From soil to sequencing; annotating phage SanaSana

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The incidence of antibiotic-resistant bacteria has increased over the past century, causing a global crisis. The present roster of known antibiotics is becoming less effective. Methicillin-resistant *Staphylococcus aureus* (MRSA) is the number two killer worldwide, and ranks fourth in the United States. Phage therapy is an emerging solution for combating antibiotic resistance. Phage SanaSana was isolated and purified using host bacterium *Microbacterium foliorum* and belongs to the phage subcluster EB. Post genome annotation of SanaSana, phylogenetic analysis of the EB subcluster was conducted using the terminase gene. Investigation into potential evolutionary trends led to the SanaSana no known function (NKF) gene 16 (Gene 16), which is flanked by genes for the tail-assembly chaperone and tape measure proteins. NKF genes, flanked in the same manner, were also present in 46 of 54 members of the EB subcluster. Further phylogenetic analysis was performed using Gene 16 as the focus. This produced a clade containing SanaSana and phage Stoor. Pairwise alignment of the two genomes illuminated a difference between SanaSana NKF gene 31 (Gene 31) and Stoor NKF gene 30. BLASTp was applied to find a potential function for Gene 31. Results from BLASTp gave hits for terminase found in phages, such as the singleton phage Spartoi. HHPRED analysis determined that Gene 31 was a segment of the terminase sequence. This finding suggests that a recombination event occurred and is capable amongst phage as a whole. This research helps provide a further understanding of phage evolution and potentially contributes to phage therapy.