**Homework # 2**

The length of the barley “spike” (inflorescence) may be under genetic control. Your assignment is to determine if spike length shows qualitative (Mendelian) inheritance or quantitative inheritance that defies simple Mendelian analysis.

Digital images of spikes in the Oregon Wolfe Barley population are shown at <http://barleyworld.org/oregonwolfe/images>. Please forgive the advertisements - collateral damage from using flickr.

* + - For this assignment, choose the n = 82 *Hordeum bulbosum*-derived doubled haploid (DH) population – the “OWB Hb Phenotypes” hyperlink. These doubled haploids are not numbered consecutively, but there are 82 of them.
    - Plan ahead and take a few minutes to become familiar with viewing these images.
    - Note the “ruler” in each image. You can use this to determine the length of the spike. When measuring the spike length, measure from the first to the last floret - do not count stem or awn. Some spikes are curved – just ignore the curve and assume length is from base to tip of the spike. Keep it simple – express your measurement to the nearest whole centimeter. See the data scoring sheet at the end of this assignment for examples.
    - You assignment is to measure the head length of each doubled haploid, develop a hypothesis for the inheritance of spike length, test your hypothesis, and interpret the results.

1. Fill in the attached scoring sheet (appended to this assignment). Doubled haploid (DH) numbers are provided, spike lengths are given for the parents and first eight DHs.
2. Draw (or use Excel to make) a frequency distribution showing spike length. In your histogram, be sure to indicate the phenotype of each of the parents.
3. Which term best describes this frequency distribution?
   1. Qualitative (Discontinuous)
   2. Quantitative (Continuous)
4. Mendel (and many after him) was able to classify some traits as ‘qualitative” even though they measured the traits using a quantitative scale. The key thing is to describe, in sufficient detail, the rationale behind the classification and the exact way that it was done.
   1. Follow their examples, and classify spike length as “long” and “short”.
   2. Briefly describe your criteria for “short” and for “long”
5. How many loci do you hypothesize are responsible for determining spike length in this population?
6. Calculate a chi square to test your hypothesis regarding the number of loci that determine spike length 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 |
| Short |  |  |  |  |
| Long |  |  |  |  |
| Totals |  |  |  |  |

1. Calculated X2 = \_\_\_\_\_\_\_ ; df = \_\_\_; probability = \_\_\_\_
2. Do you accept or reject your hypothesis?
3. How many alleles are segregating at the locus that you have determined are responsible for spike length in this population?

Spike length data sheet for the OWB *Hordeum bulbosum* (Hb) population

|  |  |
| --- | --- |
| OWB doubled haploid # | Length |
| Dominant (Dom) parent | 3 |
| Recessive (Rec) parent | 12 |
| 2 | 4 |
| 3 | 5 |
| 4 | 8 |
| 6 | 6 |
| 7 | 10 |
| 8 | 4 |
| 9 | 12 |
| 10 | 3 |
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