Genome 371, 22 February 2010, Lecture 12 Analysis of gene function

Gene knockouts



Analysis of a disease gene

Pick a model organism Find mutant(s) Map the gene that has been mutated Identify genes in the region Find which of these genes is the "culprit" Find out more about the gene's function

Gene knockout or "knockdown" in model systems

...does the phenotype mimic the disease? Strategies to understand what a gene normally does...

- » gene knockdown... reduce expression of the gene
- » gene knockout... completely delete the gene (or a critical portion of the gene)
- » "knock-in"... replace one allele (e.g., wild type) with another (e.g., a specific mutation)

A complete loss of function allele

Usually produced by **replacing** a gene or portion of a gene with some kind of selectable marker

Knock-out mutations are engineered deliberately

...by modifying a gene with recombinant DNA technology, and replacing the wild type allele with the knockout ("KO") allele.

Goal?

To understand what a gene normally does, find out what happens if the gene is missing Gene knockouts in yeast

Making a knockout ... one way to proceed:



Cut out the target gene...

...and replace it with a selectable marker (e.g., URA3)



Then cut out the larger insert...

Transform ura3 mutant yeast with this fragment



Ask... with the target gene knocked out, what phenotype do these cells have? (Besides Ura⁺)

Another way to make the disrupted gene for a knockout

design PCR primers whose 3' ends are URA3 sequence and whose 5' ends are CDC28 sequence:



Systematic ORF deletions

The deletions must be carried out in **diploids**. Why?





which are wild type gene?



Some notes on homologous recombination in yeast

In mitotic yeast cells . . .

1. How much homology is needed in the flanking sequences to ensure successful recombination?

~50 bp minimum

2. How perfect does the homology have to be?

Pretty close, 1 mismatch in 100 bp can reduce efficiency to 1/10 the level when no mismatches.

3. How big can the heterologous part be and still get successful recombination?

Pretty big (30 kb); but the bigger the difference the lower the frequency.

From QS:

After analysis of many such tetrads, "good" wine production under the conditions tested was mapped to a single gene, *ASP1*, encoding an enzyme called asparaginase, which is needed for growth when the only source of nitrogen is the amino acid asparagine. The bad wine strain has a wild type allele while the good strain has a complete LOF allele of this gene. The involvement of *ASP1* in wine quality is just a hypothesis, based on a correlation between the genotype and the phenotype. Outline an experiment that you could do (perhaps using a DNA library) to test the hypothesis.

Gene knockouts in mice





Making a mouse knockout

e.g., test hypothesis that gene YFG2 is needed for tail growth



Make crosses between the heterozygotes...

identify the knockout-homozygotes, look at their phenotypes



Problems doing a knockout in mouse

Random **insertion** of DNA much more frequent than homologous recombination



Solution?

Aside: Random insertion of the knockout allele somewhere in the genome... why is that not good enough?

How to select for homologous recombination?



outcome for homologous recombination? only Marker 1 is integrated outcome for random insertion? Both Marker 1 and Marker 2 are integrated

Selecting for homologous recombination

Select for homologous recombination by including **negative selection**



How to transform a whole mouse?

All cells in the mouse must have the knockout allele!



Not quite...

have to make knockout in stem cells, get the stem cells to develop into whole mice...

Making the mouse KO allele

Mouse gene to be knocked-out (YFG2).





Add the **<u>thymidine kinase</u>** gene (tk) from herpes virus to the end of the construct.



DNA is ready to go into mouse cells.

Mouse ES cells



Transfer of DNA to ES cells



Homologous recombination in ES cells

A rare event . . .



The need for positive <u>and</u> negative selection

Neomycin selects for: cells that have taken up the KO-PNA

Gancyclovir selects against:

 \leq

cells that have randomly inserted the KO-DNA

Clones of ES cells that grow in neomycin + gancyclovir are assayed by Southern blotting or PCR to see which ones have the correct gene replacement.

[How exactly would you do this test? What diagnostics would you look for?]

...and then injected into recipient blastocyst

develops into mouse with yfg2-ko

lssues...

» Will all cells in the resulting mouse be transformed? No. (The mouse will be chimeric... stay tuned.)

» How to tell which mice developed from modified blastocysts? transformed ES cells from non-albino (C/C) mouse recipient blastocyst from albino (c/c) mouse

Returning the modified ES cells to an embryo



Some cells are <u>C/C</u>; YFG2/yfg2-K0 Some cells are c/c; YFG2/YFG2

WhyTo distinguish host from knockout productsalbino?

Returning the embryos to an albino female



How to get from here...



All of the tissues could be chimeric; even the germ cells!



Mate the chimeric mouse to an albino \rightarrow Pick fully pigmented offspring

Looking for germ-line transmission (example)

Mate this chimeric male to <u>albino</u> females and look for <u>non-albino</u> offspring.



Predicting the offspring from the chimera



Which of these mice have the KO allele?



Which one is which? How would you test them?

Finally ... Homozygous knockouts?



Among the offspring,

there should be 1/4 that are homozygous yfg-K0/yfg-K0

How do you find them?

Q. What phenotype results?

Some KOs have obvious phenotypes

The IL-6 KO mouse is obese.



Some KOs have suprising phenotypes

Current Biology, Vol. 13, 1775–1785, October 14, 2003, ©2003 Elsevier Science Ltd

Cdk2 Knockout Mice Are Viable

cyclin gene Cyril Berthet,^{1,3} Eiman Aleem,^{1,3} Vincenzo Coppola,² Lino Tessarollo,² and Philipp Kaldis^{1,*}



...but are sterile

Working hypothesis: Cdk2 is needed primarily for meiosis, not mitosis

Some KOs have no apparent phenotypes



Conclusions about deletions with no phenotype?

If a knock-out has wild type phenotype, does that mean . . .

- 1. the gene doesn't do anything? under test conditions
- 2. there is a second gene carrying out the function?

3. there is a complex of proteins where any one protein is dispensable but the complex is needed?

Wild type complex of 6 proteins



Loss of one component—complex is still functional

or





But loss of two components results in a nonfunctional

complex



complex falls apart



Hypotheses 2 and 3 predict that certain double mutants would show a phenotype.

knockout of gene 1 doesn't give phenotype knockout of gene 2 doesn't give phenotype knockout of both gene 1 and gene 2 results in a phenotype