CONSIDER FOR TALK

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Going to the Gap for more than genes

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Bacteriophage (phage) are the most numerous and diverse biological entities on Earth. This diversity provides a reservoir of information about not only gene and genome structure and function but about mechanisms of evolution. This year we explored the genomes of two mycobacteriophage, Phaja and Pippin. Phaja is a Cluster E phage with a genome size of 75685bp. Pippin is a Cluster A1 phage with genome 52034bp in length. To explore these two genomes we focused on the gaps. One gap visible on Phamerator is created by the tRNA genes. Phaja carries two, both encoding Gly tRNAs. They do not reflect alternative codon use when comparing Phaja to Mycobacterium smegmatis. Rather they are codons used at a higher frequency by Phaja suggesting a need for a larger tRNA pool. The mismatch of codon frequency of use with the host, suggests that M. smegmatis may not be Phaja’s natural host. Another gap we explored was one created by an approximately 500bp insertion immediately upstream of the tapemeasure protein gene in Phaja. The insertion contains two overlapping reading frames. BLAST analysis shows that both reading frames have the potential to encode an endonuclease. The endonuclease has been annotated in other phage. However, the structure suggests the possibility of a reading frame shift. It is intriguing that that the structure occurs immediately downstream of the tail chaperone ORFs with their reading frame shift. Phaja also contains an endonuclease/recombinase that it shares with a small subset of the Cluster E phage, downstream of gp94. Most of the E cluster phage have a methylase at this position. The endonuclease is a candidate for horizontal gene transfer. Gaps are usually mined for promoter sequences and in Pippin we explored the promoter region of the putative repressor protein. Pippin forms lysogens at a very low frequency and the plaque morphology is essentially clear. The peptide is 100% conserved with the putative repressor of BxB1 as is the sequence in the gap. The area has a weak promoter based on sequence and the same sequence is found in other cluster A1 phage suggesting there is another reason for the clear plaques.