

Bio393: Genetic Analysis

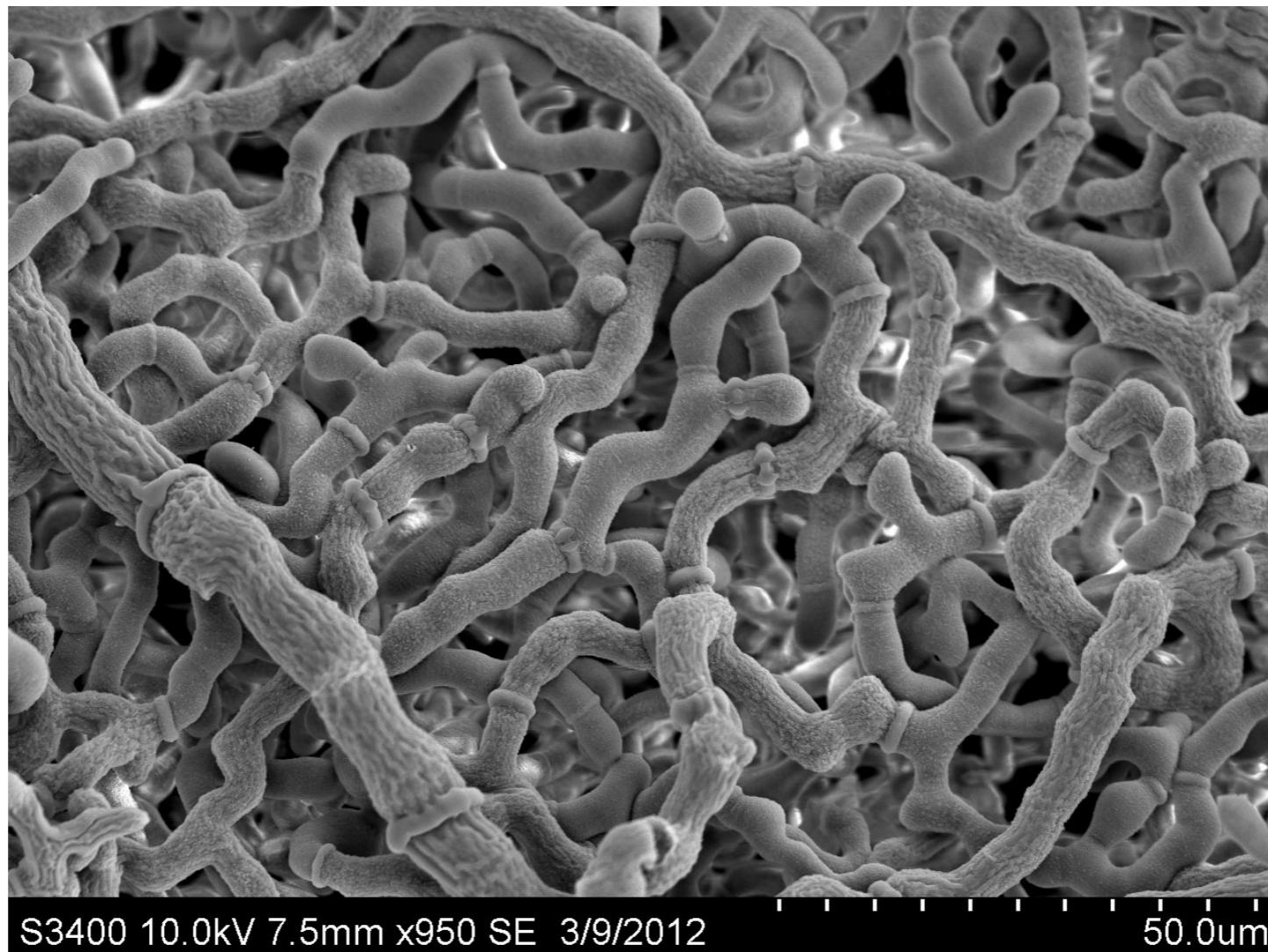
Genetic interactions: epistasis



George Beadle

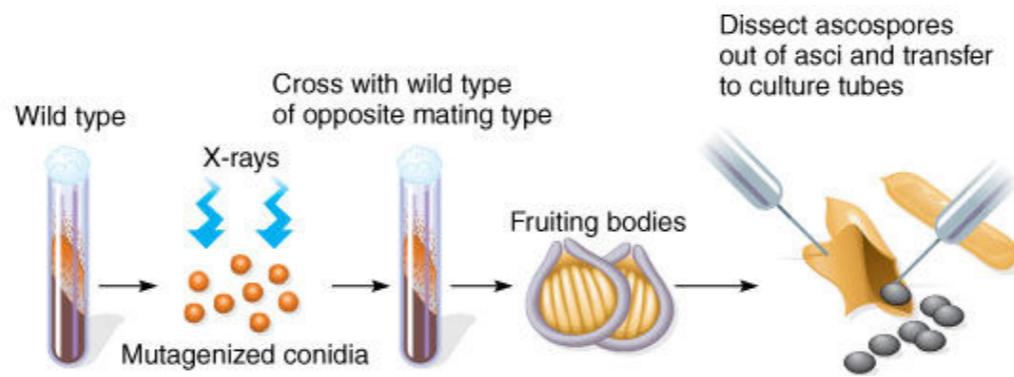


Ed Tatum

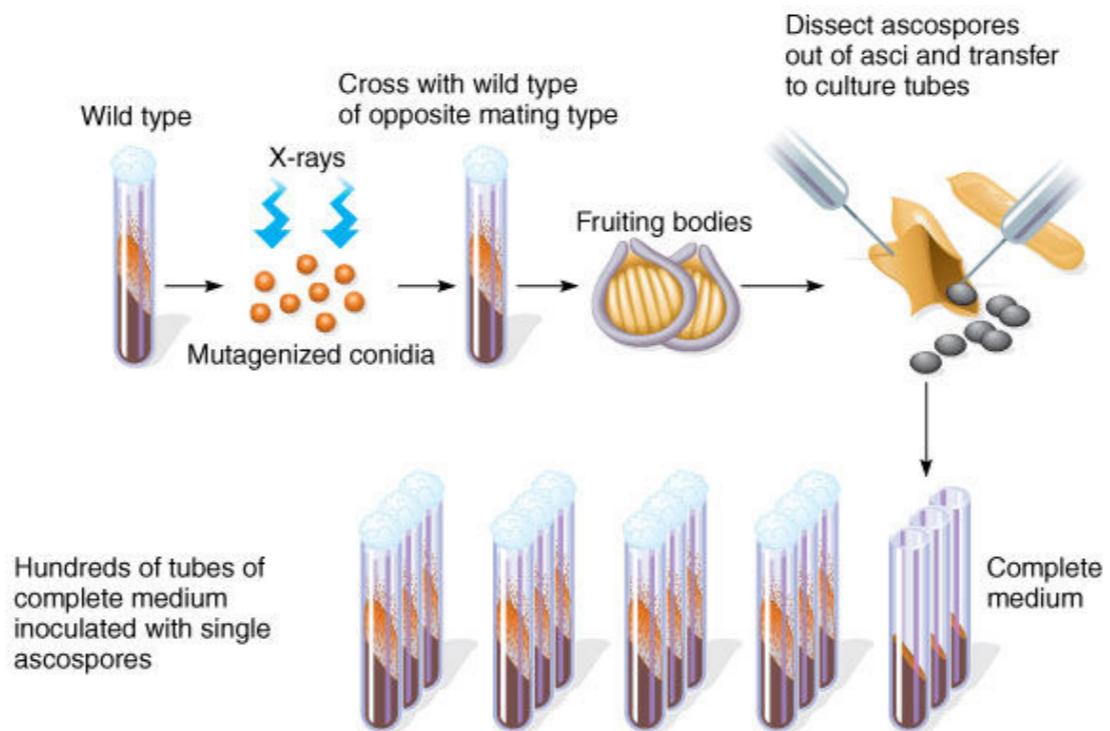


Neurospora crassa

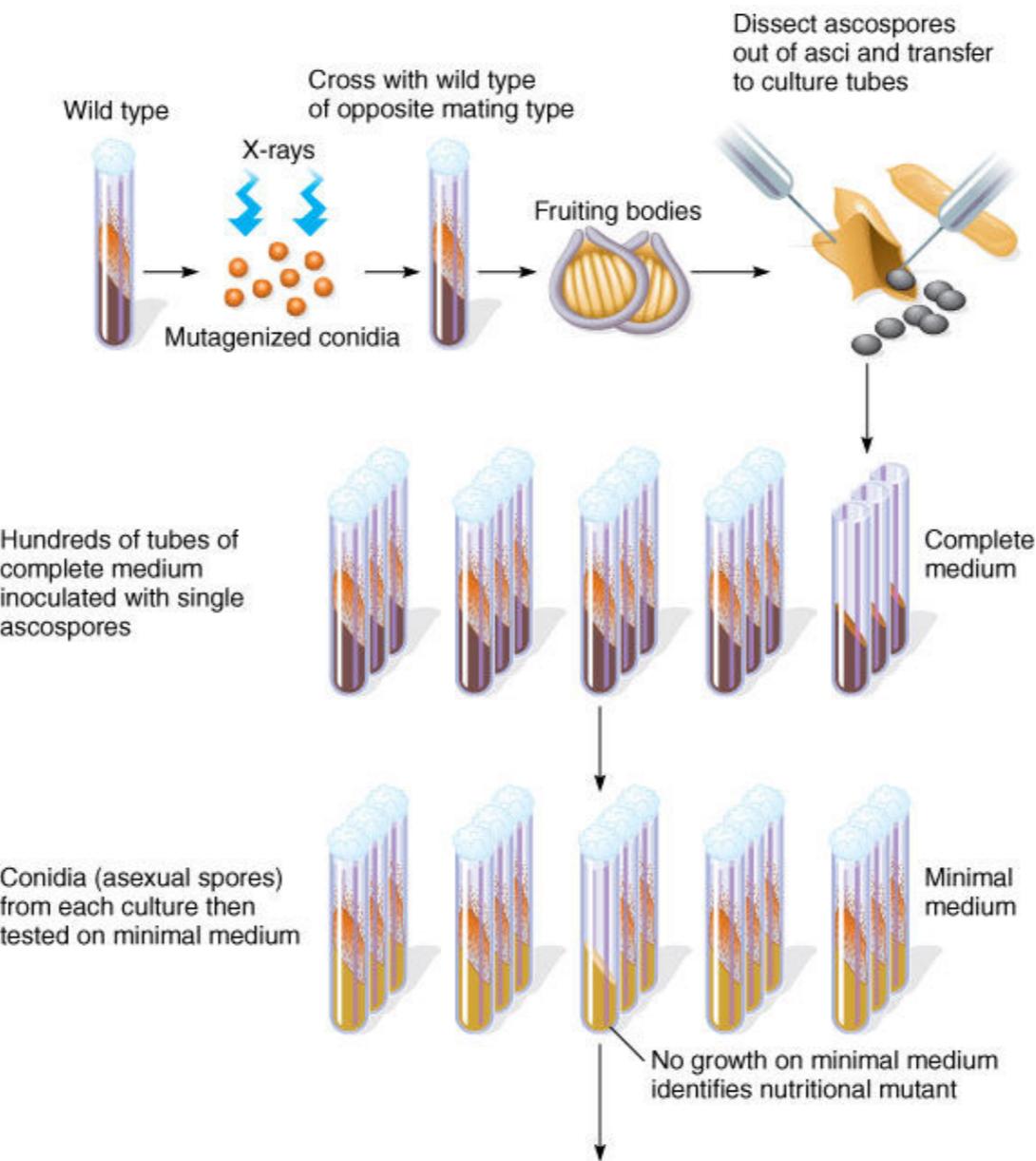
The Beadle- Tatum Experiment



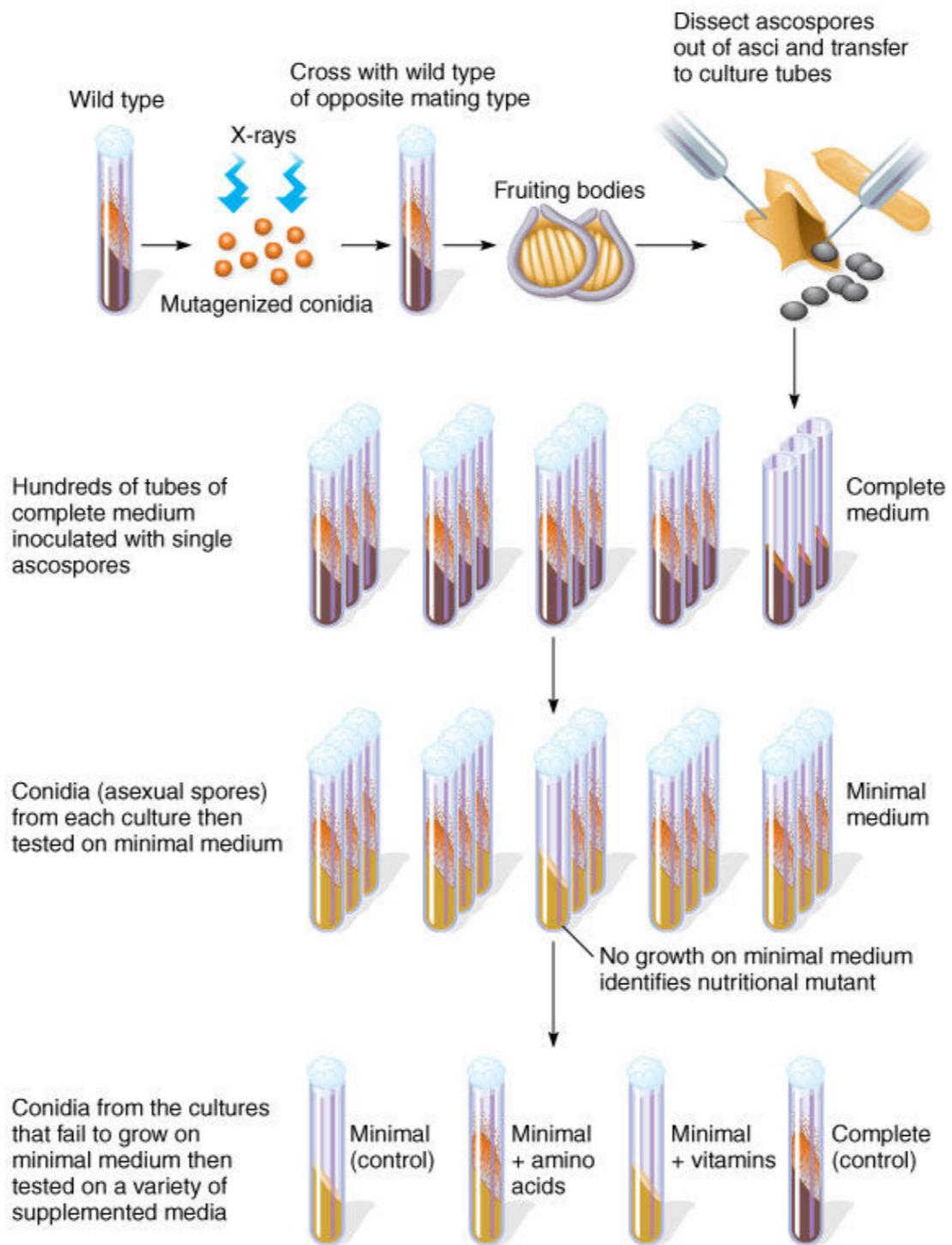
The Beadle- Tatum Experiment



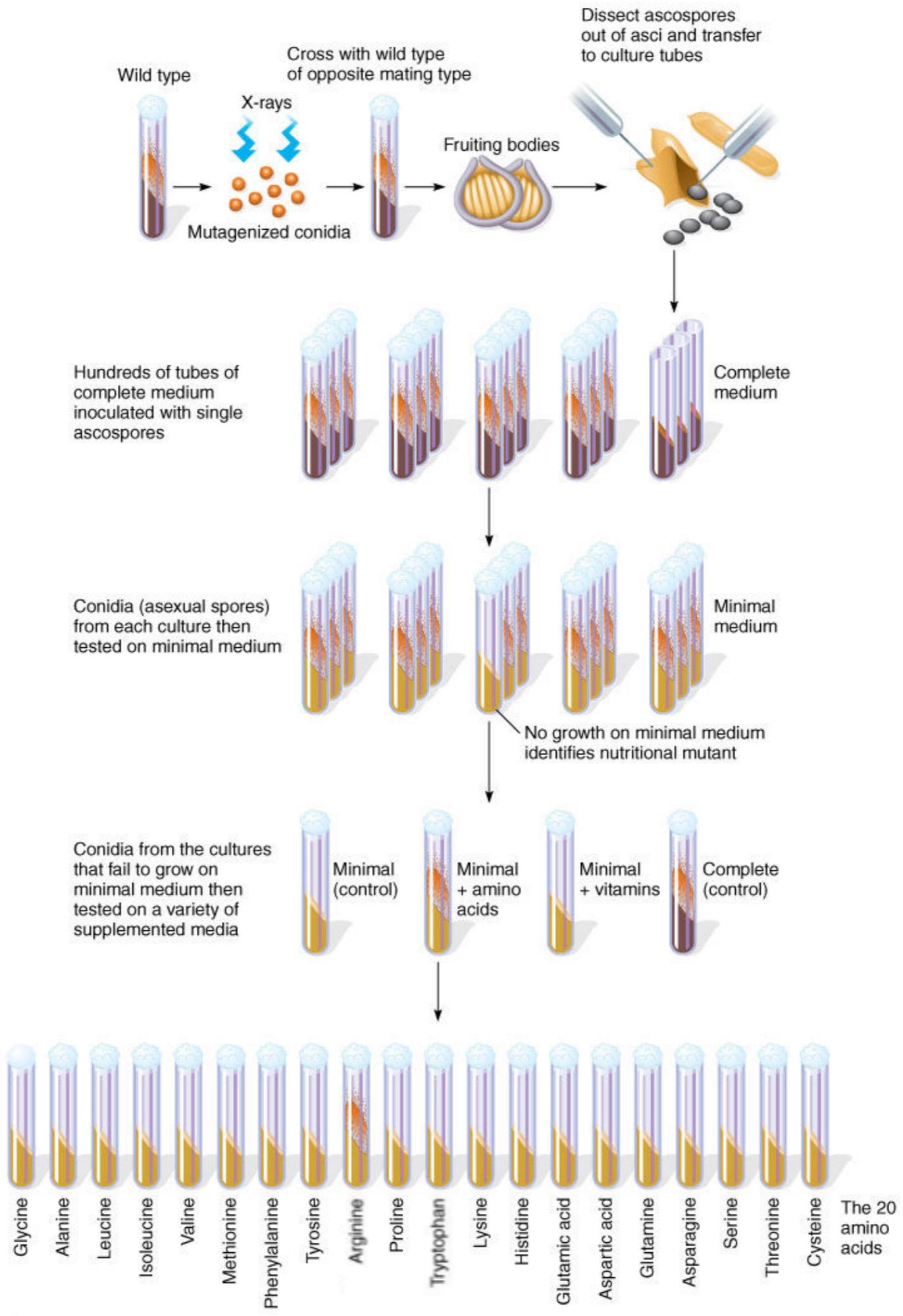
The Beadle- Tatum Experiment



The Beadle- Tatum Experiment

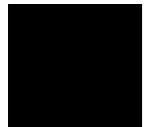


The Beadle- Tatum Experiment



Arginine mutant complementation experiment

	<i>arg-a</i>	<i>arg-b</i>	<i>arg-c</i>	<i>arg-d</i>	<i>arg-e</i>	<i>arg-f</i>	<i>arg-g</i>	<i>arg-h</i>	<i>arg-i</i>
<i>arg-a</i>									
<i>arg-b</i>									
<i>arg-c</i>									
<i>arg-d</i>									
<i>arg-e</i>									
<i>arg-f</i>									
<i>arg-g</i>									
<i>arg-h</i>									
<i>arg-i</i>									



Growth = wild type



No growth = mutant

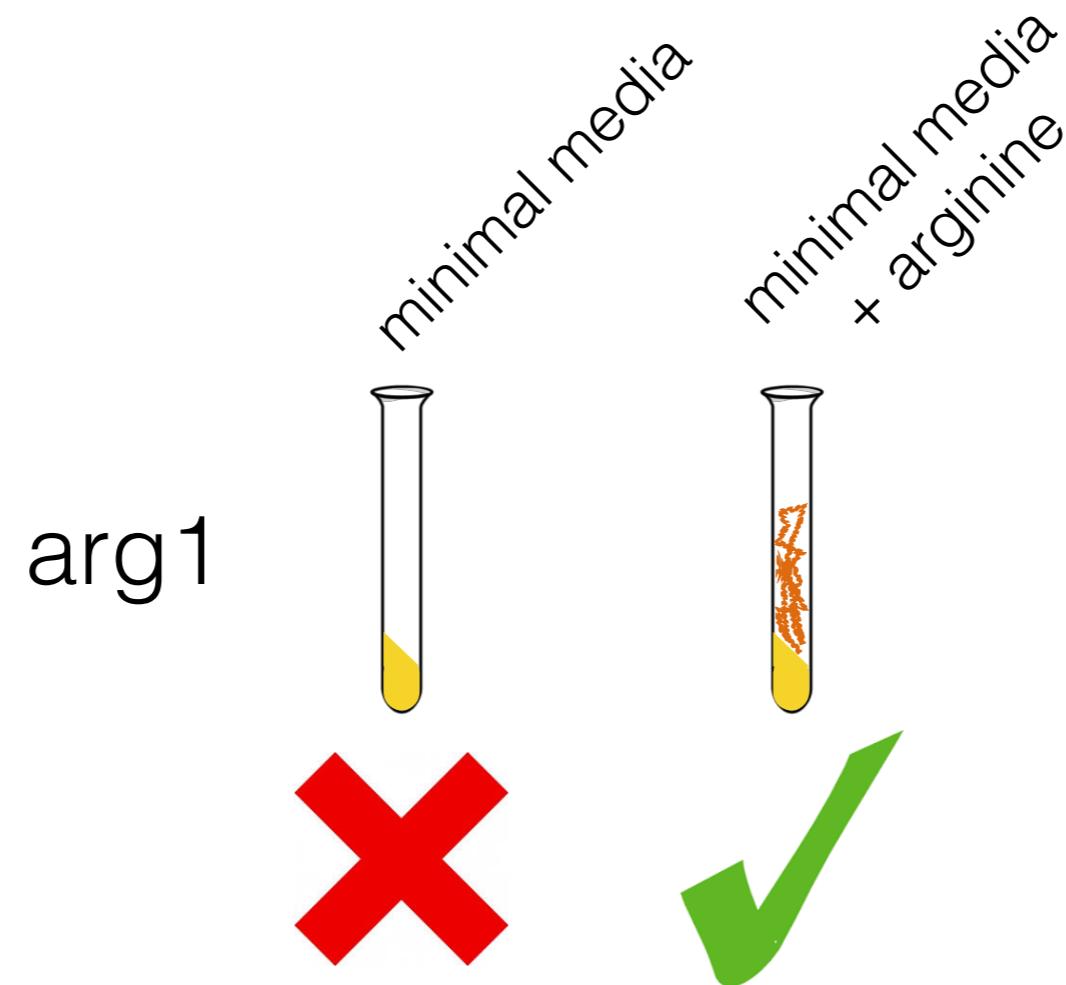
Arginine mutant complementation experiment

Three genes

arg1 = [a, d, f, g]

arg2 = [b, c]

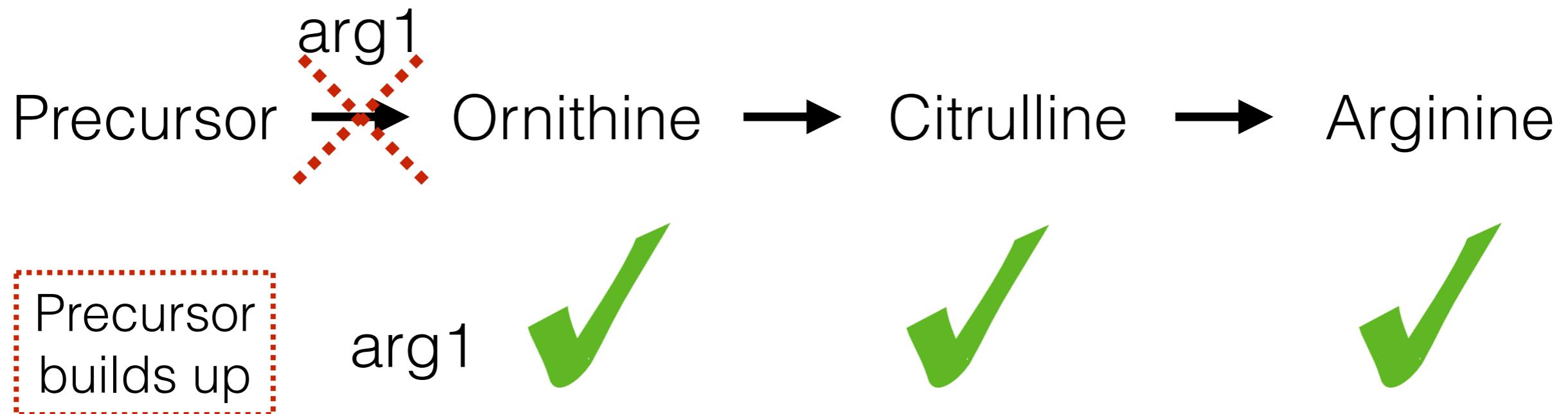
arg3 = [e, h, i]



One gene - one enzyme hypothesis

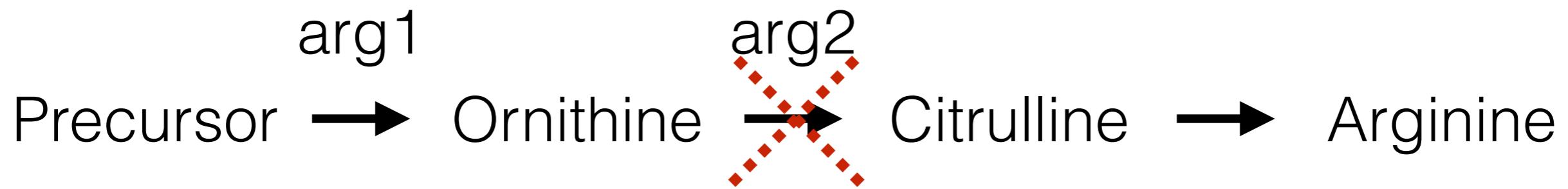
Precursor → Ornithine → Citrulline → Arginine

One gene - one enzyme hypothesis



Mutants accumulate precursor for previous step

One gene - one enzyme hypothesis



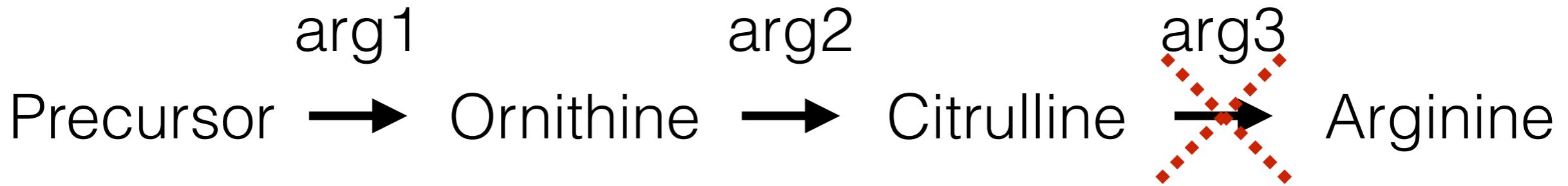
Precursor
builds up



Ornithine
builds up

Mutants accumulate precursor for previous step

One gene - one enzyme hypothesis



Precursor builds up

Ornithine builds up

Citrulline builds up



Mutants accumulate precursor for previous step

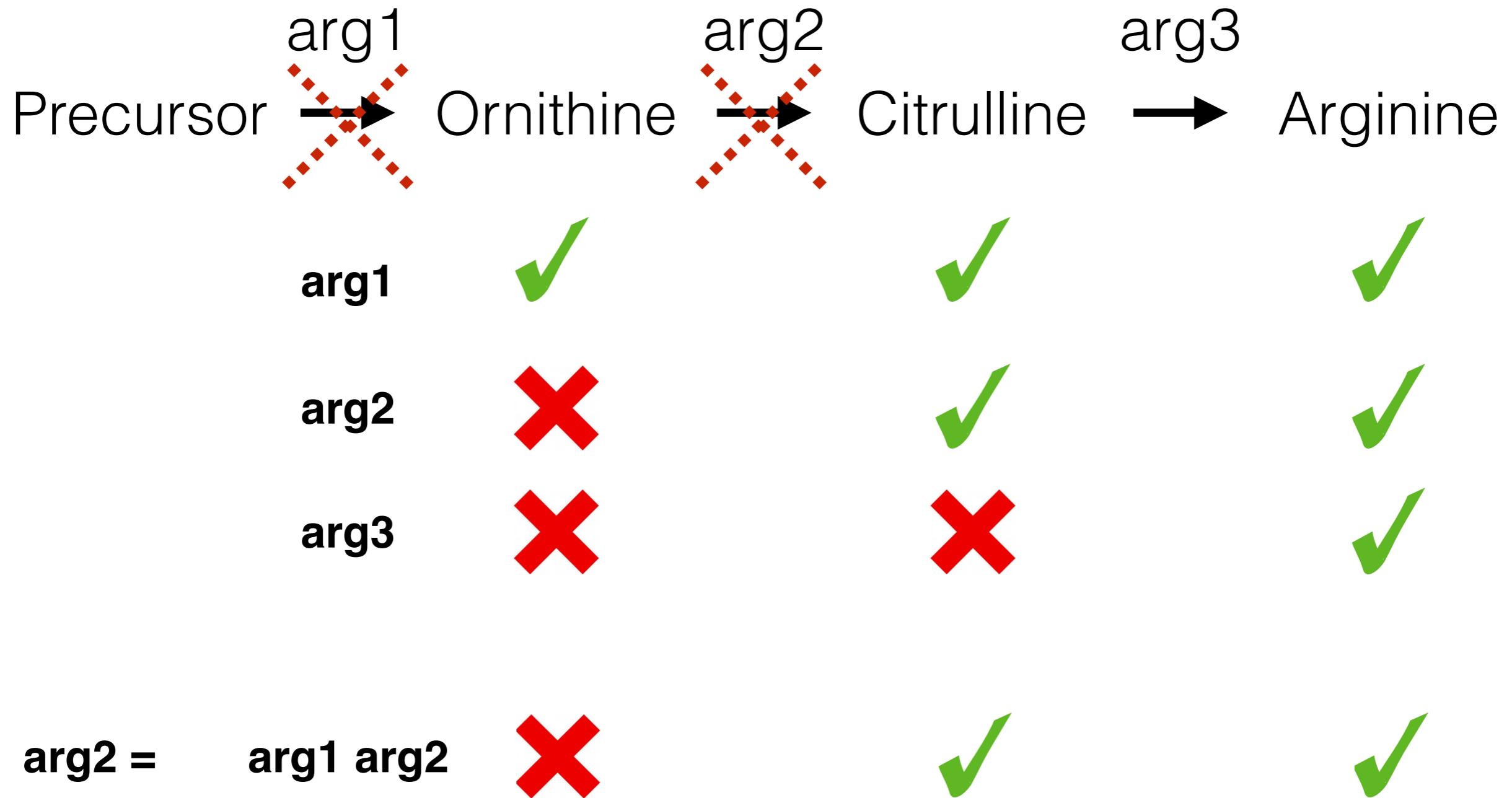
Epistasis

the effect of one gene is dependent on another gene



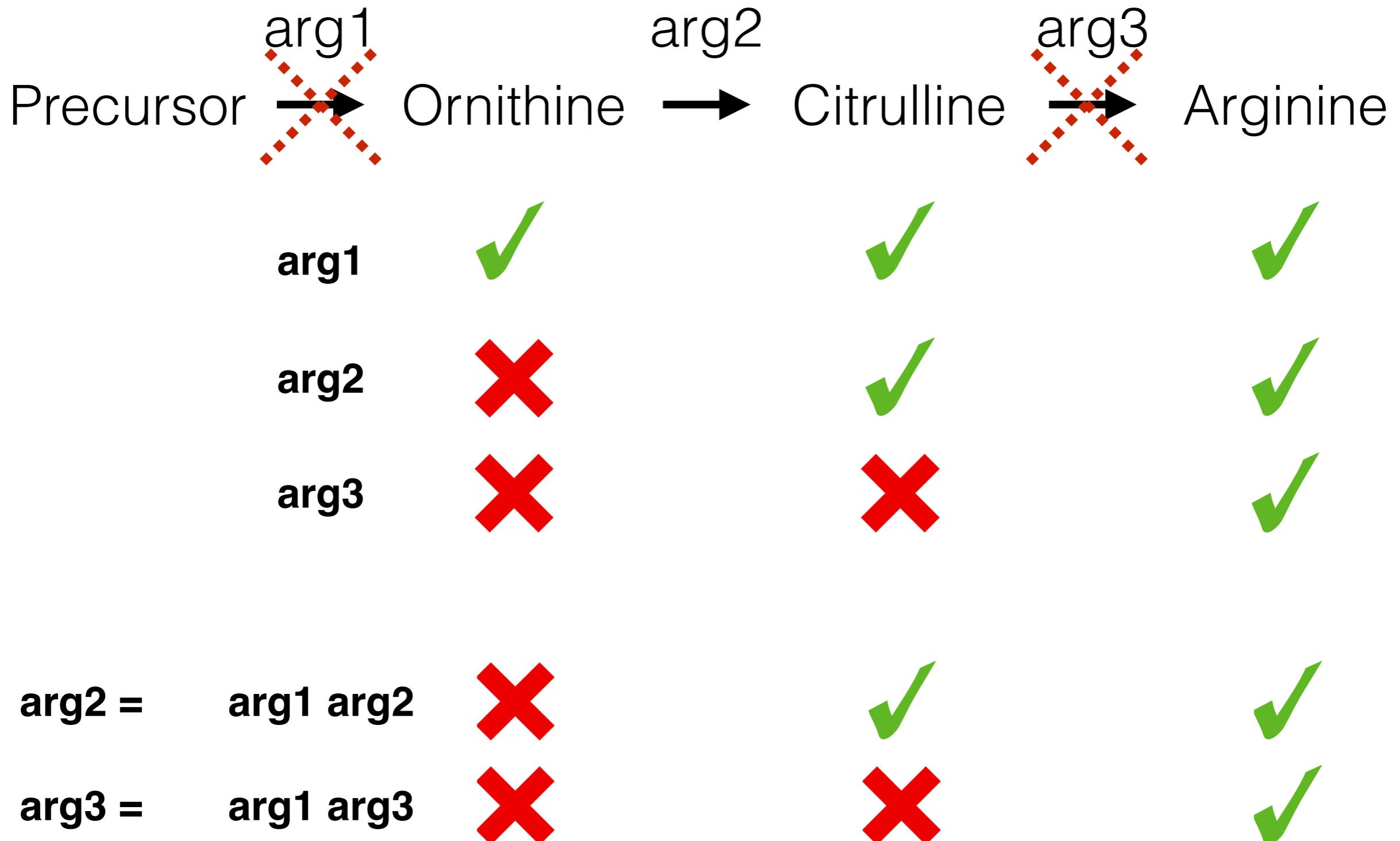
William Bateson

Biochemical epistasis



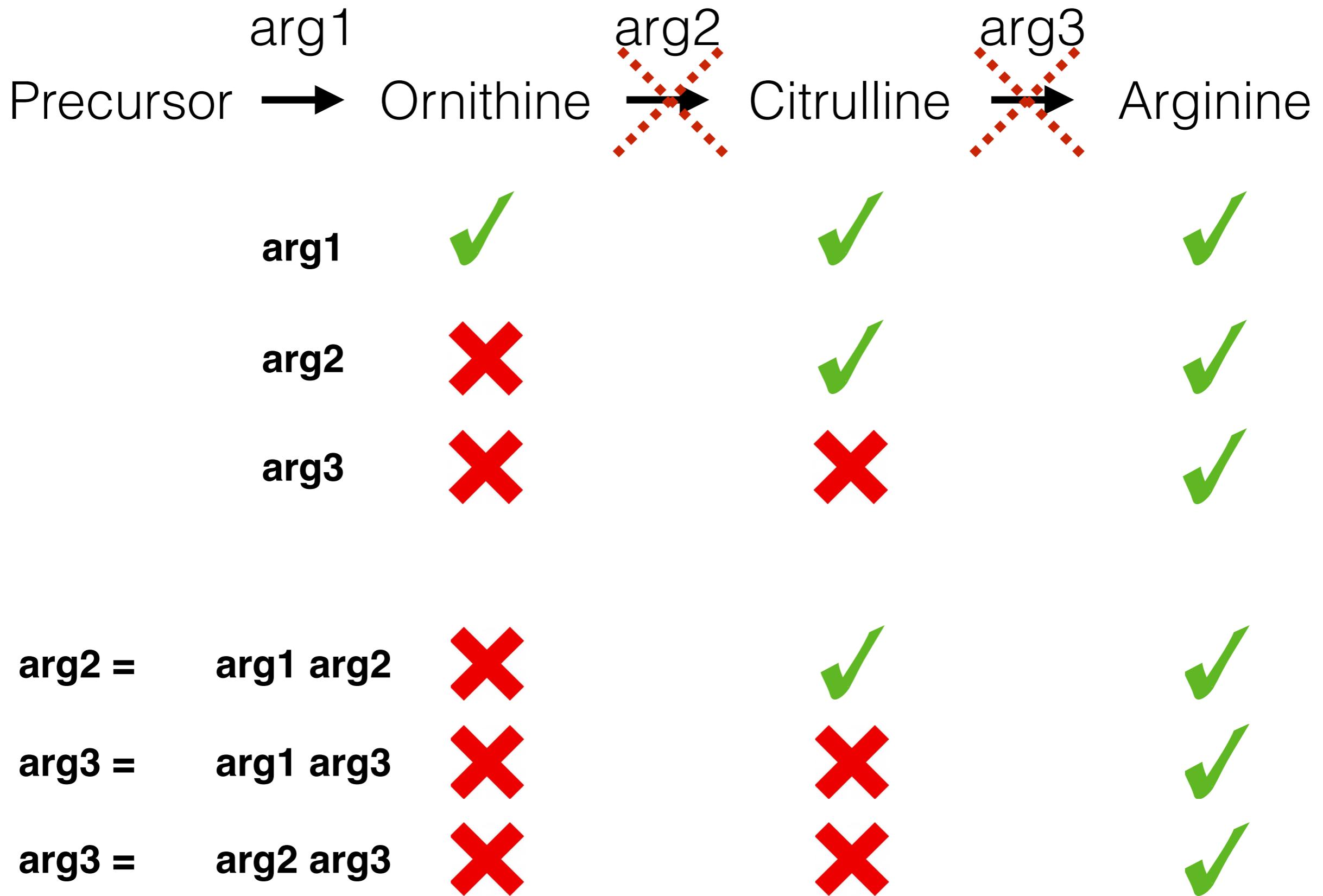
arg2 is epistatic to arg1, arg2 is downstream (or in parallel) to arg1

Biochemical epistasis



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

Biochemical epistasis



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

Approach to understanding biochemical epistasis

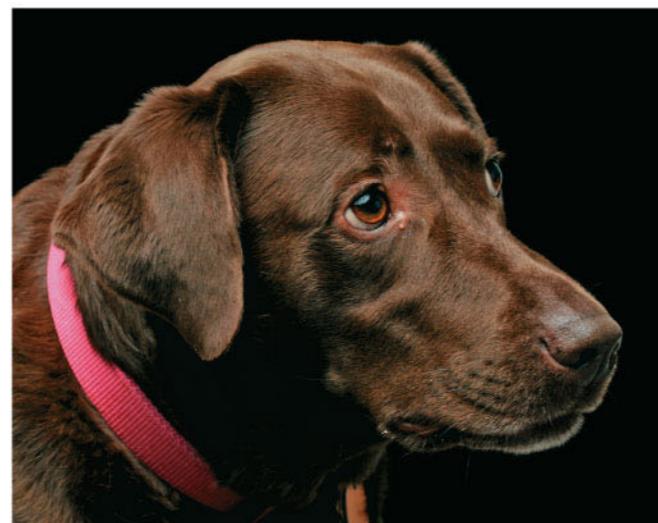


1. Single mutants fail in a step in a biosynthetic pathway
2. Double mutants fail in two steps. The phenotype dictates the most downstream gene in the pathway.
3. What will the single and double mutants accumulate?
4. Pathways can be branched

Epistasis - one mutant phenotype trumps another



(A)



(B)

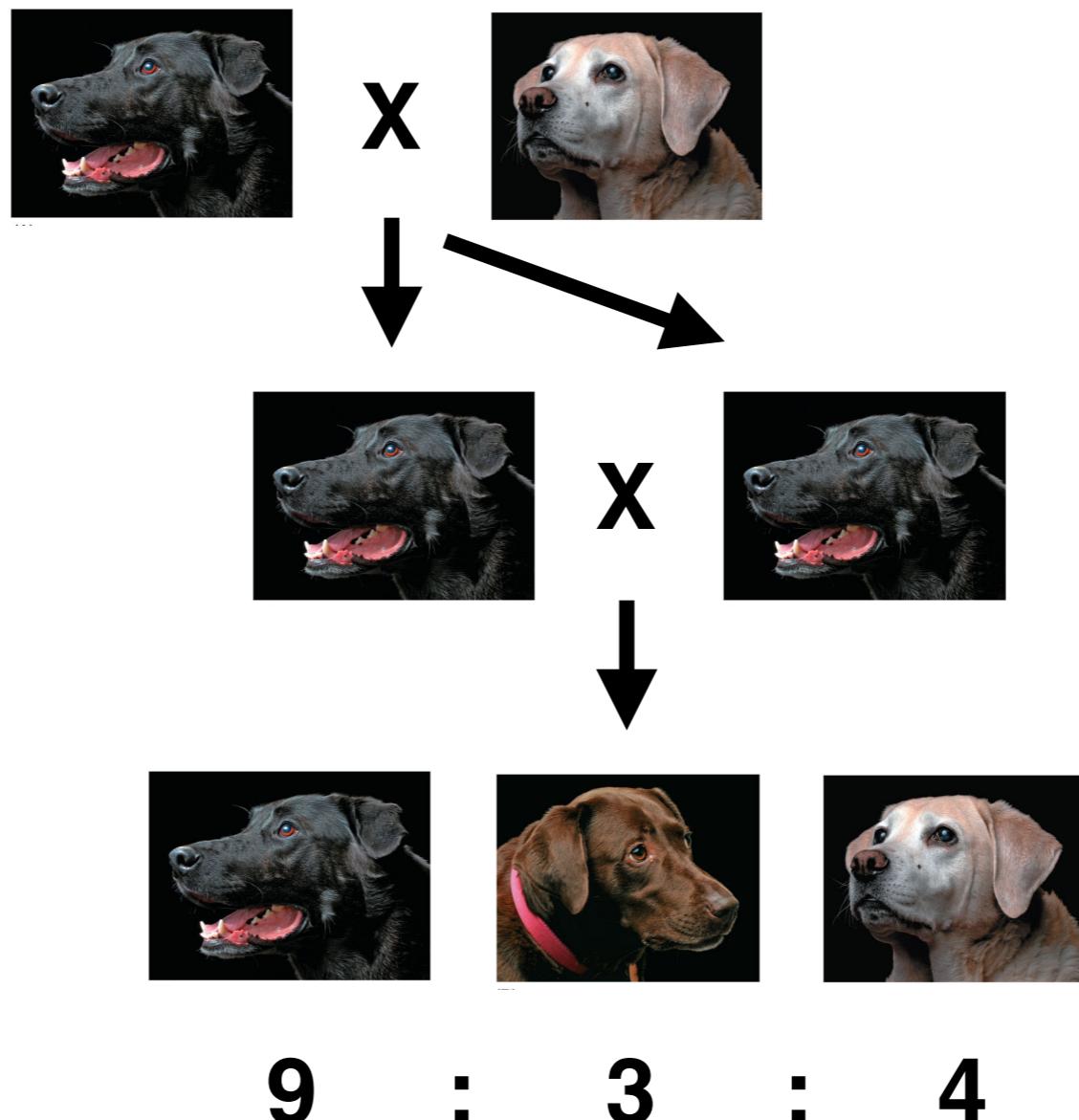


(C)

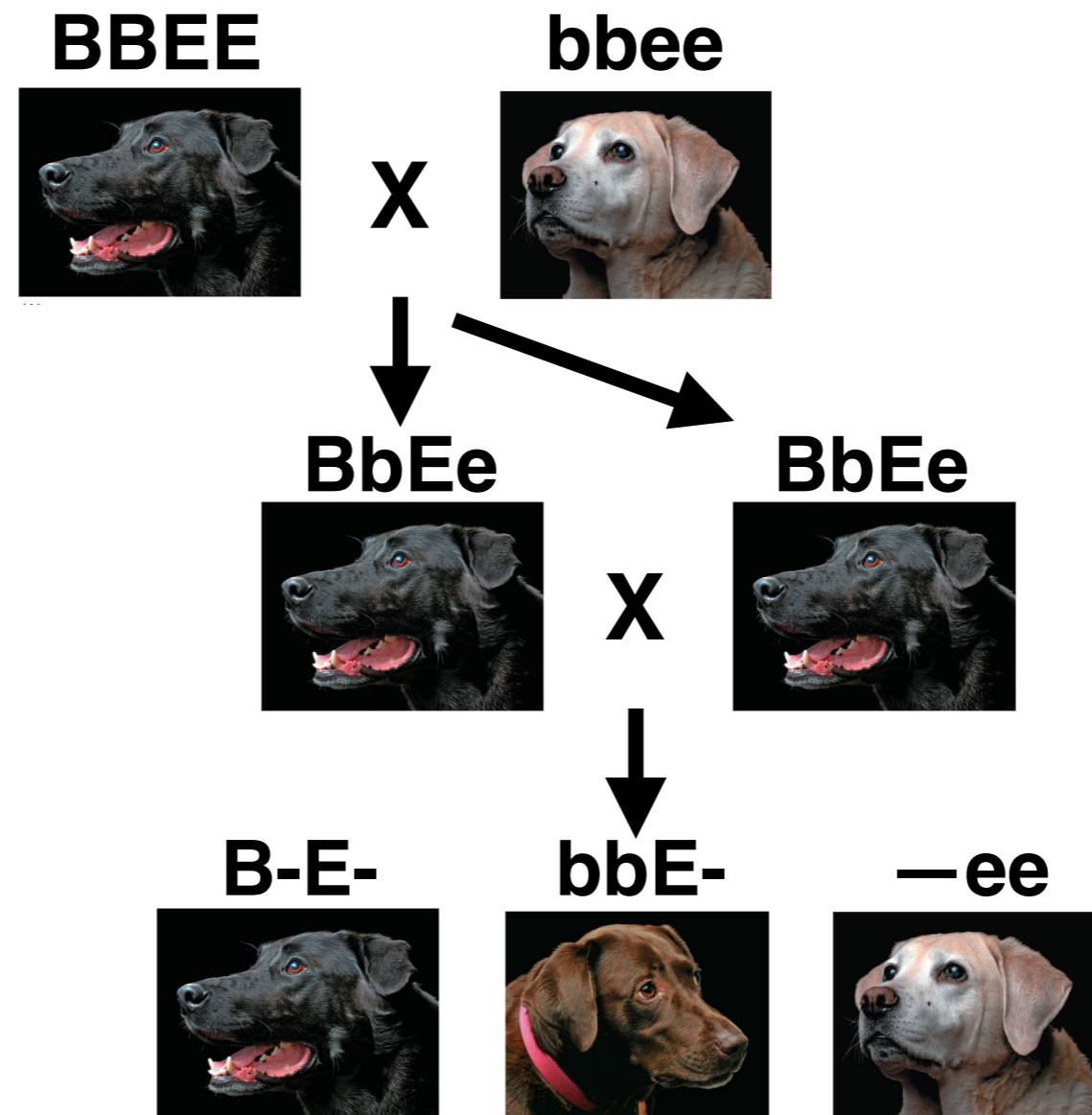
LIFE 8e, Figure 10.14

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Epistasis - one mutant phenotype trumps another



Epistasis - one mutant phenotype trumps another



B = black

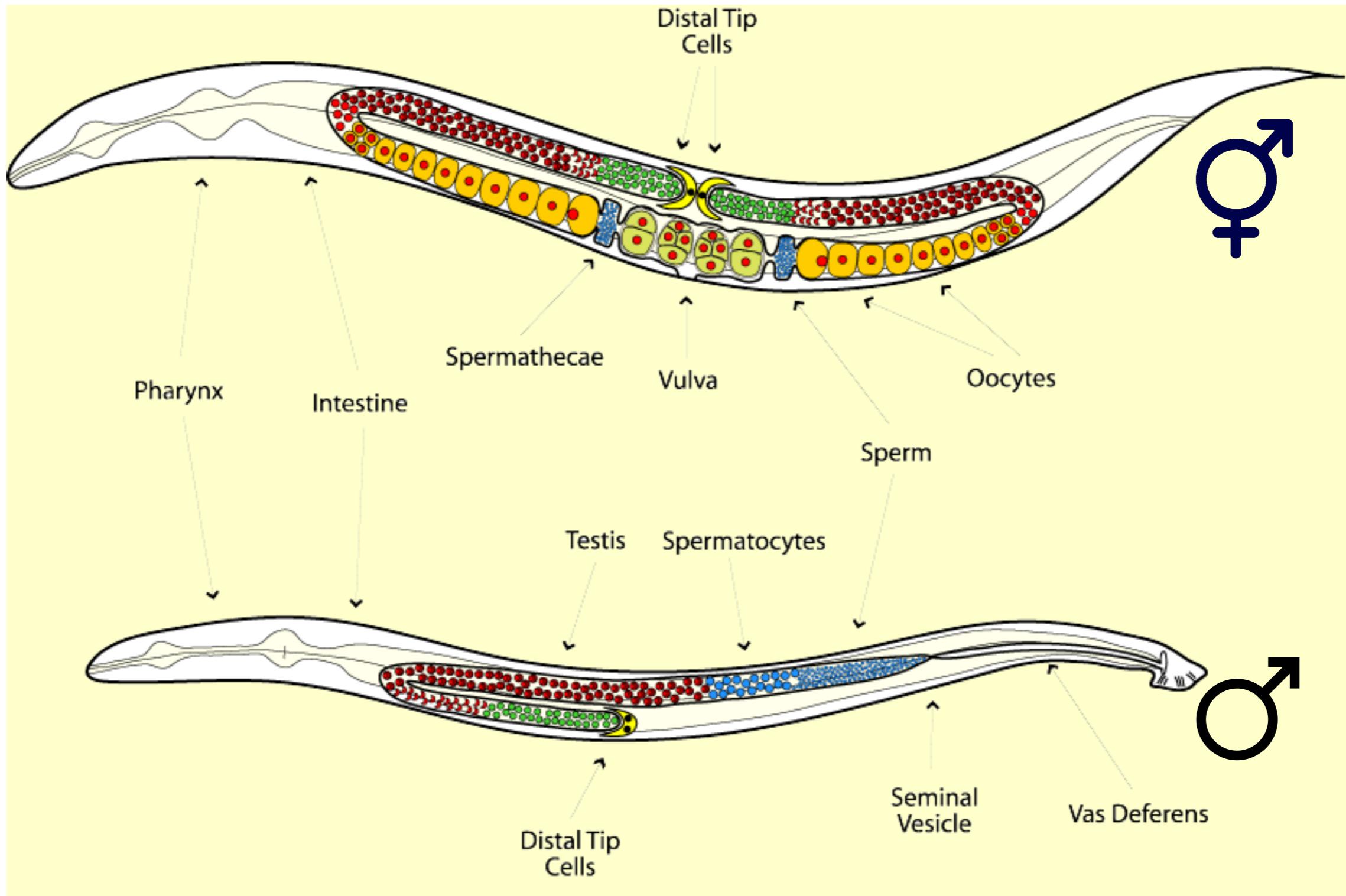
b = brown

E = color

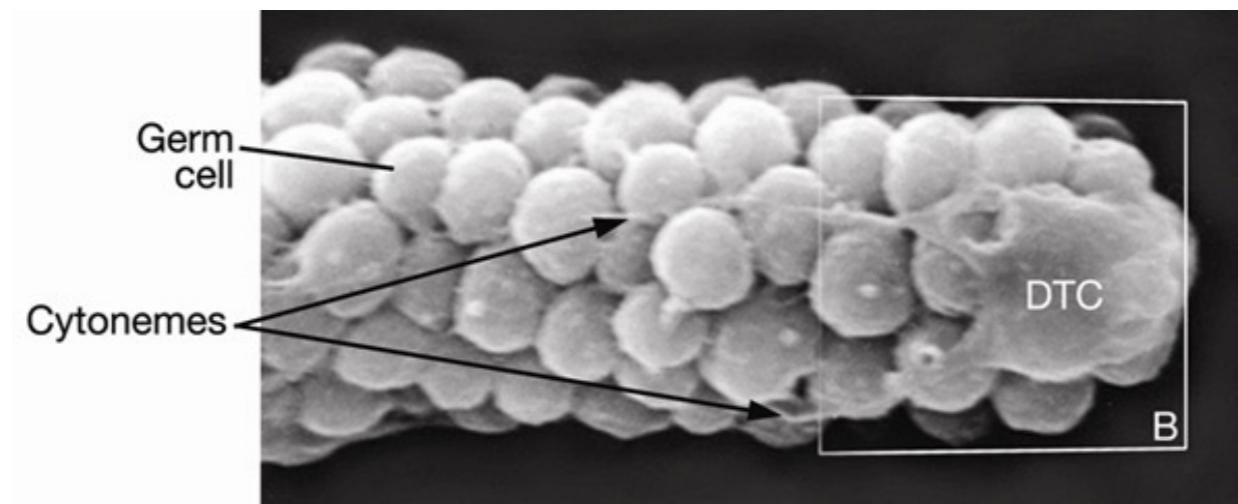
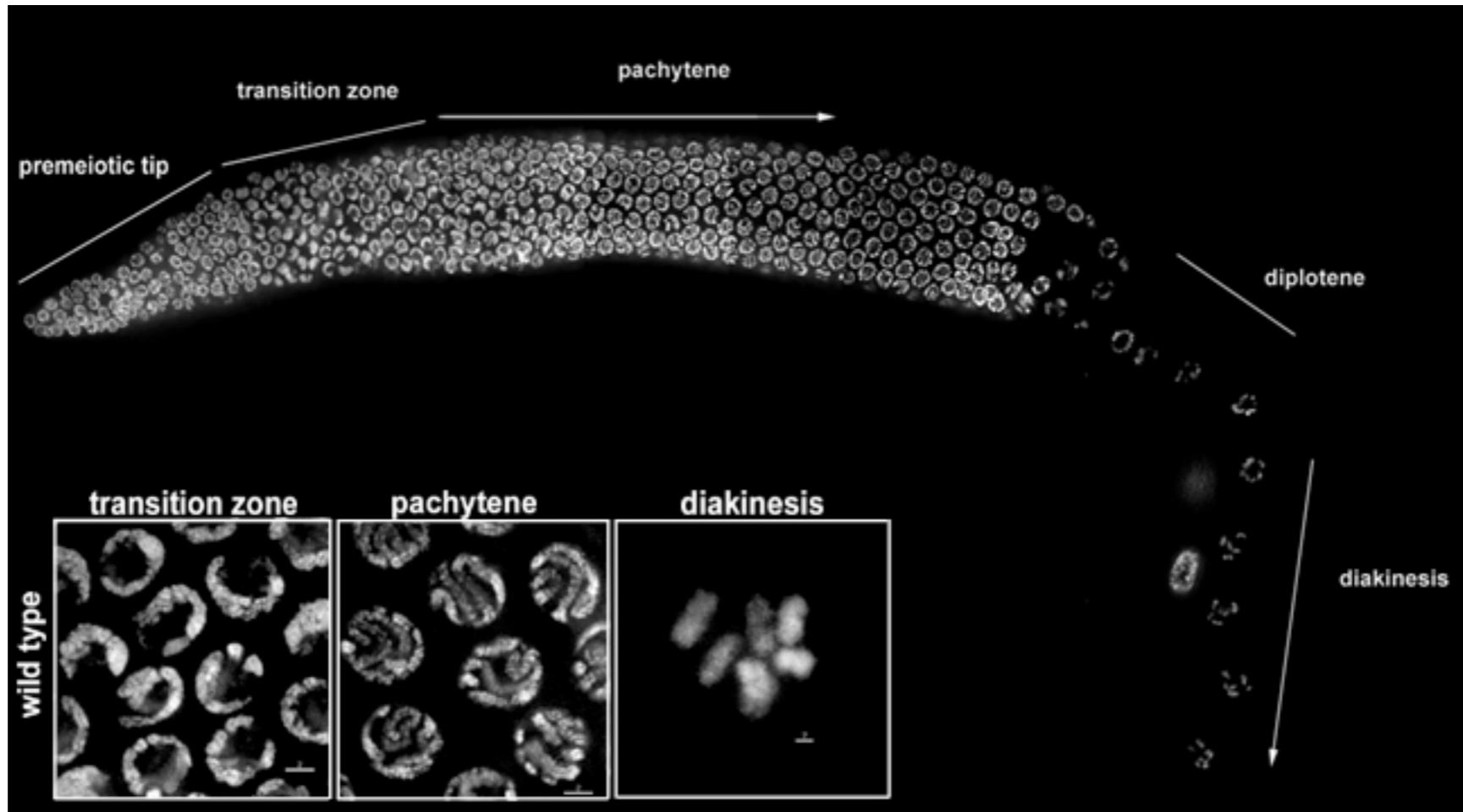
e = no color

9 : 3 : 4

The *C. elegans* germline



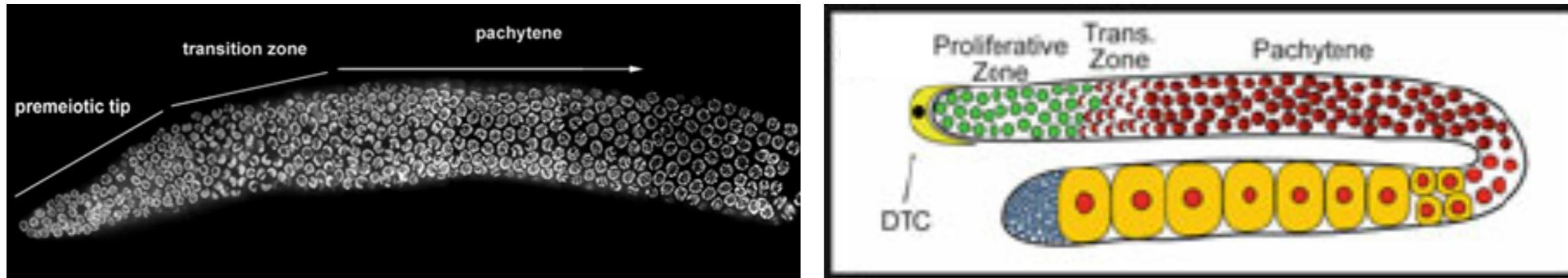
The *C. elegans* germline





Judith Kimble

C. elegans germline mutants

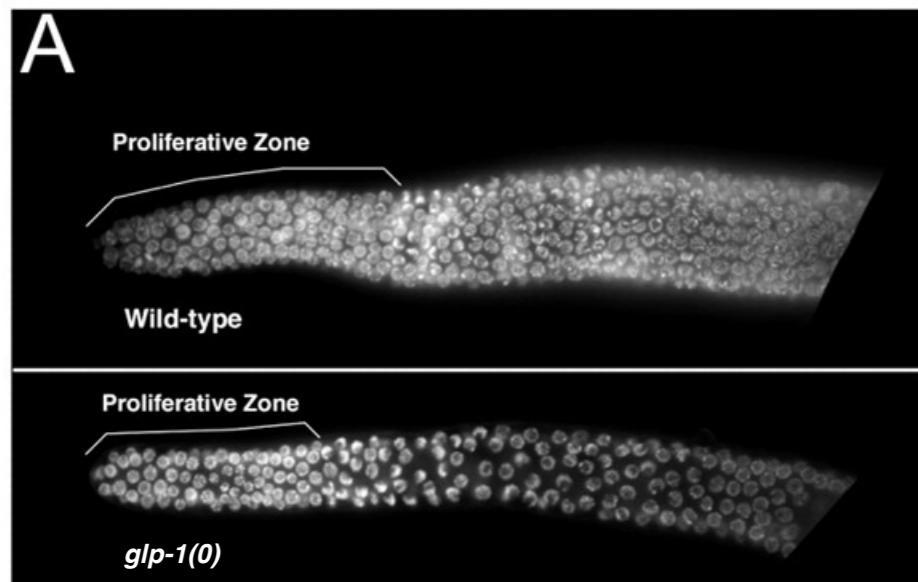


$glp-1(0)$ = all meiotic germ cells

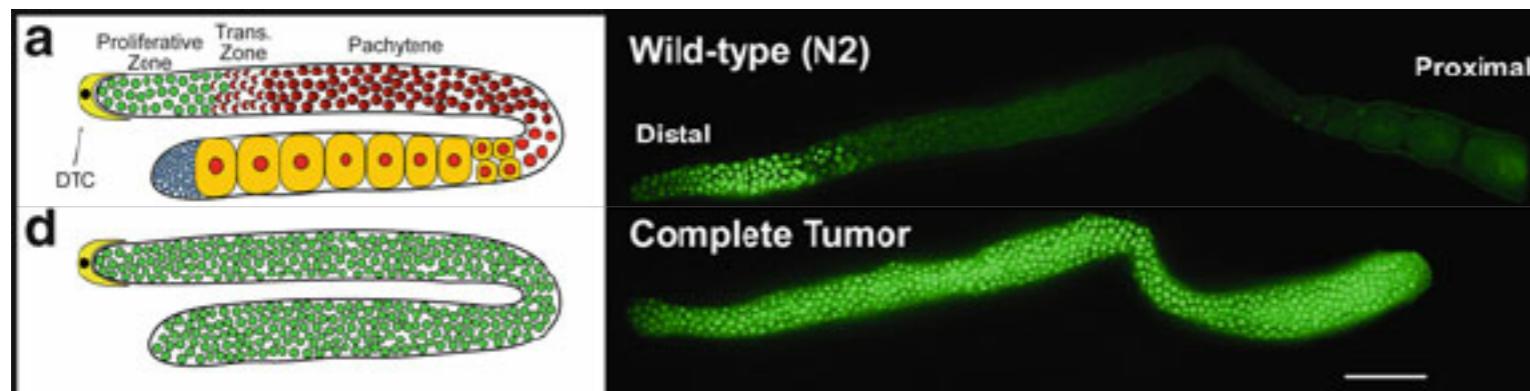
$glp-1(gf)$ = all mitotic germ cells

$glp-1$ → **germ cell proliferation**

C. elegans germline mutants



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



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

glp-1 → germ cell proliferation

C. elegans germline mutants

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

***glp-1* → GSC prolif.**

***lag-2* → GSC prolif.**

***fbf-1* → GSC prolif.**

***gld-1* → GSC prolif.**

How do these genes work together?

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

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

How do these genes work together?

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

***glp-1* → GSC prolif.**

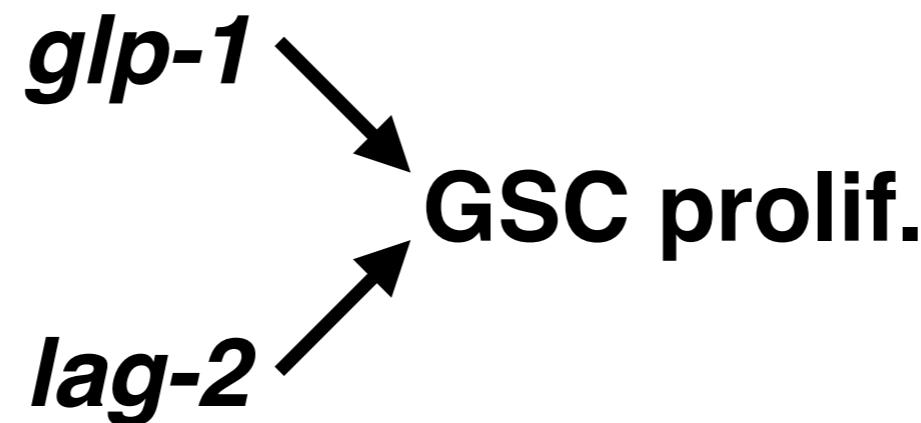
***lag-2* → GSC prolif.**

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
3. 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

How do these genes work together?

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

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How do these genes work together?

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

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

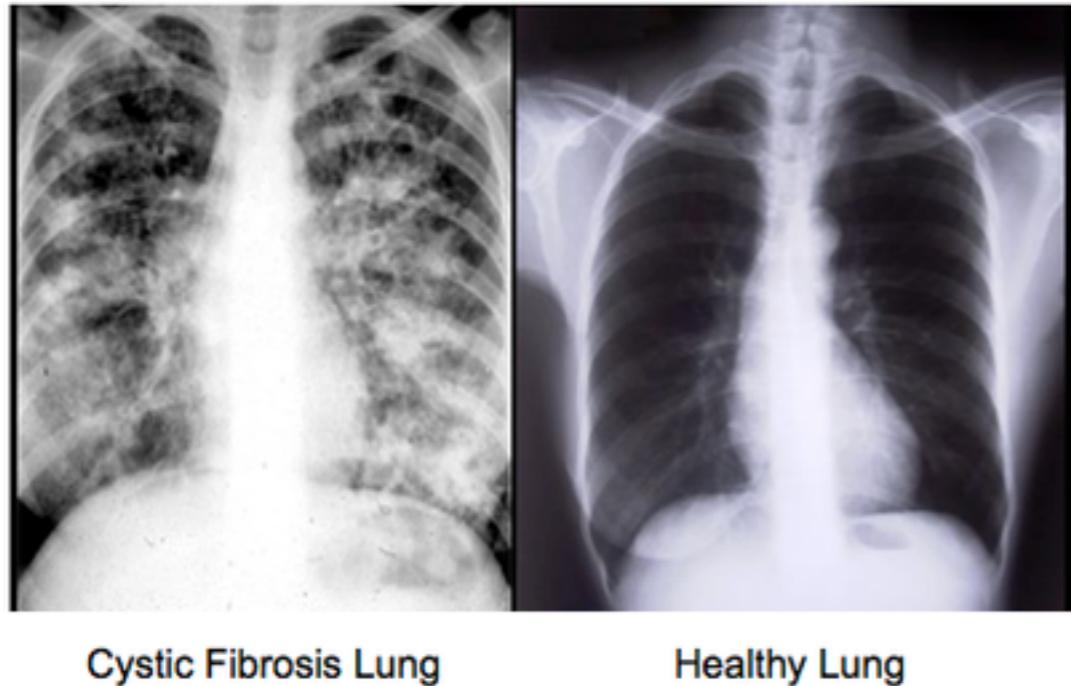
How do these genes work together?

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<i>glp-1(gf); fbf-1(0)</i>	meiotic cells
<i>glp-1(0); gld-1(0)</i>	mitotic cells
<i>fbf-1(0); gld-1(0)</i>	mitotic cells
<i>lag-2(0); fbf-1(0)</i>	meiotic cells
<i>lag-2(0); gld-1(0)</i>	mitotic cells

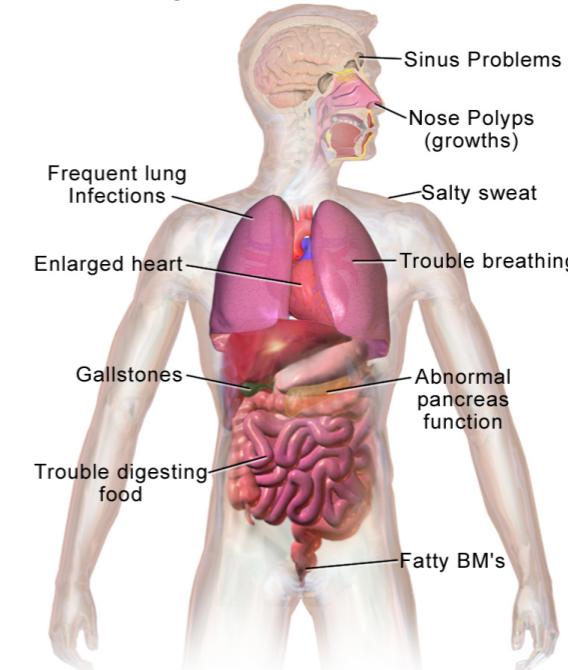
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***fbf-1* → GSC prolif.**
***gld-1* → GSC prolif.**

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

What about cystic fibrosis and today's topic?

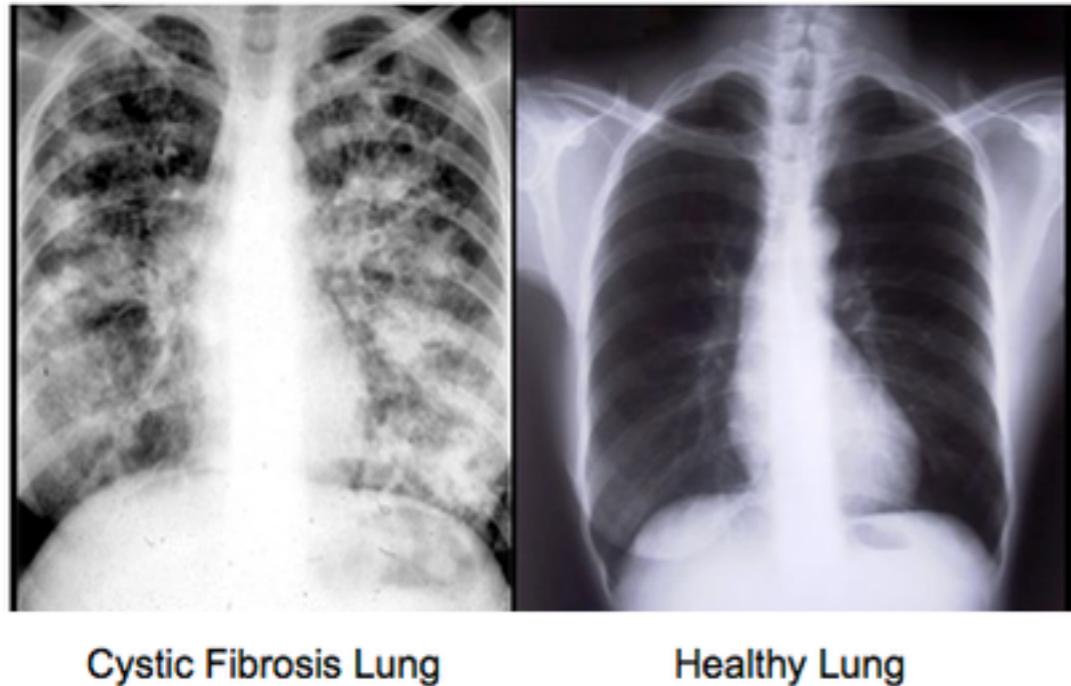


Health Problems with Cystic Fibrosis

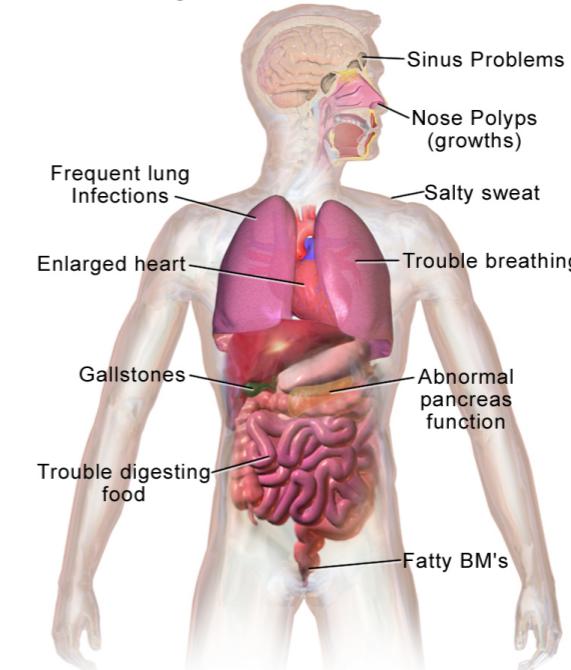


1. Autosomal recessive disorder
2. Not caused by chromosomal aberrations or meiotic NDJ
3. Mapped to chromosome 7
4. Mutations in CF gene are null or hypomorphs
5. Compound heterozygosity (failure to complement) is common

What about cystic fibrosis and today's topic?



Health Problems with Cystic Fibrosis



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