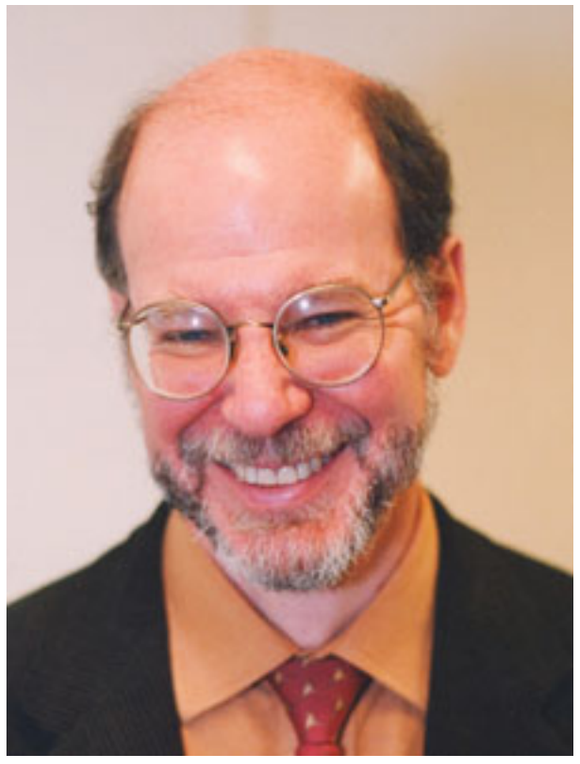
Bio393: Genetic Analysis

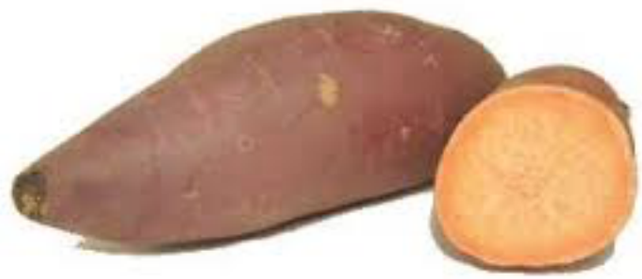
Step-wise genetic analysis

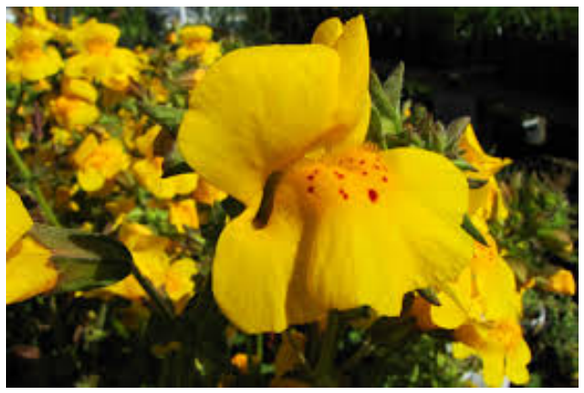


Bob Horvitz

Lecture 8

“Model organisms” are everywhere now





1. Define the problem

?

Let the question choose the organism
(not the other way around)

2. Choose an organism

Organism	Time to 10^6	Space
Bacteriaphage	1 hour	10 nL

10^6 individuals to study 10^{-6} mutation rate

$2^{20} \approx 10^6$ individuals

2. Choose an organism

Organism	Time to 10^6	Space
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Bacteria	15 hours	1 µL

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2. Choose an organism

Organism	Time to 10^6	Space
Bacteriaphage	1 hour	10 nL
Bacteria	15 hours	1 µL
Yeast	1 day	0.1 mL

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2. Choose an organism

Organism	Time to 10^6	Space
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Worm	10 days	6 cm cube

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Fly	6 weeks	0.5 m cube

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Worm	10 days	6 cm cube
Fly	6 weeks	0.5 m cube
Mouse	3 years	Half Pancoe
Human	750 years	Chicago suburbs

10^6 individuals to study 10^{-6} mutation rate

$2^{20} \approx 10^6$ individuals

3. Perform a mutant hunt

To mutagenize or not to mutagenize?

Yes	No	
10^{-3}	10^{-6}	LoF mutation
10^{-5}-10^{-6}	10^{-8}-10^{-9}	Specific mutation

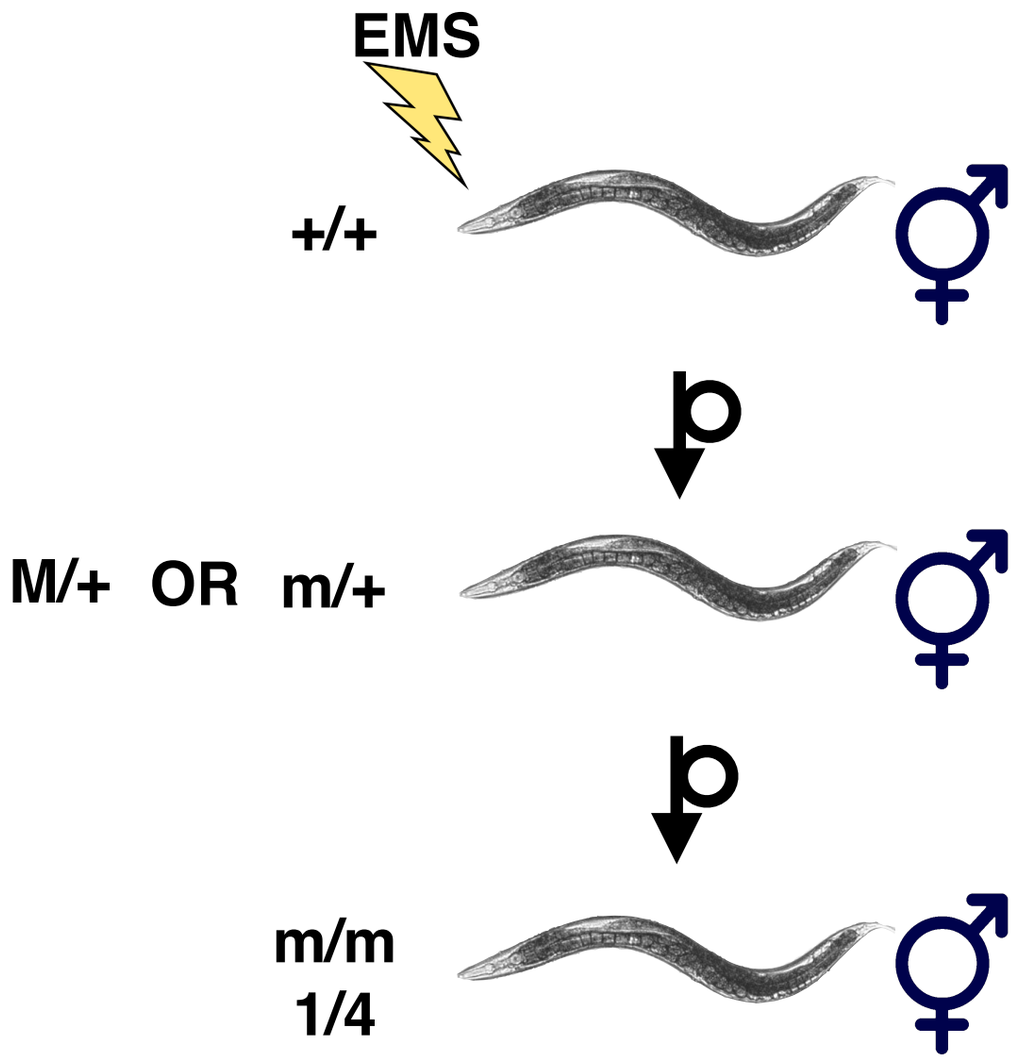
C. elegans

~20,000 genes
20 LoF mutations

D. melanogaster

~12,000 genes
12 LoF mutations

Screen or selection?



C. elegans screens for dominant or recessive phenotypes

Screen or selection?

$\frac{\pm}{+}$ ♂♂ x $\frac{Sp}{CyO}$ ☿☿

$\frac{\pm}{CyO}$ OR $\frac{m}{CyO}$ ♂ x $\frac{Sp}{CyO}$ ☿

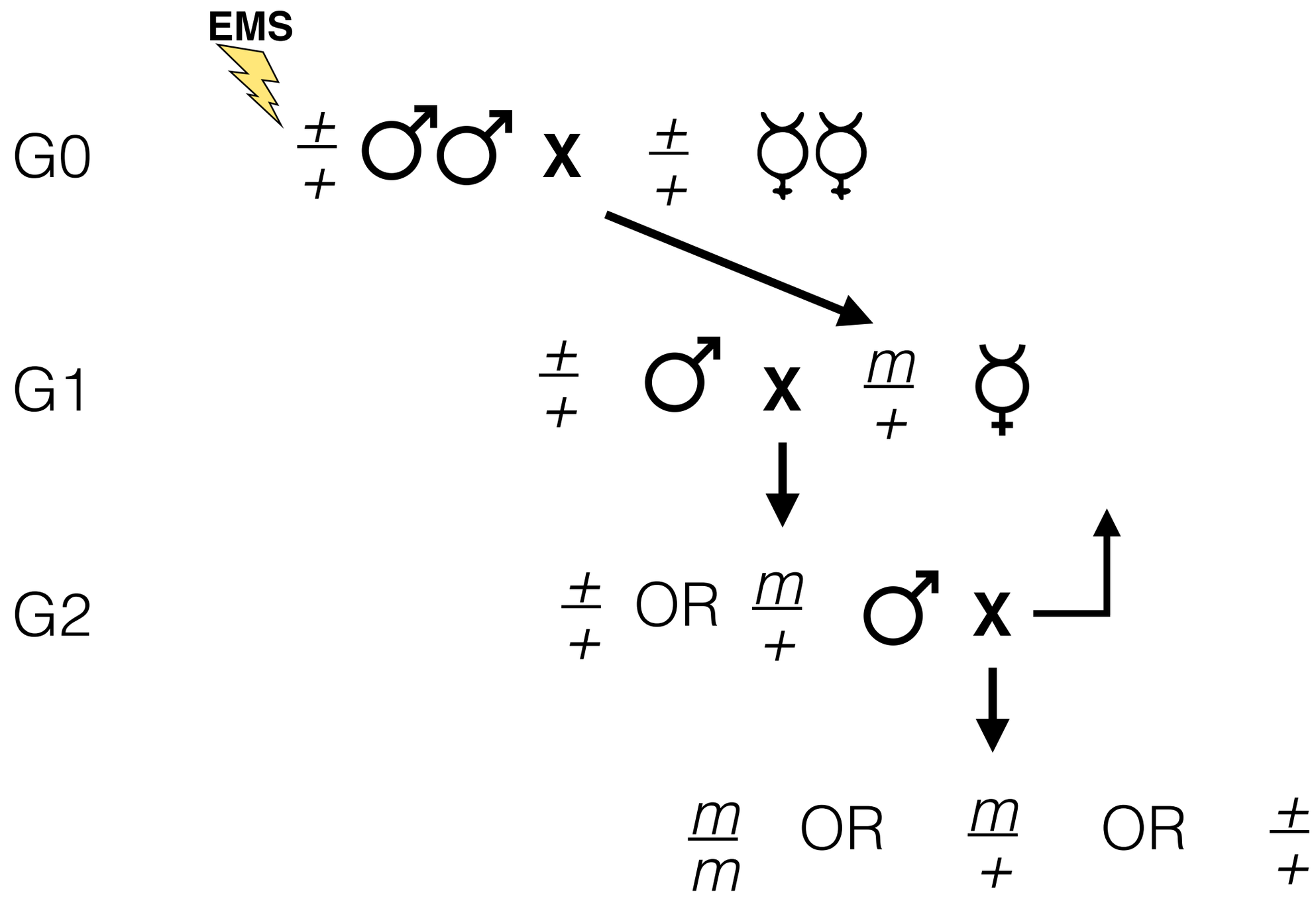
Single-pair crosses

$\frac{m}{CyO}$ ♂ x $\frac{m}{CyO}$ ☿☿

$\frac{m}{m}$ OR $\frac{m}{CyO}$ OR $\frac{CyO}{CyO}$

Mutant? **Curly wings** **dead**

Screen or selection?



Mouse screens for dominant or recessive phenotypes

Remember hemizygous screens too

4. Screen until saturation?

Use Poisson sampling and common sense

Saturation of the investigator's patience

Change mutagens

Why might we miss genes?

Numbers are too small
Pleiotropy (sterility or lethality)
Redundancy

5. Establish a strain

True-breeding stocks

Balancers, balanced stocks

Freeze organisms

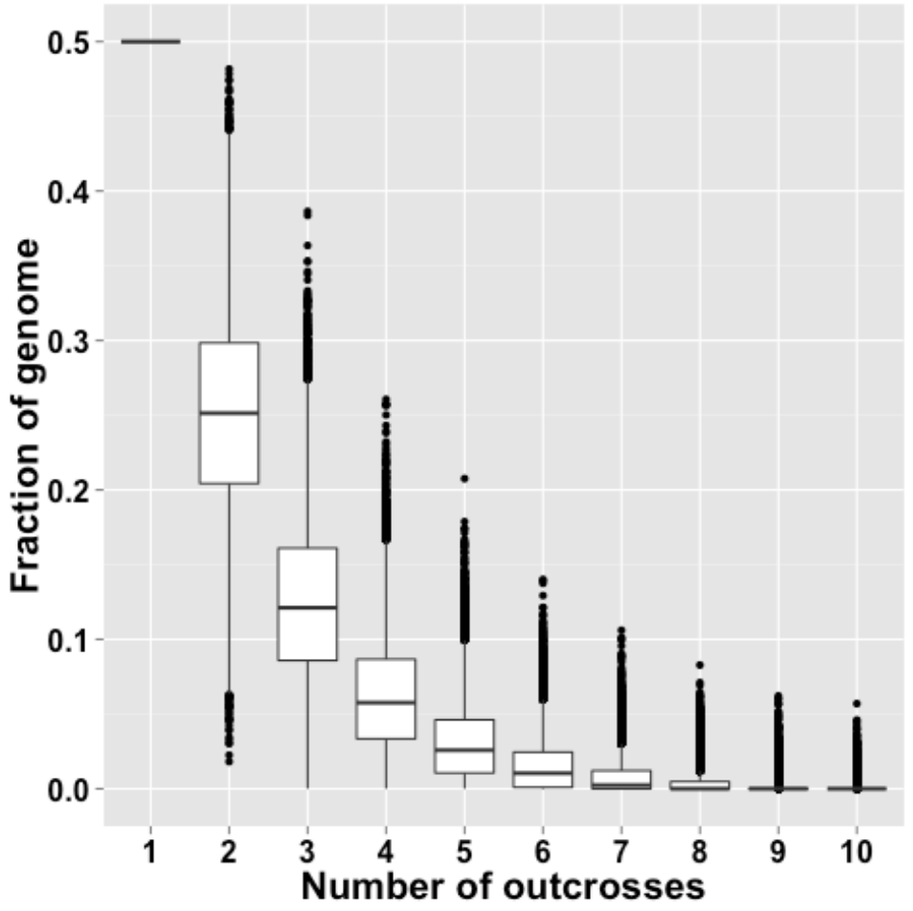
The most common phenotypes are sterile or dead!

6. Backcross and/or outcross

Mutagenesis adds hundreds of mutations randomly throughout the genome.

Backcross = cross to parent used in the screen/selection

Outcross = cross to a wild-type strain



7. Test for dominance

8. Single-gene phenotype?

9. Mapping and complementation

What have we discovered so far?

10. Characterize the phenotype

Look at the wild-type and mutant organisms *in detail*

Let's say you
screened for mutants
that failed to lay eggs

What could be
mutated?

No embryos
No vulva
No vulval muscles
No neurons
Or malfunction of any vulva, muscle, or neuron

Pleiotropy

A single mutation causes many different mutant traits

Mutation in gene X

Mutant with…

long hairs — gene X ⊣ short hair

disrupted sleep patterns — gene X → normal sleep

slow growth — gene X → normal growth

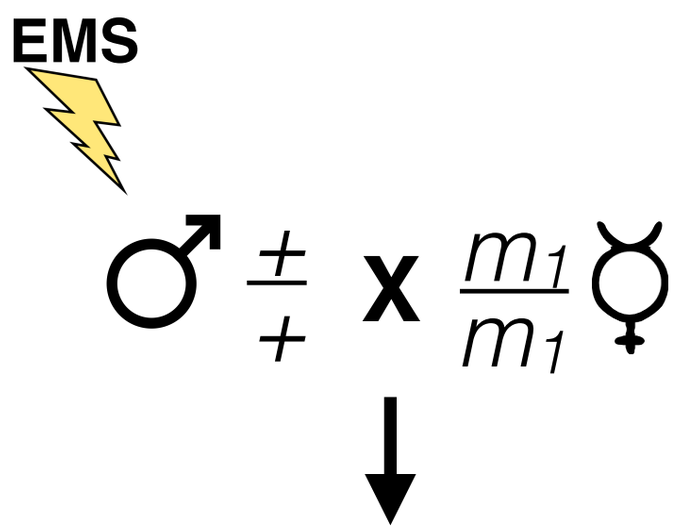
enhanced metabolism of high fat diet — gene X ⊣ fat metabolism

11. Define the nature of the mutant allele(s): gene dosage

1. Dominant or recessive?
2. Frequency of mutant?
3. Where is the mutant allele in allelic series?
4. Look at deficiency heterozygotes for haploinsufficiency
5. Antagonism by wild-type copies of gene

What if you only have one mutant?

12. Perform non-complementation screens



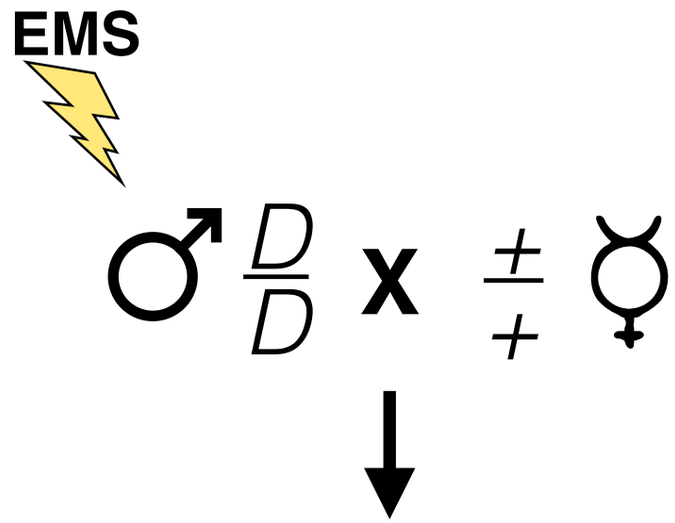
13. Define the null phenotype

What happens with a complete loss of gene function?

Dosage studies, non-complementation screens, and characterization of the mutant phenotype tell you about the null phenotype

What if you have a mutant
with a dominant gain-of-function phenotype?

Cis-dominant suppressor screen



Common (mutant) | Rare (wild-type)

What could *D** be?

Revertant, intragenic suppressor, dominant extragenic suppressor, or null mutant

How can you tell?