

LETTER TO THE EDITOR

The evolutionary ecology of SARS-CoV-2: A missing perspective in the One Health approach

Undoubtedly, the current COVID-19 (coronavirus disease 2019) pandemic is one of the greatest health crises humanity has faced. To better understand and mitigate this global crisis, and to be better prepared for similar epidemics in the future, it has been suggested to view the COVID-19 outbreak within the One Health (OH) framework (e.g. Amuasi et al., 2020; Stoffel et al., 2020). The OH concept aims at achieving optimal health for people, non-human organisms, and the environment via inter- and transdisciplinary collaborations across health and environmental sciences (Lerner & Berg, 2017). Given the zoonotic origin of SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) that spilled over to humans from wildlife, such an approach is certainly warranted. Without a doubt, linking human, animal and ecosystem health within the OH framework is a powerful approach in predicting, tackling and preventing disease outbreaks (Antoine-Moussiaux et al., 2019). However, even though the OH concept has expanded beyond its initial narrow focus on human and veterinary health and now includes wider ecological, environmental and socio-economic perspectives from EcoHealth approaches (Lerner & Berg, 2017), the stated importance of OH in the COVID-19 context often seems limited to recognizing and detecting zoonotic origins, understanding the human-animal-environment interface and avoiding the circumstances of transmission (see Villanueva-Cabezas et al., 2020). Among the multiple integrative approaches missing in the OH framework to pandemic response, the evolutionary ecology of the host-parasite system can offer a crucial perspective and valuable insight.

Although vaccination efforts will likely be a great success in tackling the pandemic (Scudellari, 2020), the virus and COVID-19 are expected to persist, potentially with regular seasonal outbreaks occurring during the coming years (Kissler et al., 2020). SARS-CoV-2 has therefore become, and will in the foreseeable future remain, part of the human host-pathogen system. From the viruses' point of view, the human host represents a resource-rich ecosystem that the virus has spilled over to, in which it replicates and evolves (Rynkiewicz et al., 2015). The emergence of new SARS-CoV-2 variants carrying different mutations highlights the pathogen's evolution within its human host system (Greaney et al., 2021). Moreover, it remains to be explored how the novel coronavirus will interact with other human parasites, pathogens or mutualists as part of a complex pathobiome (Bass et al., 2019; Siles-Lucas et al., 2021) and microbiome (Ferreira et al., 2021). Altogether, this should caution against any hopes of returning to the *status quo ante* and 'back to normal' once this crisis has been overcome. In evolutionary processes, there is no going back, and a solution that aims at restoring

a pre-outbreak situation simply does not exist. Other pathogens that have spilled over to humans from animal hosts, like the Zika virus, continue to develop, change in character and expand in geographical range (Kindhauser et al., 2016; Zohdy et al., 2019). Overall, the 'new normal' (WHO, 2021) in social contexts brought about by COVID-19 comes along with a new biological normality in a long-term host-parasite association with continuous coevolution.

Moreover, it is well likely that the human host system can serve as a 'stepping stone' for the virus to find its way into yet other host species, ecosystems and habitats, which might be the starting point of a dynamically changing host range of SARS-CoV-2 throughout its evolutionary history. After the initial wildlife-to-human transmission of SARS-CoV-2, the virus has continued to spill over to other mammals, most notably American mink *Neovison vison* in Danish and Dutch fur farms, and it has the potential to infect a wide range of domesticated and wild animals, which can serve as reservoirs and be the starting point for new animal-human transmissions and spillbacks (Gryseels et al., 2020; Munnink et al., 2021). Having been co-introduced around the world by its cosmopolitan human host, we may expect that further cross-species transmission events will occur in the future. Such spillovers are largely driven by increased exposure events and can result in the emergence of new genetic variations and novel strains of SARS-CoV-2 (Frutos et al., 2021; He et al., 2021; Parrish et al., 2008). Consequently, this epidemic should be viewed as a biological invasion and studied in the context of invasion biology, taking into account the relationship between introduced organisms and their environment (Nuñez et al., 2020; Vilà et al., 2021). As COVID-19 transits from epi- to endemicity in human populations, an ecological and evolutionary perspective will be helpful to better assess the dynamics of this host-pathogen development, both within and between-hosts (Lavine et al., 2021).

Considering human, animal and ecosystem health together under the OH umbrella can greatly benefit our understanding of zoonotic diseases but will require investigating them as novel and potentially persistent host-parasite systems including an eco-evolutionary perspective. In this context, it is especially important to point out that changes in nature, such as zoonotic spillover events, are often irreversible and that humans, while deeply embedded in ecosystems, are complex ecosystems themselves. Human health, rather than a state of well-being with the mere absence of disease, encompasses the ability to adapt and self-manage in the face of physical, social and emotional challenges (Huber et al., 2011). A better recognition and public awareness of the complex biology and evolution of human-parasite

interactions could help our understanding of this pandemic, assist the public in framing often poorly known phenomena like viral mutations, coevolution, zoonotic spillovers or biological invasions and lead to more autonomous and responsible behaviour in light of current and future health challenges.

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CONFLICT OF INTEREST

The authors declare no competing interests.

ETHICAL STATEMENT

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DATA AVAILABILITY STATEMENT

The authors do not have data to share.

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