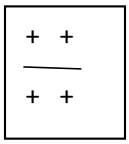
Series 2: Cross Diagrams - Complementation

There are two alleles for each trait in a diploid organism

In *C. elegans* gene symbols are **ALWAYS *italicized.***

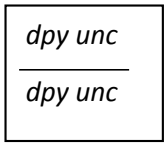
**<u>To represent two different genes on the same chromosome:</u>**

When both genes are wild-type: + is the wild type or non-mutant form of a gene:



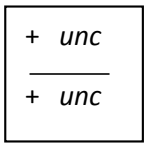

**The phenotype of this worm is wild type**

When both genes are mutant:

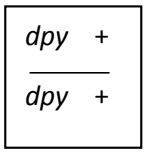



**The phenotype of this worm is double mutant Dpy and Unc phenotype.**

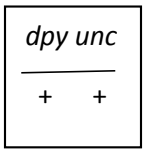
When one gene is wild type and the other mutant:

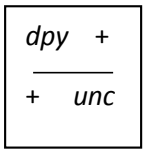



**The phenotype of this worm is Unc**




**The phenotype of this worm is Dpy**

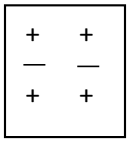



**The phenotype of these worms is wild type**

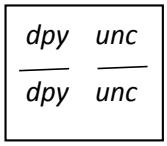
**<u>To represent two different genes on different chromosomes:</u>**

There is noticeable space between the two chromosomes



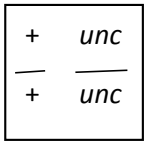

**The phenotype of this worm is wild type**

When both genes are mutant:

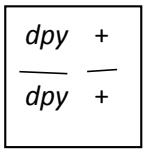



**The phenotype of this worm is double mutant Dpy and Unc.**

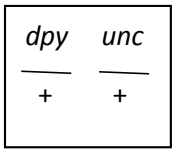
When one gene is wild type and the other mutant:

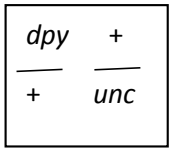



**The phenotype of this worm is Unc**




**The phenotype of this worm is Dpy**




**The phenotype of these worms is wild type**

Mating symbols:

- X – symbolizes mating between two different individuals
- Ⓧ - symbolizes a self cross – when the hermaphrodite worms fertilize their own eggs

NAME: _____

You will use **complementation analysis** to, perhaps, discover the identity of your gene of interest. You may find out whether or not your unknown *dpy* mutation has been previously characterized or is, possibly, a newly discovered functionally significant gene mutation. Complementation may also help you confirm the location of your gene of interest indicated by your linkage testing and mapping work.

There are 31 different genes discovered so far, that when mutated, give a Dpy phenotype. These genes are scattered throughout the genome.

You have identified the chromosome where your *dpy* gene is located from the linkage analysis. We will cross worms with your *dpy* gene of interest to worms with other, known *dpy* genes on this chromosome, to determine whether or not the mutations that give rise to similar Dpy phenotypes are in the same or different *dpy* genes.

**Two possible outcomes:**

1) The *dpy* mutation we are studying and a previously characterized *dpy* mutation fail to rescue the mutant phenotype to wild type (are not complementary) indicating that the two mutations are in the same gene.
2) The *dpy* mutation we are studying and a previously characterized *dpy* mutation are complementary (the mutant phenotype is rescued to wild type) indicating that the two mutations are NOT in the same gene.

Work through the expectations for each cross. Show all work and answer all questions for full credit.

**Cross 1: Creation of heterozygous males with our *dpy* gene**

$$\frac{dpy}{dpy} \quad X \quad \frac{+}{+}$$

_____ _____ List the gametes each parent can produce

_____ Give the genotype of the F1 progeny

_____ Give the phenotype of the F1 progeny

Why must we create heterozygous males?

**Cross 2: Crossing heterozygous *dpy* males with a hermaphrodite with a previously characterized *dpy* mutation in the same *dpy* gene as ours.**

$$\frac{+}{dpy} \quad X \quad \frac{dpy\text{-}k}{dpy\text{-}k}$$

*dpy-k* symbolizes the previously characterized *dpy* mutation

_____
_____ What gametes can this worm make?
_____

_____ _____ Give the genotype of the progeny

_____ _____ Give the phenotype of the progeny

We are specifically looking for the phenotype of the MALE progeny resulting from this cross. WHY?

These *dpy* genes FAIL to complement each other. Explain the concept of failure to rescue the mutant phenotype to wild type.

**Cross 2: Crossing heterozygous *dpy* males with a hermaphrodite with a previously characterized *dpy* mutation on the same chromosome but in a DIFFERENT *dpy* gene from ours.**

| | | | | |
|---|---|---|---|---|
| + + | X | + *dpy-k* | *dpy-k* symbolizes the previously |
| *dpy* + | | + *dpy-k* | characterized *dpy* mutation |
| _____ | | _____ | What gametes can this worm make? |
| _____ | | | |
| _____ | | _____ | Give the genotype of the progeny |
| _____ | | _____ | Give the phenotype of the progeny |

Why might we see some Dpy hermaphrodite progeny resulting from both of these complementation crosses?

These *dpy* genes are complementary.  Explain the concept of rescuing the mutant phenotype to wild type.