Question 12

How does a user find characterized mouse mutants corresponding to human genes?

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The NCBI provides a set of maps that show chromosomal regions homologous between mouse and human. This resource can be accessed directly at http://www.ncbi.nlm.nih.gov/Homology/. For this example using a known, mapped human gene, however, it is easier to start the search from the LocusLink entry for tyrosinase. The LocusLink query page can be found at http://www.ncbi.nlm.nih.gov/LocusLink/. Select Human from the Organism pull-down menu, enter ‘tyrosinase’ into the Query box and click Go. To view the entry for tyrosinase (TYR), click on its LocusLink ID, 7299.

On the resulting page (Fig. 12.1), links to the mouse homology maps are in the section of the LocusLink summary page marked Relationships. In this case, there are four maps available for TYR showing mouse alignments: NCBI vs MGD aligns the current NCBI assembly of the human genome with the MGD (Mouse Genome Database), at The Jackson Laboratory) genetic map, UCSC vs MGD aligns the current UCSC genome assembly with the MGD genetic map, NCBI vs. EST-based RH Map aligns the NCBI assembly with the Whitehead–MRC RH map, and UCSC vs. Hudson et al. aligns the 7 October 2001 UCSC assembly with the Whitehead–MRC RH Map. The Hs and Mm links adjacent to each map name show the mouse–human homology map with the master chromosome as human or mouse, respectively. Click on theLe link next to the NCBI vs. MGD map.

The resulting mouse–human map shows the mouse genes that are the likely orthologs of human genes on human chromosome 11 (Fig. 12.2). Depending on the browser being used, one may have to click the View as text box to obtain the output; the resulting output will appear in text format, slightly different from what is shown in Fig. 12.2. Chromosomal locations of the mouse genes are shown, where known. The green circles link to the UniSTS entry for each locus; those on the left link to the human UniSTS entry, whereas those on the right link to the mouse UniSTS entry. The cytogenetic positions are hyperlinked to either the human or mouse Map Viewer, as appropriate. Gene symbols are linked to LocusLink. The tyrosinase gene, highlighted in pink, maps to mouse chromosome 7 at 44 cM, a piece of information that will be needed in the next step.

The mouse models themselves are described at the Mouse Genome Informatics site at the Jackson Laboratory. Go to the Mouse Genome Informatics home page, at http://informatics.jax.org/, and use the Query Forms pull-down menu to select Linkage Maps. On the resulting page, customize the search to find the region around the mouse gene Tyr. Under Chromosome, set the number to 7; then set the chromosomal region to between 40 and 48 cM.

Many of the uncloned mouse mutants are not mapped in high-resolution crosses, and many are carried out with a small number of mice relative to another easy-to-score phenotype for another mouse mutant that maps to the same chromosome. It is thus necessary to be lenient in looking for potential uncloned mouse mutants (±4 cM relative to the location). In this case, as the NCBI data tells us that the gene is at 44 cM, the region from 40 to 48 cM should be searched.

Further down the page (Fig. 12.3), under Markers, set Include DNA segments to No to reduce the number of markers shown. Do include syntenic markers, which are DNA markers and mutant alleles linked to chromosome 7 that have not been finely mapped but that may be associated with a phenotype of interest relative to TYR. Under Comparative Maps, Show homologs from species, choose human (Homo sapiens). Select Show all markers. Use the default setting for all other options, and hit Retrieve.

The gene Tyr is found on page 2 of the output, at 44 cm (Fig. 12.4). The mouse chromosome is shown schematically on the left and expands as one moves to the right. In the rightmost columns are the names of the mouse markers in a particular region in blue and, if there is a corresponding human ortholog, the name of that ortholog in black. Some of the displayed mouse markers are genes, some are STSs, some are recessive mutants (all small letters) and some are dominant alleles (initial capital letter). At the bottom of the page are syntenic markers, those which have been mapped to chromosome 7 but not to an exact position.

Clicking the blue Tyr link at 44 cm opens up a summary of the Genes, Markers, and Phenotypes for that gene (Fig. 12.5). Of particular interest in this case are the phenotypic alleles. There are 99 mouse strains with mutations in the Tyr gene.

Users can also view chromosomal regions that are homologous between mouse and human by using Ensembl’s SyntenyView, available from the ContigView by clicking the Jump to→syntenyview link (Fig. 1.14, center yellow bar).
Figure 12.3

Build a Linkage Map Using Information From MGD

Generate a comparative map by selecting a species under ‘Show homologies from species.’

Figure 12.4
Figure 12.5

Mouse Genome Informatics

Genes and Markers

Query Results - Details

Type: Gene
Symbol: Atp4b
Description: ATPase, H+ transporting, mitochondrial F0 part
Chromosome: 10
cDNA Position: 64,560
GenBank Accession ID: NM_010800
Synonyms: c1 allin0

Additional Information:
- Information Complexity
- Marker Mapping (A1)
- Protein Domain (Q9)
- Bioinformatics (Q9)
- Gene Expression Data (Q9)
- Deep Expression (Q9)
- Molecular Probing and Sequencing (Q9)
- Functional Genes (Q9)
- Mouse Genome Catalog

Gene Classifications: (You can browse the Gene Ontology (GO) Classifications)

<table>
<thead>
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<th>Category</th>
<th>Classification Term</th>
<th>Evidence</th>
<th>Inferred From</th>
<th>Ratio</th>
</tr>
</thead>
<tbody>
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<td>P</td>
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</table>

Other Database Links for this Marker:

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<th>Reference</th>
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</thead>
<tbody>
<tr>
<td>NM_010800</td>
<td>EMBL, Genbank</td>
<td>45460</td>
</tr>
</tbody>
</table>
Owing to a production error, Figure 11.2 was inadvertently inserted in place of Figure 12.2 in both the print and online PDF versions of the *User's Guide*. The screen pictured in the full text version online is the correct Figure 12.2.
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