



Genetics

For Herpers

*The Reptile and Amphibian
Breeder's Guide to Genetics.*

Charles Pritzel

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Foreword

The foundation of genetics is very important to understanding all of the concepts that are built upon it. It is quite simple and tends to be easier to learn than most people suspect. However, there is still a version of genetics floating around within the reptile hobbies which does not base anything on the reality of how genes are inherited and expressed. That version tends to cause more confusion because things soon cease to make any sense, and one is required to just memorize a lot of rules that are simply random and have no rhyme or reason.

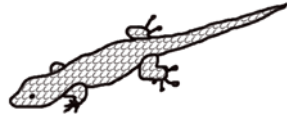
This book teaches Mendelian genetics, which is based on the way genes are propagated, inherited, and expressed in real life. The rules are very simple, and if you can:

- Add $16 + 18$, or
- Play board games with dice, or
- Play checkers, or
- Play card games,

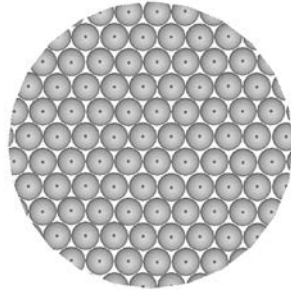
Then you can learn genetics and become a genetics wizard. Don't let the chapters ahead intimidate you, and if you start to feel lost, don't worry, it usually takes a couple of times through to sink in, even for the smartest of people. Just remember, you didn't learn addition or reading or the alphabet in the first try either.

Introduction

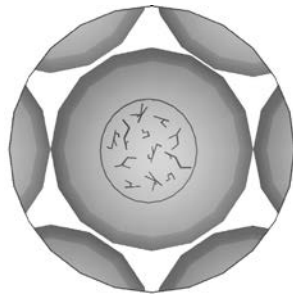
Here we see an animal. We will use a lizard for our example, but the same concepts apply to all herps: turtles, frogs, amphibians, lizards, snakes, etc.



Zooming in, we can see that animals are made up of many cells, which all have some things in common.



Zooming in on one cell, notice that each cell contains a nucleus. This is where the genetic material is found. It is divided into groups known as chromosomes, each of which is a string-like shape.



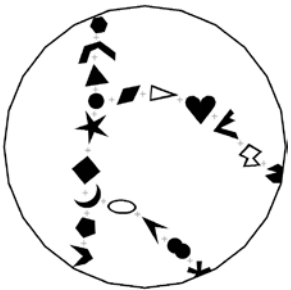


entire set (one genome) was inherited from the mother. The other entire set (one genome) was inherited from the father.

Zooming in on an individual pair of chromosomes,

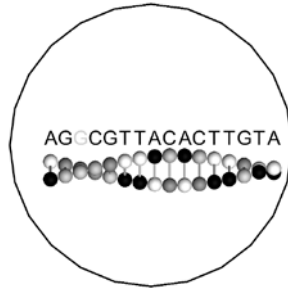


we see that each chromosome is made up of many genes strung together. Each symbol represents a place on the chromosome where an individual gene resides. These places are known as loci (loak-eye) which is plural for locus, as in "location."



In many species of animals, there are tens of thousands of loci. Notice that some of the loci, such as the star locus, contain different versions of the same gene.

An individual gene is composed of a strand of DNA. DNA is short for *Deoxyribonucleic Acid*. There are four different “nucleic acids” that make up the individual pieces in the strand, and they are abbreviated as A, C, G, and T.

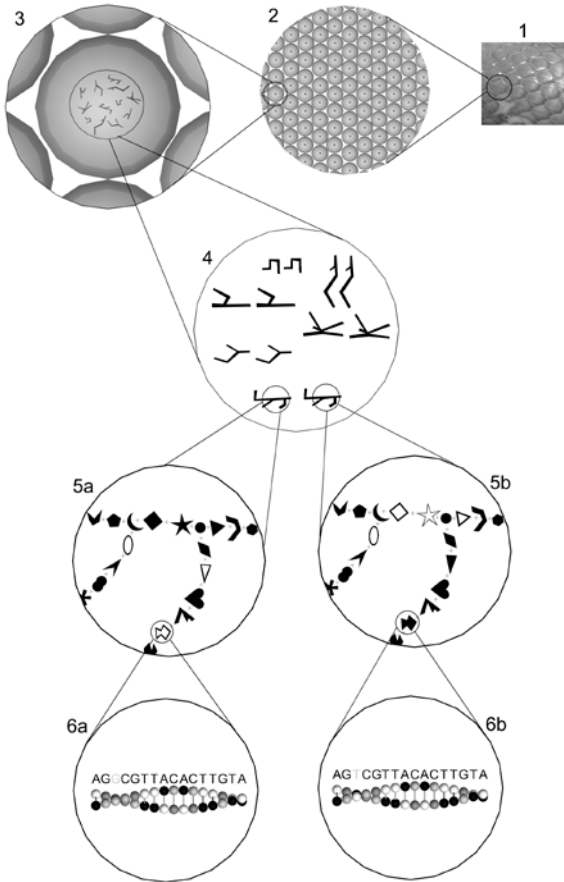


A strand of DNA can be represented as a sequence of letters, symbolizing the nucleic acids in the actual sequence. Notice that the sequence in these two genes is not identical: one starts out with AGGCG and the other starts with AGTCG. There can be different genes at the same locus. Each different gene for a locus is known as an allele. (Pronounced “uh-leel.”)



6

Summary: An animal (1) is made of (2) many cells. In each of these cells (3) is a nucleus which contains pairs of (4) chromosomes. These chromosomes (5) are made of strands of genes, and the genes (5 a&b) can be different from each other. The genes differ because of the (6 a&b) actual DNA sequence.



What Genes Do

An individual gene “codes for” a protein. This means that when the gene is activated, it produces a specific protein in that cell. Which exact protein is produced is a result of the sequence of that gene.

A protein is a group of *amino acids* stuck together. There are 23 types of amino acids. These 23 are the “alphabet” from which proteins are spelled. These serve many functions in the cell and/or in the body.

Proteins can act as enzymes, helping other chemical reactions take place. For example, a protein known as tyrosinase helps the amino acid tyrosine form into long chains. These long chains of tyrosine are the black/brown pigment melanin, which is what’s responsible for the colors in the skin/hair/feathers/scales of many animals, including humans.

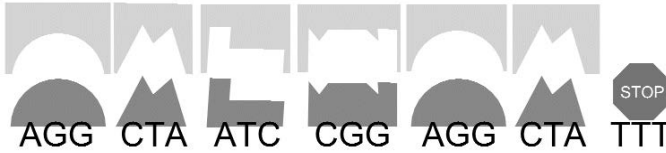


Proteins can also act as hormones, which leave the cell and signal other cells in the body. They can also act as receptors for a cell, telling that cell when a particular chemical is present.

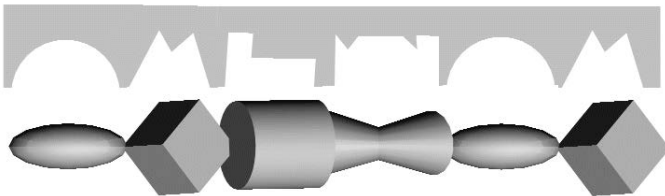
Looking again at the sequence of letters, notice that it is divided into groups of three letters. (Real genes are generally thousands of letters, but for simplicity we will use a short sequence.) Each group of three is called a *codon*.



Each codon corresponds to either an amino acid, or a “stop.” The “TTT” sequence in this example is the stop codon, and signifies the end of the gene. The other codons each match up to a specific amino acid, seen lined up above the codons.



The amino acids are chained together in the specified order, spelling out a protein. This protein then is able to fulfill its function in the cell. For example, let’s say this protein is tyrosinase, it might then go assist in the production of the pigment melanin in this cell.



Artist's conception of a protein.

When a Gene is Altered

Occasionally, a gene gets changed. Changes are known as mutations. These can happen from an error in the copying process, or many other reasons, such as the DNA sequence being altered by radiation or chemicals. Many mutations are lethal or “incompatible with life” meaning the cell (or fertilized egg) that carries it will die and never propagate this new mutant.



One type of mutation is known as a “point mutation” and changes only one letter in the DNA strand. For example, if our above “T” gene were altered by a point mutation, it could become the gene below, which produces a different protein. Notice that “AGG” at the beginning has been changed to “ATG” in the new mutant.



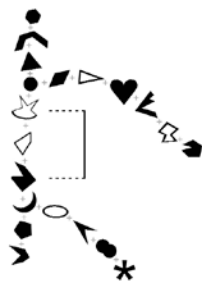
When this new sequence is activated, it will no longer produce the familiar tyrosinase protein.

Instead, it will produce a different protein. This new protein might end up doing nothing in the cell, perhaps causing an animal with this gene to be amelanistic, lacking all melanin. Or it might perform a similar function but be more or less effective than the original, causing the animal to be hypomelanistic (having less melanin than usual) or hypermelanistic (having more melanin than usual.) Or this new gene could serve a completely different purpose in the cell. (Or it could be lethal.)



Some errors will eliminate a large segment of DNA. When material is removed from the sequence,

this is known as a *deletion*. On the left is the normal configuration of a given chromosome. On the right is the chromosome after a deletion of the “star” locus and part of the diamond locus. The star locus



is gone, and the diamond locus has been changed. A deletion can remove anywhere from a few letters in a sequence, to hundreds of thousands of letters, and affect just one gene, part of one gene, or multiple genes. The opposite of a deletion can occur, and is known as an *insertion*.

An *amplification* is where one or more genes are duplicated, such as the triangle and circle in this example. This can increase the amount of a particular gene product or products.



A *translocation* is when entire segments of one chromosome, containing many loci, can detach from one chromosome, and re-attach to a different chromosome. This is illustrated below.



Notice that when these types of mutants are passed down to offspring, there can be new configurations where large parts of a chromosome are duplicated, or completely missing.



Homozygous and Heterozygous

These two terms are used to describe whether the two alleles at a locus are the same, or different. This is an either/or case, and any locus is either heterozygous, or homozygous. There are no “between” or “other” scenarios.

If they are the same, they are *homozygous* and if they are different they are *heterozygous*. Here are some examples of gene pairs:

$A^+ \cdot A^+$ - Homozygous
 $A^C \cdot A^C$ - Homozygous
 $A^d \cdot A^d$ - Homozygous
 $B^b \cdot B^b$ - Homozygous
 $B^+ \cdot B^+$ - Homozygous

$A^+ \cdot A^C$ - Heterozygous
 $A^d \cdot A^+$ - Heterozygous
 $A^C \cdot A^d$ - Heterozygous
 $B^+ \cdot B^b$ - Heterozygous
 $D^d \cdot D^e$ - Heterozygous

Homozygous and heterozygous are often abbreviated to *homo* and *het*. The term “*factored*” (such as “red-factored” or “s-factored”) is also sometimes used to indicate a heterozygous carrier of a recessive gene.

Notation and Symbols

When working with genetics problems or discussing genetics, you might see several different types of notation. This book uses several forms, to help you become comfortable with the overall idea instead of becoming set on a particular method.

The general idea is to symbolize different alleles, and be able to show them as individuals or pairs. If a gene is recessive to the wild-type it is put in lower case, otherwise it's in uppercase.

You can use a single letter. If you prefer you can use “+” for the wild-type gene for a given locus. For example: “**a**” and “+” with genotypes such as “++” and “+**a**” and “**aa**.” This is quicker to write down, but you can run out of letters or it can get confusing if there are many alleles at one locus.

You can use a locus/allele symbol for each gene. Everything at the A locus has a letter **A** or **a** and then the allele symbol in superscript. This notation looks like this: “**A**⁺ **A**⁺” and “**A**⁺ **a**^a” and “**a**^a **a**^a.” It is better for situations where there are many alleles at a given locus, but can be more work to write down.

A separator can also be used between the genes to ensure they don't get smashed together and look like a single symbol. Separators can be a space, a

slash or double slash, a dot, or anything that visually separates them.

For example, if there are three alleles at a locus, the wild-type, an albino allele, and a dilute allele, you could symbolize them in any of these ways:

Wild Type	Albino	Dilute
A	a	a ^d
+	a	d
A ⁺	a ^a	a ^d


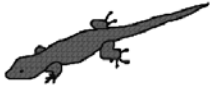

You could symbolize gene pairs in any of the following ways, or another way.

Wild-type	Het albino	Het dilute
A A	A a	A a ^d
A·A	A·a	A· a ^d
A//A	A//a	A// a ^d
+ +	+ a	+ d
+·+	+·a	+·d
+//+	+//a	+//d
A ⁺ A ⁺	A ⁺ a ^a	A ⁺ a ^d
A ⁺ ·A ⁺	A ⁺ ·a ^a	A ⁺ ·a ^d
A ⁺ //A ⁺	A ⁺ //a ^a	A ⁺ //a ^d

There may be a preferred style of notation within each species, and it's recommended to use that style for that species. When working out problems, the best notation is the one that you can most easily read. It is all a matter of personal preference. As long as you can work out the correct answers, use what you prefer.

Genotype And Phenotype

The *phenotype* is the outward appearance. This could be the skin color, the pattern, the shape or size or texture of the scales, the length of the tail, body shape, a certain disposition or behavioral pattern, blood type, and so on.

Genotype	Phenotype
$++$	
$+a$	
aa	

The *genotype* is the actual alleles present at a given locus. Often it is written in symbols to show which alleles are paired up. For example “ $A^+ \cdot A^+$ ” or “ $A^C \cdot A^+$ ”

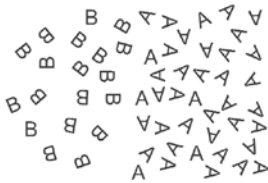
Genotypes can also be written out in plain English, such as “homozygous wild type” or “homozygous albino” or “heterozygous albino.” Homozygous and heterozygous are often abbreviated to *homo* and *het*.

In the case of mutants that are recessive to the wild-type, it is only necessary to specify the recessive gene, for example, “het for albino” would be the same as saying “het for albino and wild-type.”

Dominant, Codominant, Recessive

We know that there can be different versions of a gene, and that each animal has a pair of alleles at each locus, so the next question is what happens when the pair is made of two of these different alleles.

For any pair of alleles, there are two basic types of relationships. The first is dominant/recessive, where one of the alleles is dominant and is expressed. The other relationship is codominance, where both alleles are expressed in some way or another.

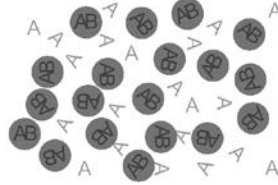


We'll look at dominant / recessive first. For this example, let's say that a black pigment is made when proteins A and B are combined.

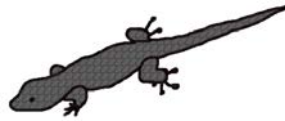
The allele normally found at locus A produces large amounts of protein A, and some protein B is already present in the cells. These proteins gather to produce our lizard's normal pigment.



We will call the normal allele A^+ . When A^+ is paired up with itself, the *genotype* is $A^+ \cdot A^+$. This individual produces plenty of protein A, enough to pair up with all of the protein B in the cells, and make a large amount of pigment.



This creates the typical (or *wild-type*) appearance for this species.



Now we'll add a mutant allele. Let's say that a new mutation occurs, and it is non-functioning. That is, this mutant allele doesn't produce any protein A at all. We will call it A^a .

When A^a is paired up with the normal A^+ allele, the genotype is $A^a \cdot A^+$. The "+" allele will continue to do its normal thing, producing large amounts of protein A. Meanwhile, the "a" allele will do its thing, and produce nothing.

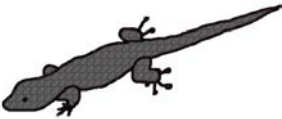




With only one functioning “A” allele, only half as much of protein A is produced. But this is still enough to combine with all of the existing protein B, so there is still the same amount of pigment.



As a result, this lizard looks the same as the other wild-type lizards that are carrying two copies of the normal allele.



Notice that the “a” allele is present, but its effect is not seen to us. This is called a dominant / recessive type relationship. The dominant “+” allele is expressed, but the recessive “a” allele is not expressed.

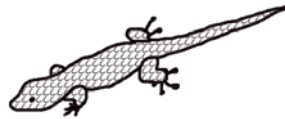
A recessive allele is not always hidden. If it is paired with itself, its effect becomes visible. Let's see what happens when the genotype is $A^a \cdot A^a$ instead.



Since both alleles in the pair are the non-functioning "a" mutant, protein A is not produced at all. Only protein B is present.



Since the pigment is made from A and B combining, there is no pigment produced. The resulting lizard would have no pigment, and would be an albino.



Any two alleles A_1 and A_2 can be paired up in three different ways:

Recessive Mutant

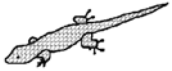
$++$



$+a$



aa



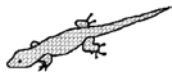
A_1/A_1 , or A_1/A_2 , or A_2/A_2 . In this case, we can only create two different appearances. The het genotype still produces the phenotype of the dominant gene.

Dominant Mutant

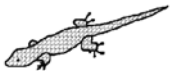
$++$



$+A$



AA



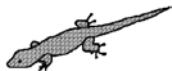
This is called a dominant / recessive relationship. The *dominant* allele is the one that is expressed whenever it is present. The *recessive* allele is the one that is only expressed when it is the only allele present.

Codominant Mutant

$++$



$+a$



aa



The other relationship is codominance. What this means is that both alleles have some amount of dominance, and whenever that allele is present, its effects can be seen. This doesn't mean the two

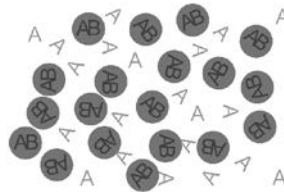
alleles have an equal amount of expression, only that neither allele is "invisible."

Let's look at what happens if our above alleles are codominant to each other, instead.

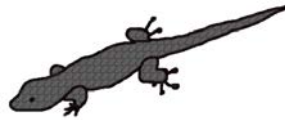
Our black pigment is made when proteins A and B are combined. The allele normally found at locus A produces protein A.



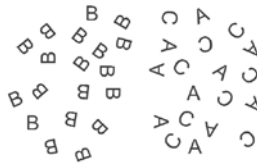
These proteins gather to produce our lizard's normal pigment.



When the genotype is $A^+ \cdot A^+$, the phenotype is normal.



Let's say our new mutant allele produces protein C instead of protein A. We'll call it A^C . Let's look at genotype $A^+ \cdot A^C$

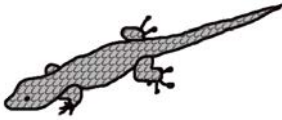


Proteins A and C are both produced. When protein C combines with protein B, it makes a light gray pigment.

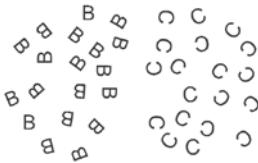




A lizard with genotype $A^+ \cdot A^C$ would produce both the dark pigment and the light pigment.



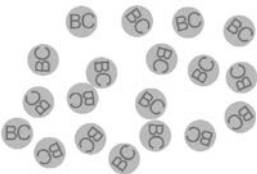
Overall its skin would be lighter than the normal type.



The remaining genotype is $A^C \cdot A^C$. This individual would produce only protein C and no protein A.

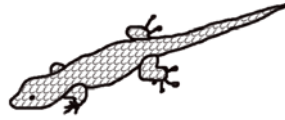


All of the pigment produced would only be protein C and B combined.



The pigment would all be light gray, and this individual would be lighter colored than the other two types.

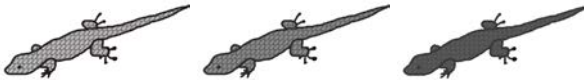
Notice that there are a total of three different looks, to go along with the three different genotypes.



This is one of the ways to determine whether you would consider two alleles to be codominant to each other. If there are three phenotypes, they are codominant. If there are only two phenotypes, they are dominant/recessive.

Many different terms are used to describe codominance: semidominant, partially dominant, incomplete dominant, the list goes on. There may be certain usages that each of these have within certain groups of people, but generally they are interchangeable, with the key being that they produce 3 possible phenotypes.

There are also many ways in which two codominant alleles can both be expressed. For example, let's say there are "black" and "white" alleles which are codominant. Many phenotypes could be produced. The effects of the two alleles might appear to blend, which would produce lizards that are a certain shade of gray.



Or they might produce lizards where one color dominates different regions of the individual, and the other color dominates the rest of the lizard.



Or there could be areas which are mostly white with black spots, and areas that are mostly black with white spots. Or the “spots” could be blended so that various shades of gray are present in different regions.



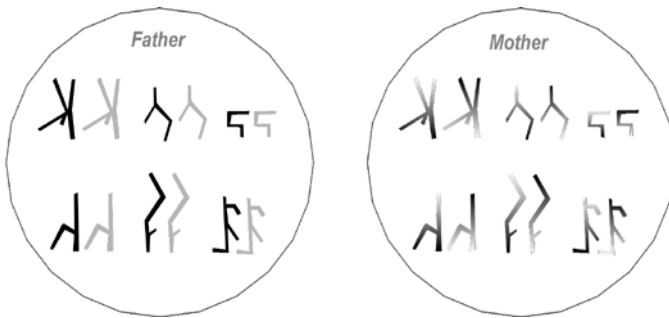
In this final example, black and white dots are present, but whether or not you see a lizard that is black and white, or a gray lizard, depends on how closely you look at it.



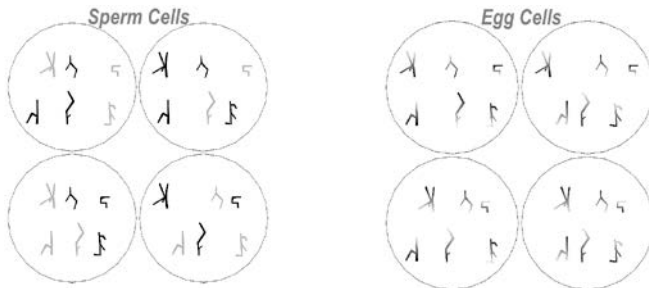
As you see, codominance can take many forms. Again, the important part of codominance is if there are three phenotypes and whether or not you are able to consistently identify the third phenotype.

Inheritance

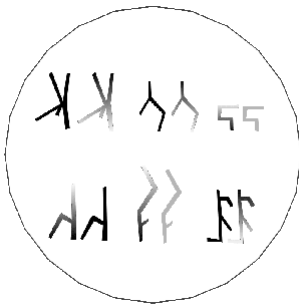
Inheritance is the process by which genes are passed down from parents to offspring. The simplified model is shown below.



Each parent has two sets of chromosomes, and each offspring has two sets of chromosomes. This is a key point of inheritance: only half of each parent's genes are passed down to a given offspring.



Offspring are produced by sperm/egg combination. The father produces sperm cells, the mother produces egg cells. Notice that each of these only carries one genome instead of two. (This is called *haploid*, and cells with two genomes are called *diploid*.)



The combined sperm/egg now has two genomes, each of the genes is paired, just like in the parents. This newly fertilized egg is called a *zygote*. (The terms heterozygous and homozygous come from this word.) It will divide

and become all of the cells in the body, so that all the cells have the same chromosomes as the zygote. Pictured below are some of the different fertilized eggs that could have come from the same breeding.



Each offspring has only half of its mother's genes, and half of its father's genes. This also means that half of its mother's genes were **not** inherited, and half of its father's genes were **not** inherited.

Predicting Outcomes

Once we know the way genes are inherited, and how they control the appearance of the animal, we can use this knowledge to predict the outcomes of any pairing.

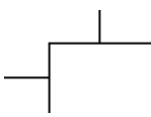
A note about predictions: all of the numbers given by predictions are probabilities. For example, if you flip two coins, the prediction is that you will get 50% heads and 50% tails. However, this does not mean that if you flip two coins, you **must** get one heads and one tails.

It should also be noted that in smaller litters, the actual results can vary wildly from the predictions. As the sample size increases, the result will tend more toward “expected.” To use the coin example again, if you flip two coins, about half the time you will get two heads or two tails, which are a huge variation from the expected. But if you flip 1,000 coins, you will almost always get a number of heads/tails reasonably close to 500 each.

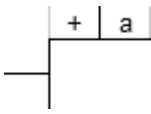
Unless otherwise stated, they are also independent events, meaning the outcome of one event has no effect on the outcome of another. For example, if you flip two coins, the result of one has no influence on the result of the other.

Punnett Squares

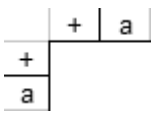
The most commonly taught method for predicting outcomes is the Punnett square. The idea here is very simple: list all possible sperm genotypes, list all possible egg genotypes, combine each sperm type with each egg type.



For a single locus (also called a monohybrid cross) the sperm types are the two genes that the male has. Remember, each sperm cell carries only one of the two genes.

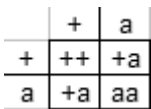


If the male's genotype at the A locus is "+ · a" then the possible sperm are "+" and "a." We will put these along the top of the square.



If the female's genotype at the A locus is "+ · a" then the possible eggs are "+" and "a." We will put these along the left of the square.

Finally, fill in each square by combining the gene from the sperm cell with the gene from the egg cell. This gives you all of the possible genotypes the offspring can inherit.



The Punnett square stays the same for all crosses at a single locus, but it can be simplified. However, the process of simplifying is more work than building the square itself. Building a single-locus square can be replaced by an easier process called “FOIL.” When

you have the two sperm types and two egg types, you make your four possible outcomes by taking the First, Outside, Inside, and Last pairs of genes.

First	+ a	+ a	= + • +
Outside	+ a	+ a	= + • a
Inside	+ a	+ a	= a • +
Last	+ a	+ a	= a • a

This method and the Punnett square method work the same way no matter what genes are placed at the locus.

When a cross involves two loci, (also known as a *dihybrid cross*) the Punnett square gets a bit larger. There are four types of sperm and four types of eggs, and a total of sixteen squares to be filled in. You can use FOIL on the father’s genotype to determine the possible sperm types. We’ll use $A^+A^+B^+b^b$ as a genotype.

First	$A^+ a^a$	$B^+ b^b$	$A^+ B^+$
Outside	$A^+ a^a$	$B^+ b^b$	$A^+ b^b$
Inside	$A^+ a^a$	$B^+ b^b$	$a^a B^+$
Last	$A^+ a^a$	$B^+ b^b$	$a^a b^b$

You can use FOIL on the mother's genotype to determine the possible egg types. We'll use $A^+A^+B^+b^b$ as a genotype.

First	$A^+ a^a$	$B^+ b^b$	$A^+ B^+$
Outside	$A^+ a^a$	$B^+ b^b$	$A^+ b^b$
Inside	$A^+ a^a$	$B^+ b^b$	$a^a B^+$
Last	$A^+ a^a$	$B^+ b^b$	$a^a b^b$

Now that we have all possible eggs and all possible sperm types, we can place them in a Punnett square.

	$A^+ B^+$	$A^+ b^b$	$a^a B^+$	$a^a b^b$
$A^+ B^+$	$A^+ A^+ B^+ B^+$	$A^+ A^+ b^b B^+$	$a^a A^+ B^+ B^+$	$a^a A^+ b^b B^+$
$A^+ b^b$	$A^+ A^+ B^+ b^b$	$A^+ A^+ b^b b^b$	$a^a A^+ B^+ b^b$	$a^a A^+ b^b b^b$
$a^a B^+$	$A^+ a^a B^+ B^+$	$A^+ a^a b^b B^+$	$a^a a^a B^+ B^+$	$a^a a^a b^b B^+$
$a^a b^b$	$A^+ a^a B^+ b^b$	$A^+ a^a b^b b^b$	$a^a a^a B^+ b^b$	$a^a a^a b^b b^b$

An alternative to combining sperm/egg with a Punnett square is to determine the results on each locus using FOIL, and then combine the loci with a grid instead.

We'll use the same cross as above: “+ a” at the A locus and “+ b” at the B locus.

First, FOIL the A locus:

First	+ a	+ a	++
Outside	+ a	+ a	+ a
Inside	+ a	+ a	+ a
Last	+ a	+ a	a a

Next, FOIL the B locus:

First	+ b	+ b	++
Outside	+ b	+ b	+ b
Inside	+ b	+ b	+ b
Last	+ b	+ b	b b

Now, put one locus across in a grid, and the other locus down.

	++	+ a	+ a	aa
+ +	++ ++	+a ++	+a ++	aa ++
+ b	++ +b	+a +b	+a +b	aa +b
+ b	++ +b	+a +b	+a +b	aa +b
b b	++ bb	+a bb	+a bb	aa bb

If you want to add another locus, you can make another grid to do so. Take all of the *results* from the previous grid, and use those down the left column, and the new locus across the top. We will add in results for a C locus.

	CC	Cc	Cc	cc
++ ++	++ ++ CC	++ ++ Cc	++ ++ Cc	++ ++ cc
++ +b	++ +b CC	++ +b Cc	++ +b Cc	++ +b cc
++ +b	++ +b CC	++ +b Cc	++ +b Cc	++ +b cc
++ bb	++ bb CC	++ bb Cc	++ bb Cc	++ bb cc
+a ++	+a ++ CC	+a ++ Cc	+a ++ Cc	+a ++ cc
+a +b	+a +b CC	+a +b Cc	+a +b Cc	+a +b cc
+a +b	+a +b CC	+a +b Cc	+a +b Cc	+a +b cc
+a bb	+a bb CC	+a bb Cc	+a bb Cc	+a bb cc
+a ++	+a ++ CC	+a ++ Cc	+a ++ Cc	+a ++ cc
+a +b	+a +b CC	+a +b Cc	+a +b Cc	+a +b cc
+a +b	+a +b CC	+a +b Cc	+a +b Cc	+a +b cc
+a bb	+a bb CC	+a bb Cc	+a bb Cc	+a bb cc
aa ++	aa ++ CC	aa ++ Cc	aa ++ Cc	aa ++ cc
aa +b	aa +b CC	aa +b Cc	aa +b Cc	aa +b cc
aa +b	aa +b CC	aa +b Cc	aa +b Cc	aa +b cc
aa bb	aa bb CC	aa bb Cc	aa bb Cc	aa bb cc

Additional loci could be added in as many times as you like. But as you can see, the work gets to be very repetitive. Another shortcut can be used to bypass the large grid and Punnett square techniques, and is advantageous because generally you are only interested in knowing the odds of one or a few of the actual results.

The odds of two or more independent things all happening are determined by multiplying the odds of all the individual events. Using this, we can determine the odds of the desired outcome at each locus, and then just multiply them all together. We'll start with something simple.

Say you are crossing “+a +b” X “+a +b” and you want to get an “aa bb” outcome. First how likely is “aa” to happen?

First, FOIL the A locus:

First	+ a	+ a	++
Outside	+ a	+ a	+ a
Inside	+ a	+ a	+ a
Last	+ a	+ a	a a

One of the four outcomes is the one you want. So the odds at A are $\frac{1}{4}$.

Next, FOIL the B locus:

First	+ b	+ b	++
Outside	+ b	+ b	+ b
Inside	+ b	+ b	+ b
Last	+ b	+ b	b b

One of the four outcomes is the one you want. So the odds at B are $\frac{1}{4}$. Just multiply all of your loci together. When multiplying fractions, you multiply all the top numbers to each other, and all the bottom numbers to each other. So $\frac{1}{4} \times \frac{1}{4} = \frac{1}{16}$. Note that this is the same answer you get with the other two methods, but it’s a lot less work.

If you want to also determine the odds of getting an offspring with “aa” but not “bb” you use the same FOIL results as above, and determine that the chance of getting “aa” is $\frac{1}{4}$, and the chance of

getting “anything but **bb**” is $\frac{3}{4}$. Multiplying again, you get $\frac{1}{4} \times \frac{3}{4} = \frac{3}{16}$.

Since there are always a maximum of 4 outcomes at any locus, this means that the odds for a locus will always be a multiple of $\frac{1}{4}$. Your numbers will always be 0, $\frac{1}{4}$, $\frac{1}{2}$, $\frac{3}{4}$, or 1. Remember, anything multiplied by zero is zero, so if you run into a zero there’s no chance of the desired outcome.

Let’s do another practice problem. When crossing $+a\ bb\ +c \times aa\ +b\ +c$, what are the odds of getting an offspring with genotype “ $aa\ bb\ cc$?”

FOIL the A locus: $(+a \times aa) = +a, +a, \mathbf{aa}, \mathbf{aa} = \frac{2}{4}$.

FOIL the B locus: $(bb \times +b) = +b, \mathbf{bb}, +b, \mathbf{bb} = \frac{2}{4}$.

FOIL the C locus: $(+c \times +c) = ++, +c, +c, \mathbf{cc} = \frac{1}{4}$.

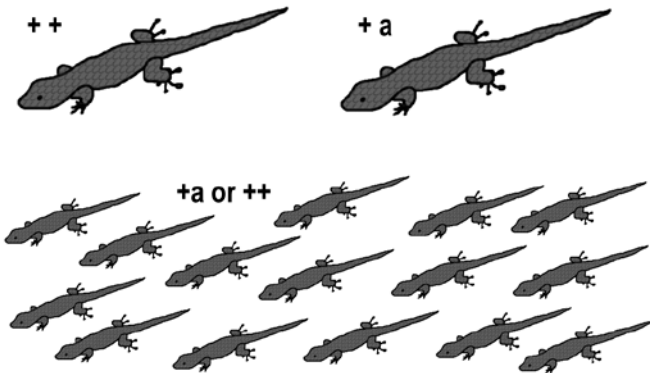
The total odds are $2 \times 2 \times 1 / 4 \times 4 \times 4$ or $\frac{4}{64}$, which simplifies to $\frac{1}{16}$.

As a final note, it should be kept in mind that the odds calculated are per offspring. If you have multiple offspring, you get multiple chances at producing the desired offspring. But remember that there are no guarantees. If you are going up against 1 in 16 odds, having 16 chances does not guarantee success, any more than flipping two coins guarantees you will get a heads.

Possible Hets

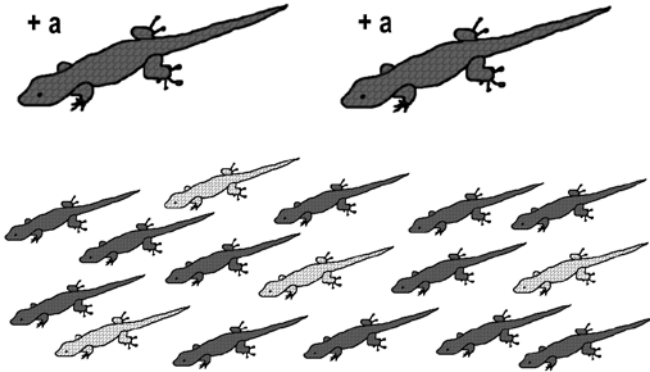
This concept is widely used among hobbyists and breeders, and you may see it often in your favorite species. These come from certain crosses involving recessive genes.

The first example is when crossing something like “+**a** X ++” which is: het for a dominant/recessive pair to a mate that is homo for the dominant gene.



FOIL gives us +**a** and ++ as results. When this litter hatches, all of the offspring will look the same, yet our prediction says approximately 50% of them will be carrying the **a** gene. Instead of ignoring that and labeling them all normal, they can be considered to have a 50% chance of carrying the **a** gene, or “50% possible het for **a**.”

The other common “possible het” is a 66% chance and also involves a recessive/dominant pair. This time it is when two heterozygous parents are bred together, such as crossing $+a \times +a$.



FOIL of the A locus for the above

F	+ a	+ a	++
O	+ a	+ a	+ a
I	+ a	+ a	+ a
L	+ a	+ a	a a

When this litter hatches, the “**aa**” offspring will be visibly expressing the recessive “**a**” gene. This leaves 3 other possibilities for the normal-looking offspring: they could be ++, +a, +a. Our prediction says that approximately 2/3 of them (the two “+a” results) are expected to carry the recessive **a** mutant. Instead of ignoring this, they can be labeled as “66% possible het.”

Another situation is when two recessive mutants exist at the same locus. This cross is “+**a** x +**a^d**.”

F	+ a	+ a ^d	++
O	+ a	+ a ^d	+ a ^d
I	+ a	+ a ^d	+ a
L	+ a	+ a ^d	a a^d

Normal-looking offspring in this litter could be considered “66% possible het for **a** or **a^d**.”

When two recessive mutants exist at the same locus, it's also possible to have offspring that are known to be hets, but it's unknown *which* of the recessive alleles it carries. Notice that all of these offspring are “het for *either a or a^d*.”

F	++	a a^d	+ a
O	++	a a^d	+ a ^d
I	++	a a^d	+ a
L	++	a a^d	+ a ^d

Remember, in reality a “possible het” always has an actual genotype and the percentages are *only the chance* of a certain outcome. So if you breed two so-called “50% hets” to each other, in reality you are either breeding two non-hets, or one het and one non-het, or two hets to each other.

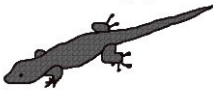
Breeding trials can be used to determine the real genotypes, by proving whether or not an individual can produce offspring with the recessive trait. This is discussed in the advanced topics.

Masking (Epistasis)

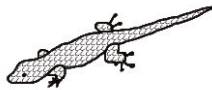
In some situations, a gene acting at one locus can hide the effects of a gene at another locus.

For example, if there is a trait that removes all color and pattern (in many species known as “leucistic”) and another trait that normally removes pigment in some areas to create a spotted pattern. The spotted pattern could have no effect on a leucistic individual even though the genes are present and it could still produce spotted offspring.

Wild-type



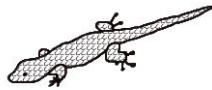
Leucistic



Spotted



Spotted Leucistic



Since the words dominant, codominant, and recessive are used to describe the relationships of genes that share the *same* locus, another term is used to describe where genes at different loci affect each other. The technical term is *epistasis* but it is often referred to as masking, where expression of one trait masks expression of the other.

Masking also can create a situation similar to the “possible het” scenario, and it isn’t just restricted to recessive genes. In the above example, it would be impossible to know just by looking at a leucistic individual if it was also expressing or carrying the spotted gene. The only way to know its genotype is by applying logic to what is known about its parents/offspring.

If the parents were both het for the spotted gene, then FOIL shows us that there are four familiar possibilities at this locus:

F	+ s	+ s	++
O	+ s	+ s	+ s
I	+ s	+ s	+ s
L	+ s	+ s	s s

In this case, 50% of the outcomes are “+ s” and another 25% are “s s.”

Depending on your preference, this could be expressed as “*possible het or homo for s*” or given with odds as “*50% possible het s, 25% possible homo s.*”

In other cases if it is only important whether the r gene is present, they could be described as “*75% possible carrier of s.*”

Advanced Topics

The Advanced section contains topics that go into more detail than the simplified presentation in the previous section of this book. These ideas are not necessarily important to every given species, but are presented for those who have discovered they wish to learn more about genetics than just the basics.

Once you have tackled the basic concepts, you should be able to grasp the rest of the topics presented here. They are not necessarily more difficult, they just require the previous concepts as a basis to build upon.

Advanced Inheritance & Linkage

In the simplified model it was shown that whole chromosomes were put into each sperm and egg cell. In reality there is an important extra step in the process of sperm/egg production: crossover.

Here a diploid cell (has two sets of chromosomes) is shown before crossover. The black chromosomes are what it inherited from one parent, the gray from the other parent.



Crossover is where the two chromosomes from a pair are each broken up in the same places, and the same parts are exchanged to form a pair of chromosomes, each of which is a mixture of both of the originals.



This allows genes to be inherited in a group that is smaller than a whole chromosome. Thus they can be mixed up more. If they were inherited as an entire chromosome, then any two genes that were on the same physical chromosome would always go

into the same sperm or egg cell. If you had an advantageous and a detrimental gene on the same chromosome, this would make it nearly impossible to get rid of the “bad” gene and keep the “good” one.

Gene Linkage



Since crossovers take place at different locations each time sperm/eggs are produced, the closer two loci are physically located to each other, the less likely it is that one of these splits will happen *between* the two, and cause them to separate.

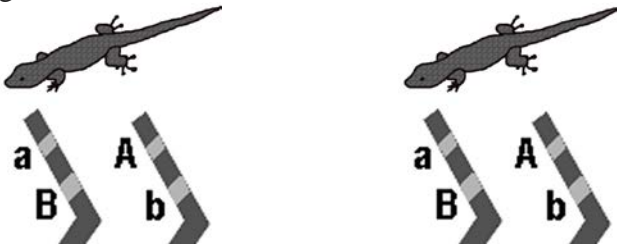


In this example, loci A and B are closer to each other than C. If they are close enough that crossovers occur only some of the time between A and B, then they will not be inherited independently from each other all the time. Their inheritance is said to be *linked*.

Let's say that A and B only separate 20% of the time, and 80% of the time they are inherited together. Let's see what happens when recessive mutant **a**, which causes the color to be a light gray, is linked to recessive mutant **b**, which causes the pattern to be spotted instead of solid.



We will cross a light gray lizard (homozygous for **a** and **B**) to a spotted lizard (homozygous for **A** and **b**) and then breed these first generation offspring together.



Our first generation (F1) offspring are normal looking and double het for the **a** and **b** mutants. Notice that the **a** and **b** mutants are on opposing chromosomes.



We picked 80% linkage for this example, so the result is that when sperm or egg cells are produced, 80% of the time **A** and **B** don't cross over, and sperm or egg cells will be one of these examples.





The other 20% of the time there is a crossover between the two loci. This will cause a sperm or egg cell with one of these two types.



This means that one out of every 10 sperm or egg cells has both mutants **a** and **b** in it. The chance of 1 in 10 sperm combining with 1 in 10 eggs is 1 in 100. Without the linkage the odds would only be 1 in 16. We can create a Punnett square showing all of the possible sperm and eggs to illustrate our outcomes.

First, list all possible sperm/egg cells, since the crossed over results are only one in five times, we would have: 4 x aB, 4 x Ab, 1 x AB, and 1 x ab.

	aB	aB	aB	aB	Ab	Ab	Ab	Ab	AB	ab
aB										
aB										
aB										
aB										
Ab										
Ab										
Ab										
Ab										
AB										
ab										

Like any other Punnett square, it is filled in by combining sperm and egg. Since large areas are the same genotype we can merge them all together to

make the results easier to see. Here is the filled-in result.

	aB	aB	aB	aB	Ab	Ab	Ab	Ab	AB	ab	
aB											
aB	aa BB				Aa Bb				Aa BB	aa Bb	
aB											
aB											
Ab											
Ab											
Ab	Aa Bb				AA bb				AA Bb	Aa bb	
Ab											
AB	Aa BB				AA Bb				AA BB	Aa Bb	
ab	aa Bb				Aa bb				Aa Bb	aa bb	

Comparing this to a regular (non-linked) cross trying to create homozygous a and b from heterozygous parents, which is 1 in 16 odds, we see that linkage can affect the expected behavior of two traits pretty drastically. The linkage can be anywhere from nothing to almost completely inseparable.

Genotype	Normal	Linked
AA BB	6	1
AA Bb	12	8
AA bb	6	16
Aa BB	12	8
Aa Bb	25	34
Aa bb	12	8
aa BB	6	16
aa Bb	12	8
aa bb	6	1

This may seem like a bad situation for someone trying to combine two genes to create a new combination. But it is a two-way street: once two linked genes have been combined, they are also equally difficult to separate. Let's use the same example, but start out with the two mutants already combined, and attempt to separate them.



This time we will cross a spotted, light gray lizard (homozygous for *a* and *b*) to a normal lizard (homozygous for *A* and *B*) and then breed these first generation offspring together.



Our first generation (F1) offspring are normal looking and double het for the *a* and *b* mutants. Notice that the *a* and *b* mutants are on the same chromosome. Last time they were on opposites.

Like any other Punnett square, it is filled in by combining sperm and egg. Since large areas are the same genotype we can merge them all together to make the results easier to see. Here is the filled-in result.

	ab	ab	ab	ab	AB	AB	AB	AB	Ab	aB	
ab	aa bb				Aa Bb				Aa bb		aa Bb
ab											
ab											
ab											
AB	Aa Bb				AA BB				AA Bb		Aa BB
AB											
AB											
AB											
Ab	Aa bb				AA Bb				AA bb		Aa Bb
aB	aa Bb				Aa BB				Aa Bb		aa BB

Notice that the linked genes almost behave like a single locus. The four results on the upper left are the same as a single-gene cross.

Compare these results to the standard outcome from this cross when the genes are not linked, when they are linked but on opposing chromosomes, and when they are linked on the same chromosome. As you can see, linkage can make two genes act somewhat like a single gene. Again, the strength of the linkage depends on how close or far away they are, and two genes can be anywhere from not linked, to almost always inherited together, or anywhere in between.

Genotype	Normal	Opposite	Same
AA BB	6	1	16
AA Bb	12	8	8
AA bb	6	16	1
Aa BB	12	8	8
Aa Bb	25	34	34
Aa bb	12	8	8
aa BB	6	16	1
aa Bb	12	8	8
aa bb	1	1	16

Comparison showing the difference of results between linked genes starting on the same chromosome versus linked genes starting on opposite chromosomes.

Proving Traits

If you want to predict the outcomes of a breeding, you need to know if a certain trait is controlled by a gene, and what type of inheritance pattern it follows. In order to do this, it needs to be shown what kinds of results occur from certain crosses, and then which mode of inheritance it matches.

The three types of Mendelian traits are recessive, codominant, and dominant.

One of the main characteristics of a Mendelian trait is its on/off nature. That is, when the trait is present, it is clearly different from specimens not expressing the trait.

Some traits can be variable in how they are expressed, but usually do not provide a smooth transition between the “on” and “off” phenotypes. If there is a smooth transition, it is more likely a result of selective breeding. Though it may be genetic, the phenotype in question may actually be controlled by a significant number of genes, which means it would not have the same predictable behavior as Mendelian traits do.

It is also a good idea to avoid using specimens that show similar tendencies to the trait in question. The

reason is that this can obscure the clear on/off indication that you are looking for.

For example, if you have lizards that are normally dark gray and you want to try and isolate a gene that reduces the gray to a lighter color, do not cross your test specimens into lizards that are already lighter gray. If you get lighter gray offspring, you have no way of knowing if they are expressing the suspect gene or if they are just like that because they are showing selective breeding influences from the other parent.

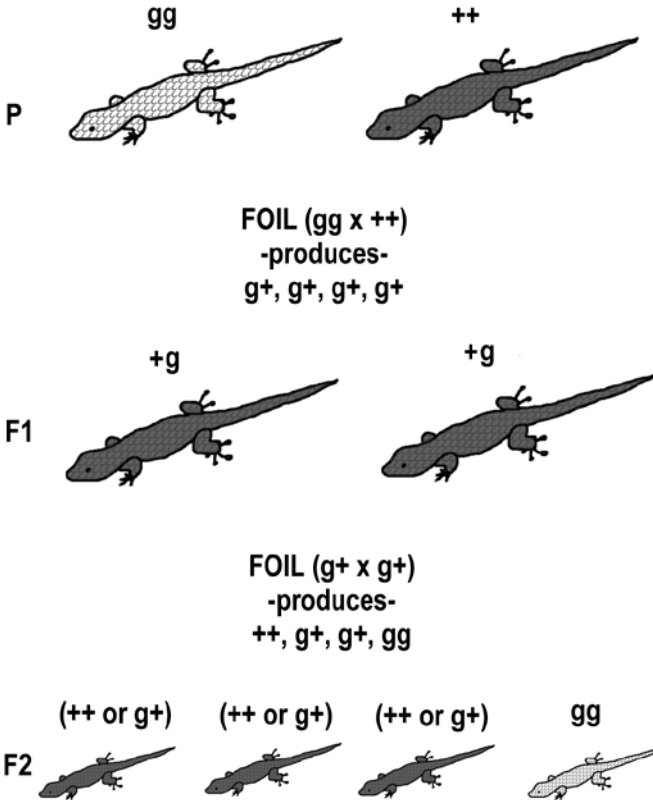
The first cross should involve the suspected individual and a typical looking unrelated specimen. It is recommended to do this in parallel to confirm the results, meaning the suspect should be bred to produce more than one litter of offspring.

You need 3 generations in order to prove a trait as one of the three types of Mendelian traits. Typically, the original generation is called the “P” and their offspring are the “F1” and the grandchildren are the “F2.” These are used to mean the “parent” and “first filial” and “second filial.”

Recessive Genes

Proving a recessive gene involves outcrossing and then inbreeding. If a gene is recessive, then the individual expressing it must be homozygous for it.

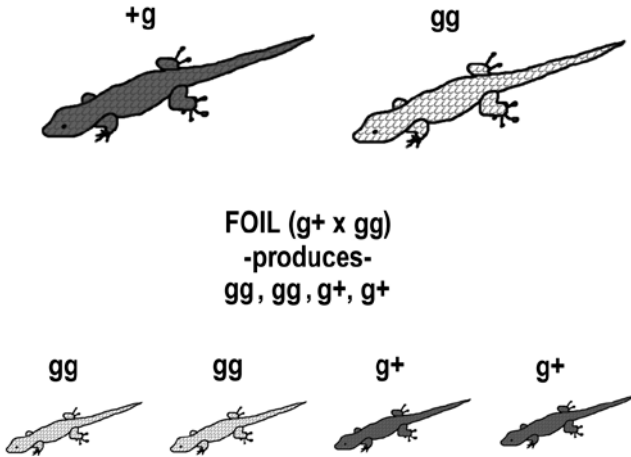
Also, any known hets you produce will not express the trait. And finally, crossing known hets produces a split litter containing approximately 25% of the offspring expressing the trait.



All three generations are necessary as proof. Sometimes an odd looking individual will occur through non-genetic means, so the F2 generation is

necessary to show if the trait can be recovered from carriers.

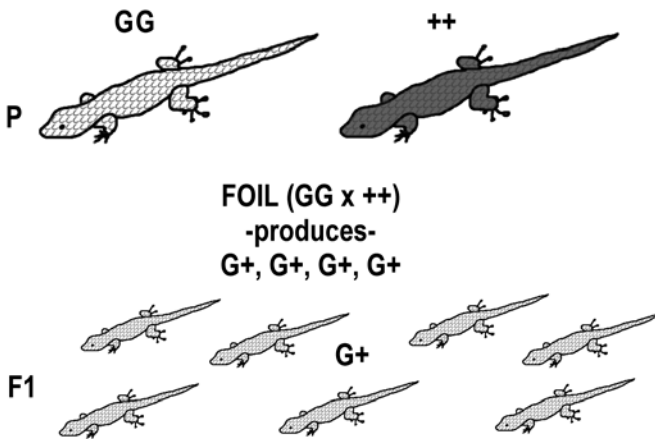
An alternate method is to cross a heterozygous specimen to a homozygous specimen. For example, cross an F1 back to the parent. The resulting clutch should be split between the two phenotypes, this time with the prediction of equal numbers of each phenotype.



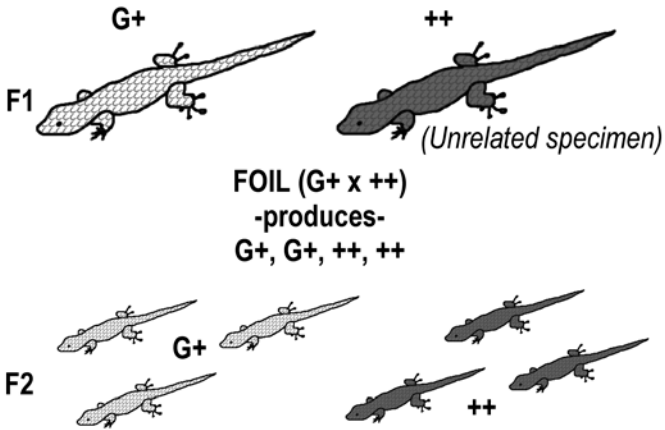
Dominant Genes

Proving a Mendelian dominant gene is a slightly different process. This time, your expected phenotype could show up in either in half or in all of the F1 generation. This depends on whether the original suspect was homozygous or heterozygous for the gene.

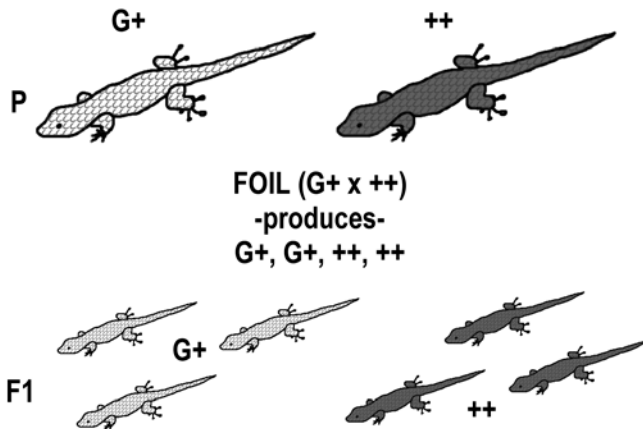
If it is homozygous, all of its offspring inherit the dominant gene and will express it.



But since this leaves only one phenotype, an on/off comparison cannot be shown, thus an additional generation must be produced to show the gene's on/off nature. Outcrossing one of the second generation (heterozygous) specimens to an unrelated non-carrier will accomplish this.



Going back to the beginning again, if the suspect is **heterozygous** for the dominant gene, the on/off indication will be present in the litter.

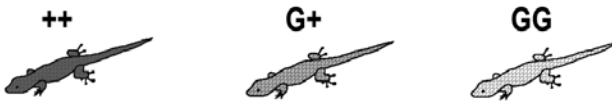


However, this result is identical to what is produced by a codominant gene, so a third generation must be

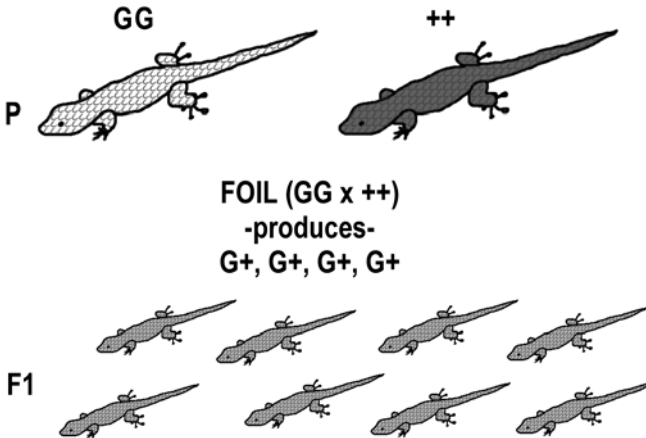
produced to show whether it is dominant or codominant.

Codominant Genes

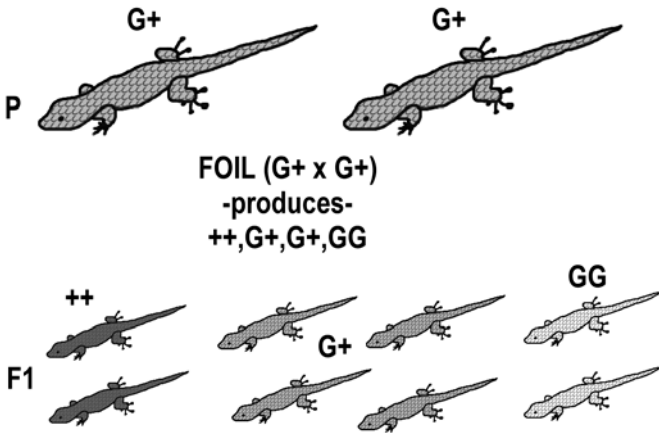
Codominant genes vary from dominant/recessive pairs in an important way: instead of two possible phenotypes, there are three. There is one phenotype to match up with each genotype. For our light gray we could use these three phenotypes:



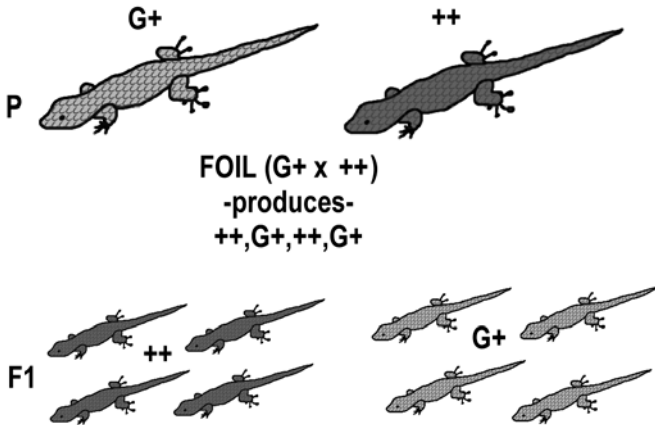
Like the situation with dominant genes, the original specimen might be heterozygous or homozygous for this mutant. If it is homozygous, then all of the first offspring will show an “in-between” phenotype.



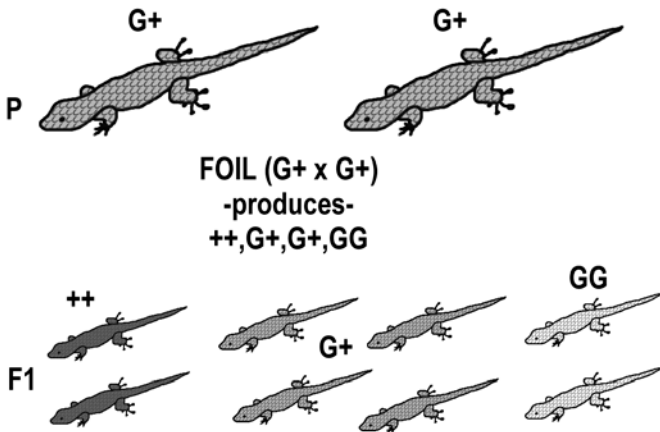
However, with selectively bred traits, many times the offspring will take on an appearance between that of the two parents. The next generation is needed to prove the three available phenotypes are clearly reproducible. Breeding het to het is an easy way to do this.



Going back to the beginning, if the original specimen is heterozygous, then the first result will resemble that of a dominant gene. Since only two phenotypes exist, there is no indicator of a codominant relationship yet.



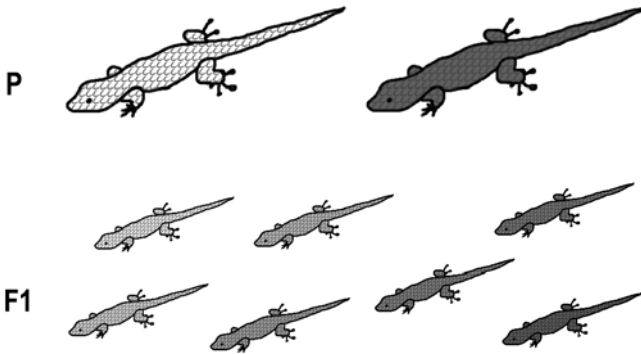
Again, breeding het to het will show whether there are two or three phenotypes.



Selective Breeding (Polygenic or multi-gene traits)

Not all looks are caused or controlled by a single gene. Some are environmental, some are simply non-reproducible flukes (basically a birth defect) and some are caused by the interactions of a larger number of genes. This last case is also known as *polygenic* which literally means “many genes.”

If the first generation in a breeding trial produces a smooth variety of looks between two types, with no clear on/off indication, then it’s likely that the trait in question is not controlled by a single gene.

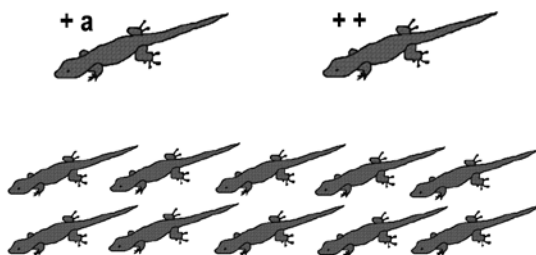


Until/unless some reliable way of separating them into clear phenotypes is found, it would be unrealistic to treat this in the same way as traits controlled by Mendelian genes.

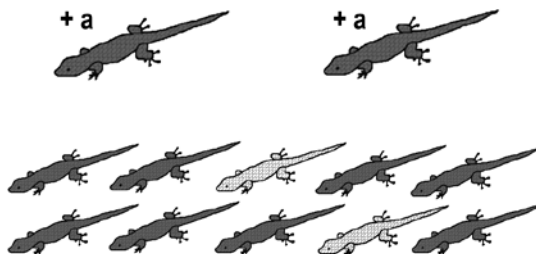
Proving Possible Hets

When working with specimens that are considered possible hets for a recessive gene, there is only one way to determine whether or not they are actually het or not het. This is through test breeding.

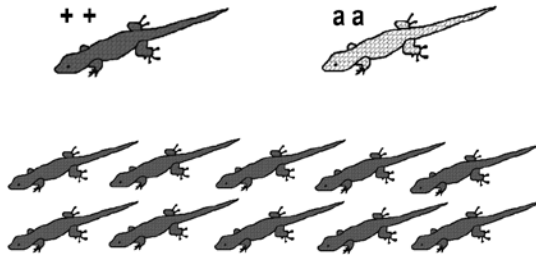
The purpose of test breeding is to determine if an individual can or cannot pass down a given gene. The way to determine this is by matching it up with a mate who carries the gene so that their offspring will provide a clear indication.



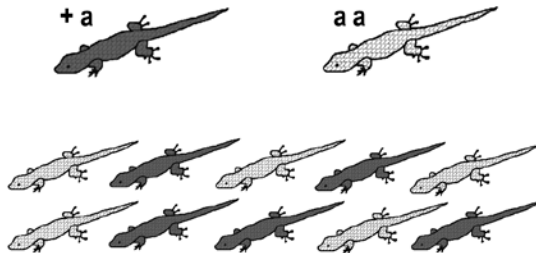
Breeding a possible het to a known het showing a negative result (above) and a positive result (below)



For example, a specimen is possible het for the recessive “a” gene. If you cross it to an individual that is known to carry the “a” gene, then some of the offspring may express the trait.



Test cross against a homozygous mate, showing a negative result (above) and a positive result (below)



If it produces offspring that you know are “aa” then the “a” gene must have come from each parent, which proves the individual is an actual carrier. When this happens you have a positive result.

Note that there is no 100% negative result, since it’s always possible you were just unlucky enough to not pair up the right genes. Larger numbers of offspring increase the accuracy of your “negative” result.

Removing Genes

Sometimes a bad gene will either appear in, or make its way into your breeding stock. It helps to know how to remove these genes from your lines, especially recessive genes.

The easiest are dominant and codominant genes. The solution is very simple: do not breed anything that carries the gene. Since the gene is always visible when present, this is an easy problem to solve.

Recessive genes, however, require more effort and planning, because it is not always possible to know which individuals carry them. For example, if you have two normal parents that produce an offspring expressing a bad recessive gene, culling the parents and all of their offspring still does not remove this gene, unless they happen to have no other relatives in your stock.

The first step is to determine who the gene carriers are. The second step is to remove all of them so that they do not contribute the bad gene any longer.

To determine who carries the gene, an individual known to carry the gene must be used in breeding trials. In many cases, a bad recessive gene is fatal when expressed, and thus a homozygous specimen

cannot be used for test breeding, therefore a heterozygous tester is needed.

Note that during breeding trials, *any* offspring that express the bad gene are proof that the parent in question is a carrier, and the trial is concluded. No matter how many healthy specimens are produced, a positive result is not reduced or erased by that. Further breeding trials that produce all “good” offspring do not disprove the previous positive result. The only exception to this is if there is reason to suspect sperm was retained from a prior mating.

#	Odds
1	50.0000%
2	25.0000%
3	12.5000%
4	6.2500%
5	3.1250%
6	1.5625%
7	0.7813%
8	0.3906%
9	0.1953%
10	0.0977%
11	0.0488%
12	0.0244%
13	0.0122%
14	0.0061%
15	0.0031%
16	0.0015%

When testing against a mate that is homozygous for the bad gene, a sample of at least 11-16 offspring is desired. The higher the number of offspring, the more definite the result. This chart shows the odds of a specimen being a non-carrier given the number of good offspring produced against a homozygous test mate.

These numbers are determined by taking 2 to the power of the number of offspring.

#	Odds
8	10.0113%
9	7.5085%
10	5.6314%
11	4.2235%
12	3.1676%
13	2.3757%
14	1.7818%
15	1.3363%
16	1.0023%
17	0.7517%
18	0.5638%
19	0.4228%
20	0.3171%
21	0.2378%
22	0.1784%
23	0.1338%
24	0.1003%
25	0.0753%

When testing against a mate that is heterozygous for the bad gene, a larger sample is needed. The chart shows the odds of an individual being a carrier, given the number of good offspring produced against a heterozygous mate.

These numbers are determined by taking $\frac{3}{4}$ to the power of the number of offspring.

Once an individual has been tested as “sufficiently negative” (which is the breeder’s decision) it can then be used with the understanding that it is unlikely to give the bad gene to any of its offspring.

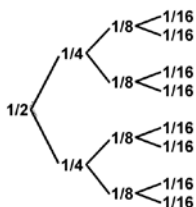
If an individual is determined to be a carrier through a positive result, it can be used as a test breeder, or culled. Keep in mind that known carriers will be needed until all of a breeder’s stock has been cleared of the bad gene.

Once all of the stock has been tested, it will be possible to remove the bad gene from the pool by culling all of the known carriers.

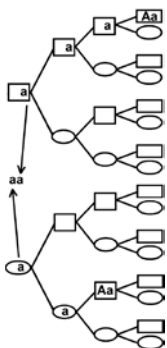
It is also sometimes suggested that these problems can be eliminated by avoiding all inbreeding, or by not breeding related individuals. But this does not provide a solution. Instead it hides the problem, which will then be a greater problem when it reappears. If carriers of the bad gene are always bred to “unrelated” individuals, then the bad gene will be propagated into more and more bloodlines, until it is present in every line, and even “unrelated” individuals are carriers. By that time, any cross might pair up two carriers, bringing out the bad gene again.

Inbreeding

Inbreeding is the breeding of “related” individuals. Generically, it means that the individuals being bred are more closely related to each other than any two random individuals from the gene pool. More specifically it is applied by breeders to crosses between siblings, parents to offspring, cousins, or similar cases.



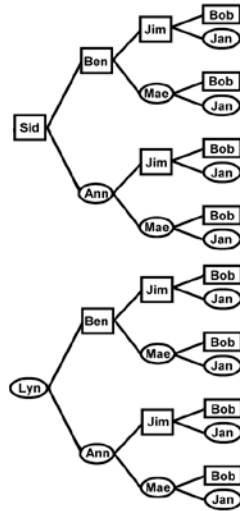
A pedigree is a way of showing the ancestors of an individual. This helps to see where genes come from. Since each parent gives half of its genes to each offspring, you can see that each grandparent contributes $1/4^{\text{th}}$ of an individual’s genes, and so on.



When the same individual appears on both the top *and* the bottom of a pedigree, this creates an opportunity for genes from that individual to be inherited from both the mother *and* the father. This situation is called “identical by descent” because the genes have actually descended from the same individual.

The farther back in the pedigree a common ancestor is, the fewer of these genes will be identical by descent. In our above example, the chance of the **a** gene being passed down from the great great grandfather to our specimen is 1 in 16. On the bottom of the pedigree, we can see that the chance of the **a** gene being inherited along that path is 1 in 8. The total odds of our specimen being “**aa**” because of this common ancestor is 1 in 128. But there is also the same opportunity with the **A** gene, which doubles the chance, so the total odds are actually 1 in 64 instead.

The most extreme example of inbreeding is breeding sibling to sibling, and repeating this for generation after generation. Notice that all of this individual’s genes have followed the same paths, and instead of sixteen great great grandparents who could contribute up to thirty two different genes, there are only two great great grandparents (Bob & Jan) who can only supply a maximum of four different genes in the gene pool.



We can see that inbreeding brings similar genes together more often than what occurs without

inbreeding. This means that recessive genes are more likely to be expressed, which can be a good thing or a bad thing, depending on which recessive gene it is.

Note that if you go far enough back in *any* individual's pedigree, there will be ancestors repeated. In order for *every* ancestor to be unique, there would have to be twice as many individuals with each generation, and doubling a number over and over creates gigantic numbers in a hurry. The far right row in a pedigree that goes back thirty generations is over one billion individuals. Forty generations back is over one trillion.

Obviously, eventually this number even exceeds the number of individuals that have existed for all time. Generally when two individuals have the same allele, it's because that allele is indeed identical by descent and at some point originated in the same individual.

Since inbreeding is such a serious taboo in human societies, it is generally taken to be a universally bad thing. But inbreeding has a good side and a bad side.

One advantage is that it's the only way a newly discovered recessive gene can be expressed in new specimens. Another is that it can be used to create a line of animals that are genetically similar, so that a

selectively bred trait behaves more predictably and breeding similar specimens produces offspring of the same type. This is known as “fixing” a trait.

The main disadvantage of inbreeding is the possibility of concentrating bad genes. This generally exposes itself after a few generations and is known as *inbreeding depression*. This can be a specific problem that appears, or a more general decrease in the quality of stock such as lower growth rates, lower disease resistance, lower fertility, and so on.

Controlled breeding programs can use outcrossing to periodically bring in fresh genes and dilute the bad ones. Thus, with a good breeding program, the advantages of inbreeding can be used while the main disadvantages can be avoided.

Hybridization

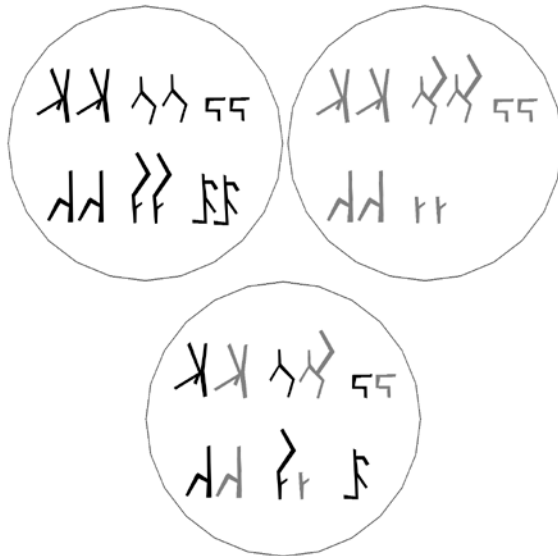
Hybridization is the breeding of individuals that are less related than the average of the population. In some cases this involves the crossing of two species. In other cases this involves simply crossing individuals of two different bloodlines or breeds.

Hybridization is basically the opposite of inbreeding, and has the opposite advantages and disadvantages.

An advantage of hybridization is known as *hybrid vigor*. Because the two lines will have many loci where their genotypes differ, their offspring will be heterozygous at many more loci than what is typically found in the population. The “vigor” can come from the fact that bad genes are most often recessive, and being heterozygous means the bad genes in either parent are much less likely to be expressed or have a bad effect.

Some hybrids are sterile, or have reduced fertility. Cross-species hybrids, and hybrids where the chromosome counts or configurations are different from each parent, can be sterile. One cause of this is that the chromosomes are not properly matched up

during crossover, during the production of egg/sperm cells.

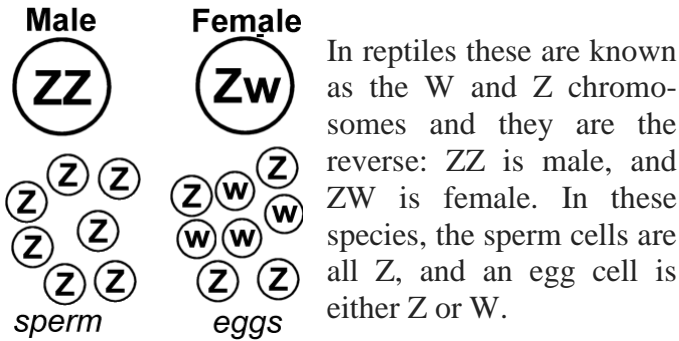


Above is a hybrid from parents with different chromosomal configurations. Notice that the parents (*above*) have a different top center and bottom center chromosome. Also the bottom right chromosome is absent in the other species.

We learned earlier that inbreeding “fixes” traits and this can be an advantage or disadvantage depending on whether the traits are good or bad. An aspect which is either an advantage or disadvantage of hybrids is the opposite of “fixed” traits. When two hybrids are bred to each other, since they are both highly heterozygous, there will be much greater diversity in their offspring.

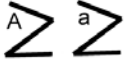
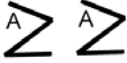
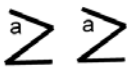
Sex-linked traits

So far all of our discussions have included genes that are on paired chromosomes. In some species the sex of an individual is determined by incubation conditions, such as temperature, and all of the chromosomes in these species are paired. However, in some species there are specialized sex chromosomes. In humans these are the X and Y chromosome. When an individual is XX they are female, and an XY is a male.

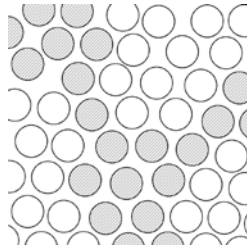


The W chromosome is much smaller and the sex-linked genes are those which only occur on the Z chromosome, or only on the W chromosome. The vast majority are expected to occur on the Z chromosome since it is usually much larger.

This causes two changes from the way we view the behavior of paired genes. First, sex-linked genes in females cannot be homozygous or heterozygous because there is only one gene present. This situation is known instead as *hemizygous*. This means there is no “dominant” or “recessive” because there aren’t two genes to fight for control of the phenotype. In males, there may be two present and they can have the same types of relationships as other paired genes.



A situation that happens in female mammals is known as X-inactivation. In short, even though all the body cells in a female have two X chromosomes, in each cell one of these is switched off and has no effect. This creates a mosaic effect, and one visible example is in female calico cats. One X chromosome has the “orange” allele and the other has the “brown” allele. The fur in each region is one color *or* the other, depending on which X chromosome has been inactivated in that particular group of cells. Meanwhile male cats normally do not have this capability because they



only have one X chromosome and thus can't carry both orange and brown at the same time, and have either one or the other. It is currently unknown whether or not Z-inactivation occurs in any herp species.

The second difference is with inheritance patterns. Normally one gene of each pair is inherited from each parent. In those species with Z and W sex chromosomes the following differences should be taken into account:

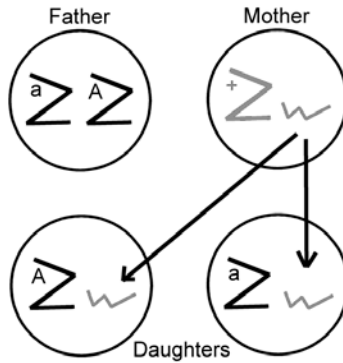
- The female passes her W chromosome to all of her daughters.
- The female passes her Z chromosome to all of her sons.
- If a female is showing a trait controlled by a gene on the Z chromosome, she inherited it from her father.
- Females cannot pass any Z-based traits to their daughters.
- Males cannot inherit or pass down the W chromosome.

	$A \text{ Z}$	$a \text{ Z}$
$+ \text{ Z}$	$+ \text{ Z} \text{ A}$ Male	$+ \text{ Z} \text{ a}$ Male
w	$w \text{ Z} \text{ A}$ Female	$w \text{ Z} \text{ a}$ Female

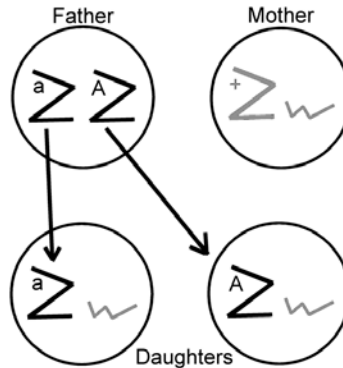
A Punnett square shows how a female that is $Z^+ w$ would not be able to pass the “+” gene to any of her daughters or w to any of her sons.

Females cannot pass any Z-based traits to their daughters. This is because they do not give their daughters their Z chromosome.

Males cannot inherit or pass down the W chromosome.



Females inherit the Z chromosome from the father, and get their w chromosome from the mother. Therefore if they are showing a Z-based trait, it came from the father.



Appendix A – Practice Problems

Determine the phenotype being expressed, given + as the wild type allele. Assume capital letters are dominant and lowercase are recessive.

1- ++

5- $A^+ \cdot a^a$

2- +a

6- a//a

3- +A

7- $A \cdot a$

4- aa

8- $A^+ \cdot A^+$

Use Punnett squares or FOIL to determine the outcomes:

9- ++ x +a

13- $a^a \cdot a^a$ x $A^+ \cdot a^a$

10- +a x +a

14- a//a x A//A

11- +a x +A

15- $A \cdot a$ x $A \cdot a$

12- aa x ++

16- $A^a \cdot A^b$ x $A^c \cdot A^d$

Use Punnett squares or the grid method to determine the outcomes:

17- +a bb x aa b+

18- $A^+a^a B^+b^b$ x $A^+a^a B^+b^b$

Use multiplication of odds at each locus to determine the odds of each outcome from the given cross:

19- +a +b +c +d x +a +b +c +d \rightarrow aa bb cc dd20- +a +b +c +d x +a +b +c +d \rightarrow +a bb ++ dd21- Aa Bb cc Dd x aa Bb Cc Dd \rightarrow aa BB cc dd22- $A^+a^a b^b b^c C^K C^+ d^+ d^+$ x $A^+a^a b^f b^g C^M C^+ d^+ d^+$
 $\rightarrow A^+a^a b^f b^e C^K C^M d^+ d^+$

Advanced:

23- Assuming a 25% chance of crossover between recessive traits **a** and **b**, determine the possibility of producing **aabb** offspring in the F₂ of a line that originates with **aa X bb**.

24- Assuming **Z** as normal Z chromosome and sex-linked trait **Z^h**, determine the number and sex of offspring from crossing a male showing the “h” trait to a normal female.

Answers:

1(Wild type), 2(Wild type), 3(Mutant A), 4(Mutant a),
5(Wild type), 6(Mutant a), 7(Type A), 8(Wild type)

9 ++, +a	13 a ^a ·a ^a , A ⁺ ·a ^a
10 ++, +a, +a, aa	14 A//a
11 ++, A+, +a, Aa	15 AA, Aa, Aa, aa
12 a+	16 A ^a ·A ^c , A ^a ·A ^d , A ^b ·A ^c , A ^b ·A ^d

17- Equal numbers of a+ b+, a+ bb, aa b+, aa bb.

18- The following 16 outcomes:

1 A⁺A⁺ B⁺B⁺, 2 A⁺a^a B⁺B⁺, 1 a^a a^a B⁺B⁺
2 A⁺A⁺ B⁺b^b, 4 A⁺a^a B⁺b^b, 2 a^a a^a B⁺b^b
1 A⁺A⁺ b^bb^b, 2 A⁺a^a b^bb^b, 1 a^a a^a b^bb^b.

19- 1 in 256.

20- 1 in 128.

21- 1 in 64.

22- 1 in 64.

23- 1 in 64. (1/8 x 1/8)

24- Z^h Z^h x Z w =

Z^h Z – Normal male

Z^h w – “h” type female

Appendix B - Glossary

Allele – Any of the variations that can occur at a given locus.

Chromosome – A group of genes that are physically attached.

Codominant – A relationship between two alleles where they are both expressed when paired together. The three possible genotypes of the pair produce three phenotypes.

Crossover – When two paired chromosomes exchange comparable material. Also used to describe the occurrence of two linked genes being swapped between chromosomes.

Dihybrid – A cross involving two loci of interest.

Diploid – A cell that contains paired chromosomes. Cells are normally diploid. See also: *haploid*.

DNA – Short for Deoxyribose Nucleic Acid or Deoxyribonucleic Acid. DNA is the substance that the genes are made of.

Dominant – A gene that controls the phenotype when it is paired with a recessive allele. The three possible genotypes of the pair produce two phenotypes. See also: *recessive*.

Epistasis – *See Masking*.

F1, F2 – The generations in a cross, the P generation is the original cross. The F1 are the offspring of P x P. The F2 are the offspring of F1 X F1. Numbers can continue indefinitely.

Factored – *Heterozygous* for a recessive gene.

FOIL – A method of determining all possible outcomes of a cross at a single locus. See also: *Punnett Square*.

Gene – A term that can be used interchangeably with locus or allele. See also: *locus, allele*.

Genome – A complete set of chromosomes for a given species.

Genotype – The alleles present at a given locus. See also: *phenotype*.

Haploid – A cell that has only one genome, such as sperm and egg cells. See also: *diploid*.

Hemizygous – Having a particular allele on a sex chromosome.

Heterozygous – When the allele pair at a locus is made of two different alleles. Opposite of *homozygous*.

Homozygous – When the allele pair at a locus is made of two copies of the same allele. Opposite of *heterozygous*.

Hybrid – A cross between two different lines, or two different species.

Hybrid vigor –The opposite of inbreeding depression. An increase in vigor resulting from pairing detrimental recessive genes with beneficial dominant genes that can sometimes occur with outcrossing.

Inbreeding – A breeding between two closely related individuals.

Inbreeding depression – An accumulation of detrimental effects that can occur with inbreeding.

Inheritance – The process by which parents pass down genes to their offspring.

Linked – Two genes that are inherited together more often than usual because of their proximity on the same chromosome.

Locus – A location on a particular chromosome, where a particular set of alleles reside.

Masking – a condition where the expression of one trait makes another trait undetectable. The hidden trait is said to be *masked* by the other.

Mendelian – A trait that is controlled at a single locus by a gene pair. *Named after Gregor Mendel, the father of genetics.*

Monohybrid – A cross involving only one locus of interest.

Mutant – An allele that is not the wild-type gene at its locus.

Mutation – Any change to a gene, or deletion, that forms a new allele.

Outcross – A breeding between two unrelated individuals.

Phenotype – The outward appearance or characteristics of a specimen. See also: *genotype*.

Polygenic – A trait that is controlled at many loci or by many genes. See also: *selectively bred*.

Possible Het – A way of expressing the possibility that a specimen has a known chance of carrying a particular recessive gene because its parents are known carriers.

66% Possible Het – Occurs when both parents are heterozygous for a dominant/recessive allele pair.

50% Possible Het – Occurs when one parent is heterozygous for a dominant/recessive allele pair and the other parent is homozygous for the dominant gene.

75% Possible Het or Homo – Occurs when both parents are heterozygous for a dominant/recessive allele pair and the expression at that locus is masked by another gene.

Punnett Square – A method of determining all possible outcomes of a cross, by combining all possible sperm cells with all possible egg cells. See also: *FOIL*.

Recessive – A gene that has no effect on the phenotype when it is paired with a dominant allele. The three possible genotypes of the pair produce two phenotypes. See also: *recessive*.

Selectively bred – A trait whose inheritance cannot be predicted in ratios, but occurs in varying amounts along a sliding scale. See also: *polygenic*.

Sex-linked - A gene that occurs on one of the sex chromosomes.

Wild-Type –

- 1-The allele at a locus that is most commonly found in wild specimens.
- 2-The “normal” gene or phenotype.
- 3-The phenotype most commonly found in wild specimens.

Zygote – The fertilized egg and thus the origin of genetic material for all cells in an animal. Zygote is the root of the terms heterozygous and homozygous.

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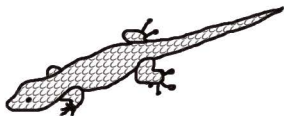
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