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Arthrobacter globiformis B-2979 Eesa lysogens promote immunity to lytic and temperate phages

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Bacteriophages are viruses that specifically infect bacterial hosts. They can replicate through either the lytic or temperate cycle. While lytic phages cause bacterial cell lysis, temperate phages integrate their DNA into the bacterial genome, allowing them to replicate alongside the host or exit at a later time. This study focuses on Arthrobacter globiformis B-2979 phage Eesa. Previous work showed that Eesa formed 1 mm cloudy plaques, which became more apparent after several days of incubation. Attempts to increase its viral concentration were challenging, leading us to hypothesize that Eesa was a temperate phage. Genome sequencing placed Eesa in the Arthrobacter phage Cluster AS, subcluster AS1. Its genome contains genes involved in both lytic (Eesa\_23 and Eesa\_24) and temperate (Eesa\_33 and Eesa\_34) infection cycles, supporting laboratory observations. Given Eesa’s temperate plaque morphology, we attempted to generate lysogens and assess their immunity. Out of six potential lysogens, two were stable and confirmed using phage release assays. Both lysogens were immune to further Eesa infection. A panel of lytic and temperate phages was used to assess lysogen sensitivity. Of eight lytic phages, only one, Salpal, infected the lysogen at levels comparable to the host strain. The lysogen was resistant to infection by temperate phages in Cluster AZ (Liebe) but sensitive to Cluster AY (Anekin and CookieBear) and Cluster FL (Hirko). Future work will expand sensitivity assays and perform comparative genomic analyses to identify genes potentially involved in immunity against specific lytic and temperate phage clusters.