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BioScience®

A Forum for Integrating the Life Sciences

American Institute of Biological Sciences

The Virus Evolves: Four Public Health Priorities for Reducing the Evolutionary Potential of SARS-CoV-2

As scientists who study evolution, we are concerned about the threat posed to public health by evolving SARS-CoV-2 variants. We celebrate the start of vaccination campaigns, enabled by remarkable scientific achievements, but these advances are now at risk of being undermined by evolution. In particular, we emphasize that—unless we keep case numbers low—novel variants will continue to emerge, increasing the chances that some will evade vaccine-induced immunity.

These dangerous consequences of SARS-CoV-2 evolution are looming, but rapid viral evolution is not inevitable. Fundamental principles of evolution provide clear guidelines for slowing down the evolutionary process. With these principles in mind and echoing the calls made by others (see the supplementary material for complete references and signatories), we urge policymakers to prioritize the following:

Reduce case counts as much as possible. One of the most well established truths of evolution is that adaptive change is more likely when populations are larger. This means that a drastic reduction in infections will not only reduce illness and save lives in the face of variants that are already present, but it will guard against the conditions that favor the evolution of new variants of concern, which may be more transmissible, more virulent, or more able to escape immunity (“escape variants”).

Urgely vaccinated people to continue mitigation measures. The emergence and spread of escape variants is favored by transmission of the virus to and from people who are immunized (whether they have been immunized by natural infection or by vaccines). Although such transmission chains may be infrequent, they become more likely when case numbers are high in areas where vaccinations are being rolled out. Therefore, in order to limit the emergence and spread of escape variants as vaccination campaigns proceed, policy-makers should encourage vaccinated people to continue to adhere to mitigation measures (e.g. masks, physical distance, ventilation) while case numbers remain high.

Increase genomic and genetic surveillance and share data quickly on public repositories. Genomic surveillance (regular sequencing of a representative sample of cases) is essential for identifying the emergence of new variants. Sharing these sequence data on public repositories as quickly as possible will enable rapid responses when new variants of concern are detected. Moreover, genomic data should be paired with patient metadata so that any variants that alter the disease characteristics can be identified. Concurrent with genomic surveillance, increased genotyping of samples from cases for known variants of concern (e.g., via RT-PCR, polymerase chain reaction, which can return test results very quickly) is needed for rapid detection so that targeted control efforts can be put in place around those cases.

Coordinate internationally. We all live on the same planet. Leaving the epidemic uncontrolled anywhere leaves the global population vulnerable to the evolution of variants that can escape immunity. Therefore, we support the scientific consensus calling for global coordination on both vaccination campaigns and genomic surveillance.

We ask leaders to seize this window of opportunity; protect the health of citizens and economies by taking swift action to guard against the threat of ongoing viral evolution.

Supplemental material

Supplemental file with a list of society signatories and full references is available at *BIOSCI* online.

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