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## **Clustering and genomic analysis of phages from Podoviridae family**

Phage genomes evolve, according to the modular evolution, by the exchange of interchangeable genetic elements. This causes that the standard hierarchical branching phylogeny of phages and their classification are unsatisfied and even impossible. To show relationships between the phage genomes by an alternative approach, we applied CLANS software which uses a version of the Fruchterman–Reingold graph layout algorithm to visualize pairwise sequence similarities in either two-dimensional or three-dimensional space. The analyses were performed on the 92 Podoviridae complete genome sequences using all-against-all TBLASTX searches on the amino acid level. Additionally, we made the pairwise comparison on the nucleotide level in BLASTN for 36 genome sequences from Autographivirinae subfamily to study relationships between these phages in detail. In the studies we also included the newly sequenced genome from *Klebsiella pneumoniae* KP34 phage. The analyses made possible to group the phage genomes in clusters and proposed some modifications in their current taxonomic classification. The applied method is very sensitive and enabled to find a signal coming from horizontal gene transfer from some Picovirinae members to *Lactococcus* phage KSY1. Detailed comparison of genomes from phiKMV viruses revealed distinct gene content and arrangement at the 3'-end genomic region which may be responsible for differences in the host recognition and infection mechanisms.