

Mapping disease risk at human-wildlife 'hotspots'

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Rhesus macaques in the city of Shimla, northern India. Credit: Dr. Krishna Balasubramaniam

New research has mapped how infectious diseases spread among wildlife populations in areas where humans and wildlife live in close proximity. The study has identified the animals, specifically wild monkeys that live in large groups alongside human settlements, that may act as "superspreaders."

It found that monkeys with the most human interactions are responsible for the largest outbreaks. This is because these locations where monkeys and humans come into close contact, typically around sources of food, can attract monkeys from different groups and sub-groups. It is at these human-wildlife hotspots that monkeys closely interact with monkeys they wouldn't regularly mix with, leading to larger outbreaks.

With a rising global population meaning that [human settlements](#) increasingly encroach on the natural ranges of wild animals, there is a growing risk from both [zoonotic diseases](#) that "spillover" from wildlife to humans and zoonanthroponotic diseases that "spillback" from humans and cause outbreaks among wildlife.

Published in the journal *Scientific Reports* and led by Dr. Krishna Balasubramaniam of Anglia Ruskin University (ARU), the research used epidemiological computer models to simulate how [infectious diseases](#) may spread among monkeys living in urban and peri-urban areas of South and South-East Asia. It is the first study to use simulations to compare disease spread through animals' social behavior, to disease spread through animals' tendencies to congregate around and interact with humans.

The team of researchers, including academics from University of California, Davis, monitored the behavior of rhesus macaques, long-tailed macaques, and bonnet macaques in northern India, Malaysia, and

southern India respectively. In these locations, wild macaques frequently share space with humans, and their interactions with people often focus around accessing food.

The researchers gathered detailed behavioral data on interactions between humans and individual monkeys as well as interactions between monkeys within the same group, within which individuals have strong social connections. This information was collected from 10 separate groups of macaques across the three Indian and Malaysian locations.

This behavioral data was fed into mathematical Susceptible-Infected-Recovered (SIR) epidemiological models to simulate the impact of outbreaks of human diseases of varying transmissibility such as the influenza virus, Coronaviruses, and the measles virus. Computer simulations were run 100,000 times in total across the 10 groups and across the different human diseases, and the vulnerability of these [macaque](#) populations to human-induced disease outbreaks was evaluated.

The study found that the size of the [outbreak](#) was positively predicted by the centrality within the group of the first-infected macaque—if that individual is better connected within its social network, it would lead to a larger outbreak.

The second key finding is that the centrality of the first-infected individual, based on both its congregations with other monkeys around humans and its interactions with humans, plays a greater role in predicting the scale of outbreak than how central it is within its own group.

This is because macaques may congregate around human-provisioned food alongside other macaques with whom they would otherwise not interact that often. The study revealed that these situations seem to create additional pathways for disease transmission and therefore lead to

larger outbreaks.

The researchers believe this work could be vital for helping to identify individual monkeys that are the most sociable, and tend to congregate around and interact with humans the most. Targeting these with vaccinations or other forms of medical treatment could potentially protect both macaque populations and humans in areas where they live in [close proximity](#).

Dr. Krishna Balasubramaniam, Lecturer in Conservation & Animal Behavior at Anglia Ruskin University (ARU), said, "COVID-19 has highlighted the importance of understanding infectious disease transmission among [wildlife populations](#) in urban and peri-urban areas. Population expansion has increased the contact between humans and wildlife, and these human-wildlife interfaces are widely recognized as 'hotspots' for the transmission of diseases across a variety of species.

"Our research focused on the potential impact of a human-borne disease spreading through wild macaque populations. Being so closely related to humans, macaques are highly vulnerable to the same diseases that infect people. Indeed, previous work by other researchers established that macaques may be infected by human gastrointestinal and respiratory pathogens. Here we showed how respiratory pathogens in particular might spread through macaque populations, and specifically how their behavior might influence such spreading.

"Through fieldwork and modeling, our research identified which individuals are most likely to act as 'superspreaders' of disease, leading to larger outbreaks. How central the individual was within its own group had an effect on the size of outbreak, but interestingly the stronger predictor of whether a macaque would go on to cause a large outbreak was its tendency to congregate around humans with macaques from other sub-groups.

"Sources of human-provided food can act as a 'honeypot' and lead to macaques coming into very close contact with individuals with whom they may otherwise have less contact, for instance monkeys from other families or sub-groups.

"As well as being 'superspreaders' within their species, these individuals with the most human contact also pose the highest risk for interspecies [disease transmission](#) events, either from humans into wildlife, or vice-versa. These would be the most effective targets for disease control strategies such as vaccination or antimicrobial treatment."

More information: Impact of joint interactions with humans and social interactions with conspecifics on the risk of zoonotic outbreaks among wildlife populations, *Scientific Reports* (2022).

Provided by Anglia Ruskin University

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