Bacteriophage phylogeny revisited

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Abstract

Bacteriophages or phages are viruses that only infect bacteria. The International Committee on Taxonomy of Viruses classified these viruses in accordance with the morphology of their free virion particles and type and size of their genome. This system fails on the classification of several phages, which have their genome already sequenced. It also requires a morphological analysis by transmission electron microscopy, which is very expensive and time consuming [1]. In 2002 Rohwer and Edward proposed the only sequence-based system existing up to this moment. Thus, it is of utmost importance to develop new systems for bacteriophage classification that take into consideration the genomic and proteomic information already available [2].

The purpose of this study is to establish a new method for the classification of phage based on the genetic information available. The principal objective is to cluster the bacteriophages in different family and types. To create a new *phylogenetic tree* we analysed all 670 available genome sequences deposited in the *GenBank* database. Sequences were aligned using the *T-coffee* program [3]. A genetic marker for the construction of the phylogenetic tree was designed by creating a *concatenate* of different gene products that presented the highest similarity. In other words, the most conserved gene products were used to form a broader genetic marker. The method allows the use of a single, created genetic marker to classify unknown phages with existing phage types and families. A comparison to existing methods is discussed.

References

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