

Genome Update: tRNAs in sequenced microbial genomes

Genomes of the month – microbial genome evolution

Eight microbial genomes have been published in the four weeks since the last Genome Update was written (Ussery *et al.*, 2004). They represent five bacterial and three eukaryotic organisms, and provide several interesting aspects of genome evolution. A very brief overview of the new genomes will be presented below; this is meant merely to wet the appetite of the reader and to provide pointers to the relevant recent literature.

Two spirochaete genomes have been published this month, bringing the total number of genomes from three to five for this phylum. The genome of *Treponema denticola* strain ATCC 35405 (Seshadri *et al.*, 2004) is more than twice the size of the previously sequenced genome of *Treponema pallidum* (2.8 Mbp vs 1.1 Mbp), although the number of tRNAs and rRNAs are about the same in both genomes. The difference in genome size appears to be the result of a combination of three types of evolution: genome reduction, lineage-specific recombination and horizontal gene transfer (Seshadri *et al.*, 2004). The other newly sequenced spirochaete genome, of *Leptospira interrogans* serovar Copenhageni strain Fiocruz L1-130 (Nascimento *et al.*, 2004), has two chromosomes and encodes 3728 genes, two rRNA operons and 37 tRNAs, as shown in Table 1. This genome is nearly identical in size to that of *L. interrogans* serovar Lai (Ren *et al.*, 2003), which has 4727 annotated genes, or nearly 1000 extra genes. This is perhaps due to the difference in cut-off values for gene-finding from the two different groups.

Members of the *Chlamydiae* are amongst the most successful bacterial pathogens of humans, and there are currently eight sequenced pathogenic chlamydial genomes, ranging in size from 1.0 to 1.2 Mbp

(see table on supplemental web page). Recently, it was discovered that *Chlamydia* and related species can also exist in free-living amoebae, and the genome of the *Acanthamoeba* sp. endosymbiont *Parachlamydia* sp. UWE25 has now been sequenced (Horn *et al.*, 2004); at 2.4 Mbp, it is about twice the size of the other chlamydial genomes. It is estimated that the last common ancestor for the pathogenic and symbiotic chlamydia was about 700 million years ago, and that this bacterium already contained many of the virulence factors found in modern pathogenic chlamydia (Horn *et al.*, 2004).

The thermophilic and halotolerant bacterium *Thermus thermophilus* has become a model organism for structural biology, as many of its proteins have been crystallized and their structures determined. Examination of the genome of *Thermus thermophilus* strain HB27, which can grow at temperatures up to 85 °C, has revealed some clues as to what it might take to live in a hot-spring environment (Henne *et al.*, 2004). Based on its genome sequence, it looks like this bacterium is a scavenger which lives on solid surfaces and takes up nutrients as they pass by.

The genome of the parasite *Wolbachia pipientis* wMel is unusual in that it is both streamlined and also contains high levels of repeats and mobile DNA elements

(Wu *et al.*, 2004). Thus, for this bacterium, natural selection appears to be a bit inefficient, probably due to repeated population bottlenecks (Wu *et al.*, 2004).

Three eukaryotic genomes have also been sequenced this month. As usual, unfortunately the quality of the eukaryotic sequences is not as good as that of the prokaryotic genomes; there are many gaps in the sequences, and also the annotation (when present) is patchy at best (in our opinion). According to Kellis *et al.* (2004), the genome sequence of the yeast *Kluyveromyces waltii* strain NCYC 2644 compared to that of *Saccharomyces cerevisiae* provides 'the first comparison across an ancient whole genome duplication event and offers the opportunity to study the long-term fate of a genome after duplication'. The intracellular pathogen *Cryptosporidium parvum* type II isolate has a genome of about 9.1 Mbp in length and encodes a mere 3800 proteins (Abrahamsen *et al.*, 2004). (Note that this is about the size of a medium to small bacterial proteome!) This parasite has undergone massive genome reduction and streamlining, even losing all of its mitochondrial DNA, which has been incorporated into the main chromosome. Finally, the genome of the alga *Cyanidioschyzon merolae* 10D (Matsuzaki *et al.*, 2004) is 16.5 Mbp long and spread over 20 chromosomes. There are very few introns, and only three rRNA operons (see Table 1). This genome

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