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Annotation and Comparative Analysis of Two New Microbacterium foliorum Bacteriophages, Figueroism and EarickHC

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Fourteen novel bacteriphages isolated from *Microbacterium foliorum* were isolated by students at La Sierra University. Thirteen phages were obtained through enriched isolation while one was isolated through direct plating. All fourteen phages had clear, medium size plaques indicative of lytic phages. Two phages, Figueroism and EarickHC, were chosen for further investigation. Both Figueroism and EarickHC have a siphoviridae morphotype based on electron microscopy analysis and their genomes were sequenced and annotated using bioinformatic tools such as PECAAN, Phamerator, NCBI Blastp, and HHPred.  
  
Figueroism’s genome is 41,847 base pairs, with a GC-content of 63.5%. Based on sequence similarity it was assigned to cluster EA1. Figuerosim encodes for 63 genes, of which 30 were assigned functions. A host range assay performed on various other Microbacterium species revealed that Figueroism can also infect *M. paraoxydans*, although at a much lower rate than *M. foliorum*.   
  
Earick HC was assigned to cluster EC and its genome is 52,992 base pairs long, with a GC-content of 68.9%. It has 91 genes, of which 40 were assigned functions. Although a holin was not assigned, EarickHC has eight different membrane proteins, including three that are immediately upstream of the lysin A gene. Moreover, it encodes for a DNA binding protein with high similarity to an RNA polymerase sigma factor. Like other members of the cluster, EarickHC also encodes for an 18 bp asymmetric sequence motif, 5’-TAgaCTATagGTgTaAgC-3’ that is repeated 12 times throughout the genome, positioned around 21-30 bp upstream of a predicted translation initiation codon.