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BNFO 301  
Research Project Rough Draft

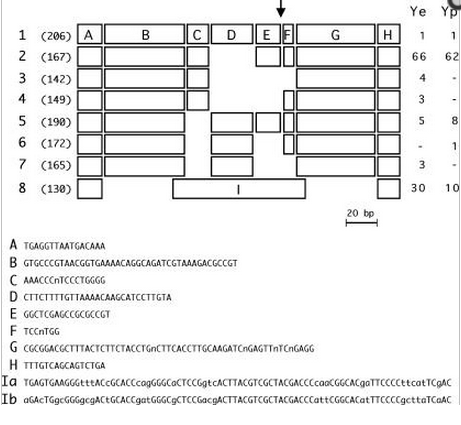
**Short dispersed palindromic repeats within *Yersinia* bacteriophages.**

# Introduction

It is imperative to understand Bacteria, as they are a very diverse domain filled with many beneficial and harmful species. In particular, most the species in the genus *Yersinia* are pathogenic to humans [1]. With increasing rise of resistance amongst ‘superbug’ bacteria using bacteriophages in novel Phage therapy is proving to be more efficient in the long run compared to antibiotics [1,2,3]. Most species in *Yersinia* contain *Yersinia* palindromic (YPALs) sequences are miniature DNA insertions that are spread across the chromosomes of *Yersinia* [2,3,4]. These sequences are about ~150 nucleotides in length and is significant for playing a role as RNA elements in posttranscriptional control [2,3,4]. The purpose of this study is to determine whether or not certain YPAL elements are present in *Yersinia* phages.

**Methods**

This study specifically focuses on subfamily 2 of *Yersinia* which includes a 167 nt YPAL [4]. This YPAL is included in Y. *enterocolittica* and Y. *pestis* [2,3,4]. These species are significant because they are extremely pathogenic to humans [4]. The analysis of phage sequences is required to obtain a better understanding as to similarities that the *Yersinia* phages share with their bacterial hosts Y. *enterocolitica* and Y. *Pestis*. Using BioBike, a tool must be created to find YPALs within the *Yersinia* phages.



**Fig 1.** Structural organization of YPAL elements. This figure includes all 8 different types of YPALs currently known in Yersinia. Elements commonly found in subfamily 2 (Y. enterocolitica, Y. pestis) contain 167 nucleotides and include an A/H terminal sites. This will be the main criteria for searching for YPALs in Yersinia phage.

Degregio et al. (2006)

A subfamily 2 YPAL sequence can be pieced together by combining the various elements of nucleotides given from **Fig. 1**. To create a YPAL-finding tool for our Yersinia phage in BioBike, a search criteria must be constructed. To do so, using the A and H terminals as a window for a search function in BioBike may find instances of subfamily 2 YPALs in the Yersinia phages obtained.

In BioBike the MATCHES-OF-PATTERN is used to find patterns in Yersinia phage that include both the A and H terminals that are found in subfamily 2 Yersinia bacteria *and* should match the length of 167 nucleotides to be considered as a subfamily 2 YPAL sequence.

Phages to be analyzed for YPALs:

TGAGGTTAATGACAAAGTGCCCGTAACGGTGAAAACAGGCAGAATCGTAAAGACGCCGTAAACCCnTCCCTGGGGGGCTCGAGCCGCGCCGTTCCnTGGCGCGGACGTTTACTCTTCTACCTGnCTTCACCTTGCAAGATCnGAGTTnTCnGAGGTTTGTCAGCAGTCTGA

**Fig 2.** Subfamily 2 YPAL sequence. Yellow represents the A and H terminals, Green represents the B and G regions of the sequence. The blue and purple regions represent the inner core regions of the YPAL sequence. The smaller region of the YPAL, F, is represented in grey.

*Y.* Berlin *Y.* L-413C *Y.* phiA1122 *Y.* phiYeO3-12 *Y.* py54 *Y.* Yepe2

Window Frame to Search:

Subfamily 2 YPAL

TGAGGTTAATGACAAA……………………………….TTTGTCAGCAGTCTGA

(A Terminal)……………………………………………………………..(H Terminal)

Algorithm:

The MATCHES-OF-PATTERN in BioBike was used to find any instances of subfamily 2 YPALs in any of the six Yersinia phage obtained. Both A and H terminals were used to find a match in each phage through BioBike.

**Results and Discussion**

Out of the six phages that were analyzed for YPALs there were no matches of the A and H terminals in all of the Yersinia phages obtained. The MATCHES-OF-PATTERN function in BioBike did not detect any instances of subfamily 2 YPALs in Yersinia phage. This confirms that there aren’t any subfamily 2 YPALs that are of known existence in Yersinia phages Berlin, L-413C, phiA1122, phiYeO3-12, py54, and Yepe2.

For further study of YPALs, it would be imperative to analyze these phages and use a MATCHES-OF-PATTERN that encapsulates more Yersinia phages. Another pathway of progressive study would be to analyze any matches of YPALs in Yersinia plasmids. In conclusion, there are no instances of YPALs *of any subfamily* in the Yersinia phages tested because each subfamily of Yersinia includes an A and H terminal, and not one A or H terminal match could be found through BioBike in any of the Yersinia phage.

**Works Cited**

**1. De Gregorio, Eliana, et al. "Enterobacterial repetitive intergenic consensus sequence repeats in yersiniae: genomic organization and functional properties."*Journal of bacteriology* 187.23 (2005): 7945-7954.**

**2. Delihas, Nicholas. "Enterobacterial small mobile sequences carry open reading frames and are found intragenically—evolutionary implications for formation of new peptides." *Gene regulation and systems biology* 1 (2007): 191.**

**3. Delihas, Nicholas. "Small mobile sequences in bacteria display diverse structure/function motifs." *Molecular microbiology* 67.3 (2008): 475-481.**

**4. De Gregorio, Eliana, et al. "Structural organization and functional properties of miniature DNA insertion sequences in Yersiniae." *Journal of bacteriology* 188.22 (2006): 7876-7884.**