

**Biology 423L**

**Sept. 15/16**

**Mouse Coat Colors: Genetic dissection of pigment pathways**

Report due Sept. 29/30.

**Readings:** Epistasis: Hartwell Chapter 3 pp. 56-71.

**Objectives:** 1) To introduce you to mice as model organisms for genetics.  
2) To use the inheritance of variation in coat color to reveal genetic pathways for pigment production.

**Introduction:** Mice fit the criteria for genetic model organisms because they are small and relatively easy to keep in a controlled place, they breed easily and have large numbers of offspring. Because they are mammals, they share more physiological pathways with humans than the other genetic models we will study in this course. Therefore, they are common models for studies of human disease. In this lab we will use natural variation in coat color in mice as a tool to investigate the genetic pathways for pigment production in mammals. We will be given several examples of mice with different coat colors. We will consider informative genetic crosses between mice with different pigmentation. From analysis of the inheritance of coat color mutations through the F1 and F2 generations, we will determine the order of genes in the pathway for dark pigment production.

**Materials and methods:**

Mice

1. Black or brown
2. Agouti
3. Albino

**Report:**

**Abstract as usual**

**Introduction:** State the goal of this experiment in your own words. Discuss what the dark pigment of mice is and how it is produced. Discuss the meaning of epistasis and how it can be used to determine the order of gene products in a biochemical pathway.

**Results:** Write down the results of all the demonstration crosses. Write down the phenotype(s) of the parents, the ratios of phenotypes in the F1 animals and the ratios of phenotypes F2 animals.

The first 4 crosses with the albino1 and albino2 mice will give you all the information you need to decide what are the genotypes of the albino1, albino2, agouti and black mice for the genes A, B and C. You were told which alleles are dominant at each locus.

One goal is to figure out the genotypes of the albino1 and albino2 mice. I would like more than just the genotypes in the report. In the results section of the report, explain what you learn from each cross about the genotypes of the parents in the cross so it is clear how you figured out the albino1 and albino2 genotypes.

The second goal is to determine the order of the genes in the pathway. The position of one gene is clear. Explain your conclusions in the discussion section.

The third goal is to explain the results of the crosses with waved mutants. In the results section, write out the crosses and the results that were presented. Which allele is dominant, which is recessive. Do they complement? Discuss an explanation for the results of the cross between waved1 and waved 2 in the discussion section (see below).

**Discussion:** What is the genetic pathway for the coat color genes presented in the exercise? Make a diagram. Look up the regulatory and biochemical pathways for melanin production in mice. Explain the role of the products made by genes A B and C in the melanin pathway. Please cite the place where you found the information. Use a standard citation in the discussion section and write out the full reference at the end of the report. When you discuss published work, cite the paper. Do the citation in the first sentence in which the study is mentioned. Eg. Seven large families with a high incidence of cystic fibrosis were surveyed for DNA markers linked to the disease (Smith et al., 1987).

References: at the end of the section: in alphabetical order

Smith J, Jones, P.A. and White, K. 1987 Family studies map cystic fibrosis to Chromosome 7 *Genetics* 130: 147-156. Use the journal "Cell" as an example of how to format the paper, the citations and the references Cite the references where you found the information.

In the discussion section, give me a reasonable explanation for the result of the cross between waved1 and waved2. We know these alleles are mutations in the same gene because the mutant alleles have been cloned. However, they complement when two homozygous mutants are crossed leading to a w1/w2 heterozygote. How could that occur? Please explain your reasoning. I am not asking you to go to research papers to find out the published reason. I want you to think about how this could happen and we will accept any reasonable explanation. I will present the published reason after you hand in your lab reports.