

OPINION¹

Parasite sharing between humans and nonhuman primates and the hidden dangers to primate conservation

GÓMEZ *et al.* (2013) argued that the centrality of a nonhuman primate (NHP) species in network analyses of host-parasite interactions represents a good predictor of its potential as a source of emerging infectious diseases (EIDs) to humans. Centrality indicates the degree of connectedness of a node (here, a primate species) with the other nodes in a network based on their similarity relative to a given variable (here, shared parasites). Regardless of our quite limited knowledge of parasite diversity in general (e.g., viruses, bacteria, fungi, protists, and helminths) (DOBSON *et al.* 2008) and wild primate-parasite relationships in particular, which is strongly dependent on sampling effort (NUNN 2012), the comparative analysis of GÓMEZ *et al.* (2013) is useful to identify NHPs that share similar parasite communities with humans. Here we discuss how a few highly terrestrial taxa drove the positive relationship between centrality and the number of EIDs in humans; additionally, we challenge the applicability of network analysis of a database composed of taxa from all over the world as a means to predict the potential of species as sources of EIDs because the flow of information (parasites) between most pairs of nodes (allopatric primate species) can only occur indirectly, via humans as hubs (connectors); finally, we call attention for the fact that publications focusing on the possible influence of wildlife on human health has potential negative implications for biodiversity conservation.

First, the positive relationships found between centrality and the number of EIDs, both in a larger sample of primate species ($n = 129$; shown in GÓMEZ *et al.* 2013: fig. 1C) and in a smaller sample of well-studied taxa ($n = 38$; shown in GÓMEZ *et al.* 2013: fig. 2B), appear to have been pushed by a few species with extreme EID values. To test this hypothesis we determined the ranks for both variables of 36 data points shown in GÓMEZ *et al.* (2013: fig. 2B; two data points could not be identified because of high or complete overlap with others) and ran Pearson correlations. We did not run correlations with the complete dataset because the data points (shown in GÓMEZ *et al.* 2013: fig. 1C) were highly overlapped. However, the reliability of our analysis is supported by the strong positive relationship found between the centrality scores of the 38 species in both datasets (GÓMEZ *et al.* 2013: fig. S2). We obtained the identities of the ten most central species from the Supporting Information Online (shown in GÓMEZ *et al.* 2013: table S12). Like GÓMEZ *et al.* (2013), we found a significant correlation between centrality and the number of EIDs in our 36-data point sample ($r^2 = 0.2656$, $t = 3.5064$, $df = 34$, $p = 0.0013$). After the species with the highest

number of EIDs – 23, chimpanzee *Pan troglodytes* (Blumenbach, 1775) was excluded from the sample, the correlation remained significant ($r^2 = 0.1441$, $t = 2.3574$, $df = 33$, $p = 0.0244$). Removal of the taxon with the second highest number of EIDs – 18, gorilla *Gorilla gorilla* (Savage, 1847) resulted in a non-significant correlation ($r^2 = 0.0692$, $t = 1.5424$, $df = 32$, $p = 0.1327$). Exclusion of the taxon with the third highest number of EIDs – 13, yellow baboon *Papio cynocephalus* (Linnaeus, 1766) totally undermined the power of centrality as a predictor of the number of EIDs ($r^2 = 0.0188$, $t = 0.7708$, $df = 31$, $p = 0.4466$).

The six most central primates, including chimpanzees (most central), gorillas (5th centrality) and yellow baboons (6th centrality), are highly terrestrial. In fact, GÓMEZ *et al.* (2013) acknowledged their ecological overlap with humans as an important element in the risk of pathogen exchange (see also COOPER *et al.* 2012). Surprisingly, however, the effect of the degree of terrestriality (estimated by COOPER *et al.* 2012) on EID richness was not tested by GÓMEZ *et al.* (2013). The potential relationship between terrestriality and risk of pathogen exchange highlights the well-known influence of contact between hosts in the exchange of parasites (LEENDERTZ *et al.* 2006, PEDERSEN *et al.* 2007, BREED *et al.* 2009, HARPER *et al.* 2013). The importance of contact is also implicit in the authors' statement that humans share more parasites with domestic animals than with wild NHPs (see also COOPER *et al.* 2012). According to TAYLOR *et al.* (2001), 75% of the known infectious organisms that are pathogenic to humans ($N = 175$) are zoonotic.

Although GÓMEZ *et al.* (2013) have focused on identifying candidate sources of future human EIDs by analyzing the network without taking into account the origin of shared parasites with NHPs and the identity (often unknown) of the reservoir host population(s) or environment(s) (*sensu* HAYDON *et al.* 2002), we can take advantage of their analyses to also discuss the potential of EID spillover from humans (and domestic animals) to the survivorship and conservation of NHPs (CLEAVELAND *et al.* 2001, NUNN & ALTIZER 2006, NUNN 2012). According to BORGATTI (2005: 69), “the importance of a node in a network cannot be determined without reference to how traffic flows through the network.” In the study of GÓMEZ *et al.* (2013), humans are by far the most likely, if not uniquely, responsible for the required node interaction (BUTTS 2009, POULIN 2010) and the flow of the mostly generalist parasite species (PEDERSEN *et al.* 2005, COOPER *et al.* 2012) that they share with NHPs, and which are not shared through common descent. The impossi-

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bility of interaction between most primate taxa included in the analysis of GÓMEZ *et al.* (2013) derives from their allopatric distributions, many of which occur in different continents.

Our possible contribution to EIDs affecting NHPs (NUNN 2012) is particularly critical because high rates of human population growth during the past few decades in countries inhabited by wild NHP populations (ESTRADA 2013) has resulted in a significant increase in human contact with wildlife and new opportunities for cross-species disease transmission, especially via habitat encroachment, bush meat hunting and pet trade (KAUR & SINGH 2009, BRINKWORTH & PECHENKINA 2013, HARPER *et al.* 2013). Evidence of the devastating effects of EIDs on NHP populations has accumulated over the past decade. BERMEJO *et al.* (2006), for example, estimated that an Ebola outbreak (whose probable reservoir is a bat, RYAN & WALSH 2011) at the Lossi Sanctuary in the Republic of Congo reduced the populations of gorillas and chimpanzees by over 90% and 80%, respectively. In the New World, populations of black-and-gold, *Alouatta caraya* (Humboldt, 1812), and brown, *A. guariba clamitans* Cabrera, 1940, howler monkeys in the Province of Misiones, Argentina, and the state of Rio Grande do Sul, Brazil, were severely affected by a recent outbreak of yellow fever (BICCA-MARQUES 2009a, BICCA-MARQUES & FREITAS 2010, HOLZMANN *et al.* 2010, FREITAS & BICCA-MARQUES 2011, ALMEIDA *et al.* 2012). The strong impact of the disease on these populations was critical in the reassessment of the conservation status of both taxa. The status of *A. guariba clamitans* deteriorated to Critically Endangered in Argentina (AGOSTINI *et al.* 2012) and to Vulnerable in Brazil, whereas the status of *A. caraya* deteriorated to Endangered in the state of Rio Grande do Sul and to Near Threatened in the Brazilian national list (federal and state decrees are not yet available).

Finally, we warn that human-biased scientific information has a strong potential to generate the delivery of sensationalist mass media messages with undesired consequences (BRADSHAW *et al.* 2007). For instance, misinformation delivered by the media during the aforementioned outbreak of yellow fever caused the killing of howler monkeys by local people in the state of Rio Grande do Sul (BICCA-MARQUES & FREITAS 2010). To reverse this scenario, a campaign entitled "Protect Our Guardian Angels" was launched to inform the media and the lay public about the crucial role that howler monkeys play as sentinels of the circulation of the pathogen of this disease (BICCA-MARQUES 2009b, BICCA-MARQUES & FREITAS 2010). The campaign was successful in changing the way the media addressed the issue, but it was probably quite ineffective in educating the public (see the news "Bugios seguem como alvo errado para evitar febre amarela" at www.crmvrs.gov.br/info488.html). With respect to the publication by GÓMEZ *et al.*'s (2013), statements made by Rachel Nuwer in the Smithsonian Institution's blog (<http://www.smithsonianmag.com/science-nature/which-primate-is-the-most-likely-source-of-the-next-pandemic-38535377/?no-ist>), for instance that "This chimp may look innocent, but he may harbor any of dozens of diseases that infect humans" below a

photo of a chimpanzee, "experts prioritize the task of figuring out which animals in which regions of the world are most prone to delivering the latest novel pathogen to hapless humanity" and "those species that occurred in the center of the diagram are the best positioned to kick off the next pandemic or horrific infectious disease", illustrate this sensationalism. The authors' recommendation for interventions on potential super-spreaders to prevent new pandemics in humans without disclosing the options may also have disastrous consequences to the world's primate species, about half of which are already threatened with extinction. Thus, we need to direct greater efforts to creating opportunities to promote the protection of remaining NHP populations and we shall be aware that the way our scientific results are presented does matter.

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Júlio César Bicca-Marques¹ & Cláudia Calegari-Marques²

¹ Departamento de Biodiversidade e Ecologia, Pontifícia Universidade Católica do Rio Grande do Sul. 90619-900 Porto Alegre, RS, Brazil. E-mail: jcbicca@pucrs.br

² Departamento de Zoologia, Universidade Federal do Rio Grande do Sul. 91501-970 Porto Alegre, RS, Brazil.

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