae | Chapare virus | Mammarenavirus chapareense |
| Arenaviridae | Junin virus | Mammarenavirus juninense |
| Arenaviridae | Lassa Fever virus | Mammarenavirus lassaense |
| Arenaviridae | Lujo virus | Mammarenavirus lujoense |
| Arenaviridae | Lymphocytic choriomeningitis virus | Mammarenavirus choriomeningitis |
| Arenaviridae | Machupo virus | Mammarenavirus machupoense |
| Arenaviridae | Venezuelan Hemorrhagic Fever virus | Mammarenavirus guanaritoense |
| Arteriviridae | Simian hemorrhagic fever virus | Deltaarterivirus hemfev |
| Astroviridae | Mamastrovirus 10 - mink | Mamastrovirus mustelae |
| Astroviridae | Mamastrovirus 13 - ovine | Mamastrovirus ovis |
| Astroviridae | Mamastrovirus 9 | Mamastrovirus virginiaense |
| Bornaviridae | Mammalian Bornavirus 1 (BoDV-1) | Orthobornavirus bornaense |
| Bornaviridae | Variegated squirrel bornavirus 1 (VSBV-1) | Orthobornavirus sciuri |
| Coronaviridae | Alpha recombinant CoV | Recombinant alphacoronavirus |
| Coronaviridae | Canine coronavirus-human pneumonia-2018 (CCoV-HuPn-2018) | Alphacoronavirus suis (CCoV-HuPn-2018) |
| Coronaviridae | Human coronavirus NL63 (Bat) | Alphacoronavirus amsterdamense |
| Coronaviridae | Middle East Respiratory Syndrome Coronavirus | Subgenus Merbecovirus |
| Coronaviridae | Porcine deltacoronavirus PDCoV | Deltacoronavirus (PDCoV) |
| Coronaviridae | Porcine hemagglutinating encephalomyelitis virus | Betacoronavirus gravedinis (PHEV) |
| Coronaviridae | Severe Acute Respiratory Syndrome coronavirus | Subgenus Sarbecovirus |
| Coronaviridae | Swine acute diarrhea syndrome coronavirus (SADS-CoV) | Alphacoronavirus porci |
| Filoviridae | Bombali viruss | Orthoebolavirus bombaliense |
| Filoviridae | Ebola virus | Orthoebolavirus zairense |
| Filoviridae | Huángjiǎo virus | Thamnovirus thamnaconi |
| Filoviridae | Lloviu virus | Cuevavirus lloviuense |
| Filoviridae | Marburg virus | Orthomarburgvirus marburgense |
| Filoviridae | Mengla virus | Dianlovirus menglaense |
| Filoviridae | Reston virus | Orthoebolavirus restonense |
| Filoviridae | Sudan ebolavirus | Orthoebolavirus sudanense |
| Filoviridae | Xilang virus | Striavirus antennarii |
| Flaviviridae | Dengue virus | Orthoflavivirus denguei |
| Flaviviridae | Ilheus virus | Orthoflavivirus ilheusense |
| Flaviviridae | Japanese encephalitis virus | Orthoflavivirus japonicum |
| Flaviviridae | Jingmen tick virus | Jingmenvirus |
| Flaviviridae | Rocio virus | Orthoflavivirus rocio |
| Flaviviridae | Spondweni virus | Orthoflavivirus spondweni |
| Flaviviridae | Tick-borne encephalitis virus | Orthoflavivirus encephalitis |
| Flaviviridae | Usutu virus | Orthoflavivirus usutuense |
| Flaviviridae | Wesselsbron virus | Orthoflavivirus wesselsbronense |
| Flaviviridae | West Nile virus | Orthoflavivirus nilense |
| Flaviviridae | Yellow fever virus | Orthoflavivirus flavi |
| Flaviviridae | Zika virus | Orthoflavivirus zikaense |

| Family | Previous Name | MSL39 Viral Species Name |
|------------------|--|---|
| Hantaviridae | Hantaan orthohantavirus | Orthohantavirus hantanense |
| Hantaviridae | Hantaan virus | Orthohantavirus hantanense |
| Hantaviridae | Sin Nombre virus | Orthohantavirus sin Nombreense |
| Hepadnaviridae | Domestic Cat Orthohepadnavirus | Orthohepadnavirus felisdomestici |
| Hepadnaviridae | Hepatitis B virus genotype C | Orthohepadnavirus hominoidi genotype C |
| Hepadnaviridae | Pomona bat Orthohepadnavirus | Orthohepadnavirus pomi |
| Hepeviridae | Hepatitis E virus | Paslahepevirus balayani |
| Nairoviridae | Crimean-Congo hemorrhagic fever virus (CCHF) | Orthonaivirus haemorrhagiae |
| Orthomyxoviridae | Influenza A | Alphainfluenzavirus influenzae |
| Orthomyxoviridae | Influenza B | Betainfluenzavirus influenzae |
| Paramyxoviridae | Hendra virus | Henipavirus hendraense |
| Paramyxoviridae | Mapuera virus | Orthorubulavirus mapueraense |
| Paramyxoviridae | Menangle virus | Pararubulavirus menangleense |
| Paramyxoviridae | Nipah virus | Henipavirus nipahense |
| Paramyxoviridae | Sosuga virus | Pararubulavirus sosugaense |
| Parvoviridae | Canine parvovirus (CPV) | Amdoparvovirus canivoran |
| Parvoviridae | Canine protoparvovirus | Protoparvovirus canivoran |
| Parvoviridae | Primate erythroviruses (SPV) | Erythrovirus primate |
| Peribunyaviridae | Oropouche virus | Orthobunyavirus oropoucheense |
| Phenuiviridae | Phlebovirus Sandfly fever virus | Phlebovirus napoliense, Phlebovirus siciliense, Phlebovirus toscanaense |
| Phenuiviridae | Rift Valley Fever virus | Phlebovirus riftense |
| Phenuiviridae | SFTS virus | Bandavirus dabieense |
| Picobirnaviridae | Human picobirnavirus | Orthopicobirnavirus hominis |
| Picomaviridae | Enterovirus A71 (EV-A71) | Enterovirus alphacoxsackie 71 |
| Picomaviridae | Enterovirus D68 (EV-D68) | Enterovirus deconjecti 68 |
| Picomaviridae | Polio virus | Enterovirus coxsackiepol |
| Pneumoviridae | Avian metapneumovirus | Metapneumovirus avis |
| Pneumoviridae | Human metapneumovirus | Metapneumovirus hominis |
| Poxviridae | Alaskapox virus | Orthopoxvirus alaskapox |
| Poxviridae | Cowpox virus | Orthopoxvirus cowpox |
| Poxviridae | Monkeypox virus | Orthopoxvirus monkeypox |
| Poxviridae | Vaccinia virus | Orthopoxvirus vaccinia |
| Poxviridae | Variola virus | Orthopoxvirus variola |
| Reovirales | Mammalian orthoreovirus | Orthoreovirus mammalis |
| Retroviridae | GALV virus | Gammaretrovirus giblet |
| Retroviridae | Human immunodeficiency virus 1 (HIV-1) | Lentivirus humimdef1 |
| Retroviridae | Human immunodeficiency virus 2 (HIV-2) | Lentivirus humimdef2 |
| Retroviridae | Human T-lymphotropic virus 3 (HTLV-3) | Deltaretrovirus priTlym3 |
| Retroviridae | Simian immunodeficiency virus | Lentivirus simimdef |
| Rhabdoviridae | Genus Ledantivirus | Genus Ledantivirus |
| Rhabdoviridae | Genus Tibrovirus | Genus Tibrovirus |
| Rhabdoviridae | Genus Vesiculovirus | Genus Vesiculovirus |
| Togaviridae | Chikungunya virus | Alphavirus chikungunya |
| Togaviridae | Eastern equine encephalitis virus | Alphavirus eastern |
| Togaviridae | Madariaga virus | Alphavirus madariaga |
| Togaviridae | Mayaro virus | Alphavirus mayaro |
| Togaviridae | Onyong-nyong virus | Alphavirus onyong |
| Togaviridae | Ross River virus | Alphavirus rossriver |
| Togaviridae | Venezuelan equine encephalitis virus | Alphavirus venezuelan |

ANNEX 1. Scientists who evaluated the evidence related to 28 Viral Families and one core group of Bacteria, encompassing 1,652 pathogens

Adenoviridae

- 1. Mária Benkő, HUN-REN Veterinary Medical Research Institute, Hungary
- 2. Renald Gilbert, National Research Council, Canada
- 3. Gregory C. Gray, University of Texas Medical Branch, United States of America
- 4. Joanne Langley, Dalhousie University and IWK Health Centre, Canada
- 5. Thomas Lion, St.Anna Children´s Cancer Research Institute, Austria
- 6. Donald Seto, George Mason University, United States of America
- 7. Jim Wellehan, University of Florida College of Veterinary Medicine, United States of America

Anelloviridae

- 1. Mariet Feltkamp, Leiden University Medical Center, Netherlands
- 2. Jelle Matthijnssens, KU Leuven University, Rega Institute, Belgium
- 3. Joaquim Segalés, Institute of Agrifood Research and Technology, Spain
- 4. Lia van der Hoek, Amsterdam University Medical Centers, Netherlands

Arenaviridae

- 1. Remi Charrel, Aix Marseille Université, Hôpitaux Universitaires de Marseille, France
- 2. Juan Carlos de la Torre, The Scripps Research Institute, United States of America
- 3. Delia A. Enria, Instituto Nacional de Enfermedades Virales Humanas, Argentina
- 4. Stephan Günther, Bernhard-Nocht-Institute for Tropical Medicine, Germany
- 5. Sylvanus Okogbenin, Irrua Specialist Teaching Hospital and Ambrose Alli University, Nigeria
- 6. Jiro Yasuda, National Research Center for the Control and Prevention of Infectious Diseases, Nagasaki University, Japan

Astroviridae

- 1. Carlos Federico Arias, Instituto de Biotecnología, Universidad Nacional Autónoma de México, Mexico
- 2. Ákos Boros, University of Pécs, Medical School, Hungary
- 3. Paola de Benedictis, Istituto Zooprofilattico Sperimentale delle Venezie, Italy
- 4. Vijaykrishna Dhanasekaran, LKS Faculty of Medicine, University of Hong Kong, China
- 5. Susana Guix, University of Barcelona, Spain
- 6. Christine M Jonassen, Norwegian Institute of Public Health, Norway
- 7. Rosa Maria Pinto, University of Barcelona, Spain
- 8. Stacey Schultz-Cherry, St. Jude Children's Research Hospital, United States of America
- 9. David Wang, Washington University School of Medicine in St. Louis, United States of America
- 10. Huachen Maria Zhu, Li Ka Shing Faculty of Medicine, University of Hong Kong, China

Bacteria

- 1. Nicholas Feasay, Liverpool School of Tropical Medicine, United Kingdom
- 2. Benjamin Howden, Doherty Institute, University of Melbourne, Australia
- 3. Ann E Jerse, Uniformed Services University of the Health Sciences, United States of America
- 4. Gagandeep Kang, Vellore Christian Medical College Foundation, India
- 5. Sam Kariuki, Drugs for Neglected Diseases initiative (DNDi) Eastern Africa, Kenya
- 6. Myron M. Levine, University of Maryland School of Medicine, United States of America
- 7. Khitam Muhsen, School of Public Health, Tel Aviv University, Israel
- 8. Javier Pizarro-Cerda, Institut Pasteur, France
- 9. Firdausi Qadri, International Centre for Diarrheal Disease Research, Bangladesh
- 10. Christoph Tang, Sir William Dunn School of Pathology, University of Oxford, United Kingdom

Bornaviridae

- 1. Markus Bauswein, Institut für Klinische Mikrobiologie und Hygiene, Universitätsklinikum Regensburg
- 2. Germany
- 3. Martin Beer, Friedrich-Loeffler-Institut, Germany
- 4. Liv Bode, Virology and Infectious Diseases. Independent Senior Research Scientist, Germany
- 5. Daniel Dunia, University Toulouse, Purpan Hospital, France
- 6. Mady Hornig, Columbia University Mailman School of Public Health, United States of America
- 7. Susan Payne, retired, Texas A&M University, United States of America
- 8. Dennis Rubbenstroth, Federal Research Institute for Animal Health, Friedrich-Loeffler-Institut, Germany
- 9. Martin Schwemmle, Institute of Virology, Medical Center - University Freiburg, Germany
- 10. Barbara Schmidt, University Hospital Regensburg, Germany
- 11. Dennis Tappe, Bernhard Nocht Institute for Tropical Medicine, Germany
- 12. Keizo Tomonaga, Institute for Life and Medical Sciences (LiMe), Kyoto University, Japan
- 13. Peng Xie, The First Affiliated Hospital of Chongqing Medical University, China

Bunyavirales

- 1. Felicity Burt, University of the Free State, Faculty of Health Sciences, South Africa
- 2. Miles Carroll, University of Oxford, Pandemic Sciences Institute, United Kingdom
- 3. Nazif Elaldi, Sivas Cumhuriyet University, Turkey
- 4. Önder Ergönül, Koç University İş Bank Center for Infectious Diseases, Turkey
- 5. Roger Hewson, London School of Hygiene & Tropical Medicine, United Kingdom
- 6. Bushra Jamil, The Aga Khan University, Pakistan
- 7. Ali Mirazimi, Karolinska Institute Research area, Sweden
- 8. Mostafa Salehi-Vaziri, Pasteur Institute of Iran, Iran
- 9. Pragya D Yadav, Indian Council of Medical Research-National Institute of Virology, India

Coronaviridae

1. Gabriel Leung, LKS Faculty of Medicine, School of Public Health, The University of Hong Kong, China
2. Kyeong-Ok Chang, College of Veterinary Medicine, Kansas State University, United States of America
3. Malik Peiris, LKS Faculty of Medicine, School of Public Health, The University of Hong Kong, China
4. Stanley Perlman, University of Iowa, United States of America
5. Kanta Subbarao, University of Melbourne, Doherty Institute, Australia
6. Zhengli Shi, Wuhan Institute of Virology, Chinese Academy of Sciences, China
7. Tim Sheahan, University of North Carolina, School of Medicine, United States of America
8. Linfa Wang, Duke-NUS Medical School, Singapore

Filoviridae

1. Stephan Becker, Institut für Virologie, Philipps Universität Marburg, Germany
2. William Fischer, University of North Carolina School of Medicine, United States of America
3. Placide Mbala, Institut National de Recherche Biomédicale, Democratic Republic of Congo
4. Sabue Mulangu, Ridgeback Bio, Congo Republic
5. Nancy Sullivan, National Emerging Infectious Diseases Laboratories, Boston University, United States of America

Flaviviridae

1. Alan Barrett, University of Texas Medical Branch, United States of America
2. Sonja Best, National Institute of Allergy and Infectious Diseases, United States of America
3. Patricia Brasil, Instituto Nacional de Infectologia Evandro Chagas – FIOCRUZ, Brazil
4. Philippe Desprès, Université de La Réunion, La Réunion
5. Mike Diamond, Washington University School of Medicine, United States of America
6. Andrea Gamarnik, Fundación Instituto Leloir, Argentina
7. Eva Harris, University of California, United States of America
8. Laura Kramer, School of Public Health, State University of New York, United States of America
9. Ira Longini, University of Florida, United States of America
10. Neelika Malavige, University of Sri Jayewardenepura, Sri Lanka
11. Lee-Ching Ng, National Environmental Agency, Singapore

Hepadnaviridae

1. Marceline Djuidje Ngounoue Epse Ndzie, University of Yaoundé, Cameroon
2. Anand Gaurav, School of Health Sciences & Technology, India
3. Neeraj Masand, LLRM Medical College (Government), India
4. Salu Olumuyiwa Babalola, College of Medicine of the University of Lagos, Nigeria
5. Vaishali Patil, Charak School of Pharmacy, Chaudhary Charan Singh University, India
6. Saroj Verma, K.R. Mangalam University, India
7. Bryan Tegomoh, University of California, United States of America

Hepeviridae

1. Qiuwei Abdullah Pan, University Medical Center, Rotterdam, Netherlands
2. Kavita Lole, Indian Council of Medical Research-National Institute of Virology, India
3. Xiang-Jin Meng, Virginia Polytechnic Institute and State University, United States of America
4. Helene Norder, Gothenburg University, Sahlgrenska University Hospital, Sweden
5. Nicole Pavio, French Agency for Food, Environmental and Occupational Health and Safety, France
6. Michael A Purdy, Centers for Disease Control and Prevention, United States of America
7. Eike Steinmann, Faculty of Medicine, Ruhr University, Germany
8. Ting Wu, National Institute of Diagnostics and Vaccine Development in Infectious Diseases, Xiamen University, China

Herpesviridae

1. Lynn W. Enquist, Dept. Molecular Biology, Princeton University, United States of America
2. Herman Favoreel, Ghent University, Belgium
3. Klaus Frueh, Vaccine and Gene Therapy Institute of Oregon Health & Science University, United States of America
4. Felicia Goodrum, BIO5 Institute, University of Arizona, United States of America
5. Eain A. Murphy, SUNY - Upstate Medical University, United States of America
6. Klaus Osterrieder, Freie Universität Berlin, Germany
7. Daniel Streblow, Oregon Health & Science University, United States of America

Orthomyxoviridae

1. Christopher Chiu, Imperial College London, Hammersmith Campus, United Kingdom
2. Hideki Hasegawa, National Institute of Infectious Diseases, Influenza Virus Research Center, Japan
3. Nailya G. Klivleyeva, Research and Production Center for Microbiology and Virology, Kazakhstan
4. Florian Krammer, Icahn School of Medicine at Mount Sinai, United States of America
5. Tommy Lam, University of Hong Kong, China
6. Quynh Mai Le thi, National Institute of Hygiene and Epidemiology, Viet Nam
7. Kanta Subbarao, University of Melbourne, The Peter Doherty Institute for Infection and Immunity, Australia
8. Richard J. Webby, St Jude Children's Research Hospital, United States of America

Papillomaviridae

1. Paul KS Chan, The Chinese University of Hong Kong, China
2. Zigui Chen, The Chinese University of Hong Kong, China
3. Koenraad Van Doorslaer, University of Arizona College of Medicine, United States of America
4. Lisa Mirabello, National Cancer Institute, NIH, United States of America
5. Fanghui Zhao, Chinese Academy of Medical Sciences, China

Paramyxoviridae

- 1. Danielle Anderson, University of Melbourne, Australia
- 2. Dalan Bailey, The Pirbright Institute, United Kingdom
- 3. Anne Balkema-Bushann, Friedrich-Loeffler-Institut, Germany
- 4. Sandra Diederich, Friedrich-Loeffler-Institut, Germany
- 5. Gabor Kemenesi, University of Pécs, National Laboratory of Virology, Hungary
- 6. Benhur Lee, Icahn School of Medicine at Mount Sinai, United States of America
- 7. Piet Maes, Zoonotic infectious diseases unit, Rega Institute, Belgium
- 8. Mustafizur Rahman, International Center for Diarrhoeal Disease Research, Bangladesh

Parvoviridae

- 1. Eric Delwart, retired, UCSF, Vitalant Research Institute, United States of America
- 2. Anna-Maria Eis-Hübinger, Institut für Virologie, Universitätsklinikum Bonn, Germany
- 3. Giorgio Gallinella, University of Bologna, Department of Pharmacy and Biotechnology, Italy
- 4. Modra Murovska, Riga Stradins University, Latvia
- 5. Colin Parrish, College of Veterinary Medicine, Cornell University, United States of America
- 6. Judit Péntzes, Rutgers University, United States of America
- 7. Maria Söderlund-Venermo, Department of Virology, University of Helsinki, Finland

Picobirnaviridae

- 1. Souvik Gosh, Ross University School of Veterinary Medicine, India
- 2. Pattara Khamrin, Faculty of Medicine, Chiang Mai University, Thailand
- 3. Yashpal Singh Malik, Guru Angad Dev Veterinary and Animal Sciences University, India
- 4. Niwat Maneekarn, Faculty of Medicine, Chiang Mai University, Thailand
- 5. Gisela Masachessi, Faculty of Medical Sciences National University of Córdoba, Argentina

Picornaviridae

- 1. Kimberley Benschop, National Institute for Public Health and the Environment, Netherlands
- 2. Edson Elias da Silva, Oswaldo Cruz Institute (Fiocruz) Rio de Janeiro, Brazil
- 3. Thea Kølsen Fischer, Nordsjaellands Hospital, Copenhagen University Hospital, Denmark
- 4. Min-Shi Lee, National Health Research Institutes, Taiwan, China
- 5. Heli Harvala Simmonds, NHS Blood and Transplant and UCL, United Kingdom
- 6. Steve Oberste, Centers for Disease Control, United States of America
- 7. Miao Xu, National Institutes for Food and Drug Control, China
- 8. Hongjie Yu, Fudan University at School of Public Health from China CDC, China

Pneumoviridae

- 1. Larry J. Anderson, Emory University School of Medicine, United States of America
- 2. Louis J. Bont, University Medical Centre Utrecht, Netherlands
- 3. Ruth Karron, Johns Hopkins Bloomberg School of Public Health, United States of America
- 4. Jerome H. Kim, International Vaccine Institute, Republic of Korea
- 5. Claudio Lanata, Instituto de Investigación Nutricional, Peru

- 6. Octavio Ramilo, St. Jude Children's Research Hospital, United States of America
- 7. John Williams, UPMC Children's Hospital of Pittsburgh, United States of America
- 8. Heather Zar, University of Cape Town, South Africa
- 9. Mohammed Ziaur Rahman, International Center for Diarrhoeal Disease Research, Bangladesh

Polyomaviridae

- 1. Chris Buck, US National Cancer Institute, United States of America
- 2. Sébastien Calvignac-Spencer, Helmholtz Institute for One Health, University of Greifswald, Germany
- 3. Michael Carr, National Virus Reference Laboratory, University College Dublin, Ireland
- 4. Yuan Chang, University of Pittsburgh, Cancer Virology Program, Hillman Cancer Research Institute, United States of America
- 5. Sayeh Ezzikouri, Institut Pasteur, Morocco
- 6. Mariet Feltkamp, Leiden University Medical Center, Netherlands
- 7. Michael Imperiale, University of Michigan, United States of America

Poxviridae

- 1. Rafael Blasco, Centro Nacional INIA, Consejo superior de investigaciones científicas, Spain
- 2. Inger Damon, retired, Centers for Disease Control and Prevention (CDC), United States of America
- 3. Clarissa Damaso, Universidade Federal do Rio de Janeiro, Brazil
- 4. Gunasegaran Karupiah, University of Tasmania, Australia
- 5. Andreas Nitsche, Robert Koch Institut, Germany
- 6. Stefan Rothenburg, University of California, Davis, School of Medicine, United States of America

Rhabdoviridae

- 1. Martin Faye, Institut Pasteur Dakar, Senegal
- 2. Anthony Fooks, Animal & Plant Health Agency, United Kingdom
- 3. Marie-Paule Kieny, Drugs for Neglected Diseases and Medicines Patent Pool Foundation, Switzerland
- 4. Matthias Schnell, Thomas Jefferson University, United States of America
- 5. Nikos Vasilakis, University of Texas Medical Branch, United States of America
- 6. Supaporn Wacharapluesadee, Thai Red Cross Emerging Infectious Diseases Clinical Center, King Chulalongkorn Memorial Hospital, Thailand

Reovirales

- 1. Terence Dermody, UPMC Children's Hospital of Pittsburgh, United States of America
- 2. Jelle Matthijnsens, Rega Institute at the University of KU Leuven, Belgium
- 3. Polly Roy, London School of Hygiene & Tropical Medicine, United Kingdom

Retroviridae

- 1. Gloria Arriagada, Universidad Andrés Bello, Chile
- 2. Alex Greenwood, Leibniz Institute for Zoo and Wildlife Research and Freie Universität Berlin, Germany
- 3. Theodora Hatzioannou, Rockefeller University, United States of America
- 4. Aris Katzourakis, University of Oxford, United Kingdom

-
5. Pontiano Kaleebu, Uganda Virus Research Institute and London School of Hygiene and Tropical Medecinet, Uganda
 6. Eric M. Poeschla, University of Colorado School of Medicine, United States of America
 7. Gilda Tachedjian, Burnet Institute for Medical Research and Public Health, Australia

Togaviridae

1. Felicity Burt, Faculty of Health Sciences, University of the Free State, South Africa
2. Naomi Forrester-Soto, The Pirbright Institute, United Kingdom
3. Kylene Kehn-Hall, Virginia-Maryland College of Veterinary Medicine, United States of America
4. Sandra López Vergès, Gorgas Memorial Research Institute for Health Studies, Panama
5. Tem Morrison, University of Colorado School of Medicine, United States of America

ANNEX 2. Prioritization Advisory Committee (PAC)

PAC Members

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Cristina Cassetti, National Institute of Allergy and Infectious Diseases, United States of America
Marco Cavaleri, European Medicines Agency, Netherlands
Zigui Chen, chairperson Papillomaviridae, The Chinese University of Hong Kong, China
Beth-Ann Collier, Retired, Vaccine Development, United States of America
Terence Dermody, chairperson Reoviridae, UPMC Children’s Hospital of Pittsburgh, United States of America
Herman Favoreel, delegate Herpesviridae, Ghent University, Belgium
Peter Figueroa, University of the West Indies, Jamaica
Naomi Forrester-Soto, chairperson Togaviridae, The Pirbright Institute, the United Kingdom
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Souvik Gosh, delegate Picobirnaviridae, Ross University, School of Veterinary Medicine, St. Kitts and Nevis, West Indies
Barney Graham, Morehouse School of Medicine, United States of America
Stephan Günther, chairperson Arenaviridae, Bernhard-Nocht-Institute for Tropical Medicine, Germany
Nivedita Gupta, Indian Council of Medical Research, India
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Laura Merson, University of Oxford, the United Kingdom
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WHO Leadership and R&D Blueprint for Epidemics Team

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Simon Allan, Gavi, the Vaccine Alliance
Derrick Sim, Gavi, the Vaccine Alliance
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Yazdan Yazdanpanah, Inserm, France
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Gladys Kalema-Zikusoka, Conservation Through Public Health, Uganda
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Martin Landray, University of Oxford, United Kingdom
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Kai Von Harbou, WHO Headquarters
Gundo Weiler, WHO Regional Office for the Western Pacific
Victoria Willet, WHO Headquarters
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ANNEX 3. Summary of Epidemiological Information on Proposed Priority Pathogens

| Family | Pathogen | Vector/ Reservoir | Mode of Transmission | Extent of person-to- person transmission | Spread | Areas with Documented Transmission |
|------------------|---|--|--|---|---------------------------------------|---|
| Arenaviridae | Mammarenavirus lassaense | Mastomys rodents | Contact with infected rodents, person-to-person transmission | Sufficient to cause outbreaks | Africa | West African countries, including Nigeria, Liberia, Sierra Leone |
| Bacteria | Vibrio Cholerae (sero 01) | Aquatic environment, human hosts | Fecal-oral transmission, contaminated water sources | Some | South Asia | Primarily in Developing countries, potential for global spread |
| Bacteria | Klebsiella Pneumonia | Humans, environmental reservoirs | Nosocomial transmission, person-to-person spread | Some | Global | Reported worldwide |
| Bacteria | Yersinia Pestis (Plague) | Rodents, fleas | Flea-borne transmission, person-to-person spread of pneumonic plague | Some | Asia, Africa, Americas | Endemic in parts of Asia, Africa, and the Americas, potential for global spread |
| Bacteria | Shigella Dysenteria 1 | Humans | Fecal-oral transmission, contaminated food/water | Sufficient to cause outbreaks | | Primarily in Developing countries, potential for global spread |
| Bacteria | Salmonella Enterica (invasive non-typhoidal) | Humans, animals, environmental reservoirs | Foodborne transmission, person-to-person spread | Sufficient to cause outbreaks | Global | Reported worldwide distribution |
| Hantaviridae | Orthohantavirus hantanense | Field mice | Inhalation of virus from rodent excreta | Little or none | Asia | Primarily confined to endemic regions in Asia |
| Hantaviridae | Orthohantavirus sin Nombreense | Deer mice | Inhalation of virus from rodent excreta | Little or none | North America | Primarily confined to North America |
| Nairoviridae | Orthonairovirus haemorrhagiae | Ticks, livestock | Tick-borne transmission, contact with infected animals | Some | Asia, Africa, Europe | Primarily confined to endemic regions in Africa, Asia, Europe |
| Phenuiviridae | Bandavirus dabiense | Ticks, small mammals | Tick-borne transmission | Little or none | Asia | Outbreaks in parts of Asia |
| Coronaviridae | Sub genus Merbecoviruses | Bats, humans | Bat-borne transmission, potential for person-to- person spread | Sufficient to cause outbreaks | Asia, Middle- East | Outbreaks in parts of Asia and the Middle East |
| Coronaviridae | Sub genus Sarbecoviruses | Bats, humans | Bat-borne transmission, person-to-person spread | Sufficient to cause outbreaks | Global | Global, already caused a PHEIC |
| Filoviridae | Orthoebolavirus sudanense | Unknown, potential animal reservoir | Contact with infected bodily fluids | Sufficient to cause outbreaks | Central and East Africa | Primarily in Central and East Africa |
| Filoviridae | Orthomareburgvirus marburgense | Fruit bats, potential animal reservoir | Contact with infected bodily fluids | Sufficient to cause outbreaks | Central and East Africa | Primarily in Central and East Africa |
| Filoviridae | Orthoebolavirus zairense | Fruit bats, potential animal reservoir | Contact with infected bodily fluids | Sufficient to cause outbreaks | Central and East Africa | Primarily in Central and West Africa |
| Flaviviridae | Orthoflavivirus flavi | Mosquitoes, non- human primates | Mosquito-borne transmission | Little or none | Africa, South America | In parts of Africa and South America |
| Flaviviridae | Orthoflavivirus denguei | Aedes mosquitoes | Mosquito-borne transmission | Little or none | | Widespread in tropical and subtropical regions |
| Flaviviridae | Orthoflavivirus zikaense | Aedes mosquitoes | Mosquito-borne transmission, potential for vertical and sexual transmission | Some | Americas, Africa, Asia, Pacific | Outbreaks in the Americas, Africa, Asia, and the Pacific |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H5,H6,H7,H10 | Avian reservoirs, humans | Respiratory transmission, potential for zoonotic transmission | Little or none | Asia, Africa, Europe | Outbreaks in parts of Asia, Africa, and Europe |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H2 | Avian reservoirs, humans | Respiratory transmission, potential for zoonotic transmission | Sufficient to cause outbreaks | Asia, Europe | Outbreaks in parts of Asia and Europe |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H1,H3 | Avian reservoirs, humans | Respiratory transmission, potential for zoonotic transmission | Sufficient to cause outbreaks | Global | Worldwide distribution |
| Paramyxoviridae | Henipavirus nipahense | Bats, humans | Bat-borne transmission, potential for person-to- person spread | Little or none | Asia | Outbreaks in parts of Asia |
| Picomaviridae | Enterovirus coxsackiepol | Humans | Fecal-oral transmission, contaminated water sources | Sufficient to cause outbreaks | Asia | Primarily confined to Afghanistan and Pakistan |
| Poxviridae | Orthopoxvirus Variola | Humans | Respiratory transmission, direct contact | Sufficient to cause outbreaks | Eradicated | Historically widespread, now confined to laboratories |
| Poxviridae | Orthopoxvirus Monkeypox | Rodents, humans | Animal-to-human transmission, person-to- person spread | Sufficient to cause outbreaks | Global | Endemic in Central and West Africa, already caused a PHEIC with global spread |
| Retroviridae | Lentivirus humimdefl | Humans | Bloodborne transmission, sexual transmission | Endemic in humans | Global | Worldwide distribution |
| Togaviridae | Alphavirus chikungunya | Aedes mosquitoes | Mosquito-borne transmission | Little or none | Asia, Africa, Americas | Outbreaks in parts of Africa, Asia, and the Americas |
| Togaviridae | Alphavirus Venezuelan | Mosquitoes, rodents | Mosquito-borne transmission | Little or none | Central and South America | Outbreaks in parts of Central and South America |

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ANNEX 4. Current landscape of candidate Vaccines and Therapeutics for proposed Priority Pathogens

Candidate vaccines

| Family | Pathogen | Vaccine name | Platform | Phase of development | Developer | Source |
|--------------|--|--|---|----------------------|--|---|
| Arenaviridae | Mammarenavirus lassaense | INO-4500 | DNA | Phase 1 | Inovio Pharmaceuticals | https://ctv.veeva.com/study/dose-ranging-study-safety-tolerability-and-immunogenicity-of-ino-4500-in-healthy-volunteers-in-gha |
| Arenaviridae | Mammarenavirus lassaense | MV-LASV | Live-attenuated Measles Virus vector | Phase 1 | Institut Pasteur, Themis Bioscience | https://clinicaltrials.gov/study/NCT04055454 |
| Arenaviridae | Mammarenavirus lassaense | rVSV-LASV | Vesicular Stomatitis Virus (VSV) vector | Phase 2 | IAVI | https://clinicaltrials.gov/study/NCT04794218 ; https://clinicaltrials.gov/study/NCT05868733?cond=rVSV%E2%88%86G-LASV-GPC&rank=2 |
| Arenaviridae | Mammarenavirus lassaense | ML29 | Reassortant virus | Preclinical | | https://www.sciencedirect.com/science/article/abs/pii/S0264410X08010062?via%3Dihub |
| Bacteria | Klebsiella Pneumonia | Ribosomal fraction | Ribosomal | Clinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8412853/ |
| Bacteria | Klebsiella Pneumonia | Klev4V | Bioconjugate | Phase 1/2 | LimmaTech Biologics AG | https://clinicaltrials.gov/study/NCT04959344?cond=Klebsiella%20Pneumonia&term=vaccine&rank=1 |
| Bacteria | Klebsiella Pneumonia | Capsular polysaccharides | Subunit | Phase 1/2 | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8412853/ |
| Bacteria | Klebsiella Pneumonia | Outer Membrane Proteins (OMP)-based vaccine | Protein | Preclinical | Various | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6656602/ |
| Bacteria | Klebsiella Pneumonia | Fimbriae Subunits | Protein | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8412853/ |
| Bacteria | Klebsiella Pneumonia | Toxins | Protein | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8412853/ |
| Bacteria | Klebsiella Pneumonia | Lipopolysaccharides | Subunit | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8412853/ |
| Bacteria | Klebsiella Pneumonia | Outer membrane vesicles (OMVs) | Subunit | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8412853/ |
| Bacteria | Klebsiella Pneumonia | Inactivated K. pneumoniae vaccine | Whole Cell Vaccines/Cell Lysates | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8412853/ |
| Bacteria | Klebsiella Pneumonia | Mixed bacterial vaccines (MBV) with heat-killed pathogens | Whole Cell Vaccines/Cell Lysates | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8412853/ |
| Bacteria | Klebsiella Pneumonia | Respivax | Whole Cell Vaccines/Cell Lysates | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8412853/ |
| Bacteria | Salmonella Enterica (invasive non-typhoidal) | iNTS-typhoid conjugate | Conjugate | Phase 1 | | https://academic.oup.com/ofid/article/10/Supplement_1/S58/7188900 |
| Bacteria | Salmonella Enterica (invasive non-typhoidal) | GMMA-based bivalent (S. Typhimurium/S. Enteritidis) | Outer membrane vesicles | Phase 1 | GSK Vaccines Ins. For Global Health (GVGH) | https://academic.oup.com/ofid/article/10/Supplement_1/S58/7188900 |
| Bacteria | Salmonella Enterica (invasive non-typhoidal) | Trivalent (S. Typhi/S. Typhimurium/S. Enteritidis) | Conjugate | Phase 2 | University of Maryland/Bharat Biotech | https://academic.oup.com/ofid/article/10/Supplement_1/S58/7188900 |
| Bacteria | Salmonella Enterica (invasive non-typhoidal) | O:4 and O:9 conjugate (S. Typhimurium/S. Enteritidis) - MAPS | Conjugate | Preclinical | Boston's Children's Hospital | https://academic.oup.com/ofid/article/10/Supplement_1/S58/7188900 |
| Bacteria | Salmonella Enterica (invasive non-typhoidal) | Trivalent (S. Typhi/S. Typhimurium/S. Enteritidis) | | Preclinical | SK Bioscience/IVI | https://academic.oup.com/ofid/article/10/Supplement_1/S58/7188900 |

| Family | Pathogen | Vaccine name | Platform | Phase of development | Developer | Source |
|----------|-----------------------------|---|--|----------------------|--|---|
| Bacteria | Shigella Dysenteriae 1 | Shigella ETEC live attenuated vaccine consisting of six Shigella strains | Live attenuated | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/31194282/ |
| Bacteria | Vibrio Cholerae (sero O139) | Shanchol | Killed whole-cell bivalent (O1 and O139) | Licensed | Shantha Biotechnics/Sanofi Pasteur | https://www.who.int/teams/immunization-vaccines-and-biologicals/diseases/cholera |
| Bacteria | Vibrio Cholerae (sero O139) | Evuchol | Killed whole-cell bivalent (O1 and O139) | Licensed | EuBiologics | https://www.who.int/teams/immunization-vaccines-and-biologicals/diseases/cholera |
| Bacteria | Vibrio Cholerae (sero O139) | Evuchol-Plus | Killed whole-cell bivalent (O1 and O139) | Licensed | EuBiologics | https://www.who.int/teams/immunization-vaccines-and-biologicals/diseases/cholera |
| Bacteria | Yersinia Pestis | rF1 and rV Antigens | Recombinant | Phase 1 | PharmAthene UK Limited | NCT00246467 |
| Bacteria | Yersinia Pestis | Flagellin/F1/V | Recombinant | Phase 1 | NIAID | NCT01381744 |
| Bacteria | Yersinia Pestis | ChAdOx1 PlaVac | Viral Vector | Phase 1 | University of Oxford | https://www.ox.ac.uk/news/2021-07-26-phase-i-trial-begins-new-vaccine-against-plague |
| Bacteria | Yersinia Pestis | rF1V Vaccine with CpG 1018 | Recombinant | Phase 2 | DynPort Vaccine Company LLC, A GDIT Company | NCT05506969 |
| Bacteria | Yersinia Pestis | plague vaccine(F1+rV) | Live Attenuated | Phase 2b | Jiangsu Province Centers for Disease Control and Prevention | NCT05330624 |
| Bacteria | Yersinia Pestis | rF1V vaccine | Recombinant | Phase 2b | DynPort Vaccine Company LLC, A GDIT Company | NCT01122784 |
| Bacteria | Yersinia Pestis | EV 76 NIEG | Live Whole Cell | Phase 4 | Scientific Research Institute of Epidemiology and Hygiene (Russian abbreviation—NIEG, Kirov) | |
| Bacteria | Yersinia Pestis | Y. pestis CO92 ΔLMA* | Live attenuated | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | Y. pestis CO92 ΔLMP | Live attenuated | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | Y. pestis EV76-B-SHUΔpla! | Live attenuated | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | Y. pestis CO92 ΔpgmΔpPst | Live attenuated | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | Calcium Phosphate based Protein-coated Microcrystals F1V | Subunit | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | Single dose F1-V polyanhydride nanoparticle coupled with cyclic dinucleotides | Subunit | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | rV10 | Subunit | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | Peptidoglycan-Free OMV (Bacterial Ghosts)-phage lytic system | Subunit | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | Manganese silicate nanoparticle rF1-V10 | Subunit | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | polymeric F1 + LcrV (ILB1)-R | Subunit | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | Y. Pseudotuberculosis-based LcrV MPLA OMV | Subunit | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | LicKM-LcrV-F1 | Subunit | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | Microvessicle (Bacteroides spp.) F1-V | Subunit | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | DNA F1-V vaccines | Vector-Based | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | Ad5-F1+ Ad5-LcrV | Vector-Based | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | Ad5-YFV | Vector-Based | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | T4-Phage | Vector-Based | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |

| Family | Pathogen | Vaccine name | Platform | Phase of development | Developer | Source |
|---------------|-------------------------------|---|--------------------------------------|----------------------|---|---|
| Bacteria | Yersinia Pestis | S. Typhimurium expressing plague antigens | Vector-Based | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | S. Typhi expressing plague antigens | Vector-Based | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | Lactiplantibacillus plantarum expressing lcrV | Vector-Based | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | F1 mRNA-LNP | Vector-Based | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | Y. pseudotuberculosis producing F1 | Vector-Based | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | Self-amplifying RNA (F1+LcrV) | Vector-Based | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Bacteria | Yersinia Pestis | F. tularensis ΔcapB + F1-LcrV/PA | Vector-Based | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/34142207/ |
| Nairoviridae | Orthonairovirus haemorrhagiae | Russian/Bulgarian Vaccine | Inactivated | Licensed in Bulgaria | | https://pubmed.ncbi.nlm.nih.gov/21142621/ |
| Nairoviridae | Orthonairovirus haemorrhagiae | KIRIM-KONGO-VAX | MVA based vaccine | Phase 1 | The Scientific and Technological Research Council of Turkey | https://clinicaltrials.gov/study/NCT03020771?cond=cchf&rank=2 |
| Nairoviridae | Orthonairovirus haemorrhagiae | DNA Vaccine | DNA | Preclinical | Linköping University | https://pubmed.ncbi.nlm.nih.gov/28250124/ |
| Nairoviridae | Orthonairovirus haemorrhagiae | mRNA-LNP vaccine | mRNA | Preclinical | Public Health Agency of Sweden | https://pubmed.ncbi.nlm.nih.gov/34817199/ |
| Nairoviridae | Orthonairovirus haemorrhagiae | Replicon particle vaccine | Replicon particle vaccine | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/30947619/ |
| Nairoviridae | Orthonairovirus haemorrhagiae | GEM-PA vaccine | Subunit Protein | Preclinical | | https://pubmed.ncbi.nlm.nih.gov/36016285/ |
| Nairoviridae | Orthonairovirus haemorrhagiae | ChAdOx2 CCHF | Viral Vector | Preclinical | University of Oxford | https://www.thelancet.com/journal/s/ebiom/article/PIIS2352-3964%2823%2900088-9/fulltext |
| Nairoviridae | Orthonairovirus haemorrhagiae | MVA CCHF | Viral Vector | Preclinical | UKHSA | https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0091516 |
| Nairoviridae | Orthonairovirus haemorrhagiae | rVSV | Viral Vector | Preclinical | University of Texas Medical Branch | https://pubmed.ncbi.nlm.nih.gov/31123310/ |
| Phenuiviridae | Bandavirus dabiense | DNA Vaccine | DNA | Preclinical | | https://www.nature.com/articles/s41467-019-11815-4 |
| Phenuiviridae | Bandavirus dabiense | rHB2912aaNSs and rHB29NSsP102A | Live attenuated | Preclinical | | www.mdpi.com/1999-4915/13/4/627 ; https://www.mdpi.com/1999-4915/16/1/128 |
| Phenuiviridae | Bandavirus dabiense | rVSV-SFTSV | Recombinant Viral Vector | Preclinical | | www.mdpi.com/1999-4915/13/4/627 ; https://www.mdpi.com/1999-4915/16/1/128 |
| Phenuiviridae | Bandavirus dabiense | LC16m8 - MVA | Recombinant Viral Vector | Preclinical | | www.mdpi.com/1999-4915/13/4/627 ; https://www.mdpi.com/1999-4915/16/1/128 |
| Coronaviridae | Merbecoviruses | MERS DNA | DNA | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8603276/ |
| Coronaviridae | Merbecoviruses | ΔCHERV-MERS-S1 pcDNA3.1-S1 pS1 | DNA | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8603276/ |
| Coronaviridae | Merbecoviruses | pSDER-pSDTM | DNA-protein | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8603276/ |
| Coronaviridae | Merbecoviruses | RBD-LSRBD-NP (cdGMP) | Nanoparticle | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8603276/ |
| Coronaviridae | Merbecoviruses | SRBD-HBD2 | Protein | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8603276/ |
| Coronaviridae | Merbecoviruses | Trivalent RBD Nanoparticle Vaccine | Recombinant protein | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10245799/ |
| Coronaviridae | Merbecoviruses | RV/MERSMERSBLPRVDP MERS/S1 | Viral or bacterial vector | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8603276/ |
| Coronaviridae | Merbecoviruses | rAd/spikePIV5/MERS-S ChAdOx1-MERS | Viral Vector | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8603276/ |
| Coronaviridae | Sarbecoviruses | VBI-2901 | eVLP (enveloped virus-like particle) | Preclinical | VBI Vaccines | vbi-vaccines.com/press-releases/vbi-vaccines-pan-coronavirus-vaccine-candidate-vbi-2901-induced-broad-and-durable-protective-titers-against-variants-of-concern/ |

| Family | Pathogen | Vaccine name | Platform | Phase of development | Developer | Source |
|---------------|-----------------------------|--|--|--------------------------------------|----------------------------------|---|
| Coronaviridae | Sarbecoviruses | Mucosal vaccine | Live attenuated | Preclinical | | https://www.nature.com/articles/s41467-023-42349-5 |
| Coronaviridae | Sarbecoviruses | Universal Sarbecovirus Vaccine | n/a | Preclinical | Shionogi & KOTAI Biotechnologies | https://www.shionogi.com/global/en/news/2023/6/230619_1.html |
| Coronaviridae | Sarbecoviruses | Mosaic-8 | Nanoparticle | Preclinical | CalTech | https://www.science.org/doi/10.1126/science.abaq0839 |
| Coronaviridae | Sarbecoviruses | IgG Fc-conjugated RBD of the original SARS-CoV-2 strain (WA1) plus a novel STING agonist-based adjuvant CF501 (CF501/RBD-Fc) | | Preclinical | Fudan University, China | https://pubmed.ncbi.nlm.nih.gov/36897979/ |
| Filoviridae | Orthoebolavirus zairense | Ad26.ZEBOV/MVA-BN-Filo | Adenovirus vector/Modified vaccinia Ankara (MVA) | Licensed | Janssen/Bavarian Nordic | https://journals.plos.org/plospathogens/article?id=10.1371%2Fjournal.ppat.1010078 |
| Filoviridae | Orthoebolavirus zairense | Ervebo (rVSVΔG-ZEBOV-GP) | Recombinant vesicular stomatitis virus (rVSV) | Licensed | Merck | https://journals.plos.org/plospathogens/article?id=10.1371%2Fjournal.ppat.1010078 |
| Filoviridae | Orthoebolavirus zairense | Ad5-EBOV | Viral Vector | Licensed in China | BIT CanSino | https://journals.plos.org/plospathogens/article?id=10.1371%2Fjournal.ppat.1010078 |
| Filoviridae | Orthoebolavirus zairense | GamEvac-Combi and GamEvacLyo Heterologous prime-boost w/ rVSV and Ad5 expressing EBOV GP (Makona) | Viral Vector | Licensed in Russia/Phase 3 in Guinea | | https://journals.plos.org/plospathogens/article?id=10.1371%2Fjournal.ppat.1010078 |
| Filoviridae | Orthoebolavirus zairense | DNA Vaccine | DNA | Phase 1 | | https://journals.plos.org/plospathogens/article?id=10.1371%2Fjournal.ppat.1010078 |
| Filoviridae | Orthoebolavirus zairense | DNA plasmid vaccine | DNA | Phase 1 | | https://journals.plos.org/plospathogens/article?id=10.1371%2Fjournal.ppat.1010078 |
| Filoviridae | Orthoebolavirus zairense | Monovalent nanoparticle | Nanoparticle | Phase 1 | | https://journals.plos.org/plospathogens/article?id=10.1371%2Fjournal.ppat.1010078 |
| Filoviridae | Orthoebolavirus zairense | Vesiculovax | Viral Vector | Phase 1 | Auro Vaccines | https://journals.plos.org/plospathogens/article?id=10.1371%2Fjournal.ppat.1010078 |
| Filoviridae | Orthoebolavirus zairense | INO-4201 | DNA | Phase 1b | Inovio Pharmaceuticals | https://academic.oup.com/jid/article/220/3/400/5395966 |
| Filoviridae | Orthoebolavirus zairense | cAd3-EBOZ/ChAd3-EBO-Z | Chimpanzee adenovirus vector | Phase 2/3 | GlaxoSmithKline | https://journals.plos.org/plospathogens/article?id=10.1371%2Fjournal.ppat.1010078 |
| Filoviridae | Orthomarbuvirus marburgense | VRC-MARDNA025-00-VP | DNA Plasmid | Phase 1 | NIAID Vaccine Research Center | https://clinicaltrials.gov/study/NCT00997607?cond=marburg&rank=9 |
| Filoviridae | Orthomarbuvirus marburgense | Ad26-MARV | Viral Vector | Phase 1 | Janssen Pharmaceuticals | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9534391/ |
| Filoviridae | Orthomarbuvirus marburgense | cAd3-Marburg Vaccine | Viral Vector | Phase 1 | NIAID | https://clinicaltrials.gov/study/NCT03475056?cond=marburg&rank=2 |
| Filoviridae | Orthomarbuvirus marburgense | rVSVΔG-MARV-GP | Viral Vector | Phase 1 | Public Health Vaccines | https://clinicaltrials.gov/study/NCT06265012?cond=marburg&rank=3 |
| Filoviridae | Orthomarbuvirus marburgense | cAd3-Marburg vaccine | Viral Vector | Phase 2 | Sabin Vaccine Institute | https://clinicaltrials.gov/study/NCT05817422?cond=marburg&rank=1 |
| Filoviridae | Orthomarbuvirus marburgense | Several | | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9560149/ |
| Filoviridae | Orthoebolavirus sudanense | HPIV3-SUDV GP | Parainfluenza virus vector | Phase 1 | NIAID | NCT03462004 |
| Filoviridae | Orthoebolavirus sudanense | rVSVΔG-SEBOV-GP | Viral Vector | Phase 1 | IAVI | https://clinicaltrials.gov/study/NCT05724472?cond=sudan&term=vaccine&rank=3 |
| Filoviridae | Orthoebolavirus sudanense | cAd3-EBO S | Viral Vector | Phase 1 | NIAID | https://clinicaltrials.gov/study/NCT04041570?cond=sudan&term=vaccine&rank=4 |
| Filoviridae | Orthoebolavirus sudanense | ChAdOx1 biEBOV | Viral Vector | Phase 1b | University of Oxford | https://clinicaltrials.gov/study/NCT05301504?cond=sudan&term=vaccine&rank=6 |
| Filoviridae | Orthoebolavirus sudanense | cAd3-Sudan Ebolavirus | Chimpanzee adenovirus vector | Phase 2 | Sabin Vaccine Institute | https://clinicaltrials.gov/study/NCT06036602?cond=sudan&term=vaccine&rank=2 |
| Filoviridae | Orthoebolavirus sudanense | MVA-SUDV | Modified Vaccinia Ankara (MVA) vector | Preclinical | | https://www.nature.com/articles/s41541-022-00512-x |

| Family | Pathogen | Vaccine name | Platform | Phase of development | Developer | Source |
|--------------|---------------------------|----------------|---|----------------------|--|---|
| Filoviridae | Orthoebolavirus sudanense | VSV-SUDV | Vesicular Stomatitis Virus (VSV) vector | Preclinical | NIAID | https://www.niaid.nih.gov/news-events/experimental-nih-sudan-virus-vaccine-protects-macaques |
| Flaviviridae | Orthoflavivirus denguei | Dengvaxia | Chimeric virus YFV/DEN1-4 | Licensed | Sanofi Pasteur | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10228381/ |
| Flaviviridae | Orthoflavivirus denguei | TV003/TV005 | Live attenuated and chimeric virus | Phase 3 | NIAID and Butantan | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10228381/ |
| Flaviviridae | Orthoflavivirus denguei | TAK-003 | Chimeric viruses | Phase 2 | Takeda | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10228381/ |
| Flaviviridae | Orthoflavivirus denguei | TDEN | Live attenuated | Phase 1/2 | WRAIR and GSK | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10228381/ |
| Flaviviridae | Orthoflavivirus denguei | DPIV | Inactivated Virus | Phase 1 | WRAIR, GSK, FIOcruz | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10228381/ |
| Flaviviridae | Orthoflavivirus denguei | TVDV | DNA vaccine | Preclinical/Phase 1 | US AMRDC, WRAIR, NMRC and Vidal | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10228381/ |
| Flaviviridae | Orthoflavivirus denguei | V180 | Recombinant protein | Phase 1 | Merck | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10228381/ |
| Flaviviridae | Orthoflavivirus denguei | DSV4 | Virus-like particles | Preclinical | International Centre for Genetic Engineering and Biotechnology | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10228381/ |
| Flaviviridae | Orthoflavivirus denguei | E80-mRNA | mRNA | Preclinical | CAS laboratory of Molecular Virology and Immunology, Institute Pasteur of Shanghai | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10228381/ |
| Flaviviridae | Orthoflavivirus zikaense | ZPIV | Inactivated | Phase 1 | NIAID/WRAIR/BIDMC | https://academic.oup.com/femspd/article/doi/10.1093/femspd/ftad036/7513202 |
| Flaviviridae | Orthoflavivirus zikaense | PIZV/TAK-426 | Inactivated | Phase 1 | Takeda | https://academic.oup.com/femspd/article/doi/10.1093/femspd/ftad036/7513202 |
| Flaviviridae | Orthoflavivirus zikaense | VLA1601 | Inactivated | Phase 1 | Valneva Austria GmbH | https://academic.oup.com/femspd/article/doi/10.1093/femspd/ftad036/7513202 |
| Flaviviridae | Orthoflavivirus zikaense | BBV121 | Inactivated | Phase 1 | Bharat Biotech International | https://academic.oup.com/femspd/article/doi/10.1093/femspd/ftad036/7513202 |
| Flaviviridae | Orthoflavivirus zikaense | VRC5288 | DNA vaccine | Phase 1 | NIAID, VRC | https://academic.oup.com/femspd/article/doi/10.1093/femspd/ftad036/7513202 |
| Flaviviridae | Orthoflavivirus zikaense | VRC5283 | DNA vaccine | Phase 2 | NIAID, VRC | https://academic.oup.com/femspd/article/doi/10.1093/femspd/ftad036/7513202 |
| Flaviviridae | Orthoflavivirus zikaense | GLS-5700 | DNA vaccine | Phase 1 | GeneOne Life Science/Inovio | https://academic.oup.com/femspd/article/doi/10.1093/femspd/ftad036/7513202 |
| Flaviviridae | Orthoflavivirus zikaense | rZIKV/D430-713 | Live attenuated | Phase 1 | NIAID | https://academic.oup.com/femspd/article/doi/10.1093/femspd/ftad036/7513202 |
| Flaviviridae | Orthoflavivirus zikaense | mRNA 1325 | mRNA | Phase 2 | Moderna Therapeutics | https://academic.oup.com/femspd/article/doi/10.1093/femspd/ftad036/7513202 |
| Flaviviridae | Orthoflavivirus zikaense | mRNA 1893 | mRNA | Phase 2 | | https://academic.oup.com/femspd/article/doi/10.1093/femspd/ftad036/7513202 |
| Flaviviridae | Orthoflavivirus zikaense | MV-ZIKA-RSP | Viral Vector | Phase 1 | Themis Bioscience GmbH | https://academic.oup.com/femspd/article/doi/10.1093/femspd/ftad036/7513202 |
| Flaviviridae | Orthoflavivirus zikaense | MV-ZIKA | Viral Vector | Phase 1 | Themis Bioscience GmbH | https://academic.oup.com/femspd/article/doi/10.1093/femspd/ftad036/7513202 |
| Flaviviridae | Orthoflavivirus zikaense | ChAdOx1 ZIKA | Viral Vector | Phase 1 | University of Oxford | https://academic.oup.com/femspd/article/doi/10.1093/femspd/ftad036/7513202 |
| Flaviviridae | Orthoflavivirus zikaense | Ad26.ZIKV.001 | Viral Vector | Phase 1 | Janssen Vaccines and Prevention BV | https://academic.oup.com/femspd/article/doi/10.1093/femspd/ftad036/7513202 |
| Flaviviridae | Orthoflavivirus flavi | YF17D | Live attenuated | Licensed | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | XRX-001 | Inactivated | Phase 1 | | https://www.mdpi.com/1424-8247/14/9/891 |

| Family | Pathogen | Vaccine name | Platform | Phase of development | Developer | Source |
|------------------|---|---|---------------------------------------|----------------------|--|---|
| Flaviviridae | Orthoflavivirus flavi | VINFLAPI001/2010 | Inactivated | Preclinical | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | Chumakov Institute inactivated YF vaccin | Inactivated | Preclinical | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | Recombinant vaccinia virus/17D YFV | Viral vector | Preclinical | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | MVA-YF and dVV-YF | Viral vector | Preclinical | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | MVA-BN-YF | Viral vector | Phase 1 | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | pYF17D-16 iDNA | DNA | Preclinical | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | pBeloBAC-FLYF and pBeloBAC-YF/ΔC | DNA | Preclinical | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | pShuttle/YFV-17D | DNA | Preclinical | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | p/YFE and pL/YFE | DNA | Preclinical | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | CJaYZ | Virus-like particles | Preclinical | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | (YF) prME mRNA | RNA | Preclinical | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | Re-encoded wild-type YF viruses | Live attenuated | Preclinical | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | YFE and YFE-LicKM | Subunit vaccine | Preclinical | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | vYF-247 | New manufacturing tools | Preclinical | | https://www.mdpi.com/1424-8247/14/9/891 |
| Flaviviridae | Orthoflavivirus flavi | YCEF-01-07 | New manufacturing tools | Preclinical | | https://www.mdpi.com/1424-8247/14/9/891 |
| Hantaviridae | Orthohantavirus sinnombreense | NONE | Multiple types | NONE | NONE | NONE |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H1,H3 | Licensed Seasonal flu vaccines | Computationally optimized HA antigens | Licensed | | |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H1,H3 | Universal Influenza Vaccine Candidate | Inactivated | Phase 2 | Sanofi Pasteur | NC103300050 |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H5,H6,H7,H10 | H5N1 influenza virus vaccine | Inactivated | Licensed | | https://www.fda.gov/vaccines-blood-biologics/vaccines/influenza-virus-vaccine-h5n1-national-stockpile |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H5,H6,H7,H10 | AS03-adjuvanted pre-pandemic H5N1 influenza vaccine | Inactivated | Licensed | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10058720/ |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H5,H6,H7,H10 | MF59-adjuvanted seasonal influenza vaccine (Fluad®) | Live attenuated | Licensed | Novartis Vaccines and Diagnostics Inc. | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10058720/ |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H5,H6,H7,H10 | H5N1 pandemic live-attenuated influenza virus vaccination | Live attenuated | Licensed | | https://pubmed.ncbi.nlm.nih.gov/26082783/ |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H5,H6,H7,H10 | Pandemic influenza vaccine H5N1 Astrazeneca | Live attenuated | Licensed | | https://www.ema.europa.eu/en/medicines/human/EPAR/pandemic-influenza-vaccine-h5n1-astrazeneca-previously-pandemic-influenza-vaccine-h5n1-medimmune |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H5,H6,H7,H10 | H7 pandemic live-attenuated influenza vaccines (pLAIV) | n/a | Phase 1 | | https://pubmed.ncbi.nlm.nih.gov/25446831/ |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H5,H6,H7,H10 | H10N8 vaccine | | Phase 1 | | https://pubmed.ncbi.nlm.nih.gov/31079849/ |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H5,H6,H7,H10 | VRC-FLUNPF0103-00-VP | Live attenuated | Phase 1 | | https://clinicaltrials.gov/study/NCT04579250?cond=h10&rank=1 |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H5,H6,H7,H10 | H5 candidate vaccine strain A/17/turkey/Turkey/05/133 | | Phase 2 | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10058720/ |
| Orthomyxoviridae | Alphainfluenzavirus influenzae H5,H6,H7,H10 | Panblok H7 | Live attenuated | Phase 2 | BARDA | https://clinicaltrials.gov/study/NCT03283319?cond=h7&rank=2 |

| Family | Pathogen | Vaccine name | Platform | Phase of development | Developer | Source |
|------------------|---|--|---|----------------------|----------------------------|---|
| Orthomyxoviridae | Alphainfluenzavirus influenzae H5,H6,H7,H10 | H7N9 LAIV | mRNA | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10058720/ |
| Paramyxoviridae | Henipavirus nipahense | mRNA- 1215 vaccine | Subunit (Hendra virus glycoprotein) | Phase 1 | NIAID | https://clinicaltrials.gov/study/NCT05398796 |
| Paramyxoviridae | Henipavirus nipahense | HeV-sG-V | Viral Vector | Phase 1 | AuroVaccines | https://classic.clinicaltrials.gov/ct2/show/NCT04199169 |
| Paramyxoviridae | Henipavirus nipahense | rVSV Nipah Virus Vaccine | Subunit (soluble F and G proteins) | Phase 1 | | https://clinicaltrials.gov/study/NCT05178901 |
| Paramyxoviridae | Henipavirus nipahense | Nipah vaccine | Subunit (stabilized prefusion F trimer, multimeric G) | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7870971/ |
| Paramyxoviridae | Henipavirus nipahense | Nipah vaccine | Viral Vector | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7300195/ |
| Paramyxoviridae | Henipavirus nipahense | VSV-NiVG | Live attenuated virus | Preclinical | | https://www.thelancet.com/journal/s/ebiom/article/PIIS2352-3964%2822%2900587-4/fulltext |
| Picomaviridae | Enterovirus coxsackiepol | Novel Oral Polio Vaccine type 2 (OPV2) | Inactivated virus | EUL | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10109087/ |
| Picomaviridae | Enterovirus coxsackiepol | Inactivated Poliovirus Vaccine (IPV) | Live attenuated virus | Licensed | Multiple | |
| Picomaviridae | Enterovirus coxsackiepol | Oral Polio Vaccine (OPV) | Inactivated Sabin strains | Licensed | Multiple | |
| Picomaviridae | Enterovirus coxsackiepol | Sabin-IPV | Inactivated virus, microneedle patch | Phase 3 | Sinovac Biotech | https://clinicaltrials.gov/study/NCT05850364?cond=polio%20vaccine&rank=16 |
| Picomaviridae | Enterovirus coxsackiepol | Microneedle Array Patch IPV | Virus-like particles | Preclinical | | https://www.nature.com/articles/s41541-022-00443-7 |
| Picomaviridae | Enterovirus coxsackiepol | VLP Polio Vaccine | Protein subunit vaccine | Preclinical | | https://www.mdpi.com/2076-0817/13/3/224 |
| Poxviridae | Orthopoxvirus Monkeypox | Ectodomains A33/B5/A27 + Alhydrogel and CpG | Protein subunit vaccine | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10186953/ |
| Poxviridae | Orthopoxvirus Monkeypox | 10 epitopes with 147 amino acid residues | Protein subunit vaccine | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10186953/ |
| Poxviridae | Orthopoxvirus Monkeypox | multi-epitope vaccine with GPGPG linkers | Protein subunit vaccine | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10186953/ |
| Poxviridae | Orthopoxvirus Monkeypox | MHC-I, MHC-II, and B-cell epitopes | Virus-like particles | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10186953/ |
| Poxviridae | Orthopoxvirus Monkeypox | Novovirus shell and VLP platform | DNA Vaccine | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10186953/ |
| Poxviridae | Orthopoxvirus Monkeypox | Plasmid DNA encoding MPOX orthologs | DNA Vaccine | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10186953/ |
| Poxviridae | Orthopoxvirus Monkeypox | Plasmid cocktail | mRNA vaccine | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10186953/ |
| Poxviridae | Orthopoxvirus Monkeypox | mRNA encoding three mABs | Live attenuated | Preclinical | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10186953/ |
| Poxviridae | Orthopoxvirus Monkeypox | IMVAMUNE | Live attenuated | Phase 3 | Bavarian Nordic | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10186953/ |
| Poxviridae | Orthopoxvirus Monkeypox | MVA-BN | Live attenuated | Phase 2 | Bavarian Nordic | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10186953/ |
| Poxviridae | Orthopoxvirus Monkeypox | Imvanex | Adenovirus vector | Licensed | | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10186953/ |
| Retroviridae | Lentivirus humimdef1 | Ad4-Env150KN/Ad4-Env145NFL + VRC-HIVRGP096-00-VP | Adenovirus vector | Phase 1 | NIAID | https://clinicaltrials.gov/study/NCT03878121?cond=HIV&intr=vaccine&ggFilters=status:rec%20act%20not,studyType:int&rank=45 |
| Retroviridae | Lentivirus humimdef1 | AdC6-HIVgp140 and AdC7-HIVgp140 | Adenovirus vector | Phase 1 | HIV Vaccine Trials Network | https://clinicaltrials.gov/study/NCT05182125?cond=HIV&intr=vaccine&ggFilters=status:rec%20act%20not,studyType:int&rank=25 |
| Retroviridae | Lentivirus humimdef1 | ChAdOx1.tHIVconsv1 prime followed by MVA.tHIVconsv3 and MVA.tHIVconsv4 boost | Bivalent subunit vaccine | Phase 1 | University of Oxford | https://clinicaltrials.gov/study/NCT04553016?cond=HIV&intr=vaccine&ggFilters=status:rec%20act%20not,studyType:int&rank=18 |
| Retroviridae | Lentivirus humimdef1 | AIDSVAX B/E+ IHV01 and A244/AHFG (w/ALFQ) | CMV Vector | Phase 1 | WRAIR | https://clinicaltrials.gov/study/NCT04658667?cond=HIV&intr=vaccine&ggFilters=status:rec%20act%20not,studyType:int&rank=5 |

| Family | Pathogen | Vaccine name | Platform | Phase of development | Developer | Source |
|--------------|------------------------|---|--------------------------------------|----------------------|---|---|
| Retroviridae | Lentivirus humimdef1 | VIR 1388 | DNA | Phase 1 | Vir Biotechnology, Inc. | https://clinicaltrials.gov/study/NCT05854381?cond=HIV&intr=vaccine&ggFilters=status:rec%20act%20not,studyType:int&rank=26 |
| Retroviridae | Lentivirus humimdef1 | Env-C Plasmid DNA and HIV Env gp145 C690 protein | Engineered immunogen | Phase 1 | NIAID | https://clinicaltrials.gov/study/NCT04826094?cond=HIV&intr=vaccine&ggFilters=status:rec%20act%20not,studyType:int&rank=15 |
| Retroviridae | Lentivirus humimdef1 | eOD-GT8 60mer | mRNA | Phase 1 | IAVI | https://pubmed.ncbi.nlm.nih.gov/37224227/ |
| Retroviridae | Lentivirus humimdef1 | mRNA- 1644/v2-Core | mRNA | Phase 1 | IAVI, Moderna | NCT05001373 |
| Retroviridae | Lentivirus humimdef1 | BG505 MD39.3 mRNA, BG505 MD39.3 gp151 mRNA or BG505 MD39.3 gp151 CD4KO mRNA | Recombinant | Phase 1 | NIAID | https://clinicaltrials.gov/study/NCT05217641?cond=HIV&intr=vaccine&ggFilters=status:rec%20act%20not,studyType:int&rank=17 |
| Retroviridae | Lentivirus humimdef1 | SOSIP v8.2 763 | | Phase 1 | Fundacion Clinic per a la Recerca Biomédica | https://clinicaltrials.gov/study/NCT05772286?cond=HIV&intr=vaccine&ggFilters=status:rec%20act%20not,studyType:int&rank=35 |
| Retroviridae | Lentivirus humimdef1 | EHVA P01 | | Phase 1 | ANRS, Emerging Infectious Diseases | https://clinicaltrials.gov/study/NCT04844775?cond=HIV&intr=vaccine&ggFilters=status:rec%20act%20not,studyType:int&rank=43 |
| Retroviridae | Lentivirus humimdef1 | CH505TF gp120, adjuvanted with GLA-SE | Adenovirus vector | Phase 1 | HIV Vaccine Trials Network | https://clinicaltrials.gov/study/NCT04607408?cond=HIV&intr=vaccine&ggFilters=status:rec%20act%20not,studyType:int&rank=16 |
| Retroviridae | Lentivirus humimdef1 | Ad26.Mos4.HIV prime and a boost with Modified Vaccinia Ankara (MVA)-BN-HIV | Bivalent subunit vaccine | Phase 1/2a | Janssen Pharmaceuticals | https://clinicaltrials.gov/study/NCT04983030?cond=HIV&intr=vaccine&ggFilters=status:rec%20act%20not,studyType:int&rank=30 |
| Retroviridae | Lentivirus humimdef1 | AIDSVAX B/E | Prime-boost (viral vector + subunit) | Phase 3 | VaxGen | NCT00006327, NCT00002441 |
| Retroviridae | Lentivirus humimdef1 | ALVAC-HIV + AIDSVAX B/E | Live attenuated | Phase 3 | Sanofi Pasteur, VaxGen | NCT00223080 |
| Togaviridae | Alphavirus chikungunya | Ixchiq | mRNA | Licensed | Valneva Austria GmbH | https://www.fda.gov/news-events/press-announcements/fda-approves-first-vaccine-prevent-disease-caused-chikungunya-virus |
| Togaviridae | Alphavirus chikungunya | mRNA- 1388 | mRNA | Phase 1 | Moderna | https://pubmed.ncbi.nlm.nih.gov/37210308/ |
| Togaviridae | Alphavirus chikungunya | mRNA-1944 | Viral Vector | Phase 1 | Moderna | https://pubmed.ncbi.nlm.nih.gov/34887572/ |
| Togaviridae | Alphavirus chikungunya | ChAdOx1 Chik | Viral Vector | Phase 1 | University of Oxford | https://classic.clinicaltrials.gov/ct2/show/NCT04440774 |
| Togaviridae | Alphavirus chikungunya | MV-CHIK | Virus-like particle (VLP) | Phase 2 | Themis Bioscience GmbH | https://pubmed.ncbi.nlm.nih.gov/30409443/ |
| Togaviridae | Alphavirus chikungunya | PXVX0317 CHIKV-VLP | DNA | Phase 2 | Bavarian Nordic | https://clinicaltrials.gov/study/NCT03483961 |
| Togaviridae | Alphavirus venezuelan | VEE DNA Vaccine | VLP | Phase 1 | US Dept of Defense | https://clinicaltrials.gov/study/NCT00582504?cond=Venezuelan%20Equine%20Encephalitis&rank=3 |
| Togaviridae | Alphavirus venezuelan | VRC-WEV VLP073-00-VP | VLP | Phase 1 | NIAID | https://clinicaltrials.gov/study/NCT03879603?cond=Venezuelan%20Equine%20Encephalitis&rank=6 |
| Togaviridae | Alphavirus venezuelan | VEE VLP Vaccine | Modified Vaccinia Ankara (MVA) | Phase 1 | SRI International | https://clinicaltrials.gov/study/NCT03776994?cond=Venezuelan%20Equine%20Encephalitis&rank=8 |
| Togaviridae | Alphavirus venezuelan | MVA-BN WEV | Multiple | Phase 2 | Bavarian Nordic | https://www.bavarian-nordic.com/investor/news/news.aspx?news=6667 |
| Togaviridae | Alphavirus venezuelan | Multiple | | Preclinical | Multiple | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7350001/ |

Candidate therapeutics

| Family | Pathogen | Treatment | Phase of development | Resource |
|---------------|----------------------------------|---|-------------------------|---|
| Arenaviridae | Mammarenavirus lassaense | Ribavirin | Off-Label Use/Phase 2/3 | NCT06212336 |
| Arenaviridae | Mammarenavirus lassaense | LHF-535 | Phase 1 | pubmed.ncbi.nlm.nih.gov/36314868/ |
| Arenaviridae | Mammarenavirus lassaense | Dexamethasone | Phase 2 | NCT06222723 |
| Arenaviridae | Mammarenavirus lassaense | Favipiravir | Phase 2/3 | NCT06212336; NCT06222723 |
| Arenaviridae | Mammarenavirus lassaense | ARN-75309 | Phase 1 | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Bacteria | Klebsiella Pneumonia | Antibiotics (multiple) | Licensed | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10960543/ |
| Bacteria | Klebsiella Pneumonia | Phage Therapy | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10960543/ |
| Bacteria | Klebsiella Pneumonia | Traditional Chinese Medicine | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10960543/ |
| Bacteria | Klebsiella Pneumonia | Antimicrobial Nanoparticle Technology | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10960543/ |
| Bacteria | Klebsiella Pneumonia | Antisense Oligonucleotides & Gene Editing Technologies | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10960543/ |
| Bacteria | Klebsiella Pneumonia | Novel Antibiotics | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10960543/ |
| Bacteria | Klebsiella Pneumonia | Antimicrobial peptides | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10960543/ |
| Bacteria | Shigella Dysenteria 1 | Antibiotics (multiple) | Licensed | |
| Bacteria | Vibrio Cholerae (sero 0139) | Antibiotics (Azithromycin) | Licensed | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5972638/ |
| Bacteria | Vibrio Cholerae (sero 0139) | Antibiotics (Erythromycin) | Licensed | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5972638/ |
| Bacteria | Yersinia Pestis (Plague) | Antibiotics | Licensed | https://www.who.int/health-topics/plague#tab=tab_3 |
| Nairoviridae | Orthonairovirus haemorrhagiae | Ribavirin | Off-Label Use/Phase 1 | https://kce.fgov.be/sites/default/files/2023-03/ADVISE_Ribavirin%20LF-CCHF_FINAL.pdf; clinicaltrials.gov/study/NCT05940545?cond=cchf&rank=1 |
| Nairoviridae | Orthonairovirus haemorrhagiae | Favipiravir | Phase 1 | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10013989/ |
| Nairoviridae | Orthonairovirus haemorrhagiae | Antibody-based therapies | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10013989/ |
| Nairoviridae | Orthonairovirus haemorrhagiae | 2'-Deoxy-2'- fluorocytidine | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10013989/ |
| Nairoviridae | Orthonairovirus haemorrhagiae | Molnupiravir | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10013989/ |
| Nairoviridae | Orthonairovirus haemorrhagiae | Corticosteroids | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10013989/ |
| Phenuiviridae | Bandavirus dabieense | Plasma Exchange | Ad Hoc use | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9510271/ |
| Phenuiviridae | Bandavirus dabieense | Favipiravir | Clinical Use | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9510271/ |
| Phenuiviridae | Bandavirus dabieense | Ribavirin | Clinical Use | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9510271/ |

| Family | Pathogen | Treatment | Phase of development | Resource |
|---------------|----------------------------------|--|----------------------|--|
| Phenuiviridae | Bandavirus dabieense | methylprednisolone/IVI G/tocilizumab/heparin | Phase 4 | https://clinicaltrials.gov/study/NCT05604859?cond=sfts%20virus&rank=1 |
| Phenuiviridae | Bandavirus dabieense | Fludarabine | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9510271/ |
| Phenuiviridae | Bandavirus dabieense | nifedipine | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9510271/ |
| Phenuiviridae | Bandavirus dabieense | Quinoline Analogues | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9510271/ |
| Coronaviridae | Sarbecoviruses | mAbs binding hACE2 | Preclinical | https://www.nature.com/articles/s41564-023-01389-9 |
| Filoviridae | Orthoebolavirus zairens | Inmazeb (Atoltivimab, Maffivimab, and Odesivimab-ebgn) | Licensed | https://pubmed.ncbi.nlm.nih.gov/31774950/ |
| Filoviridae | Orthoebolavirus zairens | mAb114 - ansuvimab (Ebanga) | Licensed | journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1012038#sec005 |
| Filoviridae | Orthoebolavirus zairens | MBP134 | Phase 1/2 | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6341996/ |
| Filoviridae | Orthoebolavirus zairens | Galidesivir | Preclinical | journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1012038#sec005 |
| Filoviridae | Orthoebolavirus zairens | GP inhibitors | Preclinical | journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1012038#sec005 |
| Filoviridae | Orthoebolavirus zairens | Bispecific antibody targeting GP and NPV-1 | Preclinical | journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1012038#sec005 |
| Filoviridae | Orthoebolavirus zairens | Adaptor-associated kinase 1 (AAK1) inhibitors | Preclinical | journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1012038#sec005 |
| Filoviridae | Orthomarburgvirus marburgense | Galidesivir | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9949811/ |
| Filoviridae | Orthomarburgvirus marburgense | Favipiravir | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9949811/ |
| Filoviridae | Orthomarburgvirus marburgense | mAbs | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9949811/ |
| Filoviridae | Orthomarburgvirus marburgense | siRNA | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9949811/ |
| Filoviridae | Orthomarburgvirus marburgense | antisense PMOs | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9949811/ |
| Filoviridae | Orthoebolavirus sudanense | Inmazeb (Atoltivimab, Maffivimab, and Odesivimab-ebgn) | Licensed for Zaire | https://pubmed.ncbi.nlm.nih.gov/31774950/ |
| Filoviridae | Orthoebolavirus sudanense | mAb114 - ansuvimab (Ebanga) | Licensed for Zaire | journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1012038#sec005 |
| Filoviridae | Orthoebolavirus sudanense | MBP134 | Phase 1/2 | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6341996/ |
| Filoviridae | Orthoebolavirus sudanense | Galidesivir | Preclinical | journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1012038#sec005 |
| Filoviridae | Orthoebolavirus sudanense | GP inhibitors | Preclinical | journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1012038#sec005 |
| Filoviridae | Orthoebolavirus sudanense | Bispecific antibody targeting GP and NPV-1 | Preclinical | journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1012038#sec005 |
| Filoviridae | Orthoebolavirus sudanense | Adaptor-associated kinase 1 (AAK1) inhibitors | Preclinical | journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1012038#sec005 |

| Family | Pathogen | Treatment | Phase of development | Resource |
|--------------|---------------------------|---|--------------------------------|---|
| Filoviridae | Orthoebolavirus sudanense | Adaptor-associated kinase 1 (AAK1) inhibitors | Preclinical | journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1012038#sec005 |
| Flaviviridae | Orthoflavivirus denguei | EYU688 | Phase 2 | https://clinicaltrials.gov/study/NCT06006559?cond=dengue&start=2020-01-01_&aggFilters=phase:0%201%203%202,status:com%20act.studyType:int&rank=2 |
| Flaviviridae | Orthoflavivirus denguei | Montelukast | Phase 2/3 | https://clinicaltrials.gov/study/NCT04673422?cond=dengue&start=2020-01-01_&aggFilters=phase:0%201%203%202,status:com%20act.studyType:int&rank=12 |
| Flaviviridae | Orthoflavivirus denguei | AV-1 (monoclonal antibody) | Phase 1 | https://clinicaltrials.gov/study/NCT04273217?cond=dengue&start=2020-01-01_&aggFilters=phase:0%201%203%202,status:com%20act.studyType:int&rank=17 |
| Flaviviridae | Orthoflavivirus denguei | Carica Papaya | Phase 3 | https://clinicaltrials.gov/study/NCT06121934?cond=dengue&start=2020-01-01_&aggFilters=phase:0%201%203%202,status:com%20act.studyType:int&rank=1 |
| Flaviviridae | Orthoflavivirus denguei | JNJ-64281802 | Phase 2 | https://pubmed.ncbi.nlm.nih.gov/37124673/ |
| Flaviviridae | Orthoflavivirus denguei | Ivermectin | Phase 2/3 | https://pubmed.ncbi.nlm.nih.gov/37124673/ |
| Flaviviridae | Orthoflavivirus denguei | AT-752 | Phase 2 | https://pubmed.ncbi.nlm.nih.gov/37124673/ |
| Flaviviridae | Orthoflavivirus denguei | Doxycycline | Phase 2 | https://pubmed.ncbi.nlm.nih.gov/37124673/ |
| Flaviviridae | Orthoflavivirus denguei | Eltrombopag | Phase 2 | https://pubmed.ncbi.nlm.nih.gov/37124673/ |
| Flaviviridae | Orthoflavivirus denguei | UV-4B | Phase 1 | https://pubmed.ncbi.nlm.nih.gov/37124673/ |
| Flaviviridae | Orthoflavivirus denguei | Zanamivir | Phase 1 | https://pubmed.ncbi.nlm.nih.gov/37124673/ |
| Flaviviridae | Orthoflavivirus denguei | VIS513 | Phase 1 | https://pubmed.ncbi.nlm.nih.gov/37124673/ |
| Flaviviridae | Orthoflavivirus denguei | Ketotifen | Phase 4 | https://pubmed.ncbi.nlm.nih.gov/37124673/ |
| Flaviviridae | Orthoflavivirus denguei | Rupatadine | | https://pubmed.ncbi.nlm.nih.gov/37124673/ |
| Flaviviridae | Orthoflavivirus denguei | Metformin | Phase 1/2 | https://pubmed.ncbi.nlm.nih.gov/37124673/ |
| Flaviviridae | Orthoflavivirus denguei | Vitamin E | | https://pubmed.ncbi.nlm.nih.gov/37124673/ |
| Flaviviridae | Orthoflavivirus denguei | Vitamin D | | https://pubmed.ncbi.nlm.nih.gov/37124673/ |
| Flaviviridae | Orthoflavivirus zikaense | Polyanion suramin | Approved antiparasitic drug | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | Brcomocriptine | Preclinical | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | Novobiocin | Clinically used antibiotic | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | Compounds 1 and 2 | Preclinical | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | Asunaprevir and simeprevir | FDA-approved | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | Sofosbuvir | FDA-approved for HCV infection | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | 4-HPR | Preclinical | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |

| Family | Pathogen | Treatment | Phase of development | Resource |
|------------------|--------------------------------|------------------------|----------------------------------|---|
| Flaviviridae | Orthoflavivirus zikaense | 3-110-22 | Preclinical | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | ZINC 40621658 | Preclinical | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | Atovaquone | FDA-approved for malaria | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | Phloretin | Preclinical | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | MTX | Clinical use for other treatment | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | JG40, JG132, and JG345 | Preclinical | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | QC, MQ, and GSK369796 | FDA approved for malaria | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | Memantine | Approved for other diseases | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | A-12 | Phase 1 for cancer | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Flaviviridae | Orthoflavivirus zikaense | MMPD | FDA approved for HCV infection | https://www.frontiersin.org/articles/10.3389/fcimb.2022.946957/full |
| Orthomyxoviridae | Alphainfluenzavirus influenzae | GP681 | Phase 3 | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Orthomyxoviridae | Alphainfluenzavirus influenzae | ZX-7101A | Phase 3 | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Orthomyxoviridae | Alphainfluenzavirus influenzae | CC-42344 | Phase 1 | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Orthomyxoviridae | Alphainfluenzavirus influenzae | HCN042 | Phase 2 | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Orthomyxoviridae | Alphainfluenzavirus influenzae | Amantadine | Licensed | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Orthomyxoviridae | Alphainfluenzavirus influenzae | Baloxavir Marboxil | Licensed | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Orthomyxoviridae | Alphainfluenzavirus influenzae | Favipiravir | Licensed | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Orthomyxoviridae | Alphainfluenzavirus influenzae | Laninamivir | Licensed | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Orthomyxoviridae | Alphainfluenzavirus influenzae | Oseltamivir | Licensed | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Orthomyxoviridae | Alphainfluenzavirus influenzae | Peramivir | Licensed | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |

| Family | Pathogen | Treatment | Phase of development | Resource |
|------------------|--------------------------------|---------------------------------|---|---|
| Orthomyxoviridae | Alphainfluenzavirus influenzae | Rimantadine | Licensed | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Orthomyxoviridae | Alphainfluenzavirus influenzae | Zanamivir | Licensed | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Orthomyxoviridae | Alphainfluenzavirus influenzae | Enisamium (VR17-04) | Licensed by other international authority | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Orthomyxoviridae | Alphainfluenzavirus influenzae | Triazavirin | Licensed by other international authority | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Orthomyxoviridae | Alphainfluenzavirus influenzae | Umifenovir | Licensed by other international authority | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Paramyxoviridae | Henipavirus nipahense | Ribavirin (antiviral) | Clinical trials | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |
| Paramyxoviridae | Henipavirus nipahense | Remdesivir (antiviral) | Preclinical | https://www.science.org/doi/epdf/10.1126/scitranslmed.aau9242?src=getftr |
| Paramyxoviridae | Henipavirus nipahense | Favipiravir | Preclinical | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |
| Paramyxoviridae | Henipavirus nipahense | Chloroquine | Preclinical | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |
| Paramyxoviridae | Henipavirus nipahense | Heparin | Preclinical | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |
| Paramyxoviridae | Henipavirus nipahense | Rintatolimid | Preclinical | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |
| Paramyxoviridae | Henipavirus nipahense | Griffithsin | Preclinical | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |
| Paramyxoviridae | Henipavirus nipahense | VIKI-dPEG4-Toco, VIKI-PEG4-chol | Preclinical | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |
| Paramyxoviridae | Henipavirus nipahense | Glilotoxin | Preclinical | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |
| Paramyxoviridae | Henipavirus nipahense | Bortezomib | Preclinical | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |
| Paramyxoviridae | Henipavirus nipahense | Balapiravir | Preclinical | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |
| Paramyxoviridae | Henipavirus nipahense | Lumicitabine | Preclinical | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |
| Paramyxoviridae | Henipavirus nipahense | CH25H | Preclinical | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |
| Paramyxoviridae | Henipavirus nipahense | KIN1408 | Preclinical | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |

| Family | Pathogen | Treatment | Phase of development | Resource |
|-----------------|--------------------------|---|-----------------------|---|
| Paramyxoviridae | Henipavirus nipahense | Sulfonamide compounds | Preclinical | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |
| Paramyxoviridae | Henipavirus nipahense | Monoclonal Antibodies | Preclinical | https://www.sciencedirect.com/science/article/pii/S147330992100400X?dgcid=author |
| Picomaviridae | Enterovirus coxsackiepol | V-7404 | Phase 1 | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Picomaviridae | Enterovirus coxsackiepol | Pocapavir | Phase 1 | https://www.intrepidalliance.org/wp-content/uploads/2024/04/INTREPID-Alliance-Antiviral-Clinical-Development-Landscape-29APR2024.pdf |
| Poxviridae | Orthopoxvirus Monkeypox | Cidofovir | Off label use | https://www.mdpi.com/1999-4915/15/4/937 |
| Poxviridae | Orthopoxvirus Monkeypox | Brincidofovir | Off label use/Phase 1 | https://www.mdpi.com/1999-4915/15/4/937 |
| Poxviridae | Orthopoxvirus Monkeypox | Tecovirimat | Off label use/Phase 3 | https://www.mdpi.com/1999-4915/15/4/937 |
| Poxviridae | Orthopoxvirus Monkeypox | VIGIV | Off label use | https://www.mdpi.com/1999-4915/15/4/937 |
| Retroviridae | Lentivirus humimdef1 | Nucleoside Reverse Transcriptase Inhibitors | Licensed | https://www.fda.gov/consumers/free-publications-women/hiv-and-aids-medicines-help-you |
| Retroviridae | Lentivirus humimdef1 | Non-Nucleoside Reverse Transcriptase Inhibitors | Licensed | https://www.fda.gov/consumers/free-publications-women/hiv-and-aids-medicines-help-you |
| Retroviridae | Lentivirus humimdef1 | Protease Inhibitors | Licensed | https://www.fda.gov/consumers/free-publications-women/hiv-and-aids-medicines-help-you |
| Retroviridae | Lentivirus humimdef1 | Fusion Inhibitors | Licensed | https://www.fda.gov/consumers/free-publications-women/hiv-and-aids-medicines-help-you |
| Retroviridae | Lentivirus humimdef1 | CCR5 Antagonists | Licensed | https://www.fda.gov/consumers/free-publications-women/hiv-and-aids-medicines-help-you |
| Retroviridae | Lentivirus humimdef1 | Integrase Strand Transfer Inhibitor (INSTIs) | Licensed | https://www.fda.gov/consumers/free-publications-women/hiv-and-aids-medicines-help-you |
| Retroviridae | Lentivirus humimdef1 | Attachment Inhibitors | Licensed | https://www.fda.gov/consumers/free-publications-women/hiv-and-aids-medicines-help-you |
| Retroviridae | Lentivirus humimdef1 | Post-Attachment Inhibitors | Licensed | https://www.fda.gov/consumers/free-publications-women/hiv-and-aids-medicines-help-you |
| Retroviridae | Lentivirus humimdef1 | Capsid Inhibitors | Licensed | https://www.fda.gov/consumers/free-publications-women/hiv-and-aids-medicines-help-you |
| Retroviridae | Lentivirus humimdef1 | Pharmacokinetic Enhancers | Licensed | https://www.fda.gov/consumers/free-publications-women/hiv-and-aids-medicines-help-you |
| Retroviridae | Lentivirus humimdef1 | Gene Therapy | Preclinical | https://medicine.wustl.edu/news/6-2-million-to-help-develop-gene-therapy-for-hiv/ |
| Retroviridae | Lentivirus humimdef1 | Immunotherapy | Preclinical | https://health.ucdavis.edu/news/headlines/clinical-trial-begins-using-car-t-cells-to-potentially-cure-hiv/2023/04 |
| Togaviridae | Alphavirus chikungunya | Several antivirals | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8310245/ |
| Togaviridae | Alphavirus venezuelan | Small molecule antiviral | Preclinical | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9958955/ |

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