CONSIDER FOR TALK

8th Annual SEA-PHAGES Symposium Abstract

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Comparative Analysis of Six Novel Streptomyces Phage: A New Host Contributes to an Increase in the Diversity and Novelty of Phage Proteins

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This year two new Streptomyces hosts were used at Washington University in St. Louis to isolate and sequence 17 bacteriophage. Of those phage, eight were isolated from plaques formed on *Streptomyces lividans* and nine from *Streptomyces viridochromogenes*. We carefully annotated six of those phage spring of 2016. These included two *S. lividans* phage, Whatever and PynkPanther, as well as the four *S. viridochromogenes* phage Stella, WRightOn, Dryad, and Rooney. Since there were no *S. viridochromogenes* phage and only 24 previously isolated *S. lividans* phage reported in PhagesDB, very few genes showed homology to previously annotated genes. We focused our annotation efforts on pairs of novel phage that showed moderate levels of similarity to each other and those with very little similarity to any previous phage. For example, comparison of phage Stella and WRightOn (ANI 79.71%), with 68 and 65 genes respectively, showed 17 differences in the mosaic pattern of their genomes. These differences are defined as the insertion or deletion of a gene as well as two genes that belong to different phamilies. Dryad and Rooney (ANI 80.97%), with 112 and 108 genes respectively, showed 25 differences. By selecting mostly novel phage we found that 78 of the 644 genes annotated for these six phage belong to orphams, phams in which they are the only member, thus providing a measure of the novelty of their genomes.