



Global cooperation for a global pandemic

The COVID-19 pandemic has highlighted the challenges and opportunities of our inter-connected world in responding to global crises.

A pervasive theme during the COVID-19 pandemic is that nothing happens in isolation. Strategies and policies decided at local and national levels often have wider global implications. Additionally, progress in researching and combatting COVID-19 has required unprecedented global cooperation. In the September 2022 issue of *Nature Reviews Genetics*, we feature three articles that highlight global aspects of responding to infectious disease outbreaks.

Niemi, Daly and Ganna¹ discuss efforts to understand the influence of human host genetics on the occurrence and severity of COVID-19. As for any complex trait, a comprehensive understanding of the underlying human genetic architecture requires many thousands of research participants and thus needs researchers to collaborate across institutions and nations. An enormously positive development from the response to COVID-19 is that the scientific community has been able to overcome the long time periods typically required to carry out major scientific projects. As for the rollout of SARS-CoV-2 testing infrastructure and vaccine development programmes, collaborations to study COVID-19 host genetics were established extremely quickly with a notable spirit of cooperation and rapid data sharing. Such global teamwork shows the enormous amount that can be achieved when the entire scientific community unites towards a common goal.

The studies discussed by Niemi, Daly and Ganna¹ also highlight the resource value of large-scale biobanks in biomedical research. By collecting data on COVID-19 incidence and severity for biobank participants, researchers were able to rapidly integrate these data with pre-existing genome sequence (and other omics) data on those participants for a timely analysis of the genetic contributions to COVID risk. Thus, biobanks will be a key resource when dealing with any future pandemics. However, to maximize their resource value it is vital to keep pushing towards ancestral diversity in biobanks, with broad data accessibility, so that they can be of value to all global populations.

Attwood et al.² focus on the first year of the COVID-19 pandemic, when control measures were often applied in ad hoc and reactive ways, and there was enormous variability in the severity of measures imposed by different nations. Although the pandemic has been beset by campaigns of misinformation, Attwood et al.² describe how the sound scientific approaches of phylogenetics and phylodynamics can provide powerful and robust evidence about the global spread of SARS-CoV-2,

including how different SARS-CoV-2 variants evolved, and the routes and timings of their local and global transmission. Such approaches are valuable for ensuring that control measures are enacted based on correct assumptions about where and how SARS-CoV-2 strains are being transmitted. One notable result they discuss concerns international travel restrictions. After variants of concern were first reported, the standard international response was to ban international travel from affected countries. However, phylodynamic approaches revealed that in some cases, these variants had already spread internationally before bans were imposed, and hence the strains still spread globally while countries subjected to travel bans suffered socioeconomic hardship. In the current pandemic, and any future ones, it will be important to ensure that countries remain incentivized to collect and share genomic data for the global good, rather than fear of stigma and damaging repercussions causing a reluctance to share.

Finally, in a Journal Club article, Musila³ reflects on a 2016 article reporting the field deployment of nanopore sequencing capacity for real-time tracking of the 2014–2016 West African Ebola outbreak⁴. Such progress is again a notable example of how technological advances and international cooperation can be leveraged to understand and combat infectious disease outbreaks. With the scientific community becoming increasingly aware of the ethical and scientific importance of appropriate and equitable engagement with local researchers⁵, a positive step forwards for future infectious disease outbreaks will be to establish and improve local sequencing and data analysis infrastructure, circumventing the need to fly in sequencing machines or export data internationally for analysis^{3,4}.

The COVID-19 pandemic has shown how connected we all are. When our connectivity is harnessed towards shared goals, great things can be achieved in rapid timescales that were once thought impossible.

1. Niemi, M. E. K., Daly, M. J. & Ganna, A. The human genetic epidemiology of COVID-19. *Nat. Rev. Genet.* <https://doi.org/10.1038/s41576-022-00478-5> (2022).
2. Attwood, S. W. et al. Phylogenetic and phylodynamic approaches to understanding and combating the early SARS-CoV-2 pandemic. *Nat. Rev. Genet.* <https://doi.org/10.1038/s41576-022-00483-8> (2022).
3. Musila, L. Genomic outbreak surveillance in resource-poor settings. *Nat. Rev. Genet.* <https://doi.org/10.1038/s41576-022-00500-w> (2022).
4. Quick, J. et al. Real-time, portable genome sequencing for Ebola surveillance. *Nature* **530**, 228–232 (2016).
5. Nature addresses helicopter research and ethics dumping. *Nature* **606**, 7 (2022).

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