

April 1 Paper 1 -- Marson et al. 2004.

"A genome-wide screen identifies genes required for centomeric cohesion." Science **303**:1367-1370, including the Supporting online material.

Background:

Chapter 7 of Hawley and Walker

Hartwell - Reference A: Genetic portrait of a yeast.

Saccharomyces Genome Database, www.yeastgenome.org/

Introduction to Yeast Genetics and Molecular Biology (Fred Sherman)

(dbb.urmc.rochester.edu/labs/Sherman_f/yeast/)

Of course, appropriate references within the paper.

Presentations (not just figures! See the syllabus for a list of how to prepare). 5 min. max each.

- 1) Overview of the paper.
- 2) Fig. 1
- 3) Fig. 2A and 2B
- 4) Fig. 2C and S2
- 5) Fig. 2D and 2E
- 6) Fig. 3
- 7) Fig. 4A and B
- 8) Fig. 4C-4E
- 9) Conclusions and reprise (what has been learned since this paper was published?)

Review:

What are GFP dots? How exactly were they constructed?

What is going on in the protocol used for screening (Fig. S1)?

How are homozygotes generated?

During normal meiosis do sister chromatids remain attached throughout their length during the first meiotic division?

Would sister chromatid cohesion in the arms be required in the absence of recombination? Explain.

Go over classical tetrad analysis problems (solved problem III in chapter 5 of Hartwell et al. and problems 5-24 to 5-33)

Define the following terms in a few words:

sister chromatid

twin spot

kinetochore (distinguish from centromere)

loss of heterozygosity

Consider the procedure shown in Fig. 1 but carried out with cells that are heterozygous for GFP spots on the centromeres of two **different** chromosomes. In the case of wild-type cells (by which I mean cells with no meiotic mutants), what fraction of tetrads would be expected to have GFP in one spore? two spores? three spores? four spores? (Look at section 7.4.3 of Hawley and Walker). How would your answers differ if one or both of the GFP spots were quite far from the centromere?

GENETICS **CBMG 688I** SPRING 2008
Homework 1 -- paper 1 (due April 1, 2008)

I will give you the yeast gene name for your gene (on Blackboard, by Monday, probably sooner).
The following five questions will be graded (2 points each).
You may turn in your answers on this sheet, in which case, be sure to provide your name!

1. (2 points) Please provide a protein **refseq** accession number for your gene in *S. cerevisiae*.
2. (2 points) What conserved domains (if any) are present in your protein?

Find your gene in the supplemental data for the Marston paper (no, please don't print the whole thing!).

3. (2 points). What is the "ORF" (a.k.a. the systematic name)? For example, the gene *SNP1* (gene name) has the systematic name ("ORF" in the table) of YIL061C.
- 4 (2 points). Is your gene essential? If not, does your gene have an effect on meiosis?
5. (2 points) What homologs of your gene (if any) are there in *Schizosaccharomyces pombe*? As a guideline, list all genes encoding proteins that are as related to your gene in *Saccharomyces cerevisiae* as the human gene is to the *Saccharomyces cerevisiae* gene. Give me the names of this gene or genes and tell me how similar it is, or they are (I want percent identity at the protein level, including any low complexity regions).

Looking ahead, you will want to find a homolog of your gene in each of the following species:
A. thaliana, *H. sapiens*, *D. melanogaster*, and *C. elegans*.
For each, list a **refseq** protein accession number.

At some point (not now) you will prepare an alignment of these five protein sequences using Bioedit or a similar program and construct a phylogenetic tree using Mega or a similar program. Bioedit can be downloaded from www.mbio.ncsu.edu/BioEdit/bioedit.html and Mega can be downloaded from www.megasoftware.net.