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The BS Cluster as Influenced by Annotation of Novel Phages Garnacho and Talos

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The first BS phage, BRock, was discovered in 2016, and the cluster was eventually designated in 2022 with the finding of phages Alone3 and LuckySocke. Cluster BS consists of four annotated and three draft phages, all of which were isolated using Streptomyces, four of which were specifically *Streptomyces lividans*. Phage Talos and Garnacho are both part of the BS cluster, with genome lengths of 114,044 bp and 114,833 bp, respectively. Phages in the BS cluster, including Garnacho and Talos, are typically Myoviridae. Both phages were extracted from soil collected on the Danforth Campus of Washington University before being isolated and amplified during the fall of 2024 and then manually annotated in the spring of 2025. In total, Garnacho has 183 protein-coding genes while Talos has 189 protein-coding genes. These final counts are typical for phage in the BS cluster, which range from 180 to 191 protein-coding genes. As the cluster is small and recently designated, most of these genes have unknown functions. Additionally, Garnacho and Talos have 32 putative tRNA genes, which is slightly higher than the average of 29.5 in the BS cluster. tRNA analysis will be conducted toward the end of genome analysis to confirm the existence and location of these tRNA genes. Other genes of interest include RecA-like DNA recombinase and Baseplate J protein, which will contribute to the larger goal of developing in-depth functional information about the BS cluster.