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- XDR-TB (drug-resistant tuberculosis), 76

Color Plates

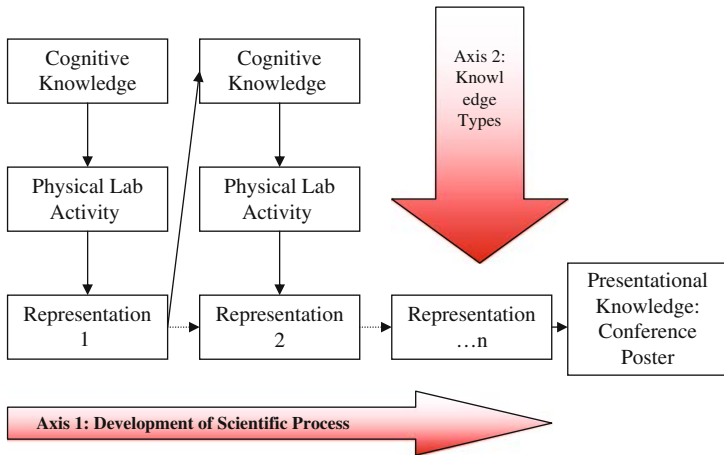


Fig. 2.2 A Schematic Representation of the Scientific Inquiry Process

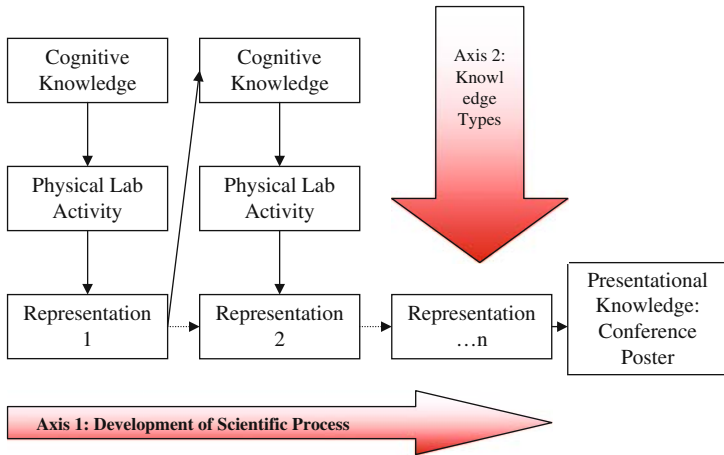


Fig. 5.2 A schematic representation of the scientific inquiry process

Color Plates

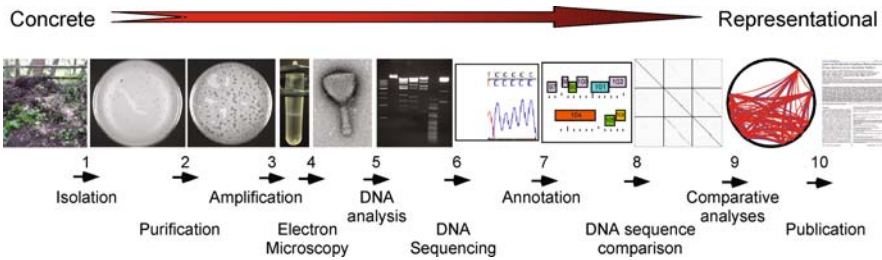


Fig. 6.3 The ten steps of the PHIRE program. Each of the ten steps in the PHIRE program are illustrated with the central arrow showing the transition from concrete to abstract comprehension from step 1 to step 10

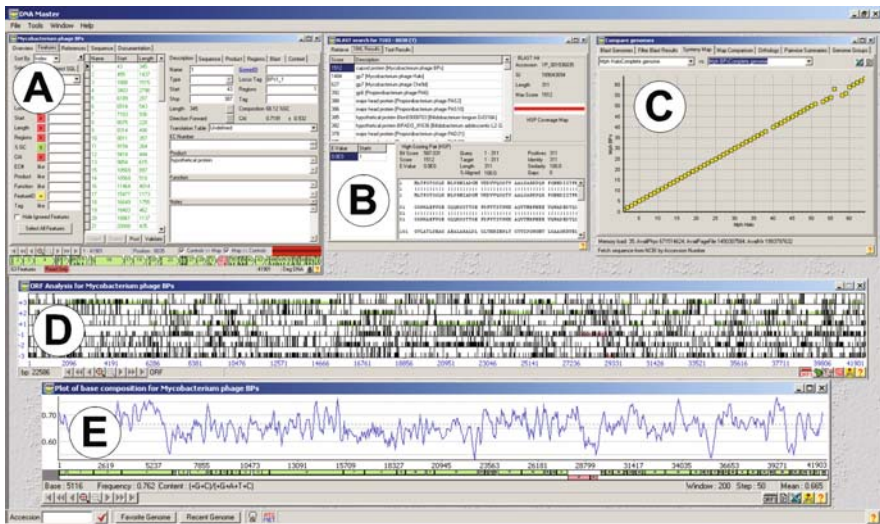


Fig. 6.6 DNAMaster: A program for phage genome annotation. Screen shots are shown from several representative windows of DNAMaster (A–E). (A) Window presenting features of mycobacteriophage BPs. The “Feature” tab is selected, showing a list of the genes with their coordinates. (B) The “Compare Genomes” window showing the results of a BlastP search of phage BPs gp7. (C) Comparison of phage BPs and phage Halo genomes, with each yellow box indicating the position of genes that are shared between the two genomes. (D) The “Frames” window showing the positions of stop and start codons in all six reading frames. The positions of identified opening reading frames are colored either *green* (forward direction) or *red* (reverse direction). (E) Plot of base composition showing the average GC% content across the BPs genome. These represent just a small subset of the available functions with DNAMaster (available as a free download from <http://cobamide2.bio.pitt.edu>)

Color Plates

L5

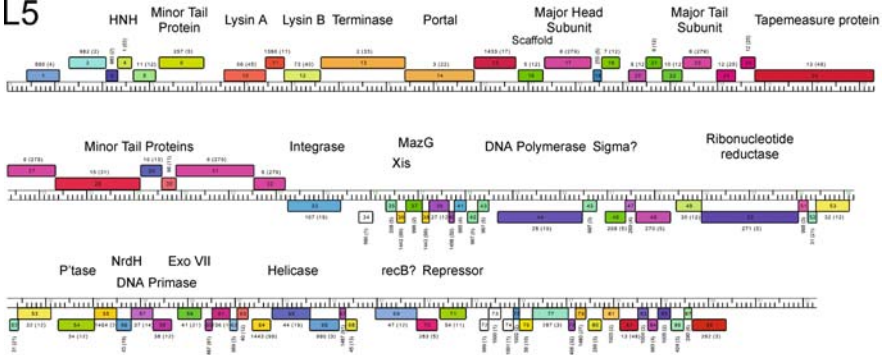


Fig. 6.8 Genome map of mycobacteriophage L5. The L5 genome is represented as a *horizontal bar* with markers spaced at 1 kbp intervals. Each of the predicted genes is shown as a colored box either above or below the genome; those above are transcribed rightward, and those below are transcribed leftward. The map was generated by the program Phamerator, which sorts the predicted genes into phamilies (Phams) as functions of their predicted amino acid sequence relatedness. The Pham number is shown above each gene with the number of Pham members in parentheses, and each gene is colored according to its Pham. Some of the predict gene functions are noted

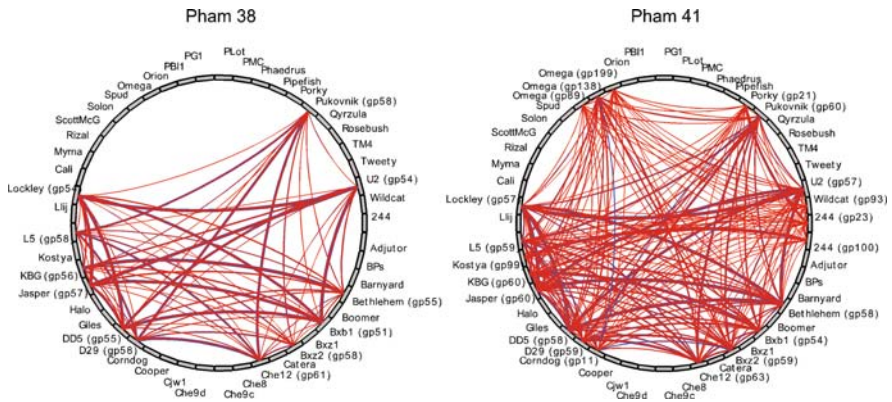


Fig. 6.9 Family circles. Family circles for Pham38 and Pham41 are shown. In the L5 genome (see Fig. 6.8), genes 58 and 59 are members of these two Phams, respectively, and the family circles suggest that they have distinct and different evolutionary histories. Each of the phages is listed around the circumference of each circle and an arc is drawn between members of each phamily with line thickness corresponding to strength of the relationship

Color Plates

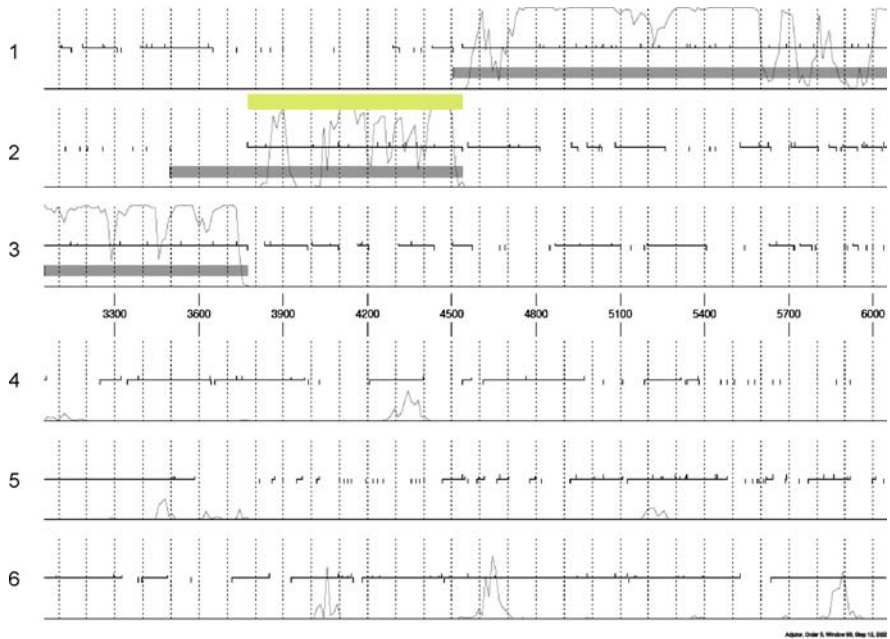


Fig. 7.1 Graphic Output of GeneMark Program. A segment of phage Adjutor genome sequence was analyzed using the program GeneMark, which generates a graph of the coding potential in each of the six possible open reading frames (ORFs) (labeled 1–6; frames 1–3 are expressed in the rightward direction, and 4–6 in the reverse direction). ORFs are identified as *horizontal lines* between translation stop codons (*down ticks*), and potential start codons are shown as *up ticks*. Coding potential is indicated by the line graph. The thick horizontal gray lines (still italicized) are considered areas of interest. One such gene is highlighted in *green*

Color Plates



```
GLIMMER (ver. 3.02; iterated) predictions:
orfID      start      end frame  score
-----
>Adjutor
orf00001      43      309  +1    5.50
orf00002     421     1524  +1   11.60
orf00003    1568    1762  +2    7.44
orf00004    1772    1936  +2   19.55
orf00005    1946    2125  +2    2.27
orf00006    2136    3776  +3    9.08
orf00008    3773    4543  +2    7.48
orf00010    4540    6306  +1   13.68
orf00011    6328    7914  +1   15.10
orf00012    7925    8137  +2    8.51
orf00013    8134    8586  +1    6.27
orf00014    8555    8734  +2    9.56
orf00015    8822    9067  +2    1.62
orf00016    9235    9636  +1    6.98
orf00017    9669   10376  +3   10.88
orf00019   10392   10811  +3   10.24
orf00020   10848   12032  +3   12.62
orf00022   12029   12397  +2   12.81
orf00023   12400   12732  +1    7.05
orf00024   12729   13136  +3    7.45
orf00025   13129   13491  +1    8.23
orf00026   13488   13907  +3    5.12
orf00027   13944   14300  +3    8.89
orf00028   14312   14512  +2    4.14
orf00029   14541   15344  +3    9.78
orf00030   15426   16079  +3   10.30
orf00032   16102   16320  +1    8.00
orf00034   16322   21094  +2   10.80
orf00036   21084   22604  +3   14.22
orf00038   22601   24256  +2   12.44
orf00039   24256   26526  +1   13.24
orf00040   26526   28574  +3   11.64
orf00043   28574   29440  +2    4.49
orf00044   29450   29770  +2   11.76
orf00046   29773   30201  +1    4.90
orf00048   30210   31193  +3   10.50
orf00049   31190   31444  +2    7.17
orf00051   31715   32254  +2    2.39
orf00053   32238   32693  +3    6.68
-----
```

Fig. 7.2 Glimmer Program Output. A segment of the phage Adjutor genome sequence was analyzed by Glimmer generating a list of potential ORFs, their start and stop codons, reading frame, and evaluative score. The *red box* designates one specific candidate gene

Color Plates

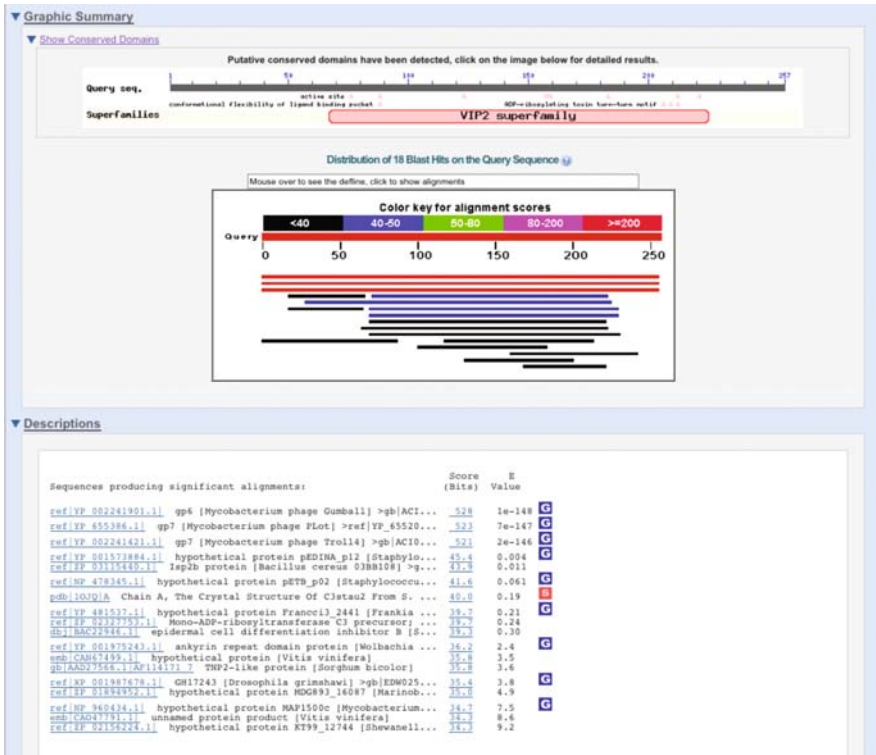


Fig. 7.3 Output of a BLASTP search using the BLAST server at NCBI. The amino acid sequence of a predicted phage protein was submitted as a search query to the server, which returned a summary of the search results; a screen shot of the results window is shown. At the *top*, a diagram shows the correspondence of a putative conserved domain identified in the search with a linear representation of the query sequence. Below that is a diagram of related sequences identified in the search, with the closest matches shown in *red*. The identities of the specific matches and their scores are shown in the *bottom panel*

Color Plates

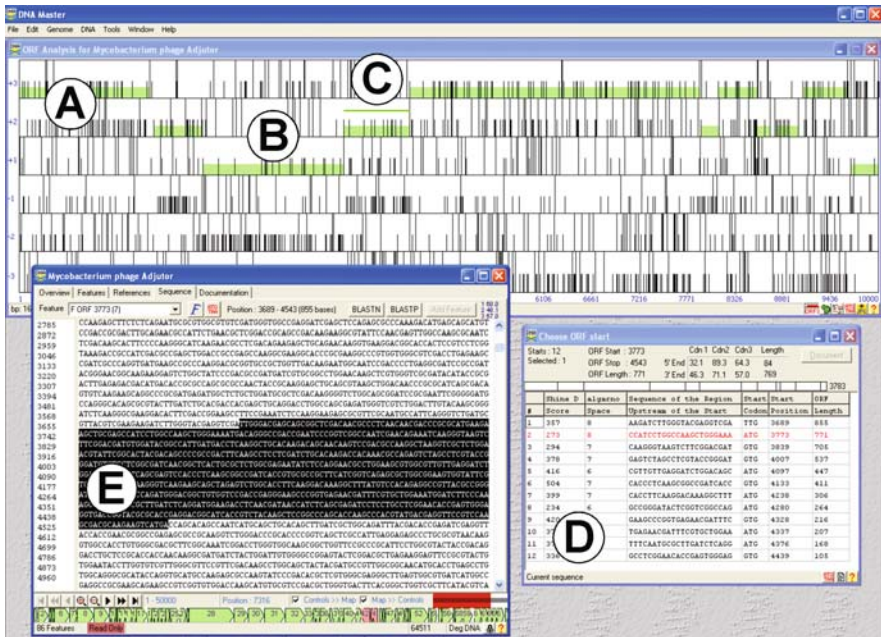


Fig. 7.4 Representations of genome analyses using DNA Master. (A) The output from the “Frames” routine in DNA Master showing six reading frames, with start (short vertical lines) and stop codons (full height lines) indicated. (B) ORFs with strong prediction for coding potential predicted by GenMark and Glimmer are designated by a thick green horizontal line. (C) Clicking on a segment of a frame of interest produces a thin green line and also links to the “choose start” routine shown in (D) the ORF and start codon corresponding to the frame segment in (C) is in red. (4). (E) The genome segment highlighted in (C) is revealed as a selected segment (black background) in the “Sequence” panel of DNA Master, and can be added to the annotation or copied as either a nucleotide or a translated amino acid sequence for BLAST analyses

