Complementation:

Complementation is a gene interaction where multiple genes can all affect the same phenotype. Two mutations are looked at during a cross to determine if they are located within the same gene or different genes. While only two genes are examined in a cross, there are not any limits placed on how many total genes can all affect the same phenotype.

Complementation has a lot of terminology to describe how mutations are related to each other. Mutations in the same gene are considered to be at the same locus (location). These mutations are considered to be allelic because they are mutations of the same gene. Mutations in different genes are at different loci (locations). These mutations are non-allelic because they are mutations of different genes. A cross of mutant individuals can result in different phenotypes. A mutant phenotype will occur when the mutant alleles the individual inherits are allelic because the individual does not have a wildtype copy of that gene. A wildtype phenotype will occur when the mutant alleles an individual inherits are non-allelic because the individual has one wildtype copy and one mutant copy of each of the two genes that have mutations. One wildtype allele for each gene in complementation is enough to produce a wildtype phenotype meaning the wildtype allele is dominant and the genes are haplosufficient.

To summarize, non-allelic mutations exist at different loci, are complementary, and when crossed result in a wildtype phenotype. Allelic mutations exist at the same locus, are non-complementary, and when crossed result in a mutant phenotype.

Complementation charts can be used to understand the relationship between mutations. These charts have all of the strains/ individuals along the left column and also the top row. The interior boxes represent the offspring phenotype from each cross. A plus sign indicates wildtype phenotype and a minus sign indicates mutant phenotype.

Learning Objectives:

- Correctly use terminology about complementation including but not limited to loci, allelic or non-allelic, complementary or non-complementary relationships between mutations.
- Understand and be able to explain why a cross of allelic mutations results in a mutant phenotype.
- Be able to understand, make, and use a complementation chart to understand the nature of mutations.
- Understand how complementation differs from other genotype to phenotype relationships in genetics.
- Be able to identify complementation and apply its ratio to explanations and offspring data.

Order of Activities:

1. Read this page explaining complementation testing https://www.ndsu.edu/pubweb/~mcclean/plsc431/mutation/mutation5.htm

2. Test yourself by completing the corresponding worksheet for this material. Attempt to first complete this on your own, then pair up with a partner or group to discuss when possible. There is an answer key provided so you can check your work and read through all explanations for the questions. Any questions you get wrong or confused about you should attempt to explain why the answer is correct and then complete again after you finish the activities in this guide.
3. After reviewing any topic, it is a good idea to have a metacognition check. Ask yourself the following questions:

    - What are my emotional responses to learning this material? Which material am I frustrated with and need aid in understanding?
    - What difficulties have I had with the learning tasks? What specific tasks will I do to master this content?
    - Do I understand all of the learning goals? Can I explain each of them out loud to someone clearly and concisely?
    - How is what I learned related to other things I have learned in this class? How is it related to other classes, my career, and my life?

4. If you would like to have more aid in learning this material, please reach out. There are numerous individuals who want to help you feel confident in your understanding. If your course has learning assistants or teaching assistant(s), you should reach out to them to review concepts you want to learn more about. Your professor is also a great resource to go to when you do not understand a topic. You can study with your peers or receive academic support through the LRC as well. If you would like help identifying how to receive the support you need, do not hesitate to contact the CU Denver Learning Resources Center at LRC@ucdenver.edu or stop by our front desk in the learning commons building.
5. Challenge: Think about how complementation compares to other ratios you have learned about. Complete the chart found here to organize your notes and have a deeper understanding of how the ratios compare to each other. Reminder, you may see problems where the type of gene interaction is not explicitly stated. For such problems, you will have to determine the gene interaction type to fully and correctly answer the question. If you need help, view table 4 of this website. https://www.nature.com/scitable/topicpage/epistasis-gene-interaction-and-phenotype-effects-460/# This features more types of ratios than you may need for your course.