

Genetics Journal Entry Two

In the last entry in our Genetics Journal we discussed many of the introductory concepts of genetics including chromosome pairs; the genes located at specific locations called loci; the different versions of genes, called alleles, that can occur at one locus on each chromosome; the concepts of heterozygous, homozygous, gene segregation, independent assortment, genotype and phenotype. We then used the pea experiments of Gregor Mendel, the father of genetics, to illustrate these concepts. Mendel found that short strains of peas when bred together always produced short offspring. He also found that some strains of tall plants when bred together always produced tall offspring and that other strains of identically appearing tall plants when bred together produce 75% tall and 25% short offspring. The short plants were determined to be homozygous for a recessive allele for “shortness” and therefore each parent could only donate one of these recessive short alleles and therefore all offspring were also heterozygous for short. The first strain of tall plants was also heterozygous, but in this instance for the dominant trait of “tallness” and therefore each parent could only donate an allele for tall and so the offspring could only be tall. The other tall strain however produced a mixture of tall and short plants. Since shortness is the recessive trait in this instance, Mendel realized that these short offspring must be homozygous for shortness (tt). Since one allele comes from each parent, then each of the tall parents that produced these short plants must be carrying one recessive gene for shortness. He also deduced that each parent must be carrying one dominant gene for tallness, which made them appear the same as the homozygous tall plants (TT). Therefore this particular strain of tall appearing plants had to be heterozygous (Tt). Being dominant, the one tall (T) gene made the parent plant appear indistinguishable from those with two tall genes. Mendel also crossed the truebreeding tall strain with the truebreeding short strain and the first generation (F1) were 100% tall plants. He hypothesized that these tall plants were all heterozygous (Tt). He proved this by breeding the F1 tall plants together and getting 75% tall and 25% short plants.

We can illustrate this with a simple but very useful diagram called a Punnett square which is a way of charting all of the possible genetic outcomes of a mating. The top row illustrates all of the possible gene contributions from one parent, and the left column shows all of the possible contributions from the other parent. The squares inside the table then represent each of the possible combinations of the genes in question from these two parents. Since we are talking about a single gene locus, each parent has one pair of genes at that position on its chromosome and so each parent has two possible contributions to the offspring. When we have two choices from each parent that can randomly combine with either of the two choices from the other parent we end up with four possible outcomes. As you can see the table has four squares representing those outcomes. In this case since the parents each contributed the same information in either random selection, because they are homozygous for this trait, the four possible outcomes are all the same.

Tall Parent Plant
TT

Short Parent Plant
tt

	T	T
t	Tt	Tt
t	Tt	Tt

The genetic code for this tall/short trait is the same for each possible offspring and the Punnett square makes it easy for us to see why. Now we can clearly understand why all of the offspring in Mendel's experiment were tall even though one half of the parents were short.

Now, we can use another Punnett square to look at what happened when Mendel took plants of this F1 generation, all of them tall, and bred them together. Remember, even though their phenotype was Tall the Punnett square showed us that their genotypes were all Tt.

Tall F1 Parent Plant
Tt

Tall F1 Parent Plant
Tt

	T	t
T	TT	Tt
t	Tt	tt

We can learn several things from this diagram. First we can see that unlike our first example each parent has two different contributions it could make. This shows us that there are three possible outcomes: TT, Tt, and tt. Two of these are homozygous TT and tt and one is heterozygous Tt. We can also see the frequency of each of these outcomes. TT is one of four or 25%, tt is also one of four or 25%, Tt, the one heterozygous outcome occurred 2 of four time or 50%. Each of these genetic combinations is called a genotype, and in this example there are three genotypes. Never the less they exhibit only two different outward appearances, either tall or short, called phenotypes. This is because the T exhibits a simple dominance effect over the t and so those plants appear tall just as the TT plants do. The end result is that three of four or 75% of the offspring in this F2 generation are tall and one of four or 25% of the F2 offspring are short. This is exactly what Gregor Mendel discovered experimentally and the Punnett square allows us to see why it happened that way. Why is that useful to us as breeders? Well, if we knew for sure what the genotype was for a particular trait in two alpacas, we could predict at least what the probable outcome of mating them would be as it regards that particular trait. It also shows us how valuable it might be to have breeding stock that is homozygous for a particular trait.

In the same way it shows us as alpaca breeders how difficult, and potentially costly, it is to select breeding stock based on the appearance of the animal, particularly when the effect of simple dominance is at work. Let us use Mendel's pea plant experiments again to explain what that means. What if only short pea plants had any commercial value to pea farmers, and there was no market at all for the tall plants. That wouldn't be too bad.

We would select only short plants, which we know are homozygous or true breeding for the short trait and cross them with other short plants. We could be sure then that all of the resulting seeds would grow short pea plants as well and 100% of our crop would have a commercial value.

Now let's turn the tables. What if there was only a market for only the tall plants, and the short plants were worthless. Well, if we knew for sure that we had a homozygous or "true breeding" strain of tall plants there would be no problem. We could cross these TT plants with each other and be sure to get only tall offspring that were also homozygous TT. Unfortunately however, we cannot know their genotype just by looking at them and seeing that they are tall. It could be that any tall plant was Tt just as well as TT if we could select only from appearances (phenotypic selection). If the stock we buy to begin our breeding program happens to be heterozygous (Tt) instead of homozygous (TT) the outcome will be much different. We could have the most beautiful looking tall pea plants that win blue ribbons at every fair and pea show, but when we cross them, 25% of the offspring are going to be tt and will be commercially worthless. As a farmer in this theoretical scenario, we will have 25% less of a crop to sell than if we had TT plants to start with. Worse yet, if we do not want to be commercial pea ranchers, but instead want to be breeders of "seedstock" to sell to the pea ranchers, then 75% of our crop will be worthless. We have just explained why. The commercial pea rancher is going to buy only homozygous TT stock, since he doesn't want to have a crop that is 25% worthless. He will prefer to pay top dollar for the quality homozygous breeding stock, and will probably insist on it if he is a knowledgeable pea rancher. So we can only sell 25% of our offspring from those heterozygous parents. But wait, it gets even worse. We can obviously tell the tt short plants and so will not sell them, but we cannot even tell by looking which one out of three tall plants are the TT ones and which two of three are the Tt ones. If we sell Tt plants to the commercial pea farmer when he thinks he is getting TT he is not going to be a happy customer. We must somehow identify the TT plants. The only way to do that however is by test mating, sometimes called progeny testing. We must take each of the tall plants and allow it to produce a crop of offspring with a minimum of five mates that are homozygous for the recessive trait (tt). If any one offspring is a short plant we know that the parent plant contributed one of the t genes and so it must have been heterozygous. However, a heterozygous parent has an equal chance of randomly contributing a T gene and then the test offspring will be a tall plant, the same result we would get if a homozygous TT plant contributed one T gene. Mathematical laws of probability tell us that we must have at least five test matings with homozygous recessive mates, all of which result in tall offspring, to say that the *probability* of the parent being homozygous for one dominant gene, in this case TT, is 95%; in order to say that the probability is 99% we would need to do test matings with seven homozygous individuals.

What does this mean to us as breeders? If we choose breeding stock based on appearance, otherwise called phenotype (tall), and they happen to be heterozygous (Tt), that look the same as the TT tall, and breed them, then on average 25% of our offspring would have no commercial value. The other 75% would have to be test mated with 7 mates each in order to determine with 99% confidence which 25% of the offspring would

be valuable to sell as breeding stock as homozygous TT parents. This costs us the time of one breeding season to determine which are our good breeding stock, as well as the cost of needing to use twenty-one homozygous recessive plants. Think of *twenty-one alpacas* for one breeding season for each three parents we are test mating! With pea plants this might not be a big expense other than the lost time, but with alpacas it could be extremely expensive.

An example that is closer to home for us as alpaca breeders would be to consider a simply inherited trait with a simple dominance effect. According to Dr. Ponzoni, the trait of fleece style, Suri versus Huacaya, is governed by one gene and with a simple dominance relationship between two possible alleles. I know there is much controversy on this topic, and that other models for the inheritance of Huacaya and Suri fleece types have been hypothesized, and it is not the scope of this article to determine whether or not Dr. Ponzoni's model is correct. It does provide us with a helpful example for alpaca breeders to visualize the genetic principles at hand and so we will pretend it is true for that purpose. The Suri fleece trait is dominant to the Huacaya trait, so we will use a capital S for suri trait and a lower case s for Huacaya trait. Any Huacaya then is by definition homozygous since the s is recessive and it requires two of them (ss) to allow the Huacaya trait to be expressed. But a Suri may be either SS or Ss and have the same phenotypic Suri fleece style. If a commercial alpaca farmer wants to produce wants to produce Suri fleece to sell, he is going to want to buy homozygous (SS) breeding stock. If he has two SS parents, then he can be sure that all of the offspring will also be SS and 100% of his fleeces will be the Suri style that he desires. If however he buys breeding stock based solely on phenotype (Suri) that are in fact Ss (genotype) they will look them same as the SS stock but his outcome will be substantially different. In fact if both parents are Ss then 25% of the offspring will be Huacayas (ss). Using the Punnett Square again will illustrate why.

	Heterozygous Suri Sire	
	Ss	
T		
Heterozygous Suri Dam		
Ss		
	S	s
S	SS	Ss
s	Ss	ss

He will on average then shear 25% less Suri fleece than if he had SS breeding stock to start with. That means it will be financially important for him to be sure he buys homozygous SS breeding stock. If he thinks he is buying homozygous breeding stock and ends up with 25% Huacaya crias from his Suri breeding stock he won't be very happy.

Now let's take it up the chain a step to the level of the breeding stock breeder, the farm that is producing breeding stock for the commercial farmer to buy. His product is the

animal, not the fleece. We have already shown that *his* customer wants to buy breeding stock that is “true breeding” or homozygous for the commercial trait he is interested in. In our example it is Suri fleece type, but you could imagine any other commercially valuable trait as well. If the stockbreeder has only homozygous SS animals to breed, then 100% of his crias will also be SS and all will be valuable as breeding stock, at least for this one trait of Suri fleece. On the other hand, if our stock breeder has chosen his foundation animals purely on phenotype, he can spend hundreds of thousands of dollars, buy beautiful, grand champion blue ribbon winning, perfectly conformed, ultra fine fleeced, ultra dense and lustrous Suris that grab every eye in the show ring, but he still doesn't know what their genotype is. If they turn out to be Ss, which no one can tell from appearance, then only one in four of the offspring will be the SS breeding stock he wants to produce. On average then they would only have one cria in every four years from these foundation animals that they could sell for Suri breeding stock. This is a significant financial disadvantage compared to the example in which he starts out with homozygous SS stock and can sell 100% of the crias each year.

But wait, it gets worse again! The breeder who has the Ss stock can't even tell which one out of four offspring are homozygous SS. He can obviously tell the one Huacaya that isn't, but he still can't identify which of the other 75% are homozygous SS. He must test mate each of these animals 7 times with Huacaya mates in order to determine with 99% confidence which animals are in fact SS. This spends at least one more breeding season to accomplish, *after* the animals are mature enough to breed, if they are males and he has 7 huacaya females available to breed each one to. So it also ties up 7 females for one season for each male being tested. If the offspring in question were female, it would take 7 years, assuming a good full term pregnancy each year, to test a female to prove she was SS. Add to all of this the fact that the offspring from these test matings will ALL be either Huacaya or Ss Suris, and even though you could sell their fleece that is small financial compensation for the fact that they are not valuable as our desired SS seed stock to sell to the commercial farmer.

I think this example not only helps make clear the concept of simple inheritance of a trait exhibiting simple dominance, it also clearly shows how expensive a mistake it might be to select our foundation stock based on phenotypic appearance, no matter how good it is. I will repeat that it is not certain that this single gene simple dominance model is correct for fleece type. But take any simply inherited commercially valuable trait and substitute for the word Suri and the result is the same. It may be much less costly in time and in money to buy more expensive foundation stock if they have been proven homozygous through test mating or progeny testing so that you know for sure what you are starting with.

In our next Genetics Journal entry we will go back to our Punnett Square again to show how the inheritance of two simply inherited traits with complete dominance can be predicted. We will also look at partial dominance and co-dominance. In the mean time, if anyone has general questions about basic genetics that you would like to see discussed in the Genetics Journal please e-mail them to the author at : journal@alpacagenetics.com