

INTRODUCTION TO QUANTITATIVE GENETICS

So far in this course we have dealt entirely either with the evolution of characters that are controlled by simple Mendelian inheritance at a single locus or with the evolution of molecular sequences. Even on Tuesday when we were dealing with population genomic data, data from hundreds or thousands of loci, we were treating the variation at each locus separately and combining results across loci. I have some old notes on gametic disequilibrium and how allele frequencies change at two loci simultaneously, but they're in the "Old notes, no longer updated" section of the book version of these notes (https://figshare.com/articles/journal_contribution/Lecture_notes_in_population_genetics/100687), and we didn't discuss them.¹ In every example we've considered so far we've imagined that we could understand something about evolution by examining the evolution of a single gene. That's the domain of classical population genetics.

For the next few weeks we're going to be exploring a field that's older than classical population genetics, although the approach we'll be taking to it involves the use of population genetic machinery.² If you know a little about the history of evolutionary biology, you may know that after the rediscovery of Mendel's work in 1900 there was a heated debate between the "biometricians" (e.g., Galton and Pearson) and the "Mendelians" (e.g., de Vries, Correns, Bateson, and Morgan).

Biometricians asserted that the really important variation in evolution didn't follow Mendelian rules. Height, weight, skin color, and similar traits seemed to

- vary continuously,
- show blending inheritance, and
- show variable responses to the environment.

Since variation in such *quantitative traits* seemed to be more obviously related to organismal adaptation than the "trivial" traits that Mendelians studied, it seemed obvious to the biometricians that Mendelian geneticists were studying a phenomenon that wasn't particularly interesting.

¹We will spend some time talking about gametic disequilibrium when we talk about association mapping in a couple of weeks.

²In fact, it involves the use of the single-locus population genetic machinery we've been using all semester.

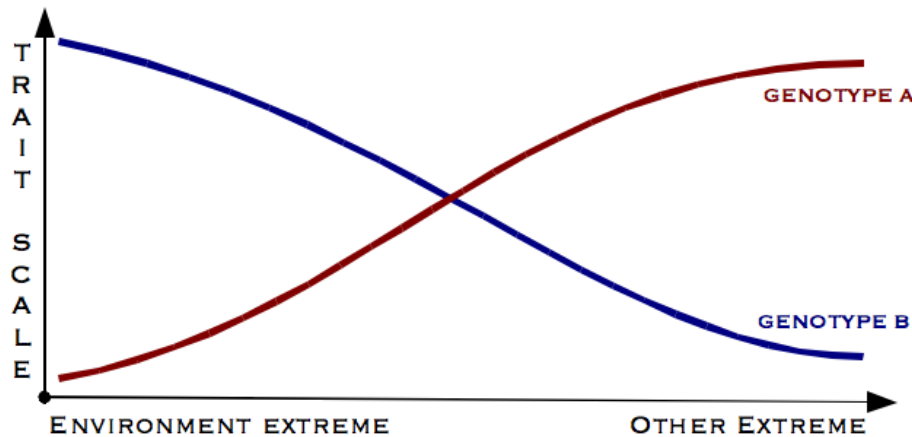


Figure 1: Hypothetical illustration of reaction norms for two genotypes across a 1-dimensional environmental gradient (from Wikipedia, Public Domain, <https://en.wikipedia.org/w/index.php?curid=3925138>, accessed 9 April 2017).

Mendelians dismissed the biometricians, at least in part, because they seemed not to recognize the distinction between genotype and phenotype. It seemed to at least some Mendelians that traits whose expression was influenced by the environment were, by definition, not inherited. Moreover, the evidence that Mendelian principles accounted for the inheritance of many discrete traits was incontrovertible.

Woltereck's [3] experiments on *Daphnia* helped to show that traits whose expression is environmentally influenced may also be inherited. He introduced the idea of a *norm of reaction* to describe the observation that the same genotype may produce different phenotypes in different environments (Figure 1). When you fertilize a plant, for example, it will grow larger and more robust than when you don't. The phenotype an organism expresses is, therefore, a product of *both* its genotype and its environment.

Nilsson-Ehle's [2] experiments on inheritance of kernel color in wheat showed how continuous variation and Mendelian inheritance could be reconciled (Figure 2). He demonstrated that what appeared to be continuous variation in color from red to white with blending inheritance could be understood as the result of three separate genes influencing kernel color that were inherited separately from one another. It was the first example of what's come to be known as *polygenic inheritance*. Fisher [1], in a paper that grew out of his undergraduate Honors thesis at Cambridge University, set forth the mathematical theory that describes how it all works. That's the theory of *quantitative genetics*, and it's what we're going to spend the rest of the course discussing.

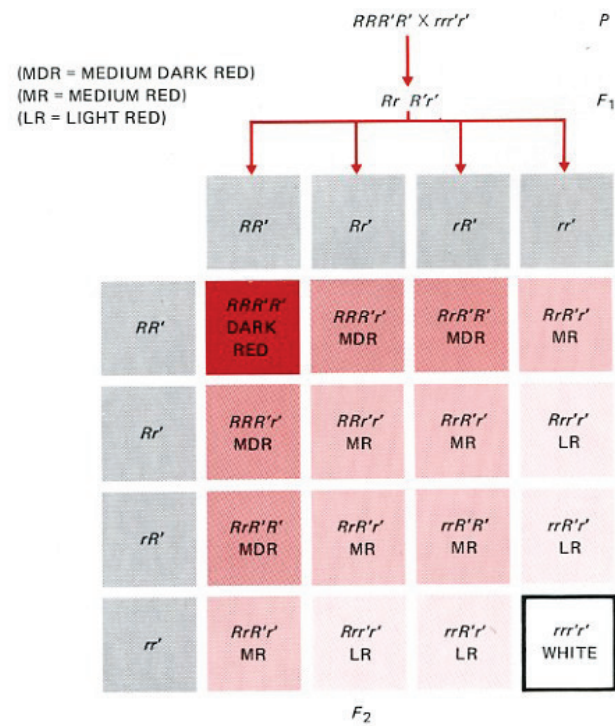


Figure 2: Results from one of Nilsson-Ehle's crosses illustrating polygenic inheritance of kernel color in wheat (from <http://www.biology-pages.info/Q/QTL.html>, accessed 9 April 2017).

An overview of where we're headed

Woltereck's ideas force us to realize that when we see a phenotypic difference between two individuals in a population there are three possible sources for that difference:

1. The individuals have different genotypes.
2. The individuals developed in different environments.
3. The individuals have different genotypes *and* they developed in different environments.

This leads us naturally to think that phenotypic variation consists of two separable components, namely genotypic and environmental components.³ Putting that into an equation

$$\text{Var}(P) = \text{Var}(G) + \text{Var}(E) \quad ,$$

where $\text{Var}(P)$ is the *phenotypic variance*, $\text{Var}(G)$ is the *genetic variance*, and $\text{Var}(E)$ is the *environmental variance*.⁴ As we'll see in just a moment, we can also partition the genetic variance into components, the *additive genetic variance*, $\text{Var}(A)$, and the *dominance variance*, $\text{Var}(D)$.⁵

There's a surprisingly subtle and important insight buried in that very simple equation: Because the expression of a quantitative trait is a result both of genes involved in that trait's expression and the environment in which it is expressed, it doesn't make sense to say of a particular individual's phenotype that genes are more important than environment in determining it. You wouldn't have a phenotype without both. At most what we can say is that when we look at a particular population of organisms in a particular environment, some fraction of the phenotypic variation they exhibit is due to differences in the genes they carry and that some fraction is due to differences in the environment they have experienced.⁶ If we have two individuals with different phenotypes, e.g., Ralph is tall and Harry is short, we can't even say whether the difference between Ralph and Harry is because of differences in their genes or differences in their developmental environment.

³We'll soon see that separating genotypic and environmental components is far from trivial. I'm also putting aside, for the moment, that genotypes may differ in their response to the environment, even though that's what I illustrated in discussing norms of reaction.

⁴Strictly speaking we should also include a term for the interaction between genotype and environment, but we'll ignore that for the time being. I illustrated the interaction between genotype and environment in discussing norms of reaction.

⁵We could even partition it further into additive by additive, additive by dominance, and dominance by dominance epistatic variance, but let's not go there.

⁶When I put it this way, I hope it's obvious that I'm neglecting genotype-environment interactions, and that I'm oversimplifying a lot.

One important implication of this insight is that much of the “nature vs. nurture” debate concerning human intelligence or human personality characteristics is misguided. The intelligence and personality that you have is a product of *both* the genes you happened to inherit and the environment that you happened to experience. Any differences between you and the person next to you probably reflect both differences in genes *and* differences in environment. Moreover, even if the differences between you and your neighbor are due to differences in genes, it doesn’t mean that those differences are fixed and indelible. You may be able to do something to change them.

Take phenylketonuria, for example. It’s a condition in which individuals are homozygous for a deficiency that prevents them from metabolizing phenylalanine (<https://medlineplus.gov/phenylketonuria.html>). If individuals with phenylketonuria eat a normal diet, severe intellectual disabilities can result by the time an infant is one year old. But if they eat a diet that is very low in phenylalanine, their development is completely normal. In other words, clear genetic differences at this locus *can* lead to dramatic differences in cognitive ability, but *they don’t have to*.

It’s often useful to talk about how much of the phenotypic variance is a result of additive genetic variance or of genetic variance.

$$h_n^2 = \frac{\text{Var}(A)}{\text{Var}(P)}$$

is what’s known as the *narrow-sense heritability*. It’s the proportion of phenotypic variance that’s attributable to differences among individuals in their additive genotype,⁷ much as F_{st} can be thought of as the proportion of genotypic diversity that attributable to differences among populations. Similarly,

$$h_b^2 = \frac{\text{Var}(G)}{\text{Var}(P)}$$

is the *broad-sense heritability*. It’s the proportion of phenotypic variance that’s attributable to differences among individuals in their genotype. It is *not*, repeat *NOT*, a measure of how important genes are in determining phenotype. Every individual’s phenotype is determined both by its genes and by its phenotype. It measures how much of the *difference* among individuals is attributable to differences in their genes.⁸ Why bother to make the distinction between narrow- and broad-sense heritability? Because, as we’ll see, it’s only the additive genetic variance that responds to natural selection.⁹ In fact,

$$R = h_n^2 S \quad ,$$

⁷Don’t worry about what I mean by *additive genotype*—yet. We’ll get to it soon enough.

⁸As we’ll see later it can do this only for the range of environments in which it was measured.

⁹Or at least only the additive genetic variance responds to natural selection when zygotes are found in Hardy-Weinberg proportions.

Genotype	A_1A_1	A_1A_2	A_2A_2
Frequency	p^2	$2pq$	q^2
Genotypic value	x_{11}	x_{12}	x_{22}
Additive genotypic value	$2\alpha_1$	$\alpha_1 + \alpha_2$	$2\alpha_2$

Table 1: Fundamental parameter definitions for quantitative genetics with one locus and two alleles.

where R is the *response to selection* and S is the *selective differential*.

As you'll see in the coming weeks, there's a lot of stuff hidden behind these simple equations, including a lot of assumptions. But quantitative genetics is very useful. Its principles have been widely applied in plant and animal breeding for more than a century, and they have been increasingly applied in evolutionary investigations in the last forty years.¹⁰.

Partitioning the phenotypic variance

Before we worry about how to estimate any of those variance components I just mentioned, we first have to understand what they are. So let's start with some definitions (Table 1).¹¹

You should notice something rather strange about Table 1 when you look at it. I motivated the entire discussion of quantitative genetics by talking about the need to deal with variation at many loci, and what I've presented involves only two alleles at a single locus. I do this for two reasons:

1. It's not too difficult to do the algebra with multiple alleles at one locus instead of only two, but it gets messy, doesn't add any insight, and I'd rather avoid the mess.
2. Doing the algebra with multiple loci involves a *lot* of assumptions, which I'll mention when we get to applications, and the algebra is even worse than with multiple alleles.

Fortunately, the basic principles extend with little modification to multiple loci, so we can see all of the underlying logic by focusing on one locus with two alleles where we have a chance of understanding what the different variance components mean.

¹⁰I used to include a joke here that I've decided not to include any more. It's not very funny, and some people might find it offensive. If for some reason you want to know what the joke is, you can find it in the 2017 version of these notes on Figshare (<https://doi.org/10.6084/m9.figshare.100687.v2>)

¹¹Warning! There's a *lot* of algebra and even a little differential calculus between here and the end. It's unavoidable. You can't possibly understand what additive genetic variance is without it. I'll try to focus on principles, and I'll do my best to keep reminding us all why we're slogging through the math, but a lot of the math that follows *is* necessary. Sorry about that.

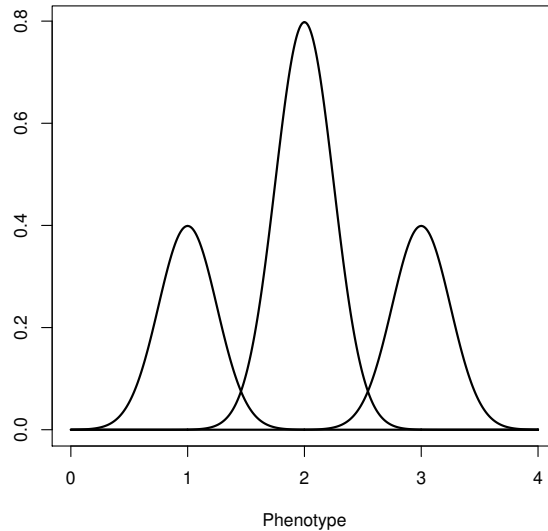


Figure 3: The phenotype distribution in a population in which the three genotypes at a single locus with two alleles occur in Hardy-Weinberg proportions and the alleles occur in equal frequency. The A_1A_1 genotype has a mean trait value of 1, the A_1A_2 genotype has a mean trait value of 2, and the A_2A_2 genotype has a mean trait value of 3, but each genotype can produce a range of phenotypes with the standard deviation of the distribution being 0.25 in each case.

Two terms in Table 1 will almost certainly be unfamiliar to you: *genotypic value* and *additive genotypic value*. Of the two, *genotypic value* is the easiest to understand (Figure 3). It simply refers to the average phenotype associated with a given genotype.¹² The *additive genotypic value* refers to the average phenotype associated with a given genotype, as would be inferred from the *additive effect* of the alleles of which it is composed. That didn't help much, did it? That's because I now need to tell you what we mean by the *additive effect* of an allele.¹³

The additive effect of an allele

In constructing Table 1 I used the quantities α_1 and α_2 , but I didn't tell you where they came from. Obviously, the idea should be to pick values of α_1 and α_2 that give additive genotypic

¹²Remember. We're now considering traits in which the environment influences the phenotypic expression, so the same genotype can produce different phenotypes, depending on the environment in which it develops.

¹³Hold on. Things get even more interesting, i.e., worse from here.

values that are reasonably close to the genotypic values. A good way to do that is to minimize the squared deviation between the two, weighted by the frequency of the genotypes. So our first big assumption is that genotypes are in Hardy-Weinberg proportions.¹⁴

The objective is to find values for α_1 and α_2 that minimize:

$$a = p^2[x_{11} - 2\alpha_1]^2 + 2pq[x_{12} - (\alpha_1 + \alpha_2)]^2 + q^2[x_{22} - 2\alpha_2]^2 \quad .$$

To do this we take the partial derivative of a with respect to both α_1 and α_2 , set the resulting pair of equations equal to zero, and solve for α_1 and α_2 .¹⁵

$$\begin{aligned} \frac{\partial a}{\partial \alpha_1} &= p^2\{2[x_{11} - 2\alpha_1](-2)\} + 2pq\{2[x_{12} - (\alpha_1 + \alpha_2)](-1)\} \\ &= -4p^2[x_{11} - 2\alpha_1] - 4pq[x_{12} - (\alpha_1 + \alpha_2)] \\ \frac{\partial a}{\partial \alpha_2} &= q^2\{2[x_{22} - 2\alpha_2](-2)\} + 2pq\{2[x_{12} - (\alpha_1 + \alpha_2)](-1)\} \\ &= -4q^2[x_{22} - 2\alpha_2] - 4pq[x_{12} - (\alpha_1 + \alpha_2)] \end{aligned}$$

Thus, $\frac{\partial a}{\partial \alpha_1} = \frac{\partial a}{\partial \alpha_2} = 0$ if and only if

$$\begin{aligned} p^2(x_{11} - 2\alpha_1) + pq(x_{12} - \alpha_1 - \alpha_2) &= 0 \\ q^2(x_{22} - 2\alpha_2) + pq(x_{12} - \alpha_1 - \alpha_2) &= 0 \end{aligned} \quad (1)$$

Adding the equations in (1) we obtain (after a little bit of rearrangement)

$$[p^2x_{11} + 2pqx_{12} + q^2x_{22}] - [p^2(2\alpha_1) + 2pq(\alpha_1 + \alpha_2) + q^2(2\alpha_2)] = 0 \quad . \quad (2)$$

Now the first term in square brackets is just the mean phenotype in the population, \bar{x} . Thus, we can rewrite equation (2) as:

$$\begin{aligned} \bar{x} &= 2p^2\alpha_1 + 2pq(\alpha_1 + \alpha_2) + 2q^2\alpha_2 \\ &= 2p\alpha_1(p + q) + 2q\alpha_2(p + q) \\ &= 2(p\alpha_1 + q\alpha_2) \quad . \end{aligned} \quad (3)$$

¹⁴As you should have noticed in Table 1.

¹⁵We won't bother with proving that the resulting estimates produce the minimum possible value of a . Just take my word for it. Or if you don't believe me and know a little calculus, take the second partials of a and evaluate it with the values of α_1 and α_2 substituted in. You'll find that the resulting matrix of partial derivatives, the Hessian matrix, is positive definite, meaning that we've found values that minimize the value of a . If you don't know what any of that means, just take my word for it that the values of α_1 and α_2 we get minimize the value of a .

That hasn't helped us figure out what α_1 and α_2 are, but it will turn out to be useful later, trust me.

Now divide the first equation in (1) by p and the second by q .

$$p(x_{11} - 2\alpha_1) + q(x_{12} - \alpha_1 - \alpha_2) = 0 \quad (4)$$

$$q(x_{22} - 2\alpha_2) + p(x_{12} - \alpha_1 - \alpha_2) = 0 \quad (5)$$

Thus,

$$\begin{aligned} px_{11} + qx_{12} &= 2p\alpha_1 + q\alpha_1 + q\alpha_2 \\ &= \alpha_1(p + q) + p\alpha_1 + q\alpha_2 \\ &= \alpha_1 + p\alpha_1 + q\alpha_2 \\ &= \alpha_1 + \bar{x}/2 \\ \alpha_1 &= px_{11} + qx_{12} - \bar{x}/2 \quad . \end{aligned}$$

Similarly,

$$\begin{aligned} px_{12} + qx_{22} &= 2q\alpha_2 + p\alpha_1 + p\alpha_2 \\ &= \alpha_2(p + q) + p\alpha_1 + q\alpha_2 \\ &= \alpha_2 + p\alpha_1 + q\alpha_2 \\ &= \alpha_2 + \bar{x}/2 \\ \alpha_2 &= px_{12} + qx_{22} - \bar{x}/2 \quad . \end{aligned}$$

α_1 is the additive effect of allele A_1 , and α_2 is the additive effect of allele A_2 . If we use these expressions, the additive genotypic values are as close to the genotypic values as possible, given the particular allele frequencies in the population.¹⁶

Components of the genetic variance

Let's assume for the moment that we can actually measure the genotypic values. Later, we'll relax that assumption and see how to use the resemblance among relatives to estimate the genetic components of variance. But it's easiest to see where they come from if we assume that the genotypic value of each genotype is known. If it is then, writing V_g for $\text{Var}(G)$

$$V_g = p^2[x_{11} - \bar{x}]^2 + 2pq[x_{12} - \bar{x}]^2 + q^2[x_{22} - \bar{x}]^2 \quad (6)$$

¹⁶If you've been paying close attention and you have a good memory, the expressions for α_1 and α_2 may look vaguely familiar. They look a lot like the expressions for marginal fitnesses we encountered when studying viability selection.

$$\begin{aligned}
&= p^2[x_{11} - 2\alpha_1 + 2\alpha_1 - \bar{x}]^2 + 2pq[x_{12} - (\alpha_1 + \alpha_2) + (\alpha_1 + \alpha_2) - \bar{x}]^2 \\
&\quad + q^2[x_{22} - 2\alpha_2 + 2\alpha_2 - \bar{x}]^2 \\
&= p^2[x_{11} - 2\alpha_1]^2 + 2pq[x_{12} - (\alpha_1 + \alpha_2)]^2 + q^2[x_{22} - 2\alpha_2]^2 \\
&\quad + p^2[2\alpha_1 - \bar{x}]^2 + 2pq[(\alpha_1 + \alpha_2) - \bar{x}]^2 + q^2[2\alpha_2 - \bar{x}]^2 \\
&\quad + p^2[2(x_{11} - 2\alpha_1)(2\alpha_1 - \bar{x})] + 2pq[2(x_{12} - \{\alpha_1 + \alpha_2\})(\{\alpha_1 + \alpha_2\} - \bar{x})] \\
&\quad + q^2[2(x_{22} - 2\alpha_2)(2\alpha_2 - \bar{x})] \quad . \tag{7}
\end{aligned}$$

There are two terms in (7) that have a biological (or at least a quantitative genetic) interpretation. The term on the first line is the average squared deviation between the genotypic value and the additive genotypic value. It will be zero only if the effects of the alleles can be decomposed into strictly additive components, i.e., only if the phenotype of the heterozygote is exactly intermediate between the phenotype of the two homozygotes. Thus, it is a measure of how much variation is due to non-additivity (dominance) of allelic effects. In short, the *dominance genetic variance*, V_d , is

$$V_d = p^2[x_{11} - 2\alpha_1]^2 + 2pq[x_{12} - (\alpha_1 + \alpha_2)]^2 + q^2[x_{22} - 2\alpha_2]^2 \quad . \tag{8}$$

Similarly, the term on the second line of (7) is the average squared deviation between the additive genotypic value and the mean genotypic value in the population. Thus, it is a measure of how much variation is due to differences between genotypes in their additive genotype. In short, the *additive genetic variance*, V_a , is

$$V_a = p^2[2\alpha_1 - \bar{x}]^2 + 2pq[(\alpha_1 + \alpha_2) - \bar{x}]^2 + q^2[2\alpha_2 - \bar{x}]^2 \quad . \tag{9}$$

What about the terms on the third and fourth lines of the last equation in 7? Well, they can be rearranged as follows:

$$\begin{aligned}
&p^2[2(x_{11} - 2\alpha_1)(2\alpha_1 - \bar{x})] + 2pq[2(x_{12} - \{\alpha_1 + \alpha_2\})(\{\alpha_1 + \alpha_2\} - \bar{x})] \\
&\quad + q^2[2(x_{22} - 2\alpha_2)(2\alpha_2 - \bar{x})] \\
&= 2p^2(x_{11} - 2\alpha_1)(2\alpha_1 - \bar{x}) + 4pq[x_{12} - (\alpha_1 + \alpha_2)][(\alpha_1 + \alpha_2) - \bar{x}] \\
&\quad + 2q^2(x_{22} - 2\alpha_2)(2\alpha_2 - \bar{x}) \\
&= 4p^2(x_{11} - 2\alpha_1)[\alpha_1 - (p\alpha_1 + q\alpha_2)] \\
&\quad + 4pq[x_{12} - (\alpha_1 + \alpha_2)][(\alpha_1 + \alpha_2) - 2(p\alpha_1 + q\alpha_2)] \\
&\quad + 4q^2(x_{22} - 2\alpha_2)[\alpha_2 - (p\alpha_1 + q\alpha_2)] \\
&= 4p[\alpha_1 - (p\alpha_1 + q\alpha_2)][p(x_{11} - 2\alpha_1) + q(x_{12} - \{\alpha_1 + \alpha_2\})] \\
&\quad + 4q[\alpha_2 - (p\alpha_1 + q\alpha_2)][p(x_{11} - 2\alpha_1)p + q(x_{12} - \{\alpha_1 + \alpha_2\})] \\
&= 0
\end{aligned}$$

Where we have used the identities $\bar{x} = 2(p\alpha_1 + q\alpha_2)$ [see equation (3)] and

$$\begin{aligned} p(x_{11} - 2\alpha_1) + q(x_{12} - \alpha_1 - \alpha_2) &= 0 \\ q(x_{22} - 2\alpha_2) + p(x_{12} - \alpha_1 - \alpha_2) &= 0 \end{aligned}$$

[see equations (4) and (5)]. In short, we have now shown that the total genotypic variance in the population, V_g , can be subdivided into two components — the additive genetic variance, V_a , and the dominance genetic variance, V_d . Specifically,

$$V_g = V_a + V_d \quad ,$$

where V_g is given by the first line of (6), V_a by (9), and V_d by (8).

An alternative expression for V_a

There's another way to write the expression for V_a when there are only two alleles at a locus. I show it here because it will come in handy later.

$$\begin{aligned} V_a &= p^2(2\alpha_1)^2 + 2pq(\alpha_1 + \alpha_2)^2 + q^2(2\alpha_2)^2 - 4(p\alpha_1 + q\alpha_2)^2 \\ &= 4p^2\alpha_1^2 + 2pq(\alpha_1 + \alpha_2)^2 + 4q^2\alpha_2^2 - 4(p^2\alpha_1^2 + 2pq\alpha_1\alpha_2 + q^2\alpha_2^2) \\ &= 2pq[(\alpha_1 + \alpha_2)^2 - 4\alpha_1\alpha_2] \\ &= 2pq[(\alpha_1^2 + 2\alpha_1\alpha_2 + \alpha_2^2) - 4\alpha_1\alpha_2] \\ &= 2pq[\alpha_1^2 - 2\alpha_1\alpha_2 + \alpha_2^2] \\ &= 2pq[\alpha_1 - \alpha_2]^2 \\ &= 2pq\alpha^2 \end{aligned}$$

An example: the genetic variance with known genotypes

We've been through a lot of algebra by now. Let's run through a couple of numerical examples to see how it all works. For the first one, we'll use the set of genotypic values in Table 2.

For $p = 0.4$

$$\begin{aligned} \bar{x} &= (0.4)^2(100) + 2(0.4)(0.6)(50) + (0.6)^2(0) \\ &= 40 \end{aligned}$$

Genotype	A_1A_1	A_1A_2	A_2A_2
Genotypic value	100	50	0

Table 2: A set of perfectly additive genotypic values. Note that the genotypic value of the heterozygote is exactly halfway between the genotypic values of the two homozygotes.

Genotype	A_1A_1	A_1A_2	A_2A_2
Genotypic value	100	80	0

Table 3: A set of non-additive genotypic values. Note that the genotypic value of the heterozygote is closer to the genotypic value of A_1A_1 than it is to the genotypic value of A_2A_2 .

$$\begin{aligned}\alpha_1 &= (0.4)(100) + (0.6)(50) - (40)/2 \\ &= 50.0\end{aligned}$$

$$\begin{aligned}\alpha_2 &= (0.4)(50) + (0.6)(0) - (40)/2 \\ &= 0.0\end{aligned}$$

$$\begin{aligned}V_g &= (0.4)^2(100 - 40)^2 + 2(0.4)(0.6)(50 - 40)^2 + (0.6)^2(0 - 40)^2 \\ &= 1200\end{aligned}$$

$$\begin{aligned}V_a &= (0.4)^2[2(50.0) - 20]^2 + 2(0.4)(0.6)[(50.0 + 0.0) - 20]^2 + (0.6)^2[2(0.0) - 20]^2 \\ &= 1200\end{aligned}$$

$$\begin{aligned}V_d &= (0.4)^2[2(50.0) - 100]^2 + 2(0.4)(0.6)[(50.0 + 0.0) - 50]^2 + (0.6)^2[2(0.0) - 0]^2 \\ &= 0.00\end{aligned}$$

For $p = 0.2$, $\bar{x} = 20$, $V_g = V_a = 800$, $V_d = 0.00$. You should verify for yourself that $\alpha_1 = 50$ and $\alpha_2 = 0$ for $p = 0.2$. If you are ambitious, you could try to prove that $\alpha_1 = 50$ and $\alpha_2 = 0$ for *any* allele frequency.

For the second example we'll use the set of genotypic values in Table 3.

For $p = 0.4$

$$\begin{aligned}\bar{x} &= (0.4)^2(100) + 2(0.4)(0.6)(80) + (0.6)^2(0) \\ &= 54.4\end{aligned}$$

$$\alpha_1 = (0.4)(100) + (0.6)(80) - (54.4)/2$$

$$\begin{aligned}
&= 60.8 \\
\alpha_2 &= (0.4)(80) + (0.6)(0) - (54.4)/2 \\
&= 4.8 \\
\\
V_g &= (0.4)^2(100 - 54.4)^2 + 2(0.4)(0.6)(80 - 54.4)^2 + (0.6)^2(0 - 54.4)^2 \\
&= 1712.64 \\
V_a &= (0.4)^2[2(60.8) - 54.4]^2 + 2(0.4)(0.6)[(60.8 + 4.8) - 54.4]^2 \\
&\quad + (0.6)^2[2(9.6) - 54.4]^2 \\
&= 1505.28 \\
V_d &= (0.4)^2[2(60.8) - 100]^2 + 2(0.4)(0.6)[(60.8 + 4.8) - 80]^2 \\
&\quad + (0.6)^2[2(9.6) - 0]^2 \\
&= 207.36
\end{aligned}$$

To test your understanding, it would probably be useful to calculate \bar{x} , α_1 , α_2 , V_g , V_a , and V_d for one or two other allele frequencies, say $p = 0.2$ and $p = 0.8$.¹⁷ Is it still true that α_1 and α_2 are independent of allele frequencies? If you are *really* ambitious you could try to prove that α_1 and α_2 are independent of allele frequencies if and only if $x_{12} = (x_{11} + x_{12})/2$, i.e., when heterozygotes are exactly intermediate.

References

- [1] R A Fisher. The correlation between relatives on the supposition of Mendelian inheritance. *Transactions of the Royal Society of Edingurgh*, 52:399–433, 1918.
- [2] H Nilsson-Ehle. Kreuzungsuntersuchungen an Hafer und Weizen. *Lunds Universitets Arsskrift*, n.s. 2, vo(no. 2), 1909.
- [3] R Woltereck. Weiterer experimentelle Untersuchungen über Artveränderung, Speziell über das Wesen Quantitativer Arunterschiede bei Daphiden. *Versuchung Deutsch Zoologische Gesellschaft*, 19:110–172, 1909.

¹⁷The easy way to do this, of course, would be to have the R Shiny app do the calculation for you. I recommend that you try it on your own and compare your answers with what R Shiny reports.

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