LABORATORY 7. *Drosophila* CLASS DATA REVIEW: GENE MAPPING AND HYPOTHESES TESTING

LEARNING OUTCOMES

At the end of this lab practice, students should be able to:

- Determine the genetics model of inheritance of four genes based on real cross data.
- Propose a scientific hypothesis (dihybrid cross) and statistically test its validity.
- Map three genes on a chromosome based on real cross data.

INTRODUCTION

The main aim of this lab exercise is to analyze and discuss the outcome of a particular cross and its further generations (**F_1** and **F_2**). Additionally, students will get familiar and comfortable at solving genetics problems and analyzing the different epistatic interactions between genes.

Based on the previous labs (#1, 2, 3 and 4), students should be familiar on the methods and analysis to determine the genetics mode of inheritance of different mutations by using the phenotypic classes and their ratios on the **F_1** and **F_2** generations. Additionally, students must be familiar with the potential epistatic interactions between some genes related with eye color variation (lab # 5). Let's use this previous knowledge and new skills to answer questions regarding your real-case genetics experiment performed in this lab.

You have been analyzing a *Drosophila* cross between **P_1 yellow body, white eyes, and miniature wing females** with a **P_2 sepia eyes males** (both **homozygous** lines). During a period of four weeks, you collected and recorded **F_1** and **F_2** data that will allow you to test some hypotheses about the inheritance and to map three genes on a chromosome.

Please **read each paragraph and question carefully.** Your understanding of the concepts is key for your success in your assignments.

X

P_1: Females (yellow body, white eyes, miniature wing mutant)

P_2: Males (sepia eyes)

Genome Wide Association Studies

Three-point mapping and genome-wide association studies (**GWAS**) both aim to identify genomic regions associated with a trait. In three-point mapping, researchers analyze recombination events in controlled crosses to determine the location of a gene relative to known markers. In contrast, **GWAS examines natural populations** and tests whether specific SNPs (Single Nucleotide Polymorphism) occur more frequently in individuals with a particular phenotype. Although the approaches differ, both rely on the same principle: genetic markers located close to a causal gene tend to be inherited together because recombination between them is infrequent. As a result, both methods can identify genomic regions linked to a trait, helping researchers narrow down the location of genes influencing phenotypes.

Procedure

The tables indicating the outcome (i.e., offspring number) of the cross performed **in your lab section** are available in front of the lab.

Please analyze those results carefully, as they are the basis to complete the lab assignment. To facilitate your understanding of the concepts and solving your assignment, please consider the following key aspects:

- The cross involves **four** genes. **Two** different genes are responsible for **white** and **sepia** eyes.

- Identify the location of genes on the chromosomes. That is, take into consideration sex-linked vs. autosomal genes. The F_1 results will provide you hints in this regard.

- Due to an epistatic interaction, the F_2 results of this cross yields 12 phenotypic classes (instead 16 classes).

-For the three-point chromosome mapping of yellow, white, and miniature, you should add up some of the **F_2** phenotypic classes together. That is, you should end up with a total of eight (8) phenotypic classes (instead of 12). Parental offspring classes (n=2), single recombinant classes (n=4) and double recombinant classes (n=2).

For the gene mapping and X2 test, you will use the **"Three Point Mapping"** virtual tool available on Canvas or here (www.ampossot.com/3point). Follow the indications on the app, complete the tables and perform your analysis.

During the second part of the lab, you will analyze data from a simulated GWAS experiment in a human population. To do so, you will use the **"GWAS virtual tool"** available at www.ampossot.com/gwas . Follow the indications in the lab manual to complete the analysis.

IMPORTANT: FILL THE TABLES WITH THE DATA PROVIDED BY YOUR TAs

Your lab section (e.g., Tuesday morning): ____

Parental flies (homozygous, pure lines)

P_1: Females, yellow body, white eyes, miniature wings.
P_2: Males, sepia eyes

F_1 results

	Males	**Females**	**Total**
	Yellow, white, miniature	Wild-type	
Total			

F_2 results

Phenotype	Sex	Amount	Total
WT	F		
	M		
y, w, m	F		
	M		
y	F		
	M		
w, m	F		
	M		
y, w	F		
	M		
m	F		
	M		
w	F		
	M		
y, m	F		
	M		
se	F		
	M		
y, se	F		
	M		
m, se	F		
	M		
y, m, se	F		
	M		