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A Comprehensive Study on the Host Range of Gordonia terrae Bacteriophages and an Analysis of Possible Genes Involved in the Process.

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Bacteriophages are generally specific to their hosts because their tail fibers recognize specific receptors on host cells. In the discovery phase of the Phage Hunters course, 39 bacteriophages were isolated from soil samples using *Gordonia terrae* as the host. After achieving high-titer lysates, these phages were tested for their ability to infect two additional hosts: *Gordonia lacunae* and *Gordonia rubripertincta*. Our results indicate that six of these phages can infect all three hosts, five phages infect *G. terrae* and *G. rubripertincta*, and three infect *G. terrae* and *G. lacunae*. The DNA of four tested phages was sequenced, and their genomes were annotated. Archidore is a temperate phage belonging to the DW cluster and was unable to infect either of the tested *Gordonia* species. Blondies, belonging to the CT cluster, is a virulent phage that infects all three *Gordonia* species tested, with an EOP of 10⁻² on both *G. rubripertincta* and *G. lacunae*. FuegoCuervo, a virulent phage in the DE1 cluster, has an EOP of 10⁻³ in *G. lacunae* but does not infect *G. rubripertincta*. Towmatter, which infects the wild host and *G. rubripertincta* with an EOP of -2, is a temperate phage associated with the DL cluster. Although the specific genes responsible for a broad host range in bacteriophages have not been clearly identified, genes such as major tail protein, tail assembly chaperone, lysin A glycosyl, holin, and DNA methyltransferase are often cited in the literature. For instance, Blondies possesses three tail assembly chaperone proteins and one lysin A glycosyl, which assist in host-cell interactions, whereas the other phages have only one or two tail assembly chaperones and no lysin A glycosyl. While *G. terrae* is more closely related to *G. lacunae*, more of the studied phages were able to infect *G. rubripertincta* as an alternative host, suggesting significant plasticity in bacteriophage host range.