WEB WATCH

Gene stories

- <http://www.bbc.co.uk/genes>

The BBC — characteristically on top of what makes its audience tick — has embraced the challenge of sating the public's thirst for stories on genetics by running a season of television and radio programmes on important issues in human genetics. For those who haven't yet had the benefit of tuning in, you can turn to the interactive web site that accompanies the broadcasts, which contains accessible and attractively presented information on genetic topics across the spectrum — from the basic rules of inheritance to why we age, and genetic diseases, through to gene profiling and human reproduction.

The site guides you aboard the 'Gene Safari', where you can learn about the cloning process and about GM organisms; or catch up with the 'DNA detectives', who reveal that Adam and Eve could never have met; or enter a courtroom debate about whether you'd want to live forever. Presenting so much about genetics as accurately and engagingly as they have done can't be easy; however, some sections border on the trivial — that genetics will tell us about our love lives, for example — or could be a bit misleading.

This web site is better suited for browsing than for systematic learning. For those wishing to venture beyond the surface, however, useful resources and links are provided. A selling feature of this site is the live debates that take place for an hour after each broadcast, allowing visitors to quiz geneticists on the programme's featured topics. And for geneticists who want a deeper insight into what the public really thinks, the 'message board' offers some veritable gems.

Tanita Casci

GENOMICS

Fission chips here we come!

The number of sequenced eukaryotic genomes has just increased from five to six. As reported in *Nature*, *Schizosaccharomyces pombe*, or fission yeast, is the second unicellular eukaryote to be sequenced — the first being its higher profile relative, *Saccharomyces cerevisiae*. The functional and comparative analysis of this new genome sequence will provide key insights into the evolution and function of eukaryotic cells.

The sequencing itself was carried out by the Wellcome Trust Sanger Institute in collaboration with several other laboratories, and the quality of the data is extremely high — less than 1 error per 10^5 bases. As for completeness — a relative term in the context of genome sequencing — the *S. pombe* sequence rates highly too. All but ~1.1 Mb (mostly tandem repeats of ribosomal RNA genes) of the 13.8-Mb genome has been sequenced.

The genome has been annotated using a mixture of *ab initio* gene prediction and sequence comparison, and from this analysis it is estimated that *S. pombe* has 4,824 genes, about 750 fewer than *S. cerevisiae*. Introns are present in 43% of genes and there are 4,730 of them in the genome, more than 20 times the number present in *S. cerevisiae*. The centromeres of the three chromosomes range in size from 35 to 110 kb and comprise arrays of tandem repeats, which makes them more similar than those of *S. cerevisiae* to the centromeres of larger eukaryotes. Interestingly, although protein-coding genes are absent from the centromeric sequences, there are quite a few tRNA genes, and, on the basis of the locations of these genes, they might delimit functional domains within the centromere.

In a comparison of the genomes of the two yeasts, the authors found that only 16% of the fission yeast genes do not have homologues in

S. cerevisiae. When this comparison included prokaryotic, as well as the other eukaryotic, genome sequences, a group of genes was found that is present only in eukaryotes. Such genes help to define the key molecules, mechanisms and functions that are unique to eukaryotic biology. The genes identified so far are involved in the cytoskeleton, intracellular compartmentalization, the ribosome and several other eukaryote-specific processes. The authors did a similar comparison to find genes that are specific to multicellular organisms, but few of these were identified. However, in an accompanying News and Views, Jonathan Eisen points out that this analysis did not take into account that multicellularity probably evolved independently in plants and animals. This question will therefore have to wait for more representative genomes to be completed.

The genome sequence of fission yeast reveals that there is a lot in common between *S. cerevisiae* and *S. pombe*. But there are some important differences as well — for example, in centromere structure and the amount of RNA splicing — which means that *S. pombe* is the better experimental system for studying some aspects of eukaryotic

EVOLUTION

Feel the fourth

In the fast-moving field of *Drosophila* genetics and genomics (see the reviews on pages 176 and 189 of this issue), chromosome 4, the smallest of the three autosomes, has often kept a rather low profile. Looking no bigger than a dot on metaphase spreads and with only ~80 genes to its name, not to mention the lack of crossing over during meiosis, most labs have shunned this dull and invariable chromosome. And with good reason, right? Wrong, say Wen Wang *et al.*, who have just published work showing that the

fruitfly's fourth chromosome leads a happening life: not only does it recombine, but also it consists of blocks of highly polymorphic regions interspersed with less variable domains. Both findings suggest that, contrary to theoretical and empirical evidence, this chromosome has been evolving, albeit at different rates in different regions.

Only ~25% of chromosome 4 is euchromatic, and it is in this portion of the chromosome that Wang and colleagues decided to look for nucleotide variation, by

sequencing a 5-kb chromosome 4 region from 33 individuals taken from either worldwide or local (Israeli) fly populations. Surprisingly, in both samples, nucleotide variation was far in excess of that seen before on a chromosome 4 gene (*cubitus interruptus*, *ci*), but was comparable with that seen on autosomes. What's more, the segregating nucleotides are organized into two haplotypes. The fact that the dimorphism occurs at all and that the frequency of each haplotype is more or less equal in local and worldwide populations probably points to the influence of balancing selection — a force that actively maintains genetic variation. Intrigued by the difference in variation at *ci*