

Using Genetic Diversity of SARS-CoV-2 to evaluate the effectiveness of specific travel measures in mitigating public health risks during the COVID-19 pandemic

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Background

Previous public health emergencies of international concern (PHEICs) show that effective global responses require coordinated action across countries. The International Health Regulations (IHR), revised in 2005, is the legal framework for the coordination of global efforts “to prevent, protect against, control and provide a public health response to the international spread of disease”. Administered by the World Health Organization (WHO), one function of the IHR (2005) is “to avoid unnecessary interference with international traffic.” Inappropriate use of travel restrictions cause avoidable economic and social impacts. Their uncoordinated use can also hinder reporting of notifiable disease events, increase disease transmission risks, and even prolong PHEICs. As adherence to, and impacts of, public health measures are not always easy to measure, genomic data provides an alternative indicator of the effectiveness of travel measures. For example, an uptick in genetic diversity indicates a new virus clade being introduced and may correspond to a lapse or failure in travel measures. We here propose to enable genomic epidemiology to a broader context incorporating epidemiological, political, and other contextual information to improve public health preventive measures.

SARS-CoV-2 Genomic Sequencing Data

- ❖ Since the first genome of SARS-CoV-2 was sequenced and released in January 2020, ~ **10 million more genomes** have been deposited to the public repository, GISAID.

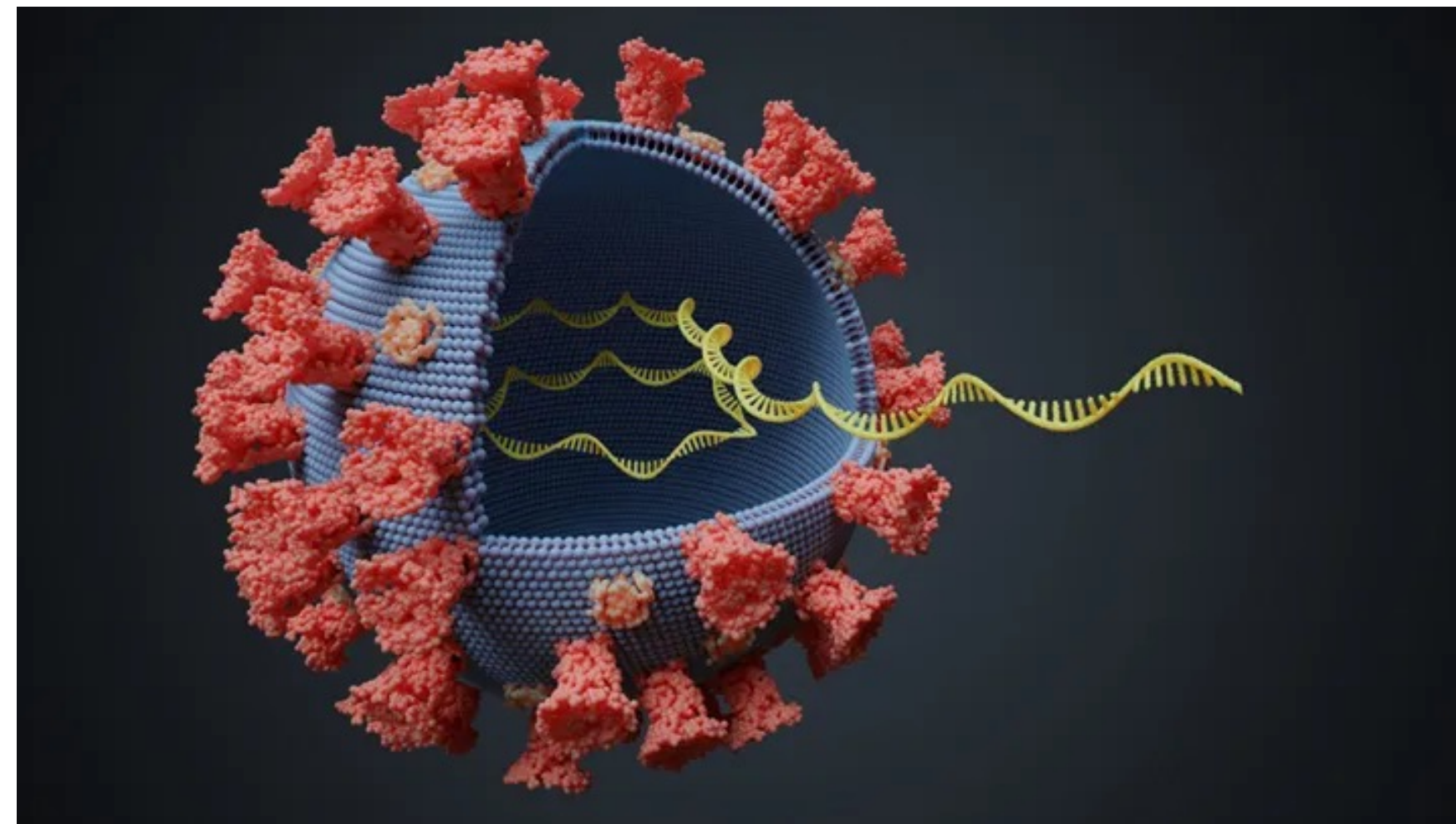
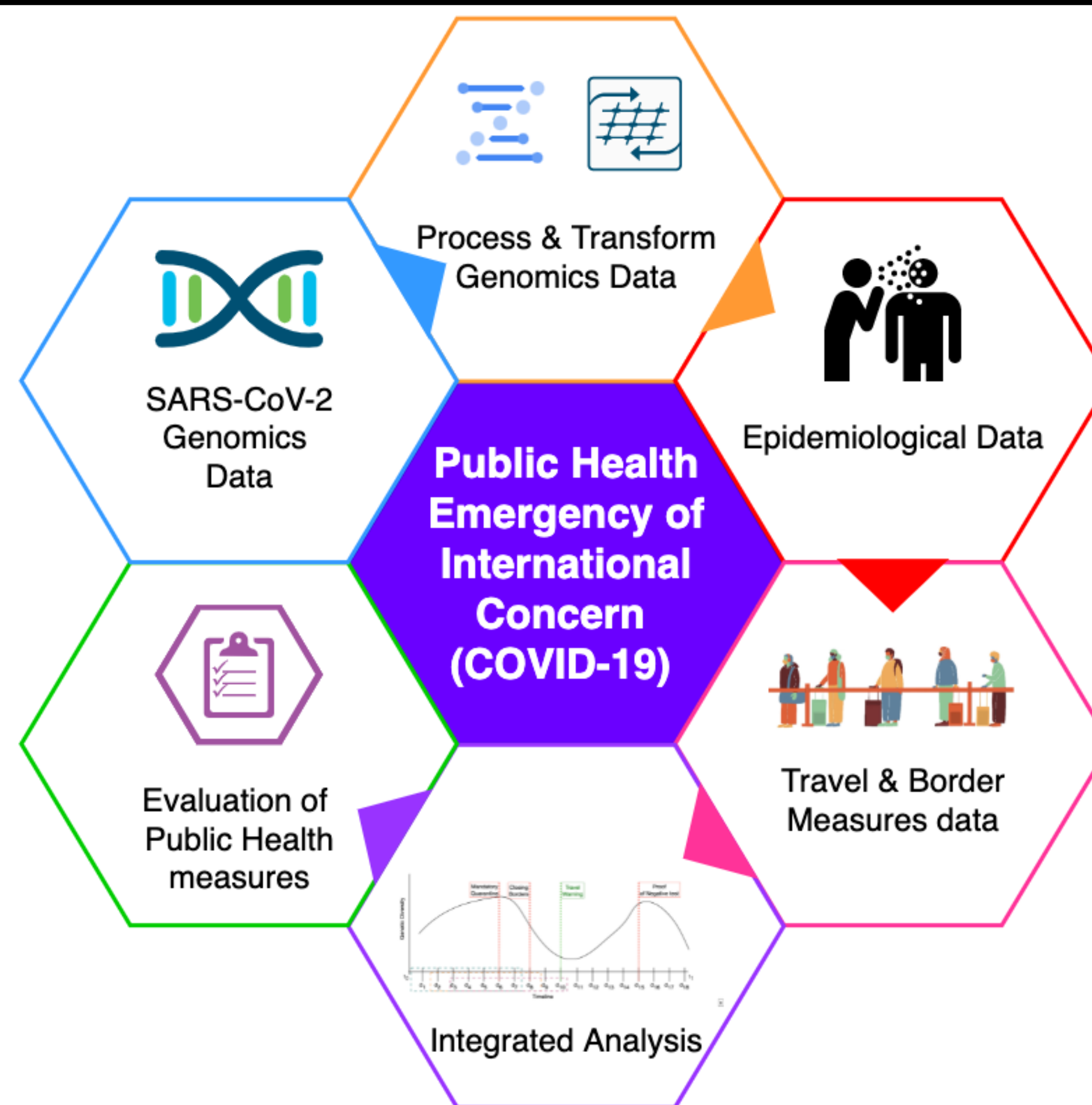


Image courtesy: iStock/vchal

- ❖ Analytical power of genomic epidemiology combined has been applied to shed light on SARS-CoV-2 *spread, dynamics of epidemics, possible sources, times, and geographic origins of emergence.*
- ❖ COVID-19 pandemic has also highlighted key gaps in our ability to use genomic epidemiology efficiently including the ability to **integrate interdisciplinary data** e.g., epidemiological or policy data.
- ❖ Integrating data from genomic sequences, case counts, information about sequencing density and how isolates are selected for sequencing, and public health measures can help in developing *methods and analyses to inform decision-making on using travel measures during major public health emergencies.*

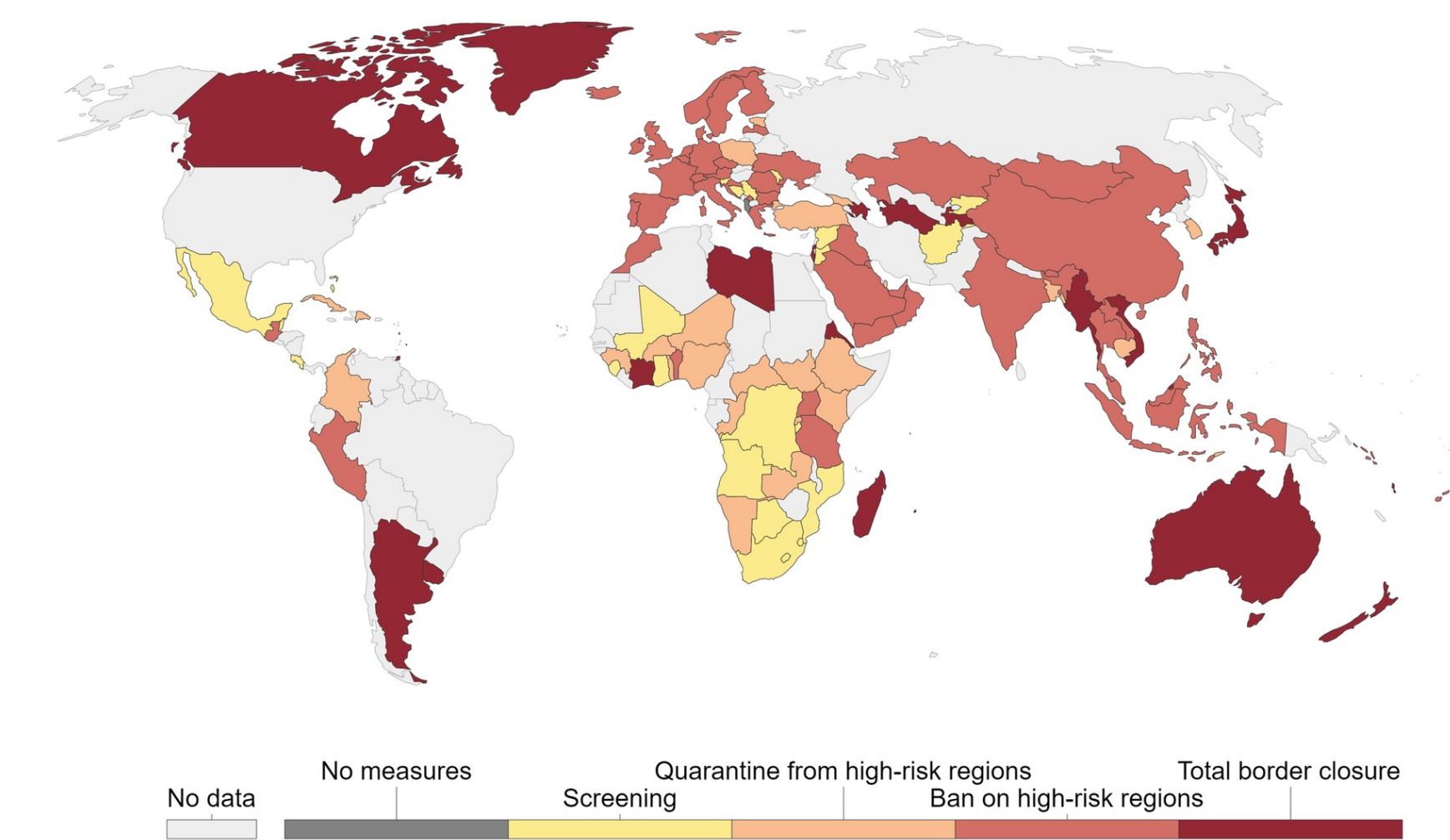
Methodology



Using the bioinformatics expertise, I aim to process genomics data and transform into a sample matrix that is able to integrate epidemiological and travel & orders measure data and evaluate public health preventive measures during COVID-19 pandemics.

Travel & Border Measures

International travel controls during the COVID-19 pandemic, Jun 6, 2021



Source: Hale, Angrist, Goldszmidt, Kira, Petherick, Phillips, Webster, Cameron-Blake, Hallas, Majumdar, and Tatlow (2021). "A global panel database of pandemic policies (Oxford COVID-19 Government Response Tracker)." *Nature Human Behaviour*. – Last updated 7 June, 00:00 (London time)
OurWorldInData.org/coronavirus - CC BY

- ❖ When declaring SARS-CoV-2 (COVID-19) a PHEIC on 30 January 2020, the WHO Emergency Committee initially did **“not recommend any travel or trade restriction based on the current information available.”**
- ❖ Despite this recommendation, travel measures have been applied to an unprecedented degree compared with previous PHEICs.
- ❖ During the H1N1 (2009) and Ebola (2014) outbreaks, up to 31% of countries adopted travel or trade restrictions. By contrast, since WHO declared COVID-19 a pandemic on 11 March 2020, and despite legal scholars warning that travel restrictions violate IHR Article virtually all countries including Canada have adopted them.

Acknowledgments

- ❖ We would like to thank members of Pandemics & Borders Project for their valuable collaboration & feedback. <https://www.pandemics-borders.org/> (Thanks to Juliet Fowler for creating project images)
- ❖ We would also like to thank New Frontiers in Research Fund and the Canadian Institutes of Health Research for funding this study.
- ❖ VirusSeq Data Portal team and Canadian Public Health Laboratory Network (CPHLN) members and staffs having contributed data to the portal.

Contact & Funding

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