

Phage Wars: Identification of a Bacteriophage 80a Lysogenic Exclusion Gene That Targets Phage f11.

1. Identify genes within the 80alpha genome not found in the phi11 genome

The two phages are known within BioBIKE under the nicknames 80alpha and phi11. The BioBIKE function COMMON-ORTHOLOGS-OF. Here are examples of its use:

The image shows three examples of the 'COMMON-ORTHOLOGS-OF' function interface in BioBIKE. Each example is a horizontal bar with a yellow background and a green arrow on the left. The first example has 'ORGANISM-NAMED' with a text box containing '"Staphylococcus"' and 'IN-PART' with a dropdown menu. The second example has 'LIST' with two text boxes containing 'sap-2' and '80alpha'. The third example has 'NOT-IN' with two text boxes containing 'stap-11' and 'stap-12'. Each example also has an 'Options' button on the right.

COMMON-ORTHOLOGS-OF ORGANISM-NAMED "Staphylococcus" IN-PART Finds genes common to all Staphylococcus phage

COMMON-ORTHOLOGS-OF LIST sap-2 80alpha Finds genes common to two phage

COMMON-ORTHOLOGS-OF stap-11 NOT-IN stap-12 Finds genes in one phage but not another

2. Identify putative functions (where possible) for the unique genes. Are they essential?

Display the annotations of the genes you found in Question 1. The function DESCRIPTION-OF may be helpful here. Sometimes the annotations aren't very helpful. Perhaps the orthologous genes in other phage have better annotations. Go further by displaying the annotations of the genes orthologs. To find the orthologs use the STAPH-ORTHOLOG-OF function, which can be placed on your FUNCTION button by running RUN-FILE, using "staph-ortholog-of.bike" as the file-name (remember the quotation marks) and selecting the SHARED option. You'll need to make many judgments as to whether an annotation indicates that the gene is essential for phage growth.

3. Assess which genes are likely to be expressed from a prophage.

The genes you're after are not part of operons under repressor control or part of operons activated during infection. The function CONTEXT-OF may be helpful, using the DRAW option.

4. Generate a prioritized list of candidate genes to be tested for phi11 exclusion