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*Commentary***Virus transmission and evolution around the world****Lalitha Bull***

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DESCRIPTION

The frequency and global impact of infectious disease outbreaks, particularly those produced by emerging viruses, highlight the need for a better understanding of how pathogen evolution and spatial ecology interact to determine epidemic dynamics. Advances in computer approaches, as well as the increased availability of genetic and geographical data, are assisting in the solution of this challenge, especially when the two data sets are merged. We look at research at the interface of evolutionary biology, human geography, and epidemiology that is aiming for a holistic perspective of viral genetic diversity, host mobility, and geographical incidence. We begin by discussing how empirical investigations have merged viral geographical and genetic data, with a special focus on evolutionary analyses' contribution to epidemiology and disease prevention. Second, we look at the relationship between virus evolution and worldwide spread for two pathogens; human influenza. A virus and chikungunya virus in further detail (Jones et al., 2008). We explore future research possibilities coming from new analyses of human mobility and commerce networks, as well as the obstacles of obtaining and sharing important spatial and genetic data.

Researchers and the general public alike recognise the effects of international trade and travel on infectious disease dynamics. Viruses have greater opportunity than ever before to spread globally in today's highly mobile society, with over half a million people in the air at any given time. Over the last century, advances in the reach, volume, and speed of human migration have linked diseases to new and expanding host populations, contributing to an increase in new and re-emerging epidemics (Holmes, 2004).

The increased interconnection of our globe has a variety of effects on transmission. More pathogen introductions result

from increased mobility due to business travel, tourism, and labour movement, whereas social and ecological changes in recipient locations may increase the risk of introductions becoming established rather than dying out. The creation of new travel routes connecting previously unconnected areas also helps now connects tropical continental regions with greater infectious disease (Pybus et al., 2009) loads and year-round transmission.

In addition to providing critical information for vaccine development, global influenza virus surveillance has resulted in an unprecedented collection of virus genome sequences sampled across space and time, allowing researchers to investigate the processes that underpin the global dynamics of this important pathogen (Brockmann et al., 2013).

Access to growing spatially linked datasets of disease prevalence, detailed satellite-based imagery, and unparalleled information on human mobility patterns are helping us better understand and assess the risks of infectious disease spread (Geisel et al., 2006). Integration of various sources of data with viral genetic data (Guillot et al., 2009) will be difficult both technically and conceptually, but it holds great potential for our ability to respond to developing viruses (Slatkin, 1993).

Infectious illness outbreaks, particularly those caused by viruses, are a common occurrence in the twenty-first century, and future trends in global mobility and trade are likely to keep or perhaps speed up their frequency. Techniques and data that may be used to characterise, analyse, and anticipate such events can aid in measuring and mitigating the dangers posed by novel and re-emerging viruses (Duffy et al., 2008). Statistical and mathematical models that combine spatially explicit data on pathogen evolution with information on human movement and environmental variability can help with epidemic control while also improving our understanding of fundamental evolutionary and ecological processes.

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