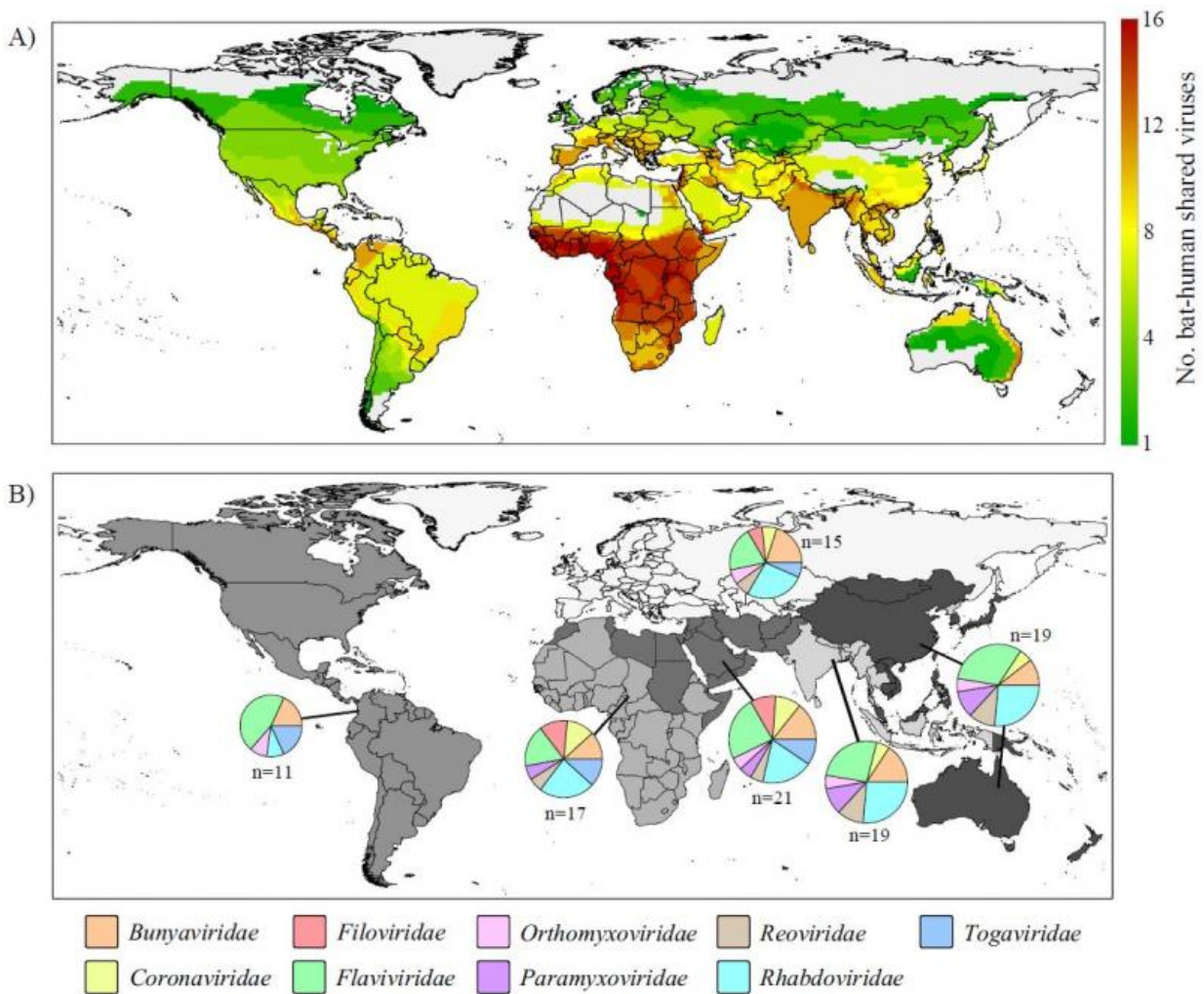


# Map shows hotspots for bat-human virus transmission risk

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Distributions of bat-human virus sharing showing a) numbers of bat-human shared viruses at one-degree grid resolution. Color represents a linear scale from 1 (green) to 16 (red); b) composition of viruses by family within the 6 WHO World Regions, where size of charts is proportional to number of viruses.

Shading denotes region (from lightest to darkest: Europe, South Asia, Africa, Americas, Eastern Mediterranean, Western Pacific) while colors denote viral family (see key). Credit: Liam Brierley et al.

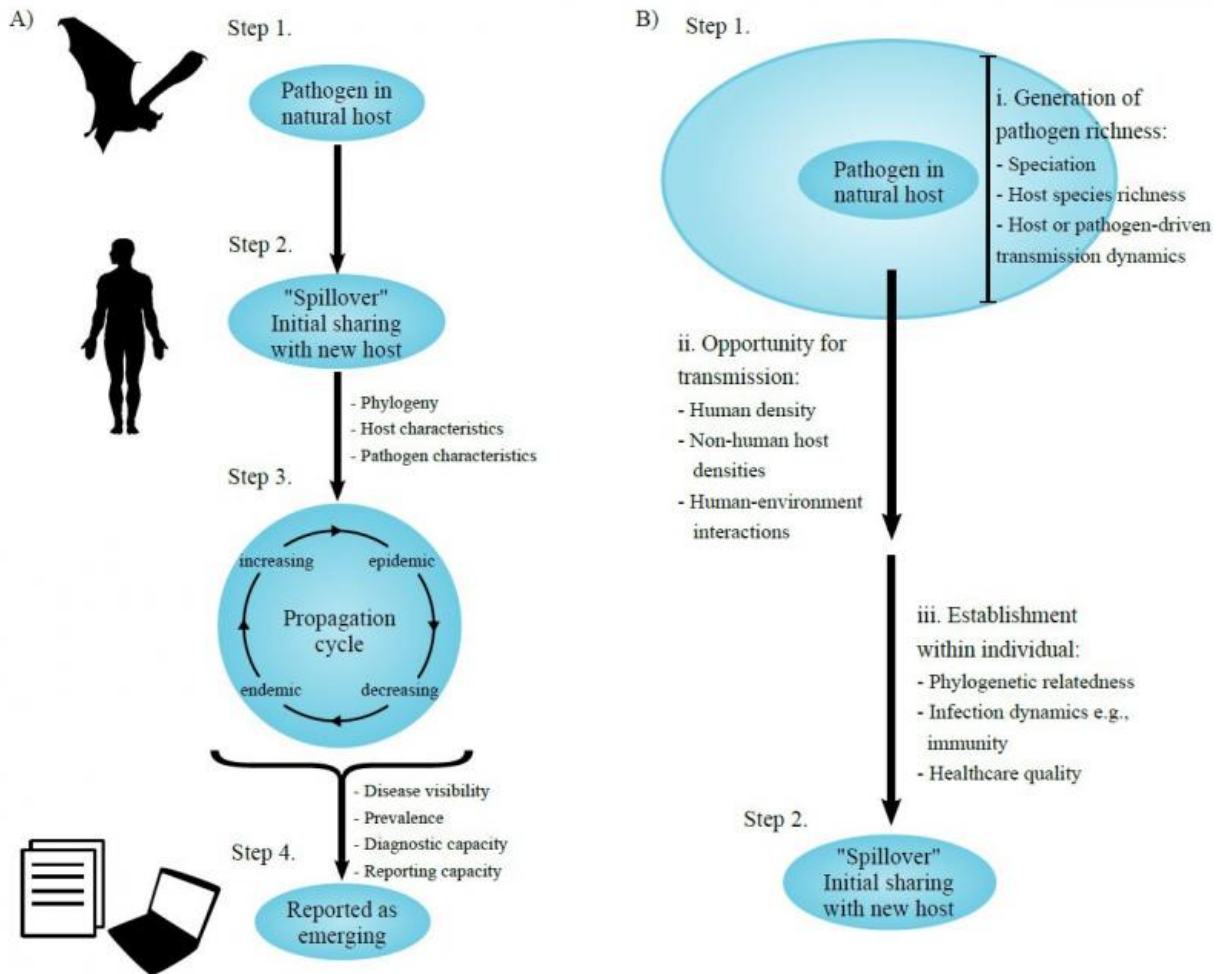
West Africa, sub-Saharan Africa and South East Asia are most at risk from bat viruses 'spilling over' into humans resulting in new emerging diseases, according to a new global map compiled by scientists at UCL, the Zoological Society of London (ZSL) and the University of Edinburgh. The map shows risk levels due to a variety of factors including large numbers of different bat viruses found locally, increasing population pressure, and hunting bats for bushmeat.

Approximately 60-75% of reported human emerging infectious diseases (EIDs) are 'zoonotic', where infectious diseases in animals are naturally transmitted to humans. The researchers chose to study bats in particular as they are known to carry multiple zoonotic viruses and are the suspected origin of rabies, Ebola and SARS (severe acute respiratory syndrome).

Lead researcher, Professor Kate Jones, Chair of Ecology and Biodiversity at UCL Biosciences and ZSL, said: "We've identified the factors contributing to the transmission of zoonotic diseases, allowing us to create risk maps for each. For example, mapping for potential human-bat contact, we found Sub-Saharan Africa to be a hotspot. Whereas for diversity of bat viruses, we found South America was at most risk. By combining the separate maps, we've created the first global picture of the overall risks of bat viruses infecting humans in different regions."

The research, using data published between 1900 and 2013, identified West Africa as the highest risk hotspot for zoonotic bat viruses. This area was outside the endemic range proposed by previous studies but has

since experienced the largest scale outbreak of Ebola virus disease seen yet.



A process-based framework of zoonotic pathogen emergence for a) the whole pathway and b) between Steps 1 and 2, expanded with necessary processes for spillover labelled i, ii, iii. Processes are verbally described to avoid conflicting terminology, e.g. 'Opportunity for transmission' has been differentially referred to as "contact" in emerging disease literature, and "exposure" in host-parasite literature. Drivers are listed next to arrows between steps. Credit: Liam Brierley et al.

Published today in *The American Naturalist*, the study developed risk maps by identifying different factors which are important for driving the early-stage of zoonosis—the transmission of viruses from bats to humans. The factors influence specific points in the process which starts with the presence of viruses in the environment and host, progressing to bats and humans coming into contact and ending with successful infection of humans.

First author, Liam Brierley, now a PhD student at the University of Edinburgh, said: "We are seeing risk hotspots for [emerging diseases](#) where there are large and increasing populations of both humans and their livestock. As a result, settlements and industries are expanding into wild areas such as forests and this is increasing contact between people and bats. People in these areas may also hunt bats for bushmeat, unaware of the risks of transmissible diseases which can occur through touching body fluids and raw meat of bats."

Information on the viruses carried by bats was collated by scientists at Western Michigan University and EcoHealth Alliance (both USA) who analysed over 110 years of data spanning 33 zoonotic bat viruses across 148 bat species from 453 literature sources. These results were then modelled by researchers at UCL and ZSL to find patterns and drivers for bat-human virus sharing and map the findings onto cells across the globe to identify areas at risk.

Liam Brierley added: "We're pleased to have collated ecology, epidemiology and public health information to identify the factors that drive virus sharing and we hope it is used to improve surveillance of emerging diseases and inform decisions about preventative action. There's still some way to go in monitoring virus diversity in wild animals and specific information on infections that would allow us to create higher-resolution maps. With advances in technology, we anticipate the way we collect and share data to improve, potentially stopping future

pandemics."

Provided by University College London

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