

V-table – the interactive structured virosphere

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Abstract

Viruses are not included in a tree of life and there is no separate structure illustrating viral diversity and evolutionary relationships. The high level of viral diversity and absence universally conserved genes do not allow presenting viral world within a structure similar to the tree of life as for cellular organisms [1]. Nevertheless, the need for a comprehensive overview on a constantly growing number of viruses raises the questions about the structure of global virosphere and the factors shaping it.

V-table is an approach to structure global virosphere. It unifies viral taxonomy, phylogeny and molecular characteristics in order to describe the principles and trends in viral diversity in easy and accessible way [2]. V-table is interactive spherical model demonstrating tabular arrangement of viral families ordered by multiple parameters simultaneously. It provides at a glance understanding on how viruses differ in terms of genome type, size and form, capsid size, symmetry and morphology, as well as host type. Moreover, it allows customized search for viruses with any specific characteristic, ranges and sets of them. Finally, the spherical shape of V-table is capable of embedding unlimited number of new viral taxa by growing at any specific place without disrupting the whole structure

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