

The Genetics Journal – Part Four

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So far in the first three entries to the Genetics Journal we have reviewed the Basic Mendelian Principles for the inheritance of simply inherited traits including the concepts of genes, alleles, dominant and recessive traits, the Mendelian laws of Gene Segregation and Independent Assortment, genotypes, phenotypes, Punnett squares and simple dominance. We also discussed modifications of Mendelian ratios such as partial dominance, co-dominance, epistasis and sex linked characteristics. These are the basic building blocks of genetics, but the genetics of animal breeding are much more complex in most cases.

Many economic traits in alpacas and in other farm animals, such as milk production, fleece weights, weaning weights, fiber diameters, etc. show continuous variations throughout a population, primarily because they are controlled by many pairs of genes. It is this continuous variation in fact that makes us realize that there are many genes involved. In the first entry of The Genetics Journal, we look at Gregor Mendel's experiments with pea plants. We saw that he observed that the plants were either tall, or short. That is because there was only one genetic locus controlling this trait, with two possible alleles or genes at that locus. One allele was for tall, the other for short. Therefore, there were only two observed values for this trait. When we looked further at his experiments, we saw that there were also two alleles for color, green or yellow, and two alleles for the shape of the peas, round or wrinkled. Each of these led to two possible expressions of the trait. When we looked at all three together then, it was possible to have 8 different phenotypic appearances of the plants, yet each of these is a distinct phenotype, not a continuous spectrum of variation. For instance, a plant might exhibit the characteristics of being tall with round, green seeds or short with round green seeds, or short with yellow wrinkled seeds, etc. However, each of these can be easily categorized. And if we were to graph the results there would be eight distinct categories on our graph. See Figure 1. With most commercially important traits in animals however, such as fiber diameter in alpacas, we don't see separate, distinct phenotypes. We see a continuous spectrum of values for fiber diameter. If fiber diameter was controlled by only three loci, with two alleles at each, we would see alpacas with only eight different fiber diameters, for example we might observe 14 microns, 16 microns, 18 microns, 20 microns, etc. but no animals with 19 microns or other intermediate values. We know that this is not true however. Therefore, since there are a great number of possible values for fiber diameter, or fleece weight, or staple length, etc. we know that these and other such traits are caused by multiple genes; hundreds or maybe even thousands of them.

Since so many production traits of livestock, including alpacas, are controlled by so many pairs of genes, we have to expand our thinking beyond inheritance involving one or two or even five or six genes. We don't know yet exactly how many genes alpacas have, but the number is likely to be greater than 30,000. Although each of these genes will behave according to the principles of Mendelian genetics as we have described them in the first three entries of this

Journal, the large number of them involved in these kinds of traits makes it impossible for us to use Punnett squares to look at possible outcomes of different matings. Let's consider a very simplified example. What if one gene pair on each of an alpaca's 37 chromosomes contributed to a fleece characteristic such as average fiber diameter (AFD)? Remember that for one pair of heterozygous genes, Tt, there are three different genetic combinations, or genotypes. (TT, Tt, tt). For two pairs of heterozygous genes, YyRr there are nine genotypes. How many different combinations for 37 gene pairs? The number of genetically different sperm or eggs for a given number of gene pairs is 2^n . The number of different genotypes (genetic combinations) is 3^n . If n (the number of heterozygous gene pairs) is 37, then $2^n = 137$ billion; $3^n = 450$ quadrillion. (450,000 billions)

Traits that are controlled by multiple genes like this are called polygenic traits. Because polygenic traits are affected by so many genes it is extremely difficult to observe the effects of specific alleles at specific loci. It is therefore impossible to explicitly identify an individual's genotype for a polygenic trait. Imagine writing out the Punnett square for all of the possible combinations of alleles for 37 different loci. Since identifying the actual genotype is out of the question, the alternative is to characterize the net effect of the individual's many genes affecting that trait. That is to say, we will add up the effect of all of the genes acting together, or in other words we will **quantify** the individual's performance and breeding value for the trait. Hence the term **Quantitative Genetics**, this deals with traits in which the phenotypes show continuous (numerical) expression.

Quantitative genetics requires the use of statistical tools including statistical concepts such as heritability and accuracy. Instead of trying to identify the animal's actual genotype for a specific trait we try to identify **breeding values** and **estimated progeny differences** for traits of importance. These breeding values are in turn used for making breeding decisions about selection and mating.

To demonstrate the breeding value (BV) concept, consider a model with only five loci affecting fleece weight. We'll call these five loci A, B, C, D and E. In our hypothetical model, the A locus can have alleles that add either -0.1kg or +0.1kg. Similar alleles exist at the B, C, D and E loci. The genetic merit of an animal for fleece weight is a sum of the effects of all of the animals fleece weight alleles. In our model of five loci, the worst possible animals would have ten inferior alleles and Breeding Values (BV) of -1.0kg

$$\begin{array}{ccccc} \text{Locus A} & \text{Locus B} & \text{Locus C} & \text{Locus D} & \text{Locus E} \\ (-0.1 + -0.1) & + (-0.1 + -0.1) & + (-0.1 + -0.1) & + (-0.1 + -0.1) & + (-0.1 + -0.1) = \\ & & & & \text{BV} = -1.0\text{kg} \end{array}$$

In the same model of five loci, the best possible animals would have ten superior alleles and Breeding Values (BV) of +1.0lb

$$\begin{array}{ccccc} \text{Locus A} & \text{Locus B} & \text{Locus C} & \text{Locus D} & \text{Locus E} \\ (0.1 + 0.1) & + (0.1 + 0.1) & + (0.1 + 0.1) & + (0.1 + 0.1) & + (0.1 + 0.1) = \\ & & & & \text{BV} = +1.0\text{kg} \end{array}$$

Let's walk through an example of using this model of quantitative genetics to help illustrate how this actually works. Our hypothetical exercise will of course only be a crude illustration because it includes only five alleles, not hundreds, and it assumes all of the alleles carry equal weight, which also may not be true in real life.

For our model I have created two hypothetical animals, Mr. Studly and Foxy Lady, and we will pretend we know the true value of the five genes controlling fleece weight on each of their chromosomes. See Figure 2. By adding, or quantifying, the values of each of these alleles we come up with the Breeding Value (BV) for each parent. Mr. Studly's BV is +0.4 kg. Breeding values in quantitative genetics are always represented as plus or minus values relative to the average for the population. This means that our Mr. Studly has a breeding value for fleece weight that is 0.4 kg, or 0.88 lbs for those of you who prefer that measure, higher than the average fleece weight. Foxy Lady's BV is -0.2kg or 0.2 kilograms less than the average for fleece weight.

Mendel's laws tell us that when the male and female produce gametes, sperm and eggs, that they will contribute one gene from each pair, and that these genes will segregate and sort randomly. In other words, each of these parents will contribute a combination of five genes consisting of either Allele number one or Allele number two from *each* of our five loci: A, B, C, D and E.

We saw previously that the genetically different sperm or eggs for a given number of gene pairs is 2^n . In our example "n", the number of gene pairs, is five. There are therefore a total of $2^5 = 32$ genetically different sperm or eggs that could possibly be formed from the five gene pairs in our model.

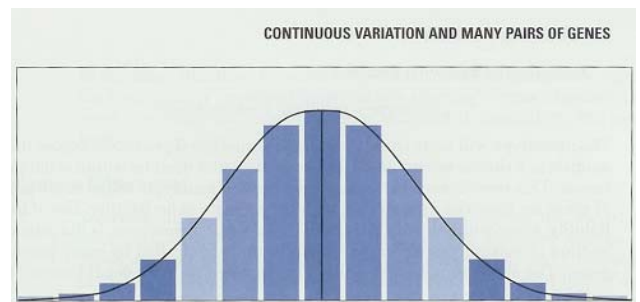
We are going to walk through an example where we will breed these two animals and look at the resulting cria's fleece weight. With just these five genes, there are 153 genetically different crias we could get from this one mating. By randomly selecting either allele number one or allele number two at each of the loci A through E we can come up with a possible gamete, sperm or egg, which each parent could contribute. See Figure 3. Remember, these gametes each represent only one of the thirty two possibilities for each parent. In this particular mating we got a sperm from Mr. Studly whose alleles has a total value of +0.3kg and Foxy Lady contributed an egg with a value of -0.1kg which created a cria with a BV of +0.2kg.

There are a number of things we can say about this one mating. First, the resulting cria has a breeding value of +0.4kg greater than the mother. Obviously this was a successful example of corrective mating, otherwise called negative assortive mating. The second thing we can say is that this cria is also better than the average cria we would expect to get from this mating. How do we know that? It is because mathematically the mean BV of all of the progeny should equal the average of the BV of the two parents. In this example the parents were +0.4 and -0.2. The average between the two would be +0.1kg. See figure 4. In this case the cria was between the values of the two parents, which would statistically be the most likely result. However,

the range of *possible* results show us that a single offspring from any mating has a slight mathematical chance of being much better than the best parent and much worse than the worst parent.. The mating of a single macho with a single hembra can result in widely different genetic merit (BVs) of progeny. In our model the best possible cria would have a BV of +0.8kg, twice as good as the best parent. The worst possible offspring could have come out with a BV of -0.6kg. How do we know this? If we go to figure 2 and choose the best possible alleles for Mr. Studly at each of the five loci we can create a possible sperm with a BV of +0.5kg. If we do the same for Foxy Lady we can get a best possible gamete of +0.3kg. The resulting cria from these two gametes would have a BV of +0.8kg. If we repeat the example for the worst possible outcome the resulting offspring would have a BV of -0.6kg. This is a range of 1.4 kg. This means that the variability of possible outcomes from breeding these two alpacas would be crias that in exactly the same environment and with exactly the same management and with the same two parents could have fleece weights that differ by 3lbs! Is that possible? Have you ever seen two alpacas from the same mating pair that looked totally different? Have you ever seen two children from the same two parents that look totally different? If not, just look at my five daughters. They all have the same two parents, yet my wife was once asked if we adopted them all!

Of course these extreme results, often referred to as outliers in livestock breeding, are rare even though possible. The science of statistics can help us understand what the chances are of having these and other kinds of results from any mating situation.

Figure 1



To demonstrate the breeding value (BV) concept, consider a model with only five loci affecting fleece weight. We'll call these five loci A, B,C,D and E. In our hypothetical model, the A locus can have alleles that add either -0.1kg or +0.1kg. Similar alleles exist at the B,C,D and E loci.

Figure 2

True Fleece Weight Genotypes

Mr. Studly	A	B	C	D	E
Allele 1	+0.1	+0.1	-0.1	-0.1	+0.1
Allele 2	-0.1	+0.1	+0.1	+0.1	+0.1

$BV_{\text{Studly}} = +0.4\text{kg}$

Foxy Lady	A	B	C	D	E
Allele 1	+0.1	+0.1	-0.1	-0.1	-0.1
Allele 2	-0.1	-0.1	+0.1	-0.1	+0.1

$BV_{\text{Foxy}} = -0.2\text{kg}$

Figure 3

Value of Alleles in Gametes

Mr. Studly	Locus				
	A	B	C	D	E
	Allele	1	1	1	2
Value	+	+	-	+	+

Sperm

= +0.3

Foxy Lady	Locus				
	A	B	C	D	E
	Allele	1	2	1	2
Value	+	-	-	-	+

Egg

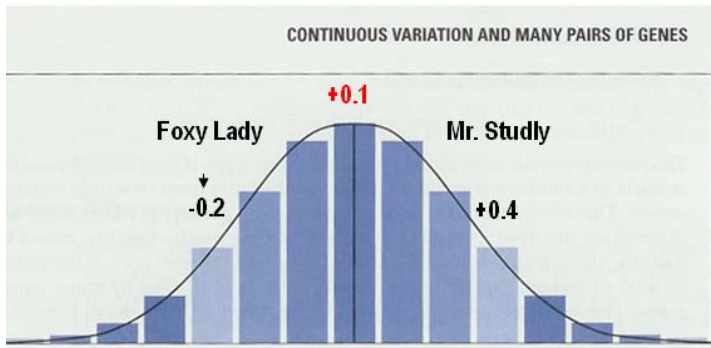
= -0.1

Cria

+0.2 kg

Total BV

Figure 4



Progeny mean BV = Average of Parents BV