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7th Annual SEA-PHAGES Symposium Abstract

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Investigating the Relationships of Bacteriophages with a Class Reveals Obvious Boarders Between Bacterial Orders

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With an estimated greater than 1031 bacteriophages in the earths biosphere, and only a small fraction studied, our understanding their diversity and evolutionary relationships is just beginning to emerge. The ability of bacteriophages to rapidly evolve through genetic mutation or exchange with their hosts and with one another adds complexity to discerning their evolutionary origins. In an attempt to understand the natural boundaries for such genetic exchange, 337 bacteriophages that infect the Enterobacteriaceae Order of bacteria (18 genera and 31 species) were recently analyzed. This analysis revealed 56 diverse clusters of related phages (32 lytic and 54 temperate). Although little correlation between the bacteriophage host and its cluster assignment was seen, most bacteriophages naturally divided into subclusters with a 78% correlation with their host genera. The fact that so few clusters correlated with the bacterial host lead us to investigate whether clusters correlated with bacterial orders rather than genera. Bacteriophages that infect the Pseudomonadales, another order within the Gammaproteobacteria class, were then compared with those that infect the Enterobacteriaceae. The correlation with cluster when comparing these different orders was remarkable, at greater than 90% for many clusters. These results suggest that although a bacterial Genus may not describe strong boundaries for genetic exchange, a bacterial order may.