

Take-out # 2
Due Friday 1/27 at beginning of class

1. Alleles at the *Blp* locus in barley determine if the mature inflorescence (the “head”) is black or white. See <http://barleyworld.org/oregonwolfe/images> for pictures of the Oregon Wolfe Barley (OWB) populations. For this assignment, choose the n = 82 *Hordeum bulbosum*-derived doubled haploid population. Note: The OWB DH progeny are not numbered consecutively, but there are 82 of them.
 - A. Draw (or use Excel to make) a frequency distribution showing the number of *BlpBlp* (black-headed) and *blpblp* (white-headed) doubled haploid progeny. Please attach on a separate page. In your histogram, be sure to indicate the phenotype of each of the parents.
 - B. Which term best describes this frequency distribution?
 - a. Discontinuous
 - b. Continuous
 - C. How many loci do you hypothesize are responsible for determining head color in this population?
 - D. Calculate a chi square to test your hypothesis regarding the number of loci that determine head color in this population – fill in the following table. Note: Parents are NOT used for calculating the chi square test.

Phenotype	# Observed (O)	# Expected (E)	O - E	(O-E) ² /E
Totals	82	82		

- E. Calculated $X^2 = \underline{\hspace{2cm}}$; df = $\underline{\hspace{2cm}}$; probability = $\underline{\hspace{2cm}}$
- F. Do you accept or reject your hypothesis?
- G. How many alleles are segregating at the locus (or each of the loci) that you have determined are responsible for head color?

2.

	Theobroma	Fragaria	Your favorite plant (common name; Genus, species)
Describe how having a complete genome sequence will facilitate breeding for one specific trait in each of the three plants.			
Describe who funded the genome sequencing of Theobroma and Fragaria. Who do you think should fund genome sequencing of your favorite plant, and why?			
Give the genome formula for each of the three plants ($2n = \underline{\quad}$ $X = \underline{\quad}$)			
Give the genome size (in Mb at the n level) for each of the three plants.			
Estimate the number of genes (at the n level) for each of the three plants.			