Genome Update: promoter profiles

Genomes of the month
Ten new genomes have been published since last month’s Genome Update. The list includes six bacterial and four yeast genomes, as listed in Table 1. A brief overview of each genome will be given below.

Acinetobacter belongs to the family Moraxellaceae of the γ-Proteobacteria, and is a neighbour of the family Vibrionaceae. The genome of Acinetobacter sp. ADP1 has been sequenced (Barbe et al., 2004); this organism is a soil isolate which can be transformed easily. The genome of Acinetobacter sp. ADP1 is 3.6 Mbp long, with an A+T content of 65% (see Table 1).

Bacillus thuringiensis has been used commercially for the biological control of insect pests, and this insecticidal activity is due to the ability of the organism to synthesize a large amount of protein that forms a parasporal crystal during sporulation (Schnepf et al., 1998). The Bacillus thuringiensis genome is 5.2 Mbp long, with an A+T content of 65%.

There are 105 tRNA genes (a high number for bacterial genomes) and the 14 rRNA genes is the highest number so far found, out of 171 sequenced bacterial genomes. It is likely that the large number of rRNA and tRNA genes are useful for high growth rates.

Two Bartonella genomes have been published recently (Alsmark et al., 2004). Bartonella quintana (1.6 Mbp) and Bartonella henselae (1.9 Mbp) are facultative intracellular bacteria and human pathogens. Bartonella quintana is the causative agent of trench fever, a disease that affected more than 1 million soldiers during World War I, and it is transmitted by human body lice. It has a low coding density of 73% compared to the other sequenced bacteria; the genome encodes a total of 1308 predicted genes (see Table 1). Bartonella henselae infects both humans and cats (30–60% of domestic cats in the USA are infected with this organism). Transmission among cats is mediated by the cat flea and to humans by cat scratches or cat bite. Bartonella henselae has a similar coding density of 73%, and a slightly larger genome which encodes 1612 predicted genes. The primary difference between these closely related strains is their reservoir ecology.

Erwinia carotovora is a plant-pathogenic enterobacterium and the causative agent of soft rot and blackleg potato diseases. E. carotovora differs from the sequenced enterobacterial human pathogens by about a third of its genome, and some of these genes are predicted to facilitate nitrogen fixation and opine catabolism. E. carotovora has an A+T content of 49%, which is similar to that of Escherichia species, and the genome encodes a total of 4492 predicted genes, including 9 and 7 of 5S and 16S, respectively (Bell et al., 2004).

Mesoplasma florum is a non-pathogenic organism and a non-motile mycoplasma species, but it is not closely related to Mycoplasma genitalium or Mycoplasma pneumoniae. It has the characteristic small genome of Mycoplasma species, with only 793 kbp, and an A+T content of 73%; there are only 29 predicted tRNAs for this slow-growing organism.

Finally, four yeast genomes have been published (Dujon et al., 2004) which represent a quite diverse set of organisms within the phylum Ascomycota. The four yeast genomes shown in Table 1 are from four different branches of the ascomycete lineage. Although all four genomes contain about 6000 genes, the genome size ranges between 10 Mbp and 20 Mbp. The Yarrowia lipolytica genome is the largest (20.5 Mbp) and has the lowest coding density; the Debaryomyces hansenii genome is only 12.2 Mbp long, yet it has about 200 more genes than that of Y. lipolytica (see Table 1). Although the exact number of rRNAs is not known, the number of clusters is given, and Dujon et al. (2004) report that there are more than 105 copies of rRNA genes scattered throughout the genome of Y. lipolytica, in addition to the seven clusters. These four genomes, when compared to each other and other yeast genomes, shed light on possible evolutionary routes taken by each branch of the ascomycete lineage.

Method of the month – promoter profiles
By looking at the average value of DNA structural parameters for all the genes in a genome, aligned at translation start sites, it is possible to construct a ‘promoter profile’. There is a general trend for the upstream regions to be AT-rich, more rigid and more easily melted than on average for the whole chromosome (Pedersen et al., 2000). Different genomes can have different promoter profiles.

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Chris Thomas, Editor-in-Chief
reflecting various environmental and other aspects of genome organization. Fig. 1 shows the promoter profiles for four of this month’s genomes. For all the genomes, there is a strong difference between the first half of the plot (upstream from translation start sites) and the second half (downstream). As discussed in a previous Genome

Table 1. Summary of the published genomes discussed in this Update

<table>
<thead>
<tr>
<th>Name</th>
<th>Strain</th>
<th>Length (bp)</th>
<th>AT content (%)</th>
<th>No. of genes</th>
<th>tRNAs</th>
<th>rRNAs*</th>
<th>Accession no.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Acinetobacter sp.</td>
<td>ADP1†</td>
<td>3 598 621</td>
<td>59-6</td>
<td>3 325</td>
<td>76</td>
<td>7</td>
<td>CR543861</td>
</tr>
<tr>
<td>Bacillus thuringiensis</td>
<td>97-27</td>
<td>5 237 682</td>
<td>64-6</td>
<td>5 117</td>
<td>105</td>
<td>14</td>
<td>AE017355</td>
</tr>
<tr>
<td>Bartonella henselae</td>
<td>Houston-1</td>
<td>1 931 047</td>
<td>61-8</td>
<td>1 612</td>
<td>43</td>
<td>4</td>
<td>BX897699</td>
</tr>
<tr>
<td>Bartonella quintana</td>
<td>Toulouse</td>
<td>1 581 384</td>
<td>61-2</td>
<td>1 308</td>
<td>42</td>
<td>4</td>
<td>BX897700</td>
</tr>
<tr>
<td>Erwinia carotovora</td>
<td>SCRI1043</td>
<td>5 064 019</td>
<td>49-0</td>
<td>4 492</td>
<td>76</td>
<td>7</td>
<td>BX950851</td>
</tr>
<tr>
<td>Mesoplasma florum</td>
<td>L1</td>
<td>793 224</td>
<td>73-0</td>
<td>683</td>
<td>29</td>
<td>2</td>
<td>AE017263</td>
</tr>
<tr>
<td>Candida glabrata</td>
<td>CBS 138</td>
<td>12 280 357</td>
<td>61-4</td>
<td>5 272</td>
<td>207</td>
<td>2 clusters</td>
<td>CR380947–CR380954</td>
</tr>
<tr>
<td>Debaryomyces hansenii</td>
<td>CBS 767</td>
<td>12 220 823</td>
<td>61-6</td>
<td>6 896</td>
<td>205</td>
<td>3 clusters</td>
<td>CR382133–CR382139</td>
</tr>
<tr>
<td>Kluyveromyces lactis</td>
<td>NRRL Y-1140</td>
<td>10 689 156</td>
<td>61-2</td>
<td>5 331</td>
<td>162</td>
<td>1 cluster</td>
<td>CR382121–CR382126</td>
</tr>
<tr>
<td>Yarrowia lipolytica</td>
<td>CLIB99</td>
<td>20 502 981</td>
<td>50-9</td>
<td>6 666</td>
<td>510</td>
<td>7 clusters</td>
<td>CR382127–CR382132</td>
</tr>
</tbody>
</table>

*The rRNA column refers to the number of operons; ‘clusters’ indicates the number of clusters of tandem repeated rRNA operons reported.
†Based on information from Tatiana Tatusov, from GenBank (see also http://www.genoscope.cns.fr/externe/English/Projets/Projet_DY/DY.html).

Fig. 1. Promoter profiles for the genomes of the bacteria Mesoplasma florum strain L1 (a), Bacillus thuringiensis strain 97-27 (b) and Erwinia carotovora strain SCRI1043 (c); also shown is the promoter profile for chromosome 1 of the yeast Yarrowia lipolytica strain CLIB99 (d). Each gene from the chromosome was aligned at the translation start site, and the average DNA structural property was calculated for each position in the alignment. Differences from the chromosomal average are plotted in the figures.
Update (Ussery & Hallin, 2004), for nearly all bacterial genomes sequenced, the region right before translation start is more AT-rich than the coding sequences. In the three bacterial genomes shown in Fig. 1, there is a general increase in deviation from the chromosomal average for most of the structural parameters up to the translation start site (‘0’ on these plots), whilst downstream the signal intensities are close to average for the whole genome. This general trend is true for most bacterial genomes, although for eukaryotes the downstream region can vary significantly from the average, as can be seen for the Y. lipolytica chromosome 1 plot in Fig. 1. This could be due to the much lower coding density (less than 50 %) compared with the bacterial genomes (typically around 85 % or larger). Along these lines, it is interesting to note that the Mesoplasma florum genome has the highest coding density of the genomes in Table 1, and it also has a more narrow range of high AT content upstream, probably reflecting a shorter distance between transcription +1 and the translation start sites. In summary, promoter profiles can be used to extract useful information about the structural characteristics of promoters from various genomes.

**Supplemental web pages**

Web pages containing material related to this article can be accessed from the following url: http://www.cbs.dtu.dk/services/GenomeAtlas/suppl/GenUp008/

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**David W. Ussery, Nikolaj Tindbæk and Peter F. Hallin**

Center for Biological Sequence Analysis, Department of Biotechnology, Building 208, The Technical University of Denmark, DK-2800 Kgs. Lyngby, Denmark

Correspondence: David W. Ussery (dave@cbs.dtu.dk)


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