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Genomic Analysis of Gordonia rubripertincta bacteriophage Sampudon

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Sampudon was discovered by Sampurna Lamichhae and Barak Adler, students of St. Luis Community College in Saint Louis, MO in 2020. The virus was isolated from Gordonia rubripertincta. Queensborough Community College students are were very grateful for the opportunity to adopt Sampudon. Its genome length is 68,500 nucleotides and it has 100 predicted protein coding genes. Sampudon belongs to the cluster DV with 26 other viruses. The average DV cluster member has length of 67,356 and GC content of 58.2%. The most similar to Sampudon is Jalebi, their major differences are outside of the protein coding segments, and they differ by 1 nucleotide in length. All Sampudon’s genes are in forward direction and the genome follows typical to DV cluster architecture. Within the DV cluster the most diversity is in the first part of the genome after gp3. Sampudon and Jalebi have their esterase and minor tail protein, many others lipase or orphams of unknown function. DNA primase/polymerase region towards the end of the genome is also very diverse. We are going to explore those regions in more detail.