

A sea change for virology

This issue marks the publication of a Consensus Statement that proposes the integration of viruses that are only characterized by metagenomic data into virus taxonomy.

According to the evolutionary biologist Stephen Jay Gould “...classifications both reflect and direct our thinking. The way we order represents the way we think. Historical changes in classification are the fossilized indicators of conceptual revolutions” (REF. 1). One might also add to this statement, in particular when reflecting on recent microbiological taxonomy, that changes in classification are an indicator or a consequence of technological revolutions.

The history of virus taxonomy has seen quite a few changes, some of which have been accompanied by heated discussions. What should be defined? Virus names? Classes? And how? The International Committee for Virus Taxonomy (ICTV), which was formed ~50 years ago², although under a different name (International Committee on Nomenclature of Viruses (ICNV)), was instrumental for answering such questions and defining the frameworks that are used to classify viruses. We are proud to publish a Consensus Statement (see page 161) by Peter Simmonds and 25 fellow virologists, which is endorsed by the Executive Committee of the ICTV and argues for and proposes how to incorporate viruses that are only characterized by metagenomic sequence data into virus taxonomy.

This Consensus Statement marks one of these ‘conceptual revolutions’ that Gould was referring to. Sequence data have been important for virus taxonomy for many years, but, so far, to define a new species of virus, direct phenotypic data were also required; for example, data about host range or pathogenicity. However, for many, if not most viruses, such direct data on their biological characteristics are not available. Sequencing and analysis methods have improved tremendously, which has led to the description of unprecedented virus diversity. For example, a recent analysis of metagenomic data from diverse samples that were collected globally identified more than 120,000 viral DNA genomes and when these viruses were clustered into groups, more than 95% of the groups did not contain any previously isolated and classified viruses³.

There is clearly a huge amount of virus diversity that is not captured in current taxonomy, much of which comes from environmental habitats, which are unlikely to receive the same amount of biological characterization as viruses that infect humans, animals or crops. The proposals that are outlined in the Consensus Statement will

enable the incorporation of this diversity into the existing virus taxonomy. Phenotypic data are still important, if they come from direct biological observations they still can be used, but phenotypic characteristics can also be inferred from sequence data alone, such as genome organization and replication strategy, and, potentially, host range and vector. Including ‘metagenomic-only’ viruses into taxonomy recognizes the importance of viruses in all hosts and environments; for example, by influencing global biogeochemical cycles or host evolution. Hopefully, it will also help to further improve taxonomy itself and elucidate relationships between different virus taxa.

Virology is not the only field that is grappling with how to include sequencing data into traditional taxonomy. For example, 16S rRNA data have shown that some bacteria that were thought to belong to different species are in fact the same. Prokaryotic taxonomy does enable the inclusion of bacteria and archaea for which no isolate is available, although only with the qualifier *Candidatus*, and most environmental prokaryotic diversity, similar to viruses, is not captured in current taxonomy. Fungal taxonomy is dealing with similar issues and, in addition, historically, different morphological types of the same fungus have often been assigned to different species. It will be interesting to see how the inclusion of metagenomic data is handled in virology and whether other fields will take similar steps.

Virology might be particularly well suited for making such a change, as studying viral genome sequences has been central for many virological studies. In addition, with the ICTV, virology has a large group of experts that dedicate some of their time to resolve taxonomic questions. We would also like to highlight that continued funding is essential for such efforts. The ICTV is supported by the International Union of Microbiological Societies, the American Society for Virology, the Microbiology Society and the Wellcome Trust. We applaud and encourage funders and researchers to support efforts that not only generate new data but also help to make sense of these data and make them understandable, available and useable for a broad research community.

“Including ‘metagenomic-only’ viruses into taxonomy recognizes the importance of viruses in all hosts and environments”

1. Gould, S. J. *Hen's Teeth and Horse's Toes*. (W.W. Norton, 1983).
2. Adams, M. J. *et al. Arch. Virol.* <http://dx.doi.org/10.1007/s00705-016-3215-y> (2017).
3. Paez-Espino, D. *et al. Nature* **536**, 425–430 (2016).