

## HIGHLIGHTS

## WEB WATCH

### Bugs galore

- <http://www.tigr.org/CMR>

The Comprehensive Microbial Resource pages from The Institute for Genomic Research provide a mine of useful information on the genomes of all microbes that have been completely sequenced and annotated — at present, 57 genomes, 120 DNA molecules and ~140,000 genes.

There are many graphical representations of each genome showing, for example, %G+C, location and function of predicted genes, and even a clickable simulation of a 2D protein gel. But the real strength of this resource lies in the facility to conduct any query against many genomes at once.

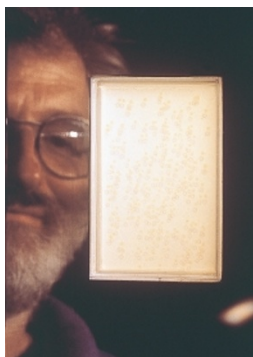
Mark Patterson

### A portrait genome

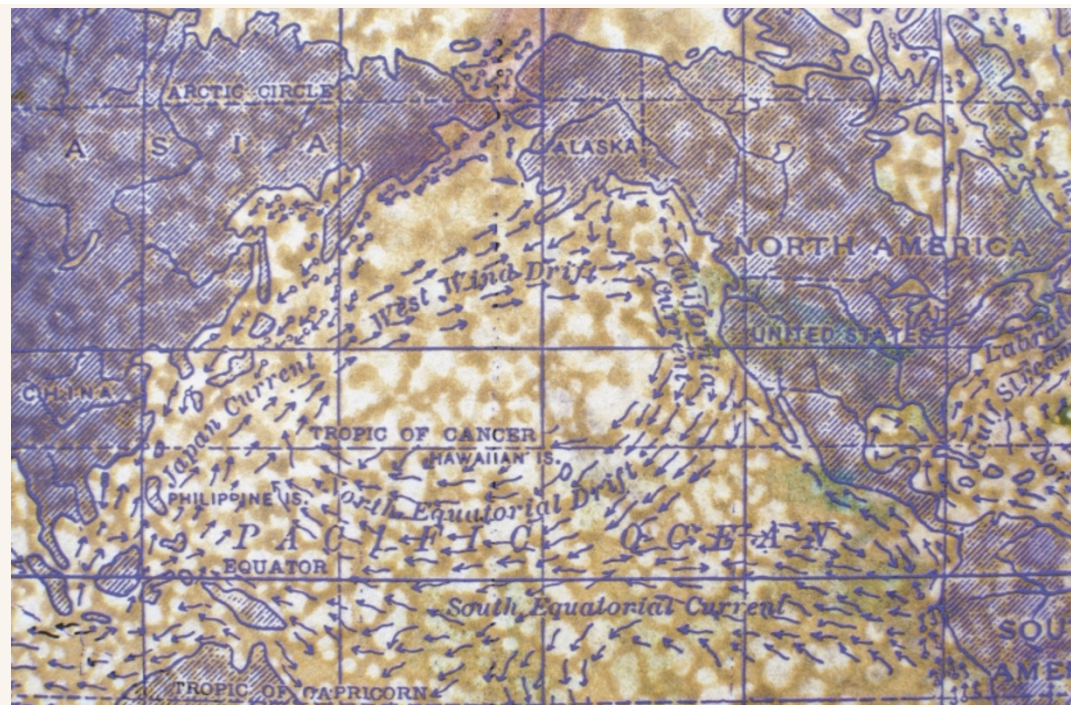
- <http://www.npg.org.uk/live/genome.asp>

The URL above won't take you to a genome database but to the National Portrait Gallery in London. It's not so much the site that we'd like to bring to your attention but a portrait of Sir John Sulston that is on display there and at the gallery. This unique portrait is actually an agar plate on which have grown bacterial clones containing Sir John's DNA. The portrait was commissioned with the support of the Wellcome Trust from Marc Quinn, who describes it as "a portrait of his [Sulston's] parents and every ancestor he ever had...".

Jane Alfred



Courtesy of the National Portrait Gallery.



## EVOLUTION

# Sticklebacks finally get a map

Of all the big questions in evolutionary biology, the problem of what makes organisms unique would probably rank among the top five. If only it were possible, the most direct approach to answering this question would be to cross species such as the elephant and mouse and then do genome scans on their grand-offspring. But given that this is not possible, understanding the genetic basis of morphological evolution is perhaps best tackled by turning to more closely related animals. The threespine stickleback — a small bony fish only about 10 cm long — is the perfect contender for such a project owing to its many, recently evolved, morphological forms. By generating a genome-wide linkage map of this fish, Peichel and colleagues have created a valuable resource for discovering the genetic loci that are responsible for adaptive change.

When the glaciers melted at the end of the last ice age, ocean sticklebacks invaded many newly created freshwater lakes and streams in coastal areas, where, over the past 15,000 years, they have rapidly diverged into hundreds of well-documented forms. Two phenotypically distinct stickleback species, the limnetic and the benthic fish, are peculiar in having adapted to different niches within single lakes of British Columbia: limnetics live in open water, have extensive skeletal armour and many gill rakers to filter ingested food, whereas benthics live near the shore, have less body protection and fewer gill rakers. Although they are reproductively isolated in the wild, Peichel *et al.* were able to cross the two fish in the lab to produce fertile progeny in which to map the loci that underlie the parent fishes' morphological differences.

In gene mapping, requirement number two after picking the species to study, is an extensive set of genetic or molecular markers. As stickleback markers

were scarce, Peichel *et al.* began the arduous task of constructing a molecular map, first by identifying 1,176 new microsatellite loci and then by designing PCR primers to map 410 of them — that's over 20 times the number already known. Most of the 281 markers they tested on the backcross progeny between benthics and limnetics were variable between the two, and so could be used to follow the segregation patterns of each marker in 92 backcross progeny. Genotypic data were then converted into a high-density linkage map, in which markers were assigned to 26 linkage groups. Having developed the new map, Peichel *et al.* tested it by doing linkage analysis of important evolutionary traits — many of which, such as the length of the first and second dorsal spines, mapped to only one or a few QTL. Overall, the results obey the general observation that a handful of QTL of large effect determine a large proportion of the variance in a certain trait.

Discovering the evolutionary path from mice to elephants is likely to stay on biologists' wish lists for some time. However, work such as this suggests it will be possible to identify the genetic events that lead to morphological differences during vertebrate evolution.

Tanita Casci

### References and links

**ORIGINAL RESEARCH PAPER** Peichel, C. L. *et al.* The genetic architecture of divergence between threespine stickleback species. *Nature* **414**, 901–905 (2001)

**FURTHER READING** Bell, M. A. & Foster, S. A. *The Evolutionary Biology of the Threespine Stickleback* (Oxford Science, New York, 1994)

#### WEB SITES

David Kingsley's lab:

<http://www.hhmi.org/research/investigators/kingsley.html>

Dolph Schluter's lab: <http://www.zoology.ubc.ca/~schluter>

Stickleback research bibliography:

<http://www.geocities.com/CapeCanaveral/Hall/1345/stickbibl.html>