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Microbacteriophage Magritte: analysis of a new singleton

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The goal of this study was to annotate the novel Microbacteriophage Magritte which is a Singleton phage. This phage was found in a soil sample under a sewage pipe in Columbia, TN.  
As of now, there are 63 Singleton phages reported on phagesdb.org with an average genome size of 60,866 bp and an average number of genes of 83.1. Phage Magritte, isolated on the Microbacterium foliorum host, utilizes the lysogenic cycle as evident from the production of consistently small opaque plaques formed in a lawn of bacterial host cells on Petri plates. Electron microscopy imaging indicates that Magritte exhibits the Podoviridae morphotype showing a short tail. In comparison to other known Singletons, Magritte has a very long genome of 133228 bp and an estimated 252 genes. One of the Magritte’s unique genome features is that it is circularly permuted so it does not have any expected biological "ends." In addition, phage Margitte has an unusually large number of tRNAs, with 24 tRNA genes confirmed by Aragorn (version 1.2.41) and tRNAscan-SE (version 2.0) out of 30 tRNAs projected by PECAAN genome analysis tool. The infernal score as a measure of the quality of the tRNA for these genes was >35. Magritte tRNAs localize between genes 86 and 92, forming “tRNA clusters” in the genome. There were also three particularly long genes present in the genome: 17, 37, and 39. The length of these genes is 5975, 4697, and 4358 base pairs respectively. Gene 17 does not belong to any known phams and its function is unknown. Gene 37 and 39 are likely to be tape measure and minor tail proteins, respectively. The genome analysis, performed using PECAAN, Phamerator and GeneMark, demonstrated that Magritte is a unique and complex bacteriophage with an unusual genome organization which can provide invaluable insights toward future bacteriophage discoveries.