

Video Tutorial 8.1: Solving a gene interaction problem

One of the earliest examples of gene interactions was found by the British geneticists Bateson and Punnett more than a century ago. They noticed that different pure breeds of chickens have different shaped combs, which they referred to as single, rose, and pea. You can see these phenotypes in this picture from Bateson's book *Mendel's Principles of Heredity*, published in 1913. When pure breeds of chickens with a rose comb were crossed to pure breeds with a pea comb, all of the F_1 chickens had a different shape comb, which they referred to as walnut. The F_1 walnut-combed chickens were mated among themselves to produce an F_2 generation. Let's diagram this cross.

Rose is crossed with pea, and all of the F_1 are walnut.

When these walnut F_1 chickens were mated among themselves, the F_2 had 113 walnut, 39 pea, 36 rose, and 12 were a different phenotype altogether called single.

Using these data, let's work through the questions below, taken from Problem 8-23 in the book.

- a) First, what is the evidence that these phenotypes are due to the interactions of two genes rather than to multiple alleles at a single locus?
- b) Explain how these phenotypic ratios arose by representing the genotype responsible for each phenotype.

So let's think about whether this is one gene or two genes.

Since pea comb and rose comb are true-breeding traits, my immediate assumption is that pea comb and rose comb are both homozygotes for some allele or some gene and that walnut comb is the heterozygote between the two. Let's write this out as if it is one gene or it is two genes. One thing we notice is that we have four phenotypes here. The F_2 includes single comb, which did not appear in previous generations, suggesting that there is also a genotype that was not present in the previous generations.

Let's write it

If it is one gene, we can write it like this. [Could make this just appear—not need to show the writing process unless you think it helps.]

If it is two genes, one parent could be like this, which we will call pea. The other parent could be like this, which we will call rose. We could make designate either gene for the phenotypes, but the important thing is that the two parents were homozygous dominant for one and homozygous recessive for the other. So in each case, they would be true breeding but they would be homozygous for different genes. And the F_1 would be heterozygous for both.

So in either case, one or two genes, we can get the phenotype seen in the F_1 generation. But it is the F_2 that we need to look at in each case. If it is one gene, we will see this outcome in the F_2 , but there are only three possible phenotypes.

In this case, with two genes, we would expect 9/16 to have a dominant allele for each of the genes, and we said that was walnut. We would expect 3/16 to be homozygous recessive for one gene and have the dominant allele for the other. We said that one was pea and this one is rose. Then we have 1/16 that is homozygous recessive for both genes. That would give us an additional genotype that we have not seen before, and that would be the single phenotype.

So I think that this is going to be two genes. Here is the most likely scenario. It is two genes, with pea homozygous recessive for one and homozygous dominant for the other, rose is homozygous dominant for one and homozygous recessive for the other. Walnut has one dominant allele for each gene, and single is homozygous recessive for both. This fits the ratios

Let's move to the next Part C.

c) In order to prove their hypothesis about the genotypes giving rise to each phenotype, Punnett and Bateson crossed each of the original breeds - one with pea comb and one with rose comb - to a breed with a single comb. What was their strategy in performing this cross, and what would be the expected outcome?

These are both test crosses, since single comb chickens have the genotype $aa\ bb$ and therefore homozygous recessive. When the original pea comb variety $AA\ bb$ is crossed to single comb variety $aa\ bb$, all of the F_1 will be $Aa\ bb$, which is pea comb. When the original rose comb variety $aa\ BB$ is crossed to a single comb variety $aa\ bb$, all of the F_1 will be $aa\ Bb$ with is rose comb.

Here is a more challenging question: Bateson and Punnett also took individual chickens with a walnut comb from the F_2 generation and crossed them to a breed with a single comb. What proportion of these crosses involving a single walnut comb chicken will give all four phenotypes in the offspring?

This question is a bit different. Bateson and Punnett took single F_2 chickens with walnut combs and crossed them to a single comb variety—so they test-crossed them. But these F_2 walnut comb chickens will have different genotypes, as shown here.

To have a walnut-shaped comb, they need to have a dominant allele for each gene, but they could be homozygous or heterozygous. The offspring that do not have dominant alleles are grayed out. Nine different genotypes will have the dominant allele for both genes.

In order for the test-cross of a walnut comb chicken with a single comb chicken to produce all four phenotypes, the walnut comb chicken must have the genotype $Aa\ Bb$. What fraction of the walnut comb chickens are heterozygotes like this?

Here are nine genotypes that will produce a chicken with a walnut comb among the F_2 generation. [Show the blue Punnett square at 6:09] Of those 9, four of them are heterozygous for both genes, as shown in blue. So 4/9 of the walnut comb chickens will give all four phenotypes when they are test-crossed to chickens with a single comb.