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Fun with Donkeykong: more phaging on (or at least near...) the bayou

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Phages were isolated from a variety of locales in and around the Greater New Orleans, Louisiana area using standard microbiological techniques. Genomic DNAs from two phages were sequenced and one genome, that of Donkeykong, was chosen for analysis. The sequenced genome is 59,478bp in length, with cohesive ends showing a ten base pair overlap. BLASTn analysis reveals considerable nucleotide homology with the genomes of other known mycobacteriophages in cluster F, subcluster F1. Automated annotation employing Glimmer, GeneMark and Aragorn in the DNAMaster environment calls about 106 features, all presumptively encoding protein; no tRNA genes are predicted. Presumed lack of tRNAs and tmRNAs is confirmed by analyses run with both “external” Aragorn (i.e. via the World Wide Web external to the DNAMaster environment) and tRNAScanSE. With the help of BLASTp analysis and similar tools, it is possible to make at least tentative proposals for the functions of possible gene products in the case of a significant minority of putative protein-encoding ORFs. The structure of the genome appears to be similar to that of many mycobacteriophages, with ORFs that at least potentially encode structural products at the left end, while the right end has a more complex and difficult to predict functional picture.