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Characterization of a Novel Gordonia Phage Isolated From Sewage From Spanish Fork, Utah

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Genome annotation has enabled massive leaps forward in the scientific community’s understanding of the proteins that phage contain, their various functions and how they compare to other organisms. Gordonia rubripertincta, which are known to disrupt agriculture, are highly similar to Mycobacterium tuberculosis that cause the disease tuberculosis, thus we believe that Gordonia bacteriophages will be good candidates for agricultural phage therapy as well as understanding the evolution of these two important bacterial hosts. Our phage hunters research team isolated Gordonia phage PushinP from local sewage treatment plants, in contrast to soil isolation. Genomic analysis was performed on Gordonia Bacteriophage PushinP to determine its similarity to other Gordonia bacteriophage using Gepard dot plot. The dot plots made for this phage showed remarkable similarity to the Gordonia bacteriophages BigChungus, Feastonyeet, Vine, Lauer, SheckWes, Mayweather, Pons and CherryonLim. Furthermore, the function of novel proteins was determined using the bioinformatic programs BLASTp, HHPred, Phyre2 and PePPER to gather this data. For example, it was determined that the structure of the hypothetical protein gp19 was highly related to an endopeptidase of Serratia marcescens. In conclusion, the Gordonia Bacteriophage PushinP, in conjunction with related phages, may be of use in agricultural phage therapy as well as further research into the evolution of Gordonia and Mycobacterium.