Complementation

Complementation is a relationship between mutations that can affect the same phenotype. Through breeding individuals with mutations, looking at phenotypes, and understanding complementation charts one can determine which mutations exist in the same gene and which mutations exist in different genes.

Analogy:

If you buy two identical cookbooks from a store, you can use either one to make food using the recipes. If you were to rip out pages 1-30 of the first cookbook and pages 60-100, you can still make all of the recipes because you have all of the pages when you look at the two cookbooks together. You only need one copy of each recipe to be able to cook the food.

This situation is an analogy for complementary mutations. The mutations exist in different locations (different genes) and thus a cross results in one wildtype (functional) copy of each gene and one mutant (broken) copy of each gene. These mutations are considered non-allelic because they are at a different locus (location) from each other. Such individuals would have a wildtype phenotype.

However, you can imagine the other option for the relationship between mutations. If the mutations are at the same locus, they are considered allelic and mutations of the same gene. A cross of allelic mutations results in offspring with a mutant phenotype. In our cookbook analogy, this would be represented by ripping out pages 1-30 from both cookbooks. Because both cookbooks are missing readable copies of these pages, it is impossible to follow the recipe in these pages to make the food.

Terminology:

It is important to be able to use the words allelic/ non-allelic, complementary/ non-complementary, wildtype phenotype/ mutant phenotype, and same locus/ different loci.

Mutations that exist in the same gene are at the same locus. They are allelic and are non-complementary. These mutations result in a mutant phenotype. A mutant phenotype is denoted by a – sign in a complementation chart.

Mutations that exist in different genes are at different loci. They are non-allelic and complement each other. These mutations result in a wildtype phenotype. A wildtype phenotype is denoted by a + sign in a complementation chart.

Practice:

Fill in the missing information in the chart. Try this first by just using what you remember to quiz yourself, then use your notes and the information above if needed.

Separate or same gene	Same locus or different loci	Allelic or non-allelic	Complementary or non-complementary	Wildtype or mutant phenotype
Mutations are in two separate genes	Different loci	Non-allelic	Complementary	Wildtype phenotype
Same gene	Same locus	Allelic	Non-complementary	Mutant phenotype
Same gene	Same locus	Allelic	Non-complementary	Mutant phenotype
Different genes	Different loci	Non-allelic	Complementary	Wildtype phenotype
Different genes	Different loci	Non-allelic	complementary	Wildtype phenotype

Complementation charts:

Complementation charts are a way to show information about crosses of mutants. Each row represents a strain (a colony of bacteria that are clones of each other) that has a mutation. The columns in a complementation chart represent the same strains as the rows do so you can see the result of a cross.

"+" represents a wildtype phenotype and "–" represents a mutant phenotype.

Because the columns and rows represent the same individuals, only half of the chart contains new information. While some created charts will show the phenotype in all boxes, it is also appropriate to shade out either the top or bottom and only illustrate the crosses' resulting offspring phenotype once.

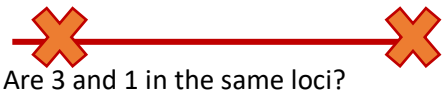
When attempting to understand complementation charts, it can be useful to draw a pseudo gene map to show which mutations are allelic. Crosses with a + indicate wildtype and a different location for those mutations and should be drawn as such on the pseudo gene map. All crosses with a – indicating a mutant phenotype mean those mutations are at the same locus together and so a pseudo gene map should indicate that these mutations are at the same location. Having an image of the location of mutations can allow you to count how many genes are in the complementation relationship and allow you to quickly answer questions about allelic/non-allelic, complementary/non-complementary, and same locus/different loci relationships between mutations.

Practice:

1. Use the complementation chart to answer the following questions.

	1	2	3	4	5
1	-	-	-	-	+
2		-	-	-	-
3			-	-	-
4				-	-
5					-

Space for pseudo gene map (aka which of these genes are in the same loci):
(1,2,3, & 4) 5



a. Are 3 and 1 in the same loci?

Yes

b. Are 2 and 4 complementary?

No

c. How many genes of interest are in this chart?

2. *Hint: This is how many different locations the mutations are at. There can be more than 2.*

d. What would be the phenotype of a cross of 3 and 4?
Mutant phenotype

2. Fill out a complementation chart using the following information and then answer the follow-up questions. 1, 2, and 5 are allelic to each other. 3 and 4 are allelic to each other.

	1	2	3	4	5
1	-	-	+	+	-
2		-	+	+	-
3			-	-	+
4				-	+
5					-

a. Are 3 and 1 in the same loci?
Yes

b. Are 2 and 4 complementary?
Yes

c. Are the mutations of strains 4 and 5 in the same gene?
No

3. Use the complementation chart to answer the following questions.

	1	2	3	4	5	6
1	-	-	+	+	+	-
2		-	+	+	+	-
3			-	+	-	+
4				-	+	+
5					-	+
6						-

Space for pseudo gene map (aka which of these genes are in the same loci):

*Explanation: 1,2,and 6 all are marked as a minus in any cross with each other. This means they are all at the same location. 3 & 5, when crossed together, also result in a minus. This means they are also at the same location. When 4 is crossed with anything besides itself, a + is seen. This means it cannot be at the same location as any of the other mutations.

a. Are 1 and 3 allelic?
   No
b. Are 2 and 4 allelic?
   No
c. Are 3 and 5 allelic?
   Yes
d. Are 1 and 2 complementary?
   Yes
e. Are 2 and 6 complementary?
   No
f. How many genes are involved in the expression of this phenotype?
   3. This is the number of separate locations that these genes are at. If confused, please see the pseudo gene map above.
g. Is the mutation in strain 4 at the same locus as any other mutation? If yes, which ones?
   No, when 4 is crossed with any other strain, a wildtype phenotype is expressed. This means that 4 is complementary and non-allelic to all other mutations and thus does not reside at the same locus as any other mutation.
h. In the lab, you cross strains 2 and 5. Then, you have their offspring reproduce. Out of 80 offspring, how many would you expect to have a mutation? How many would you expect to have a wildtype phenotype?
   A cross of 2 and 5 results in a dihybrid. This individual has one wildtype allele and one mutant allele for two genes of interest. They are heterozygous for both genes.
   The expected ratio for complementation when mating dihybrid parents is a 9:7 ratio where 9/16 individuals have a wildtype phenotype and 7/16 individuals have a mutant phenotype. You should expect the same ratio to apply to this instance of dihybrid parents mating in a complementation gene interaction; approximately 45/80 offspring will have the wildtype phenotype and 35/80 offspring will have a mutant phenotype.