



## SPEAKER

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## Ordering the Viral Universe

### [Abstract]

. Viruses are the most abundant living entities in the biosphere, outnumbering their host organisms by one to two orders of magnitude. It is conceivable that they cause the highest selective pressure their hosts encounter. As obligate parasites, viruses are dependent on their hosts, but their origins seem to deviate from that of cellular life.

What are the possible structural principles to build viruses is an open question. However, structural studies on virus capsids and coat protein folds suggest that there are only a limited number of ways to construct a virion. This limitation may be based on the limited protein fold space. Consequently, relatedness of viruses is not connected to the type of cells they infect, and the same architectural principle of the capsid has been observed in viruses infecting bacteria as well as humans. Using the viral capsid architecture, it is possible to group viruses to several structure-based lineages that may have existed before the three cellular domains of life (bacteria, archaea and eukarya) were separated. This would mean that viruses are ancient and that early cells were already infected with many different types of viruses, implying that the origin of viruses is polyphyletic as opposed to the monophyletic origin of cellular life. To test the hypothesis of limited viral structure space, we have collected information on globally sourced environmental viruses infecting archaea and bacteria, and compared the obtained information to known viral structures. The latest approach is to work on extending the comparison to viral protein *sequences*, as their number is increasing most rapidly, and often only a few compare to anything known before. To achieve this, we have joined forces between the University of Helsinki (viral expertise) and OIST (mathematics and bioinformatics expertise).

Hosted by: Mathematical Biology Unit (Sinclair Unit)

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