Evolution goes viral

The rise of SARS-CoV-2 variants with altered virus biology is bringing viral evolution into the public spotlight.

The second wave of the COVID-19 pandemic is well under way, with the tightening of restrictions and the return of lockdowns in many countries. This resurgence has all the same unwelcome effects on society that were seen in the middle of 2020. With the appearance of several mutations that may alter the biology of SARS-CoV-2, conversations about viral evolution are now common not just in research labs, but at policy forums, board meetings and dinner tables alike.

Like all viruses, SARS-CoV-2 mutates and evolves. There does not appear to be anything particularly abnormal about this virus in this respect, and its mutation rate is thought to be lower than that of influenza or AIDS. Those mutations that arise may spread by chance (such as drift and founder effects) or through selection. The diversification and spread of lineages through either mechanism are routinely used to study the origin and biogeography of the disease, as has been done with COVID-19[1]. Fairly early in 2020, one SARS-CoV-2 mutation — D614G — spread rapidly to become the dominant circulating variant of the virus. However, whether this was because of any selective advantage is not clear and has been widely debated[2].

More recently, however, several variants have arisen with more obvious evolutionary implications, and several of the mutations involved have arisen convergently in multiple lineages. The B.1.1.7 variant, first detected in the United Kingdom, has 17 mutations, the most significant possibly being N501Y[3]. The B.1.1.7 variant has increased transmissibility but not virulence, providing an example of the classic virulence–transmission trade-off common to other human and wildlife diseases[4]. While this increase in transmissibility is contributing to the scale of COVID-19 resurgence in the United Kingdom and other European countries, it is not the only factor, and governments should not be allowed to blame evolution rather than their own poor pandemic management. Indeed, new variants will arise more frequently if there is a substantial quantity of the virus in circulation, emphasizing the importance of controlling the disease. Fortunately, the effectiveness of current vaccines is not thought to be measurably weaker for B.1.1.7.

By contrast, a mutation (E484K) that has been seen in new variants in South Africa and Brazil might have implications for vaccination. It is important to stress upfront that this concern is just informed conjecture at this stage. However, preliminary in vitro results suggest that this mutation can reduce antibody binding[5] and be part of a selective escape from a polyclonal immune response[6]. These studies are both far removed from studies of vaccination in actual human populations, and even if the variants were to compromise the efficacy of current vaccines, it may be that modifying those vaccines that are based on genome sequences to target these variants would be relatively straightforward. As a further note of caution, the studies on this variant are currently preprints and therefore yet to be peer reviewed, which we view as critically important before relying on such work as a basis for long-term science and policy decisions (although preprints have unarguably played an important role in the pandemic by allowing the rapid sharing of results and data, and this journal encourages authors to make use of them).

While epidemiologists have been successful at explaining and predicting the course of the pandemic in the short to medium term, uncertainty about the new variants reveals how little we truly know about viral evolution, especially when the hosts are humans. Human actions, such as lockdowns, social distancing and vaccination, and natural effects, such as immunity, both exert selective pressures. Selection is expected to reduce virulence over time, but we don't know exactly how this relates to evolutionary change in transmissibility[7]. The iterative complexity of these processes, on a background of ever-changing global human behaviour, means we can't fully predict whether we can expect regular flare-ups of the disease, how bad these might be, whether the virus's ability to survive in the external environment may change, or whether regular re-vaccination will be required (the latter is affected by the nature of the immune response as well as viral evolution). On the other hand, we do know that the virus will continue to evolve and that many more variants will be detected, some of which may make the situation worse.

We are in a Red Queen-style race with the virus: rampant transmission may have allowed for the rapid trialling of vaccines, but it also allows the virus to adapt rapidly to its new host via mutation. The most important evolutionary lesson at this stage is therefore that we need to continue applying everything we have already learnt about viral control and surveillance — with heightened vigilance — to stem the rise of all SARS-CoV-2 lineages. ❐

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