Identifying potential disease-transmission sources in animal species by calculating risk to humans

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Chlorocebus aethiops, a primate species highly likely to transmit emerging diseases.

Spanish and US scientists have successfully identified animal species that can transmit more diseases to humans by using mathematical tools

similar to those applied to the study of social networks like Facebook or Twitter. Their research—recently published in the prestigious journal *PNAS*—describes how parasite-primate interactions transmit diseases like malaria, yellow fever or AIDS to humans. Their findings could make an important contribution to predicting the animal species most likely to cause future pandemics.

Professor José María Gómez of the University of Granada Department of Ecology is the principal author of this research, in collaboration with Charles L. Nunn (University of Cambridge, Massachusetts, US) and Miguel Verdú (Spanish National Research Council Desertification Research Center, Valencia, Spain). They propose a criterion to identify disease-transmission agents based on complex network metrics similar to those used to study social networks.

As Prof Gómez explains, "most emerging diseases in humans are zoonotic, that is, they are transmitted to humans by animals. To identify animal species that are potential high-risk sources of emerging diseases it's essential we set up mechanisms that control and observe these diseases".

Study of 150 primate species

To conduct their study, the researchers constructed a network in which each node represented one of the approximately 150 non-human primate species about which we have enough data on their parasite fauna. "Each primate species is connected to the other primates as a function of the number of parasites they share. Once the network was constructed, we studied each primate species' position—whether central or peripheral. A primate's centrality is measured by its connection intensity with many other primates that are, in turn, closely connected", says the University of Granada researcher.
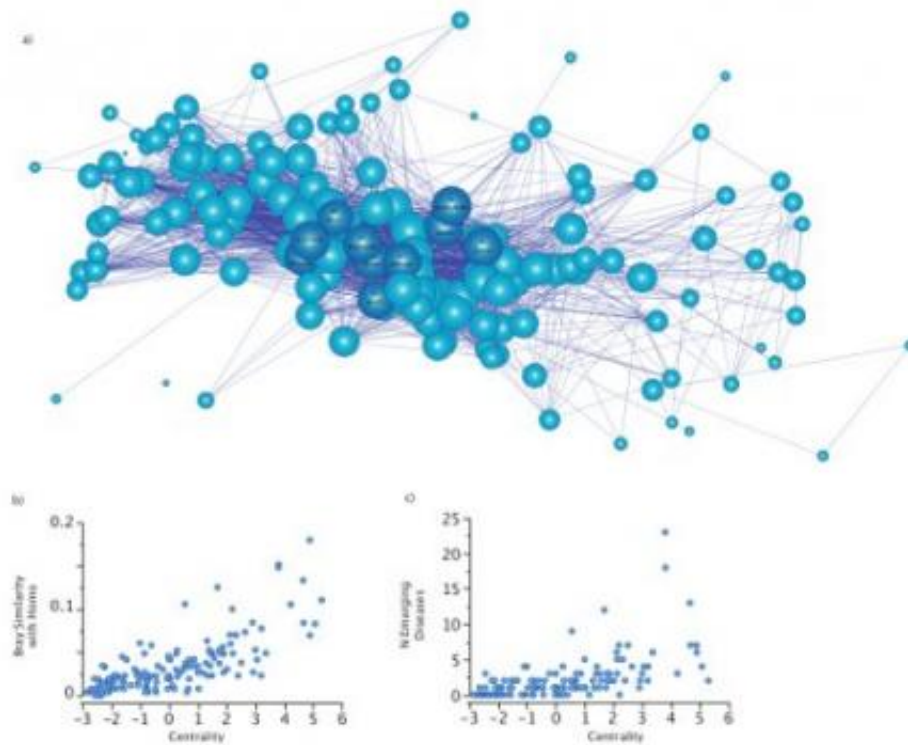
The diagram shows how primates share parasites. Each bubble represents a primate species and the lines connect species that share parasites. The larger the diameter of the bubble, the higher the number of emerging infectious diseases they share with humans. In dark blue, the ten primate species with the highest numbers of emerging pathogens shared with humans.

The article published in *PNAS* reports the researchers' discovery that the most central primates could be more capable of transmitting parasites to other species and, therefore, to humans, than the rest. "This is comparable to the idea that, in social networks, web pages that are central and have links to many other pages, spread their contents all through the Web", José María Gómez affirms.

The researchers have confirmed their hypothesis by relating the centrality value of each primate with the number of emerging pathogens

shared with humans. And, in effect, they have found that the most central primates were those that share more emerging pathogens with humans.

In conclusion, the study proposes a simple criterion to detect potential zoonotic agents of emerging disease transmission to humans: the centrality of these agents in their network interaction with their parasites. "The only information needed to construct these networks is the diversity and type of parasite infecting each host—and we already know about many zoonotic organisms. This is why we think that our approach will be useful in developing early warning plans for emerging disease in humans", Prof Gómez concludes.

Provided by University of Granada

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