

Problem set 5 answers

1. You are given five true-breeding hermaphrodite strains of *C. elegans*, each carrying a dumpy mutation, which makes the animals short and fat. All five strains are known to carry single gene mutations. You cross wild-type males with dumpy hermaphrodites of each strain and obtain F1 progeny of the following phenotypes.

<u>Dpy strain</u>	<u>F1 progeny</u>	
	<u>hermaphrodites</u>	<u>males</u>
P	wt or Dpy	wt
Q	Dpy	Dpy
R	wt or Dpy	Dpy
S	Roller or Dpy	Roller

wt= phenotypically wild-type

Dpy=phenotypically dumpy

Roller= twisted body that causes animals to roll along their longitudinal axis as they move.

For each cross, what is the phenotype of the self progeny?

i. List the recessive mutation(s)

P, R

ii. List the dominant mutation(s)

Q, S

iii. List the incompletely dominant mutation(s)

S

iv. List the mutation(s) that could be sex linked

Q (R is sex linked)

2. The three deficiencies *Df1*, *Df2* and *Df3* remove genes on the *C. elegans* fourth chromosome. In mapping experiments you cross males hemizygous for these three deficiencies (*Df/+*) to hermaphrodites that are doubly mutant for recessive mutations in *dpy-5*, which is on chromosome I, and one of four mutations on chromosome IV: *ced-3*, *ham-1*, *unc-30* and *unc-31*. The phenotypes of the progeny of these crosses are shown in the below.

<u>m parent</u>	<u>h parent</u>			
	<i>dpy-5; ced-3</i>	<i>dpy-5; ham-1</i>	<i>dpy-5; unc-30</i>	<i>dpy-5; unc-31</i>

<i>Df1</i> /+	+	-	-	+
<i>Df2</i> /+	+	+	-	-
<i>Df3</i> /+	-	+	+	+

“+” indicates complementation for the *ced-3*, *ham-1*, *unc-30* or *unc-31* mutations; “-” indicates failure to complement

The *dpy-5* mutation causes a Dumpy phenotype; the *ham-1* mutation causes a cell differentiation defect; the *unc-30* and *unc-31* mutations cause an uncoordinated phenotype

a) In these crosses, why are all of the hermaphrodites made homozygous for the *dpy-5* mutation?

To distinguish self (*dpy-5/dpy-5*) from cross (*dpy-5/+*) progeny.

b) What are the phenotypic classes and sexes of the progeny produced when *Df1* / + **m** are crossed with *dpy-5*, *unc-31* **h**?

Dpy, Unc h

Wild-type (or NonDpy, NonUnc) m and h.

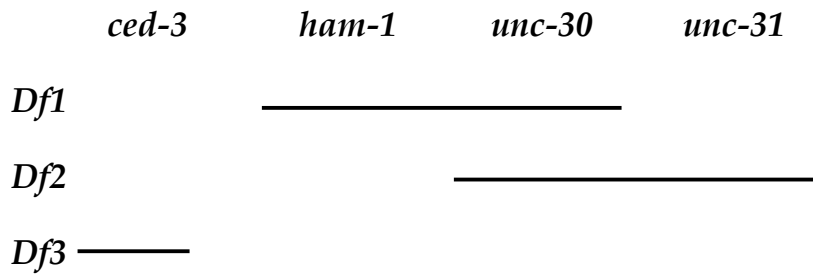
c) What are the phenotypes of the progeny produced when *Df1* / + **m** are crossed with *dpy-5*, *unc-30* **h**?

Dpy, Unc h

Unc (or NonDpy, Unc) m and h

Wild-type (or NonDpy, NonUnc) m and h

d) Draw a map showing the positions of the three deficiencies and the *ced-3*, *ham-1*, *unc-30* and *unc-31* genes.



OR

