## COMBATTING EMERGING BIOLOGICAL THREATS – PREPARING FOR THE FUTURE TODAY

# Using Open Source Data To Characterize And Identify Gaps In Viral Family Research And Medical Countermeasures

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Viral outbreaks–especially zoonosis of rarely studied viruses–represent a growing threat to public health and national security as humans increasingly encroach on animal habitats and society deals with a changing climate. Effective government responses will require better understanding—and information–on the depth and breadth of viral research worldwide, as well as gaps in that research. Our efforts are geared towards generating actionable information for policymakers and the warfighter that will help decision-makers understand the potential threats of both naturally occurring zoonosis and potential lab accidents.

Methodology: As a way to characterize the current state of viral research worldwide we investigated the research and development landscape of viral families with vertebrate hosts using CSET's open source data holdings. In this approach we examine research publications, patent datasets, clinical trials, and medical countermeasures using viral family taxonomy from the International Committee on Taxonomy of Viruses. We further analyze this body of research by country and year to examine trends in virus research and development to highlight the focus of different viral families over time.

Objective: Our study focuses on viral families rather than individual viruses because it provides a more complete picture for researchers of both those viruses that have pandemic potential and what countermeasures and therapeutics are either available, in development or are lacking. Historically, viruses that have jumped from animals to humans are within the same viral families as current human-infecting viruses. However, current vaccines and other biological countermeasures address only known viruses that infect humans, but not other viruses in known families that have similarities and also have the potential to cause pandemics or public harm. Our initial research illustrates that the U.S and China lead the world in studies on viral families, specifically respiratory viruses. However, the U.S lags behind China and Europe in studies on respiratory viral families that have caused previous pandemics: coronaviridae (SARS, MERS, COVID-19) and orthomyxoviridae (influenza viruses). Additionally, work on viruses in the coronaviridae family prior to 2020 accounted for only 423 studies, 86 clinical trials, and 0 U.S vaccines, but in 2022 now total over 1,200 publications, 6,800 clinical trials, and 2 approved U.S vaccines.

As a central part of DTRA's mission is to deter emerging biological threats, our work–by characterizing the current landscape and gaps of work on viral families—will provide decision space and generate actionable information to both protect the war fighter in exotic locales, as well as contribute to pandemic preparedness. This information will aid policymakers and the war-fighter to create actionable strategies that focus on viral families and to develop a robust medical countermeasure for future viral outbreaks and pandemic.  By focusing on countermeasures for viral families instead of individual variants, our pandemic prevention efforts will be more flexible and better suited to future challenges.