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Graham Hatfull's Lecture Part 2:
Bacteriophages: Genomic insights

Teaching Tools were prepared by Welkin Pope with Graham Hatfull.

Contents

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1. Keywords and Terms

Virion, Siphoviridae, genome, sequence similarity, DotPlot, genome defined ends, circularly permuted genome, genome architecture, genome mosaicism, homologous recombination, targeted homologous vs non-homologous (illegitimate) recombination, recombinase

2. Lecture Notes

Organization of the bacteriophage genome is discussed. Comparison of phage genomes can provide insight into the evolution of viruses.

3. Review Questions

1. We find evidence of _____ recombination in bacteriophage genomes (choose as many as you like):
   a. homologous
   b. targeted homologous
   c. illegitimate
2. Do bacteriophage particles have linear or circular genomes?
3. Does targeted homologous recombination occur during the bacteriophage lifecycle?
4. What kinds of information do genome DotPlots display?
5. If a phage has a circularly permuted genome, how do the individual chromosomes of a group of these phage particles compare to each other?

4. Answers to Review Questions

1. All three
2. Linear
3. Yes, integration of a prophage into the host's genome is an example of targeted homologous recombination.
4. DotPlots show a direct comparison of all the nucleotides in a genome to all the nucleotides of another genome. Areas of identity appear as diagonal lines.
5. Phage particles have a linear chromosome and each particle contains all the same genes as other particles in the same order, however, the first gene on the chromosome may be different. For example: phage particle one's genome might be A-B-C-D-E while phage particle two's genome may be C-D-E-A-B.

5. Discussion Questions

1. How can lytic infection contribute to phage genetic diversity?

2. What is the evidence that phage genome “modules” have different evolutionary histories?

3. How is it possible for illegitimate recombination, a process that would seem to yield few viable progeny, to be the driving force behind the genome architecture of bacteriophages?

6. Answers to Discussion Questions

1. Simultaneous infections of the same cell allows illegitimate recombination to occur between unrelated phages

2. When comparing the genomes of two different phages, it is possible to find DNA regions with high levels of sequence identity and common to both phages, next to regions of little sequence identity.

3. With an enormous global population, and a rapid infection rate, it is possible for a very rare process to occur millions of times per second.

7. Explain or Teach These Concepts to a Friend

1. Explain the difference between homologous and illegitimate recombination.

2. Explain the difference between circularly permuted genomes and genomes with defined ends.

3. Explain what genome mosaicism means.

4. Explain what genome architecture means.

8. Papers for Journal Club

1. CELL. Vol 113, Issue 2, Pages 171-82, 2003. Origins of highly mosaic mycobacteriophage genomes. Marisa L Pedulla, Michael E Ford, Jennifer M Houtz, Tharun Karthikeyan, Curtis Wadsworth, John A Lewis, Debbie Jacobs-Sera, Jacob Falbo, Joseph Gross, Nicholas R Pannunzio, William Brucker, Vanaja Kumar,

Jayasankar Kandasamy, Lauren Keenan, Svetsoslav Bardarov, Jordan Kriakov, Jeffrey G Lawrence, William R Jacobs, Roger W Hendrix, Graham F Hatfull.

2. JOURNAL OF MOLECULAR BIOLOGY. Vol 397, Issue 1, Pages 119-43, 2010. Comparative genomic analysis of 60 Mycobacteriophage genomes: genome clustering, gene acquisition, and gene size. Graham F Hatfull, Deborah Jacobs-Sera, Jeffrey G Lawrence, Welkin H Pope, Daniel A Russell, Ching-Chung Ko, Rebecca J Weber, Manisha C Patel, Katherine L Germane, Robert H Edgar, Natasha N Hoyte, Charles A Bowman, Anthony T Tantoco, Elizabeth C Paladin, Marlana S Myers, Alexis L Smith, Molly S Grace, Thuy T Pham, Matthew B O'Brien, Amy M Vogelsberger, Andrew J Hryckowian, Jessica L Wynalek, Helen Donis-Keller, Matt W Bogel, Craig L Peebles, Steven G Cresawn, Roger W Hendrix.

3. JOURNAL OF BACTERIOLOGY. 2002. Imbroglios of viral taxonomy: genetic exchange and failings of phenetic approaches. Lawrence JG, Hatfull GF, Hendrix RW.