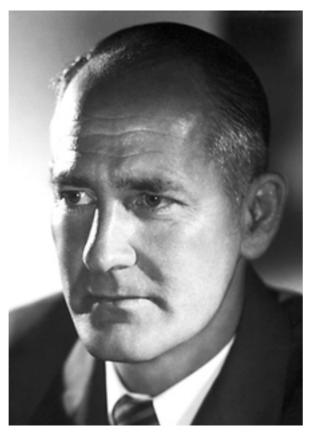
Bio393: Genetic Analysis

Genetic interactions: epistasis

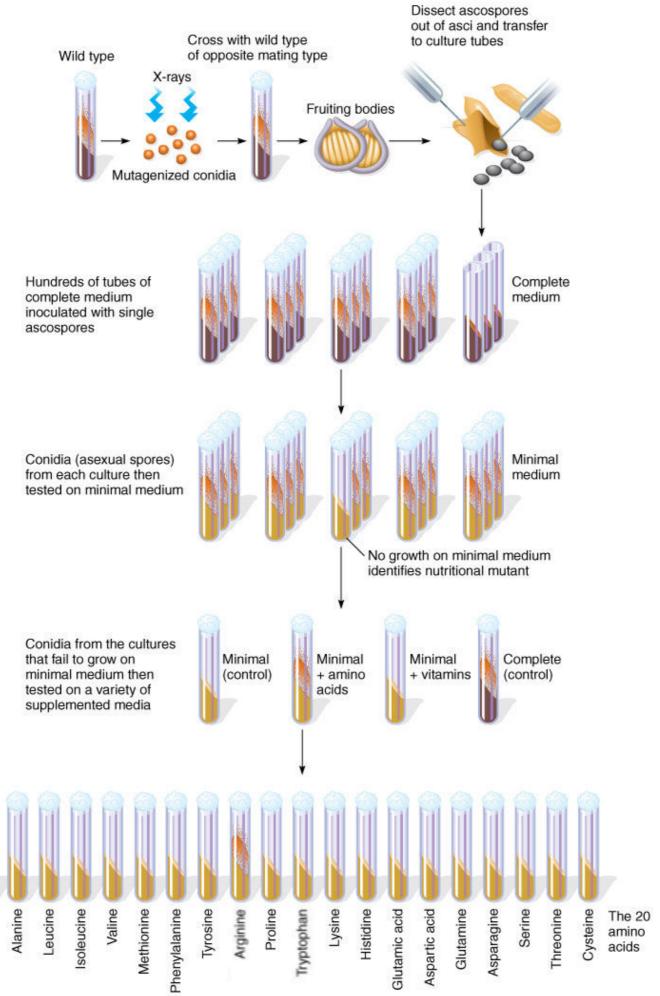


George Beadle



Ed Tatum

The Beadle-Tatum Experiment



Arginine mutant complementation experiment

	arg-a	arg-b	arg-c	arg-d	arg-e	arg-f	arg-g	arg-h	arg-i
arg-a									
arg-b									
arg-c									
arg-d									
arg-e									
arg-f									
arg-g									
arg-h									
arg-i									

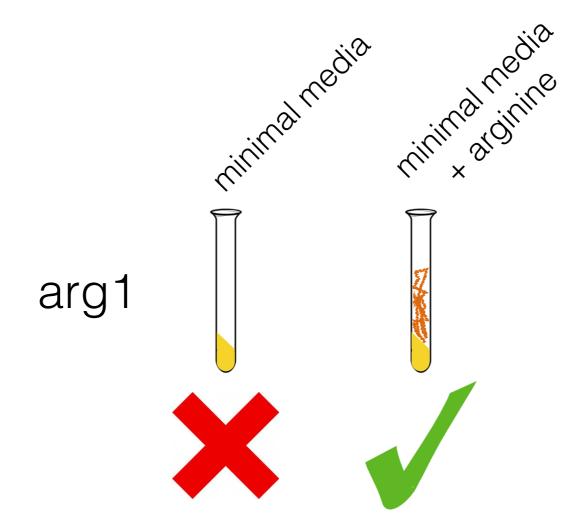
Arginine mutant complementation experiment

Three genes

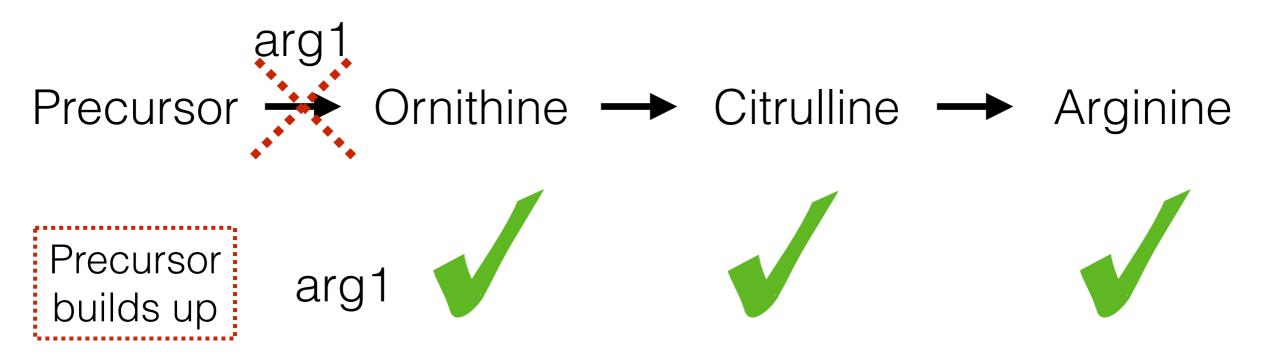
$$arg1 = [a, d, f, g]$$

$$arg2 = [b, c]$$

$$arg3 = [e, h, i]$$

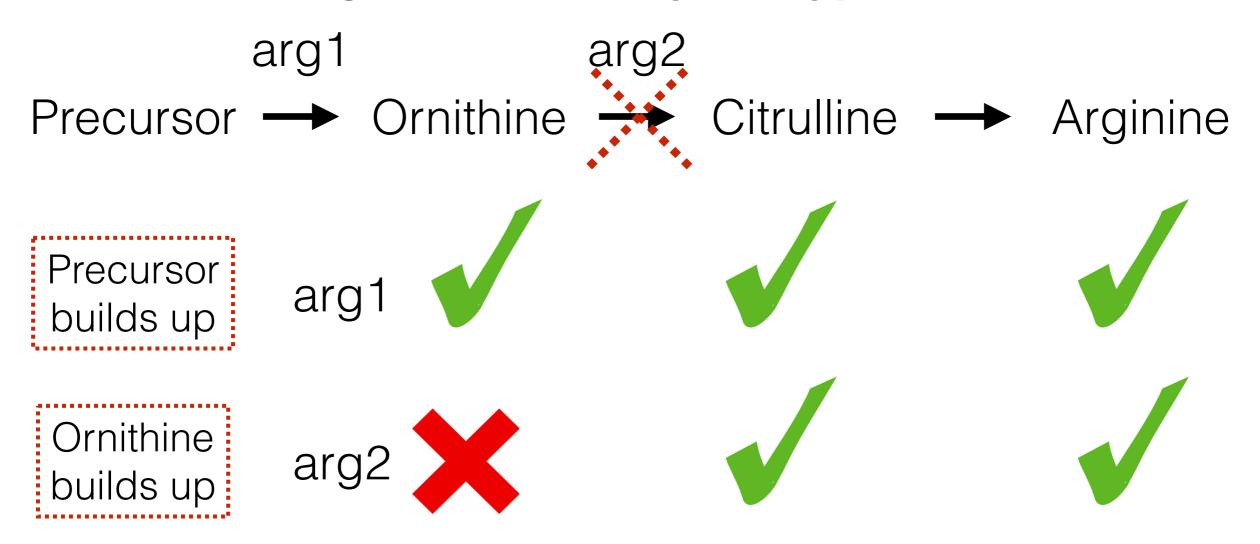


One gene - one enzyme hypothesis



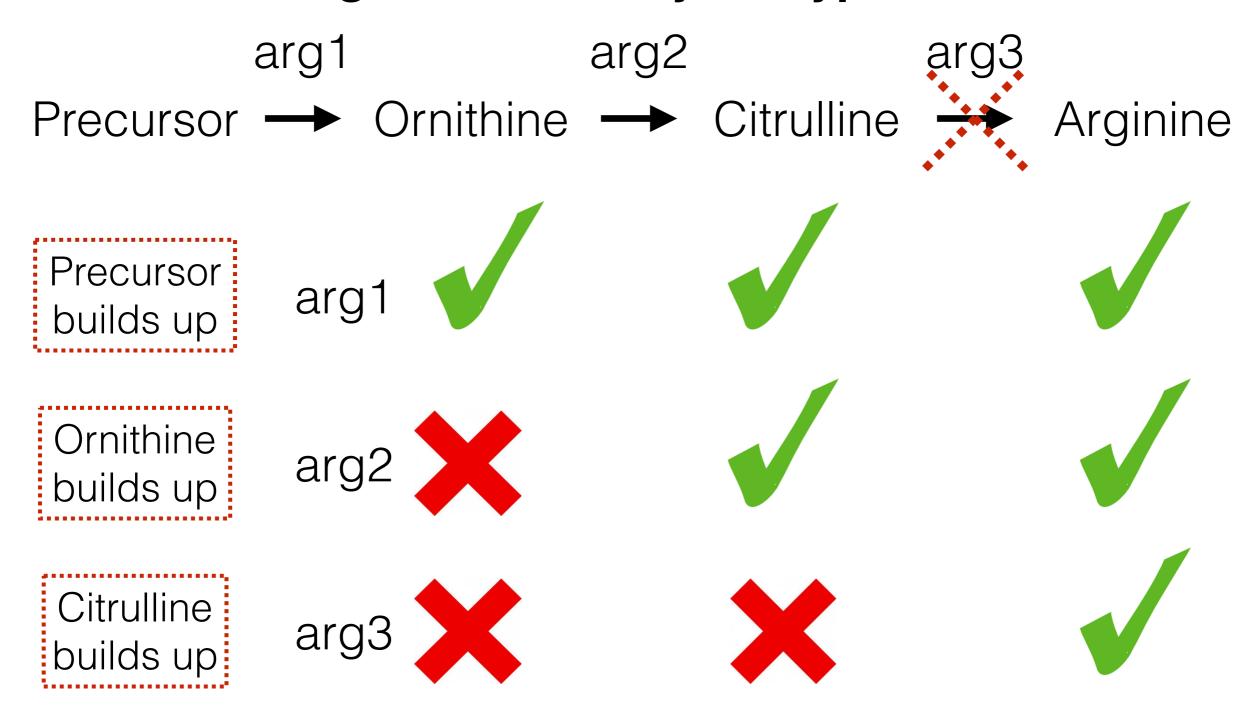
Mutants accumulate precursor for previous step

One gene - one enzyme hypothesis



Mutants accumulate precursor for previous step

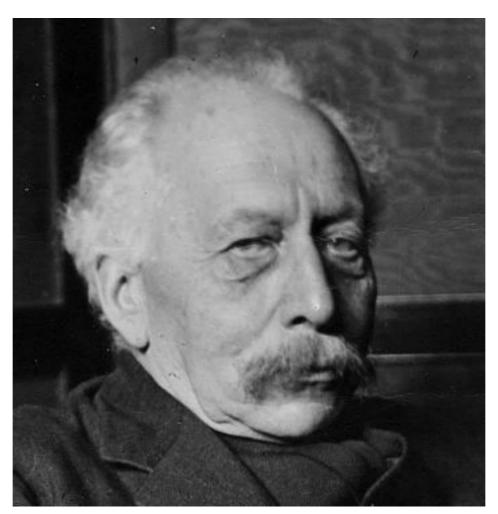
One gene - one enzyme hypothesis





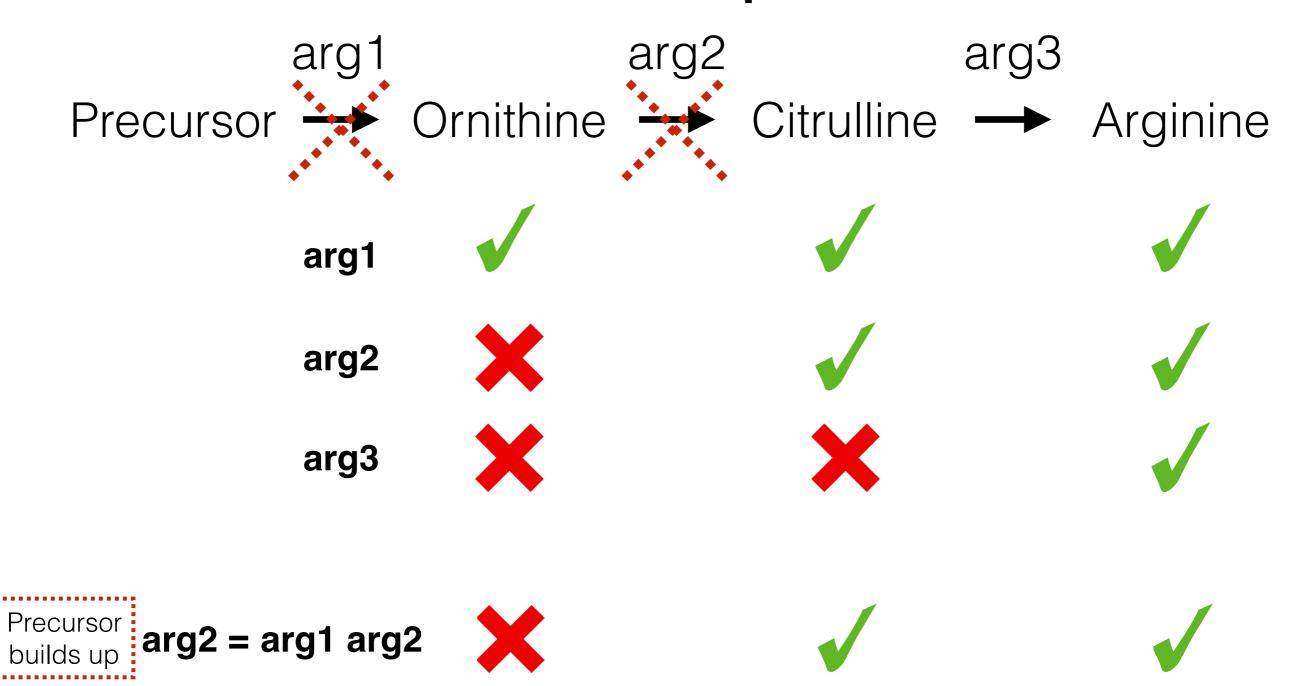
Mutants accumulate precursor for previous step

Epistasis the effect of one gene is dependent on another gene

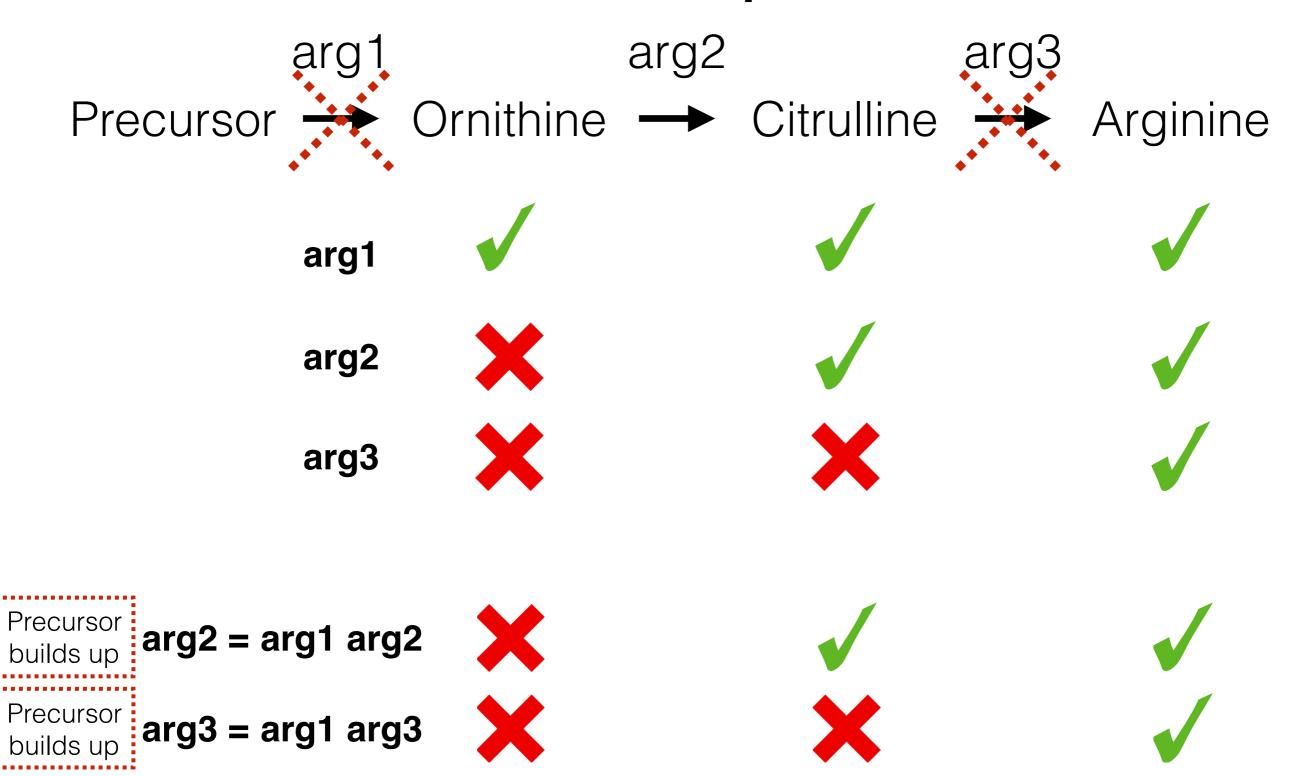


William Bateson

Biochemical epistasis

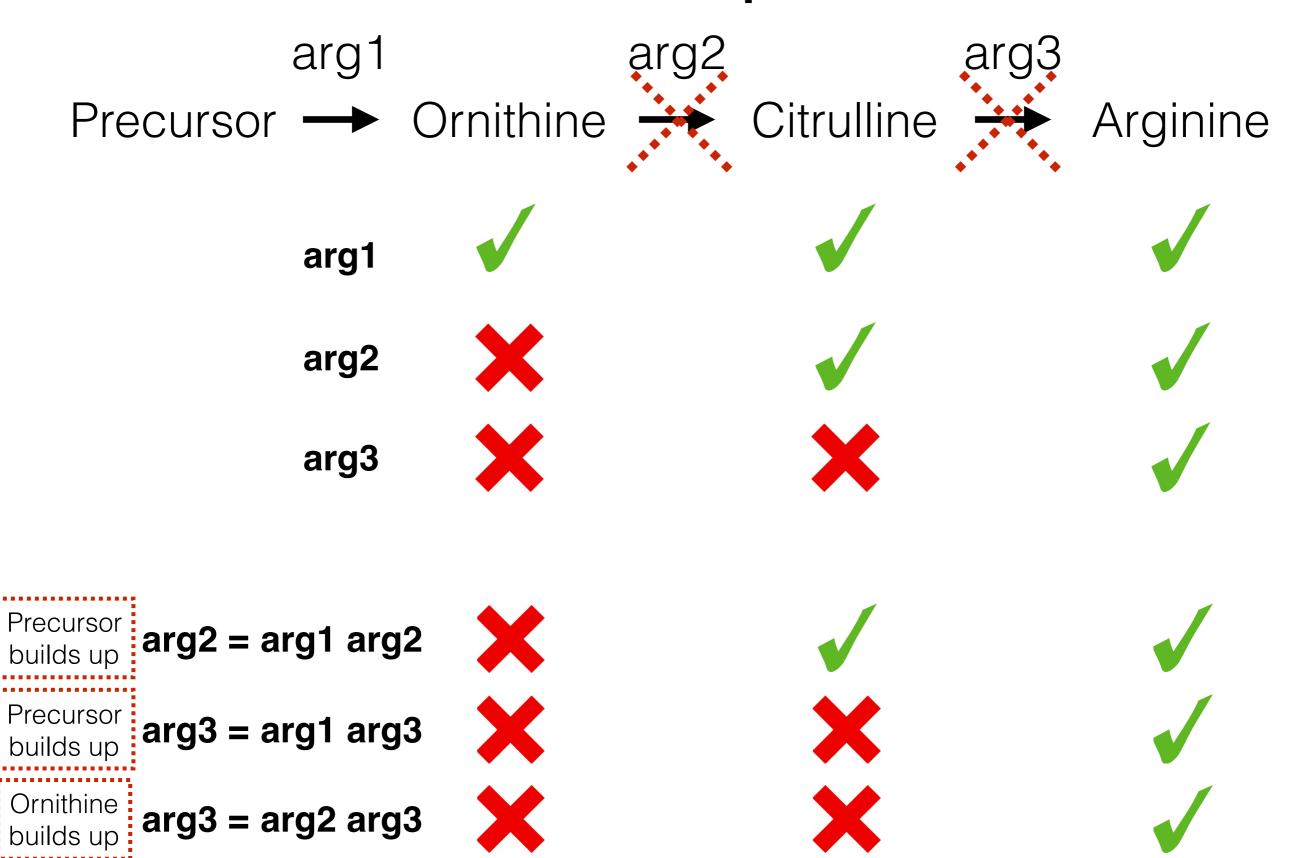


Biochemical epistasis



arg3 is epistatic to arg1, arg3 is downstream (or in parallel) to arg1 Lecture 6

Biochemical epistasis



arg3 is epistatic to arg2, arg3 is downstream (or in parallel) to arg1 Lecture 6

Approach to understanding biochemical epistasis

arg1 arg2 arg3
Precursor → Ornithine → Citrulline → Arginine

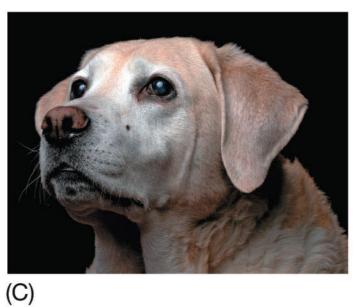
- 1. Single mutants fail in a step in a biosynthetic pathway
- 2. Double mutants fail in two steps. The growth phenotype dictates the most downstream gene in the pathway. The compound built up dictates the most upstream gene in the pathway.
- 3. What will the single and double mutants accumulate?
- 4. Pathways can be branched

Epistasis - one mutant phenotype trumps another



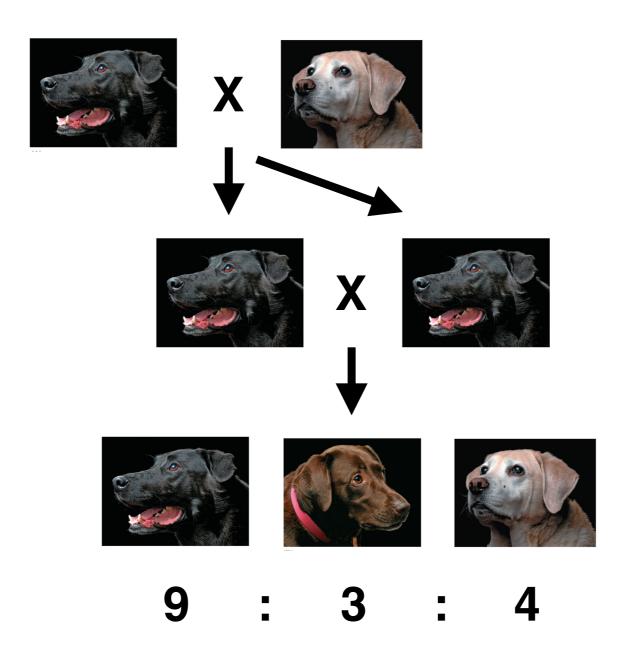




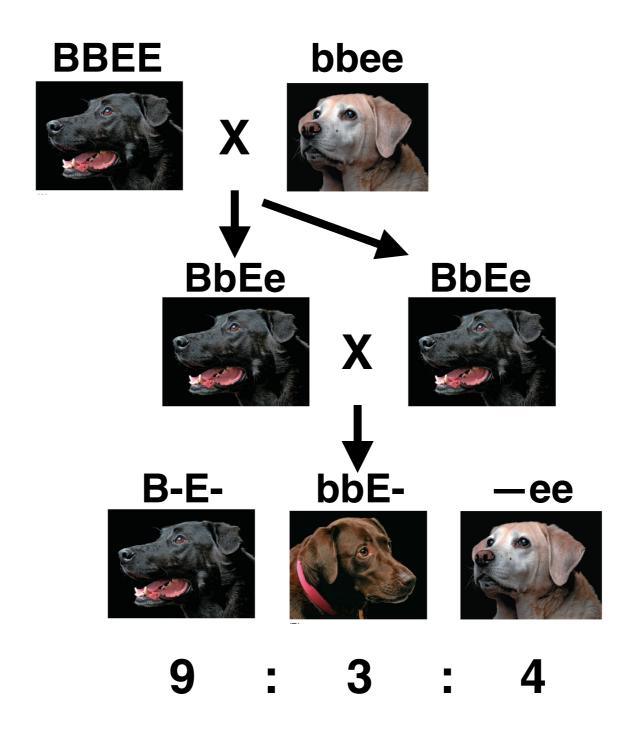


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Epistasis - one mutant phenotype trumps another



Epistasis - one mutant phenotype trumps another



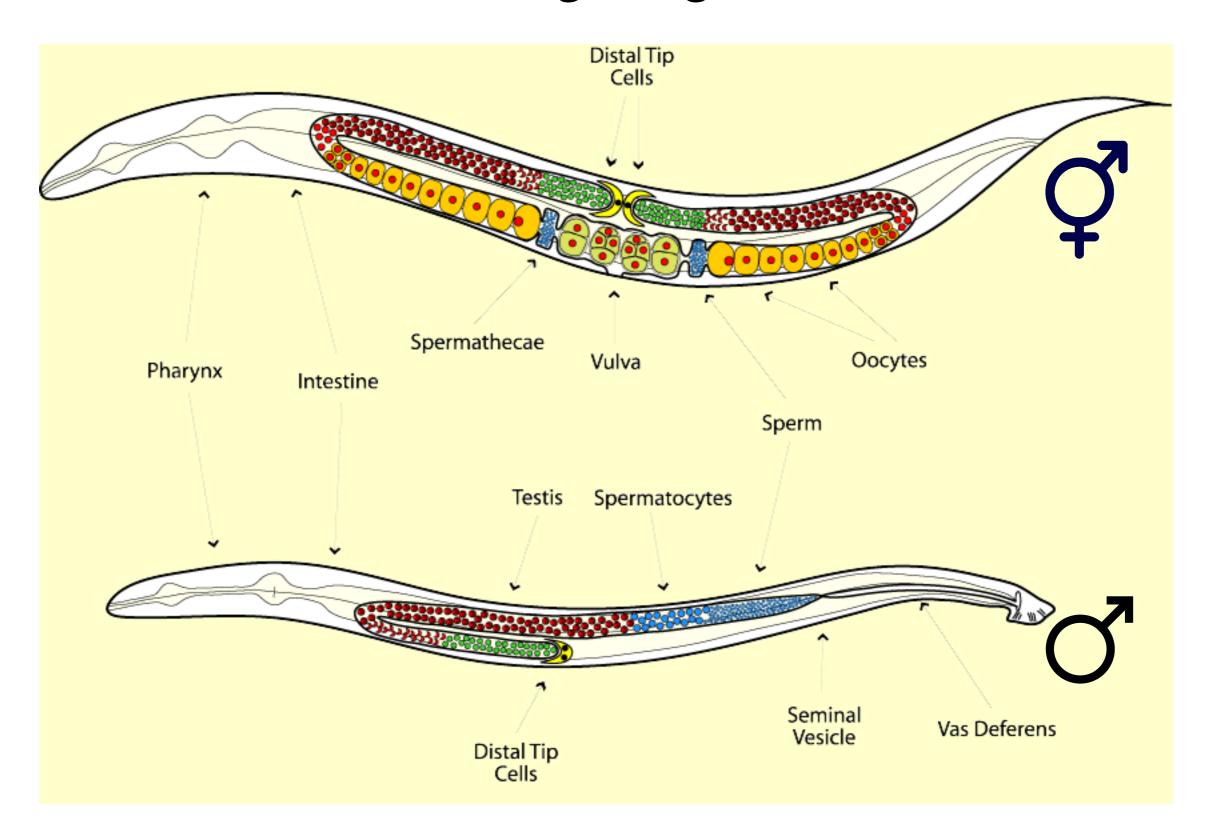
B = black

b = brown

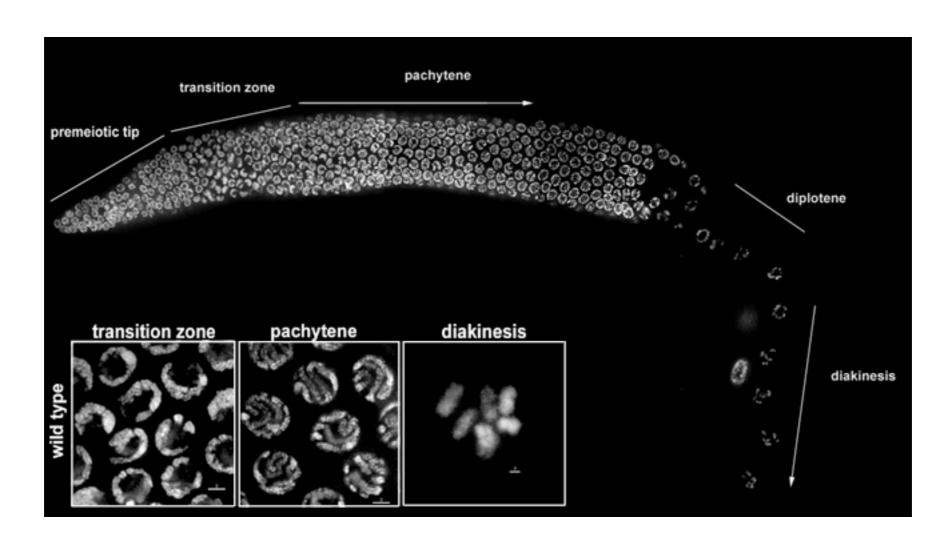
E = color

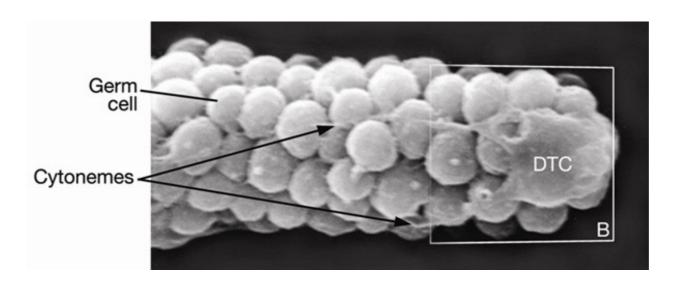
e = no color

The *C. elegans* germline



The *C. elegans* germline

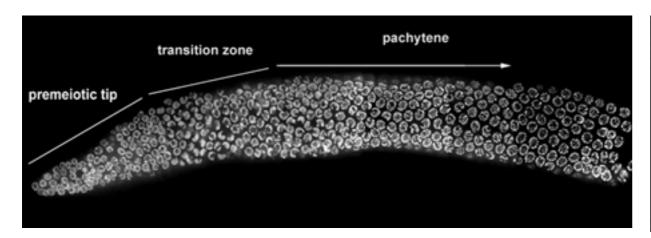


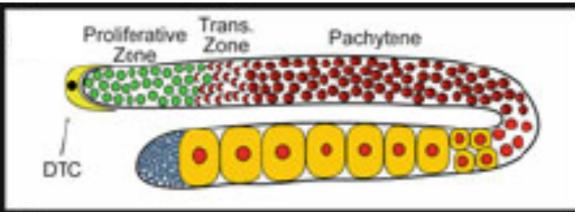




Judith Kimble

C. elegans germline mutants

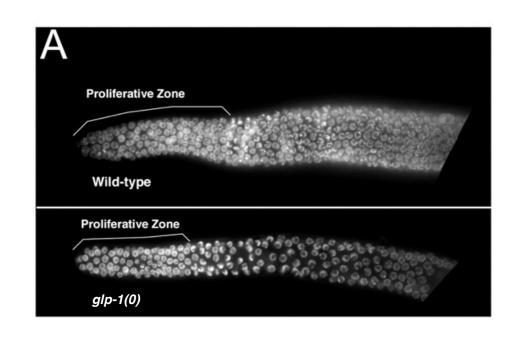




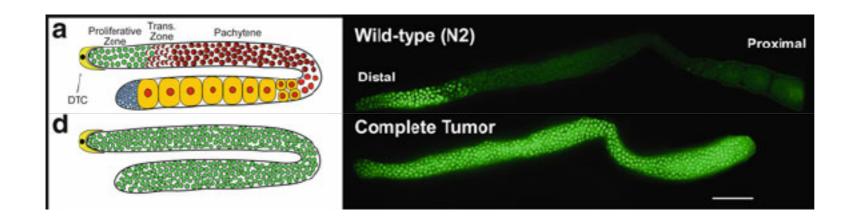
glp-1(0) = all meiotic germ cells

glp-1(gf) = all mitotic germ cells

C. elegans germline mutants



glp-1(0) = more meiosis, less mitosis



glp-1(gf) = more mitosis, less meiosis

C. elegans germline mutants

	Phenotype	Mutant
glp-1→GSC prolif.	meiotic cells	glp-1(0)
	mitotic cells	glp-1(gf)
<i>lag-2</i> → GSC prolif.	meiotic cells	lag-2(0)
fbf-1 → GSC prolif.	meiotic cells	fbf-1(0)
gld-1 — GSC prolif.	mitotic cells	gld-1(0)

Mutant	Phenotype
glp-1(0)	meiotic cells
glp-1(gf)	mitotic cells
lag-2(0)	meiotic cells
fbf-1(0)	meiotic cells
gld-1(0)	mitotic cells
glp-1(0); lag-2(0)	meiotic cells

You can only do epistasis tests with mutants that have different phenotypes

Mutant	Phenotype
glp-1(0)	meiotic cells
glp-1(gf)	mitotic cells
lag-2(0)	meiotic cells
fbf-1(0)	meiotic cells
gld-1(0)	mitotic cells
glp-1(gf); lag-2(0)	mitotic cells

glp-1 → GSC prolif.

lag-2 → GSC prolif.

Which phenotype is epistatic?

lag-2 → glp-1 → GSC prolif.

Parallel gene action can NEVER be formally excluded by phenotype alone

$$lag-2 → glp-1 → GSC prolif.$$

Null alleles have to be used for this reason.

Approach to understanding regulatory epistasis

- 1. Decide what is the output phenotype; keep it consistent
- 2. Look at single mutants and make a model with output
- Look at double mutants and make a model with output and respect to single mutant models - epistatic gene acts downstream
- 4. Remember parallel but don't assume it is always parallel (*i.e.* make linear models for regulatory epistasis)
- 5. Remember two negatives make a positive

Mutant	Phenotype
glp-1(0)	meiotic cells
glp-1(gf)	mitotic cells
lag-2(0)	meiotic cells
fbf-1(0)	meiotic cells
gld-1(0)	mitotic cells
glp-1(gf); lag-2(0)	mitotic cells
glp-1(gf); fbf-1(0)	meiotic cells
glp-1(0); gld-1(0)	mitotic cells
fbf-1(0); gld-1(0)	mitotic cells
lag-2(0); fbf-1(0)	meiotic cells
lag-2(0); gld-1(0)	mitotic cells

glp-1 → GSC prolif. lag-2 → GSC prolif. fbf-1 → GSC prolif. gld-1 → GSC prolif.

 $lag-2 \rightarrow glp-1 \rightarrow GSC prolif.$

Mutant	Phenotype
glp-1(0)	meiotic cells
glp-1(gf)	mitotic cells
lag-2(0)	meiotic cells
fbf-1(0)	meiotic cells
gld-1(0)	mitotic cells
glp-1(gf); lag-2(0)	mitotic cells
glp-1(gf); fbf-1(0)	meiotic cells
glp-1(0); gld-1(0)	mitotic cells
fbf-1(0); gld-1(0)	mitotic cells
lag-2(0); fbf-1(0)	meiotic cells
lag-2(0); gld-1(0)	mitotic cells

glp-1 → GSC prolif. lag-2 → GSC prolif. fbf-1 → GSC prolif. gld-1 → GSC prolif.

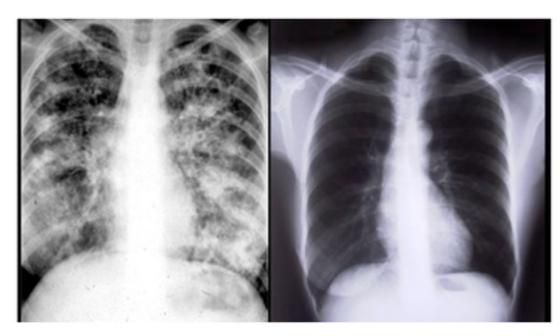
 $lag-2 \rightarrow glp-1 \rightarrow fbf-1 \rightarrow GSC$ prolif.

Mutant	Phenotype
glp-1(0)	meiotic cells
glp-1(gf)	mitotic cells
lag-2(0)	meiotic cells
fbf-1(0)	meiotic cells
gld-1(0)	mitotic cells
glp-1(gf); lag-2(0)	mitotic cells
glp-1(gf); fbf-1(0)	meiotic cells
glp-1(0); gld-1(0)	mitotic cells
fbf-1(0); gld-1(0)	mitotic cells
lag-2(0); fbf-1(0)	meiotic cells
lag-2(0); gld-1(0)	mitotic cells

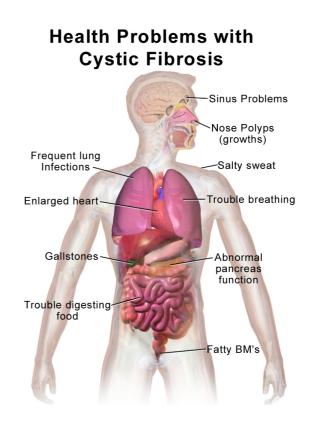
glp-1 → GSC prolif. lag-2 → GSC prolif. fbf-1 → GSC prolif. gld-1 → GSC prolif.

 $lag-2 \rightarrow glp-1 \rightarrow fbf-1 \rightarrow gld-1 \rightarrow GSC prolif.$

What about cystic fibrosis and today's topic?

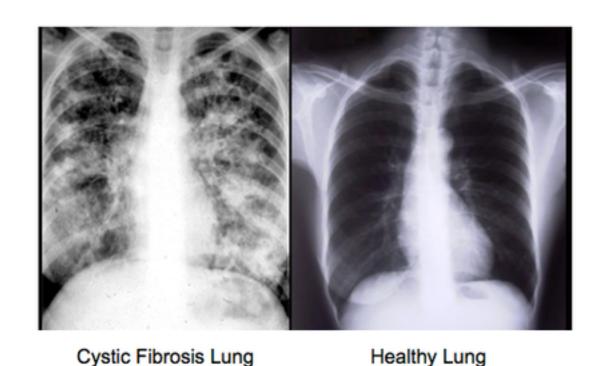


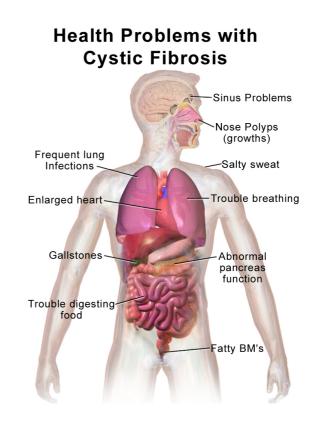
Cystic Fibrosis Lung Healthy Lung



- 1. Autosomal recessive disorder
- 2. Not caused by chromosomal aberrations or meiotic NDJ
- 3. Mapped to chromosome 7
- 4. Mutations in CF gene are null or hypomorphs
- 5. Compound heterozygosity (failure to complement) is common

What about cystic fibrosis and today's topic?





What data do we need to understand genetic interactions with the CF disease phenotype?