

WEB WATCH

Interactive evolution

- <http://www.evotutor.org/>
- <http://www.pbs.org/evolution/>

Do those dry evolutionary genetics formulae fail to leap off the page? If so, then *EvoTutor* — a free online resource for interactive simulations of evolutionary processes — might be a site that you'll greet with open arms.

By clicking on 1 of 12 evolutionary processes, such as drift or adaptation, you can access a selection of subtopics, which provide background information on the process and explanations of its associated formulae. Alternatively, you can go straight from a subtopic to an interactive simulation of a process. To illustrate gene flow, for example, individuals in two starting populations are depicted as coloured dots; by altering the rate of migration between populations and the strength of selection against migrants and hybrids, you can watch the make-up of the populations change as the coloured dots intermingle.

Although you won't become an evolutionary genetics buff just by visiting this site (having a textbook to hand might help), the simulations do help bring to life what formulae and your imagination might not. Stay tuned for *PhyloTutor* and *GenTutor*, sister sites that are now under construction.

If you're after a broader picture, then make the *Evolution* web site — linked to a US PBS television miniseries — your first stop. In seven episodes, the series explored evolution from the life of Darwin to the struggle between science and religion. Going beyond the series, the site offers video previews of each programme, links to hundreds of online sites and movies, a glossary, and courses and manuals for teaching. The *Evolution* project's goal is to heighten public understanding of evolution, and how it works. In this respect, it certainly makes the grade.

Tanita Casci

MICROBIAL GENOMICS

Bugs inside out

The genomes of important human pathogens are under intense scrutiny — the goals being to understand the basis of their virulence and to design more effective antimicrobial drugs. Important steps towards unravelling the secrets of virulence evolution are described in recent articles that report the genome sequences of two microbial pathogens — *Yersinia pestis*, the agent of plague, and *Rickettsia conorii*, which causes Mediterranean spotted fever. In a third study, which takes a more functional approach, Yinduo Ji *et al.* have devised a method to find potential virulence genes in *Staphylococcus aureus*.

The 4.6-Mb genome of *Y. pestis* seems to be in flux. Parkhill *et al.* found signs of old genomic expansions — probably a result of horizontal transfer — that preceded the split of *Y. pestis* from its close cousin *Yersinia pseudotuberculosis*. This expansion has been followed by the first signs of genome downsizing, associated with a decay of previously active genes into pseudogenes. In part, this seems to reflect a change in the pathogen's lifestyle: the genes necessary for the enteropathogen *Y. pseudotuberculosis* in its environment within the host's gut, such as adhesion genes, have become pseudogenes in the bloodstream-dwelling *Y. pestis*. Adaptation to different environments is also reflected in the accumulation of mutations in genes responsible for the uptake and transport of different nutrients in the two species.

Similar studies were conducted by Ogata *et al.*, who sequenced the *R. conorii* genome (1.2 Mb) and compared it with that of its close relative, *Rickettsia prowazekii*. These intracellular parasites diverged 40–80 million years ago, so this comparison provided interesting insight into adaptations associated with different intracellular lifestyles. As expected, there seems to be a tendency to streamline the genome. For example, the authors discovered evidence of decaying orthologues — a group of 229 genes in *R. conorii* had homology to non-coding sequences in *R. prowazekii*. Nevertheless, some gene families do exist, and they point to processes, such as importing the host cell's ATP, which represent important adaptations of these pathogens.

In an independent approach to identifying essential genes in *S. aureus* (the sequence of which was published last year), Ji and colleagues subcloned random 200–800-bp fragments of *S. aureus* DNA into plasmids, downstream of a tetracycline-inducible promoter. Bacteria transformed with these constructs were replica plated and grown in the presence or absence of a tetracycline analogue. This allowed the authors to look for constructs that prevented bacterial growth as a result of induced antisense RNA expression. Of the 600 constructs that were identified, ~200 contained an open reading

frame in an antisense orientation, and 30% of these had no known function. To test whether this approach could be extended to an *in vivo* context, Ji *et al.* infected mice with bacteria that contain a construct expressing antisense RNA to a known essential gene. Whereas control mice developed a heavy kidney infection within 72 h, mice induced to express the antisense construct suffered no infection.

Comparative and functional genomics of pathogenic species and their relatives will continue to provide invaluable insights into the evolution of pathogenicity and adaptation. The potential for substantial benefits to human health is tantalizing.

Magdalena Skipper

References and links

ORIGINAL RESEARCH PAPERS Parkhill, J. *et al.* Genome sequence of *Yersinia pestis*, the causative agent of plague. *Nature* **413**, 523–527 (2001) | Ogata, H. *et al.* Mechanisms of evolution of *Rickettsia conorii* and *R. prowazekii*. *Science* **293**, 2093–2098 (2001) | Ji, Y. *et al.* Identification of critical staphylococcal genes using conditional phenotypes generated by antisense RNA. *Science* **293**, 2266–2269 (2001)

FURTHER READING Cole, S. T. *et al.* A plague o' both your hosts. *Nature* **413**, 467–470 (2001)

WEB SITES

Yersinia pestis: http://www.sanger.ac.uk/Projects/Y_pestis/

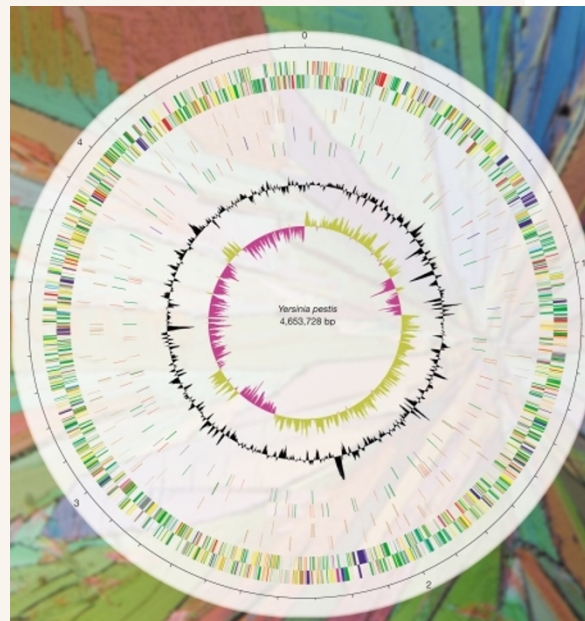
Rickettsia conorii: <http://www.ncbi.nlm.nih.gov/cgi-bin/Entrez/eframik?db=Genome&gi=199>

Staphylococcus aureus: <http://www.tigr.org/tigr-scripts/CMR2/GenomePage3.sp?database=ntsa01>

Yersinia pseudotuberculosis: <http://bbrp.llnl.gov/bbrp/html/y.pseudo.htm>

Rickettsia prowazekii: <http://www.tigr.org/tigr-scripts/CMR2/GenomePage3.sp?database=ntrp01>

Comprehensive Microbial Resource at TIGR: <http://www.tigr.org/tigr-scripts/CMR2/CMRHomePage.sp>



Circular representation of the *Yersinia pestis* genome. (Modified with permission from Parkhill, J. *et al.* *Nature* **413**, 523–527 © (2001) Macmillan Magazines Ltd.)