The Use of Pedigrees in the Study of Human Genetics

Objectives:
1. Understand how pedigrees can be used to study genetics.
2. Understand common genetic terms: recessive, dominant, heterozygote, homozygote, allele, gene, phenotype, genotype

I. Introduction

It is often valuable to know whether or not a particular trait has a genetic basis, and if it does, the extent of its genetic basis. However, it’s not easy to know what specific genes an organism has in its DNA.

Scientists have used domesticated plants and animals, and fruit flies, and various other organisms to study the genetic basis of traits, and gene transmission. With organisms like this, hypotheses can be formulated, and controlled breeding experiments can be done to test those hypotheses. Long before modern DNA technology was developed, it was possible to know whether some traits had a genetic basis.

The peas used by Mendel and the fruit flies used by Morgan and others are relatively easy to work with as far as breeding experiments go. Humans do not make such convenient research animals. First, it is obviously not acceptable to carry out controlled breeding experiments with humans. Also, the long generation times and the relatively few offspring per parent are not convenient to creating large sample sizes.

However, there is a powerful incentive to understand the genetics of humans. For instance, understanding the genetic basis of particular diseases is worthwhile. The genetic basis of human traits can be discovered through analyzing the results of matings that have already occurred, i.e. through pedigree analysis. Pedigrees are family trees which show the parents and offspring across generations, as well as who possessed particular traits.

Pedigrees of individual families are used by genetic counselors, to aid them in providing information to families who may be at risk for various genetic conditions. Members of the Church of Jesus Christ of Latter Day Saints have kept extensive genealogies which have been very useful in studying human genetics. Their records were useful in finding the location (chromosome 17) of a gene (BRCA1) that is thought to be the cause of 5 - 10% of all human breast cancers. Such genealogical databases (like those kept by the Huntsman Cancer Institute) continue to be used in medical research.

In this lab we are going to see how people do research on genes in humans. Specifically, we are going to try to find out if a particular trait is the product of dominant or recessive alleles.

Before looking at your particular pedigree, do a couple of practice problems. Some of the symbols that are conventionally used in pedigrees are shown in Figure 1. Review these, and then do the practice problems which follow.
II. Practice

A. Inferring parents from offspring.

There's a gene that controls whether hair, even the slightest amount, grows on the middle phalange of a digit on the hand. Mid-digital hair is caused by a dominant allele; absence of hair is caused by a recessive allele.

Filled in = hairy phenotype; open = not hairy phenotype

In this pedigree, the grandfather could be HH or Hh, so there are 2 possible crosses occurring.

HH X hh \( \rightarrow \) all ____ (phenotype: ________) offspring. Could this be his genotype? ________

Hh X hh \( \rightarrow \) expected: 1/2 Hh (hairy) and 1/2 hh (nonhairy) offspring. Could Hh be the genotype of the grandfather? ___________
Is one genotype more likely than the other? 

What if he had 5 kids, all with mid-digital hair? 

This pedigree also shows how a trait can "skip generations." But the gene doesn’t skip, only the phenotype does. Everybody is carrying H or h alleles.

**B. How do we know if a trait is dominant or recessive?**

**Example:** We can test ability to taste PTC with the pedigrees provided. (You may taste some PTC paper to see whether or not you have this trait.)

i. On the pedigree, dark equals taster,

ii. We'll test two hypotheses: 1) taste is caused by a dominant allele and 2) taste is caused by a recessive allele. First, Hypothesis 1, we'll test "taste is recessive." TT or Tt = not a taster, tt = is a taster. Write all possible genotypes beside each person in the pedigree.

Hypothesis 1: ■ ■ is a recessive trait. TT or Tt = not a taster, tt = is a taster.

iii. Now go through and see which possible genotypes you can eliminate. Is the above pedigree possible, if tasting is caused by a recessive allele? 

iv. You can't automatically conclude that the other hypothesis is right, so test Hypothesis 2.
Hypothesis 2: is a dominant trait or, TT or Tt = taster, tt = no taste.

III. Now do your own pedigree. With each pedigree, you study only one trait at a time

A. Build your pedigree
1. Make a line dividing paper in half.
2. Draw your pedigree in top half. Draw it big with spaces to be able to write.
Just include the people for whom you have survey data. You may want to have your instructor check it for accuracy. People without pedigrees, help out in this process.
3. Blacken in circle and squares for the first trait you wish to follow.
4. Copy the same thing onto the bottom half of the page.

Go to the other characters: for each trait, you need a separate page, with 2 pedigrees.

If you do not have a pedigree, your instructor may provide you with one.

B. Individually analyze your pedigree, as you did in Problem B, above. Start with widow's peak.

Finish both charts for each trait.
  a. See whether or not either hypothesis can be rejected.
  b. Often neither will be, but for your report you will study 3-4 families of your group and maybe one will allow you to reject one of the hypotheses.
  c. Sometimes both hypotheses may be rejected. In that case, question your data.
C. **Group analyze all pedigrees.**
   1. Exchange pedigrees, check out your partners' work.

   2. Once you are sure all are accurate, decide what hypothesis is best supported by the SET of pedigrees. Because of the small sample sizes involved, one pedigree is often ambiguous. You may accept both or reject both hypotheses. You may need to look at several pedigrees to make a final decision.

   3. If you have conflicting results, ask
      - What crosses are most likely?
      - Use reasoning we used in pedigree example.
      - What data, if any, is suspicious?
      - What data would be more likely to be wrong?

   4. Write a paragraph saying which hypothesis is more likely and explaining your reasons in detail.

A **special note about eye color.** Not all traits are simply caused by one gene with a dominant allele and a recessive allele. Eye color is actually due to multiple genes. One allele causes pigment in the iris (so non-blue); the other allele does not cause the production of pigment (an iris without pigment is blue). Multiple alleles determine the amount of pigment in the eye so irises may vary from gray-green-brown. To follow this trait on the pedigree, record it as blue and non-blue.

**References:**

