CONSIDER FOR TALK

2023 SEA Symposium Abstract

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Grand Rapids MI

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Phun for the Whole Orphamily: exploring Rhodococcus equi phages

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Twenty-three phages were isolated from soil collected in Grand Rapids, MI using *Rhodococcus equi* NRRL B-16538, a new bacterial strain for SEA-PHAGES. Visualization by TEM showed all are Siphoviridae morphology. The genomes of eleven phages were sequenced, increasing the number of known *Rhodococcus* phage genomes to 67, and revealing notable diversity within the cohort. We annotated the genome of Jflix2, which forms the new cluster CF with phage REQ1, a phage sequenced in 2011, along with two more of our 2023 phages. Over one-quarter of the genes in our CF phages are orphams. Seven of our other phages belong to the CR cluster, making them the first *Rhodococcus* phages in this otherwise *Gordonia* phage cluster. However, the *Rhodococcus* CR phages are dissimilar enough to not be placed within any of the CR subclusters (CR1-CR5). We annotated one of these CR phages, Braxoaddie, and nearly half of its genes are orphams. Finally, we annotated Reynauld, a singleton with orphams for almost two-thirds of its genes, though it does share many structural genes with two other *Rhodococcus* singletons, DocB7 and Trogglehumper. The tapemeasure genes in these phages are nearly 10,000 nucleotides and correspond to tail lengths over 500 nm.