CONSIDER FOR TALK

9th Annual SEA-PHAGES Symposium Abstract

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Cornucopia and Piper2020: A Clear Choice

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Cornucopia and Piper 2020 are two cluster F1 Mycobacterium smegmatis phage with distinctly different plaque morphologies. Cornucopia is a temperate phage that produces cloudy plaques, while Piper2020 appears to be lytic, producing only clear plaques. These phenotypes correlate with the presence of an integrase gene in Cornucopia and the absence of one in Piper2020. Cornucopia was discovered in the soil collected from an active vermiculture compost bin, a few inches under the surface. Piper2020 came from the soil of a tomato plant that was watered daily throughout the summer. Both of these phages have between 95-97% of their genes transcribed in the forward direction. Blast comparison between these two phages showed a >90% sequence homology throughout the first 30,000 bp and the last 3000 bp of their genomes. The region in between had much lower homology, many different genes and some similar genes arranged in different patterns. The Cornucopia integrase gene is 1128 bp and has a >95% homology to five other cluster F1 phage integrases throughout the entire gene. However, in many other F1 phages, the 5’ portion of the Cornucopia integrase gene is missing. MooMoo, a singleton, with a similar halo plaque morphology to Cornucopia, contains a similar integrase that includes this 5’ region. Nucleotide tblastx of this 5’ region of Cornucopia’s integrase gene showed that this is a common motif found in many phage genomes. Further analysis will determine whether this domain is found in other integrases, or proteins with other functions.