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Tail Assembly Chaperone Proteins of Microbacterium foliorum Cluster EE Phages

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Tail assembly chaperone proteins (TACP) help to create the tail structures in bacteriophages and are found adjacent to one another in bacteriophage genomes. TACP sequences are encoded for with a characteristic translational frameshift. We compared nucleotide sequence, amino acid sequence, and 3-Dimensional structures of these proteins to related phage TACPs. Because these genes have obvious functional similarity, we hypothesized that there would be considerable similarity in tail assembly chaperone encoding sequences of EE cluster phages. To explore our hypotheses we used DNA Master, Phamerator, and GeneMark to annotate and develop gene maps of bacteriophage Bri160, a novel Microbacterium foliorum bacteriophage. We then compared these results to similar genes of 26 EE cluster phages. Using Phamerator, we compared gene location and size. We created 3-dimensional structures of the proteins using I-TASSER. Bri160 showed a similar sequence organization to that of other EE cluster phages. However, our data show that Bri160 has coding potential for three tail assembly chaperones, whereas most other EE cluster phages encode for two. Evidence both for and against the existence of a third, overlapped, reverse gene was found.