MEETING ABSTRACT



Open Access

Comparison of codon usage in mycobacteriophages with and without tRNAs in their genomes

Ethan S Gill¹, Claire A Rinehart^{2*}

From 12th Annual UT-ORNL-KBRIN Bioinformatics Summit 2013 Buchanan, TN, USA. 22-24 March 2013

Background

Mycobacterium smegmatis is a soil bacterium. Over 448 mycobacteriophages specific for *M. smegmatis* have been sequenced and grouped into clusters of related genomes based on the similarity of their products and genome organization [1]. Eighty-one of these sequenced phage genomes contain at least one tRNA.

Materials and methods

In this study we compared the codon frequencies between the phages that carry tRNA in their genome (Clusters A2, A3, A5, A6, A9, C1, C2, E, J, K1, L1, L2, M) to those phages without tRNA in their genome (Clusters A1, A4, B1, B2, D, F1, G) in order to determine whether the tRNAs being carried by the mycobacteriophages were needed to survive in *M. smegmatis*. The phages with embedded tRNAs were drawn from http:// phagesdb.org/data/. The coding sequences for the mycobacteriophages were obtained from NCBI GenBank [2]. Codon frequencies were derived for each mycobacteriophage and a BoxWhiskerChart (Figure 1) was made using a program written in Mathematica[®].

To determine which codons may require expression of phage tRNAs, Figure 1 plot regions for phages containing tRNA (red) that show frequencies in excess of those not containing tRNA (blue) have been circled in magenta. Only a few codons meet this criteria: ACT, ATG, CAG***, CGT, GAC**, GAG*, TAC, TAT, TGG. A significant number of mycobacteriophages lay outside the non-tRNA phage boundaries for codons CAG, GAC



Figure 1 BoxWhiskerChart of codon frequencies in phage without tRNA (blue boxes) and those with tRNA in their genomes (red boxes). Colored boxes encompass the 25%-75% quantile while the whiskers encompass the 0-25% and 75-100% quantiles. Dark dots are outliers while gray dots are far outliers. The brown line is the mean and the cyan line is the median. The numbers on the left margin represent the number of observations, n.



© 2013 Gill and Rinehart; licensee BioMed Central Ltd. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/2.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

^{*} Correspondence: claire.rinehart@wku.edu

²Department of Biology, Western Kentucky University, Bowling Green, KY, 42101, USA

Full list of author information is available at the end of the article

and GAG, therefore, these phages may be dependent on internally coded tRNAs.

Authors' details

¹Department of Computer Science, Western Kentucky University, Bowling Green, KY, 42101, USA. ²Department of Biology, Western Kentucky University, Bowling Green, KY, 42101, USA.

Published: 22 October 2013

References

- Hatfull GF: Mycobacteriophages: genes and genomes. Annu Rev Microbiol 2010, 64:331-356.
- Benson DA, Karsch-Mizrachi I, Clark K, Lipman DJ, Ostel J, Sayers EW: GenBank. Nucleic Acids Res 2012, 40(Database issue):D48-D53.

doi:10.1186/1471-2105-14-S17-A9

Cite this article as: Gill and Rinehart: **Comparison of codon usage in mycobacteriophages with and without tRNAs in their genomes**. *BMC Bioinformatics* 2013 **14**(Suppl 17):A9.

Submit your next manuscript to BioMed Central and take full advantage of:

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

BioMed Central

Submit your manuscript at www.biomedcentral.com/submit