

Investigation

A Study of Human Gene Frequencies:

All of us have genes in pairs. We received one gene of each pair from each of our parents. For example, whether or not you have lots of room for earrings is determined by the pair of genes you received from your parents. In the case of earlobes, you can see below that you may inherit either attached or unattached earlobes.

Earlobes

Free ear lobes (dominant trait) vs. **Attached Earlobes** (recessive trait)

Free earlobes are those that hang below the point of attachment to the head.



Free Earlobes

Attached ear lobes are attached directly to the side of the head.



Attached Earlobes

Pair up with another student and look at each other's earlobes. Once that is done, count all the students in your class who have the dominant gene (free earlobes, and all of those with the recessive attached earlobes. If a student has attached earlobes, then they have two recessive genes, often represented by two small letters. Let us use aa for attached earlobes, and a A for unattached earlobes. Why can't we just write two big A's for a person with attached earlobes? (Remember, everyone has two parents!) Is it possible for someone to have one big A and one little a? How could that happen?

Photos from Our Lady of Peace Young Scientist Club. mkiss.star64.com/traits.html

In a large population, if you have two possible genes for earlobes, either attached or unattached, and if the attached only shows when there are two of them, what are the chances of a person having attached earlobes? Here are the possible combinations: AA, Aa, aA, or aa. In the first case, the gene given by each parent to the child is a "A". In the second case, the mother gives the child a "A" and the father gives the child a "a". In the third case, the father gives the child a "A", while the mother provides a "a". In the fourth case, both parents provide a "a". Therefore, the chances of getting a "AA", a "Aa", or a "aA" are .75 or 75%, while the chances of getting a "aa" are only 25%.

Count as many students in your school as you can.

Once you are done, you should make a data table like the one below:

Column I	Column II	Column III	Column IV
Name of trait	Number with trait	Frequency of Trait (Column II ÷ total)	Expected Frequency (3 to 1)
aa Attached Earlobes			.25
AA or Aa Unattached Earlobes			.75
Total Number Counted			1.00

Now you have the gene frequency of a population. If the numbers counted were large, if no one moves in or out of the school, if no genes are mutated or none of the group is selected out by disease or disaster, and mating is random in the community, then the population frequencies should stay the same year after year. How likely do you think this is? Any frequency change means that evolution, or change over time, is occurring.

The Big Question

Now, the big question. Can we relate all the studies we have done and read about to our own human population? Do we follow the rules that govern other organisms?

Obviously, we do not go out and mark and recapture humans for study unless we do it as a science experiment as you may have done earlier.

We can, however, use the Hardy-Weinberg equations to see if the gene frequencies of human populations are changing. Here is an example of a recent study.

The data below, collected during the 1940s and 1950s, showed the relationship between the percentage of the population found to have a sickling gene (i.e., individuals with one sickle cell gene and one normal gene) and the frequency of individuals with sickle cell disease, meaning they have two genes for the disease):

Location	%Sickle-cell Trait	% Sickle-cell Disease
Africa	20	2
United States*	6	4

<http://www.nslc.wustl.edu/courses/Bio296A/allen/sicklecell/part3/biogeography.html>