

CHAPTER 2

Passing Traits from One Generation to the Next

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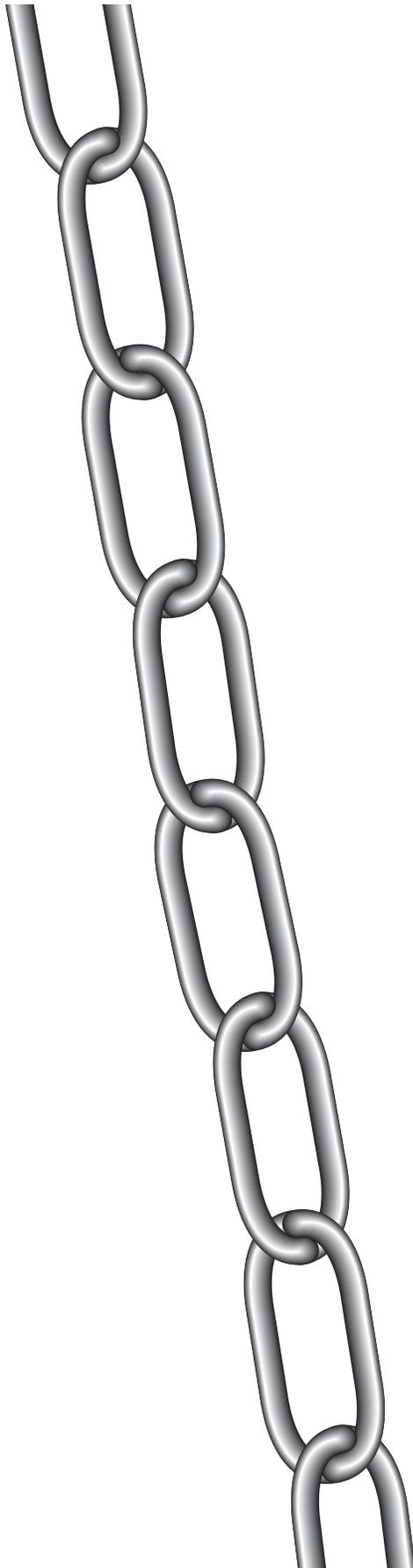
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CHAPTER 2

**Passing Traits from
One Generation
to the Next**

SECTION A

**What is
Inheritance?**

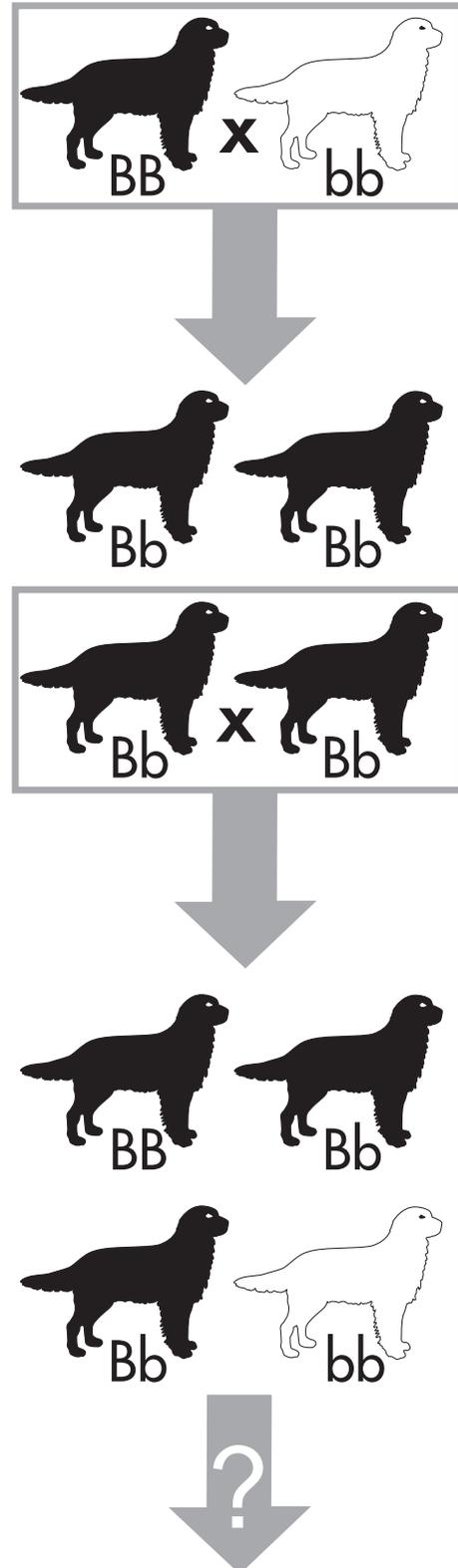
An Introduction to Inheritance

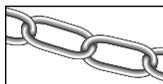
YOU INHERIT YOUR TRAITS, or characteristics, from your parents, and your parents inherited their traits from their parents. Each of us is a unique blend of traits that have been passed on from one generation to the next.

Very simple organisms like bacteria usually pass on a complete and exact copy of their own DNA to their offspring. As a result, their offspring are usually indistinguishable from themselves. Fortunately, humans don't do this, or we'd all be extremely similar to each other in every way.

Humans and other animals have a life cycle that involves the production of specialized egg and sperm cells that must be combined to form a member of the next generation. The nucleus of each egg and each sperm cell contains a copy of just one-half of the DNA of the adult who produced it. When the sperm and egg nuclei fuse after the egg has been fertilized, a new nucleus is produced that contains a copy of one half of the mother's DNA and one half of the father's DNA. It is this combination of DNA molecules, in which genes from the mother and father are now intermingled, that will direct the development of a new individual.

Although everyone inherits half of their DNA from their mother and half from their father, no one ever turns out to be exactly halfway between their two parents in their heritable features. In some of your traits you may resemble your mother, while in others you may resemble your father. And in some of your traits you may resemble one of your grandparents more than either of your parents. When we were growing up, some of us may have heard statements like "He has his mother's eyes and his father's nose, but he sure inherited Grandpa Bill's big ears!"



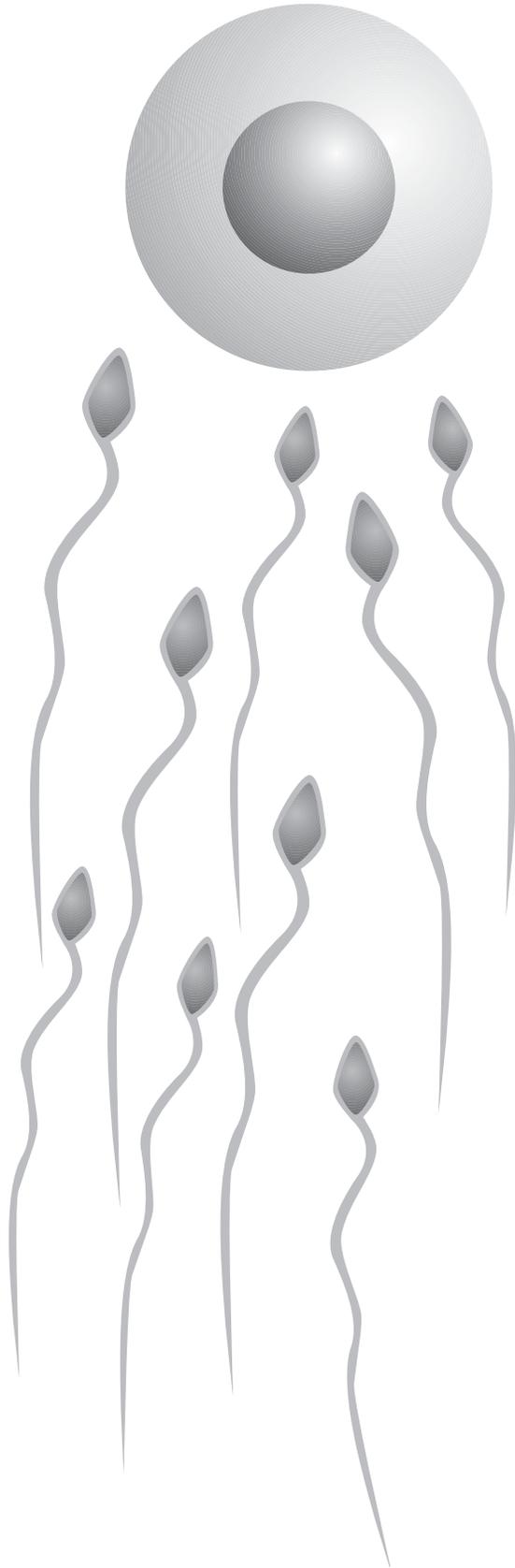
 **A.1**

The reason that each of you develop your own unique mixture of family traits is that the pair of genes for each trait that you inherit from your parents often do not have equal effects on your development. For example, as your hair follicles were developing, the gene for curly hair that you got from your mother may have been **dominant** over the gene for straight hair that you got from your father. In this case your hair will be curly, like your mother's. In the development of some other body parts, however, the reverse may have been true, and your father's genes may have been dominant over those of your mother. Genes that did not reveal their presence during development of your visible traits are said to be **recessive** to their dominant counterparts. Recessive genes are passed on from generation to generation just like dominant genes, but they only reveal their presence in individuals that did not happen to inherit a copy of a dominant gene for that trait.

The dogs in the diagram on the opposite page can be used to illustrate this sort of dominant-recessive relationship between two versions of a single gene. The top part of the diagram indicates that when a particular black and white dog mated, all of their offspring were black. However, the middle part of the diagram indicates that when two of those black dogs mated, about 1/4 of their puppies were white! We can account for this inheritance pattern by assuming that every dog inherits one copy of the gene for coat color from each of its parents, and that this coat-color gene comes in two forms: a **B** form that causes black hair, and a **b** form that sometimes causes the hair to be white. The reason that the **B** form of this gene is said to be dominant is because dogs having only one copy of it (dogs symbolized **Bb** in the diagram) are just as black as dogs having two copies of it (dogs symbolized as **BB**). In contrast, the **b** version of the gene is said to be recessive, because it only has an effect on coat color in dogs that lack a **B** gene (such as the **bb** dogs at the top and bottom right).

What sort of difference between two different forms of a gene causes one to be dominant and the other to be recessive, you ask? GREAT QUESTION! For the answer we need to refer back to things we learned in Chapter 1. Recall that the function of most genes is to specify the amino acid sequence of a particular protein, and that many of these proteins act as enzymes that mediate particular chemical reactions. The genes involved in determining the coat color of the dogs in our diagram encode alternative forms of an enzyme that is required to make "melanin," the pigment that is present in black hair. Whereas the **B** gene encodes an active form of this enzyme, the **b** version of the same gene encodes a damaged, inactive form of the enzyme. The reason that the **B** gene is dominant is that one copy of **B** is all that is necessary to make enough enzyme – and thus enough melanin – to turn the hair black. Since one copy of **B** is enough to make the hair black, the **b** version of the gene is recessive, because it can only exert an effect on hair color when the active form of the enzyme encoded by the **B** version of the gene is absent. Many dominant-recessive relationships between gene pairs have a similar basis.

In this chapter, you will use a variety of organisms – real and imaginary – to study (a) the patterns in which genes are sorted out during the formation of egg cells and sperm cells, (b) how those genes recombine when sperm and egg fuse, and (c) how they then determine the traits of the offspring. Before doing that, however, we will take a minute to consider how biologists who are interested in studying heredity decide which organisms to use for their studies.



CHAPTER 2

**Passing Traits from
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to the Next**

SECTION B

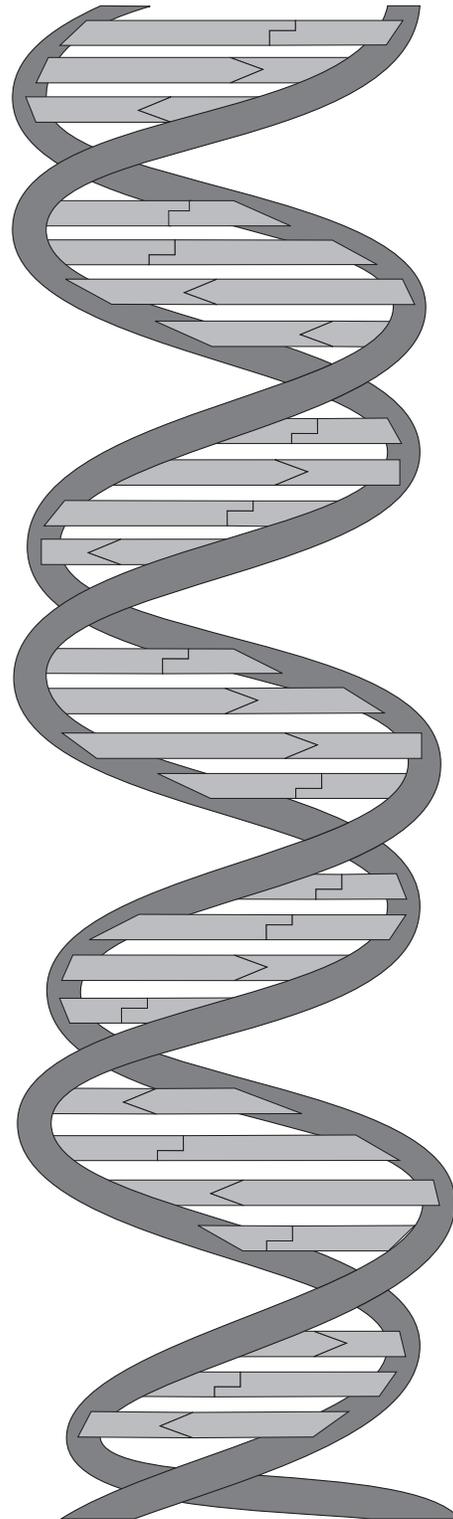
**How Does
a New
Generation
Get Started?**

Model Systems for Studying Heredity and Development

THE DNA PRESENT IN a human egg and sperm cell at the moment that they fuse contains enormous potential: the potential to direct formation of the most complex form of life the world has ever known – a human being. But the potential residing in DNA is of little significance until it becomes transformed into a physical reality. This happens through a long, slow process known as **development**. Human development begins as soon as egg and sperm fuse, while the individual is still a tiny one-cell **zygote**, and continues long after an **embryo** (a developing, unborn individual) has been transformed into a squawking newborn baby.

By now we know that genes code for proteins. But how do the proteins encoded by human DNA direct the transformation of a fertilized egg into an adult with blood and guts, muscles, and nerves, all in the right places, properly connected, and working together? And in the process, how do particular versions of certain genes that have been passed on in an egg or sperm give rise to the heritable traits that distinguish one human being from another?

Although no one can give completely satisfying answers to all such questions, enormous progress towards answering them has been made recently. Indeed, more has been learned about the twin processes of human heredity and human development during the period of time in which you have been alive than in all the prior centuries of human history combined.



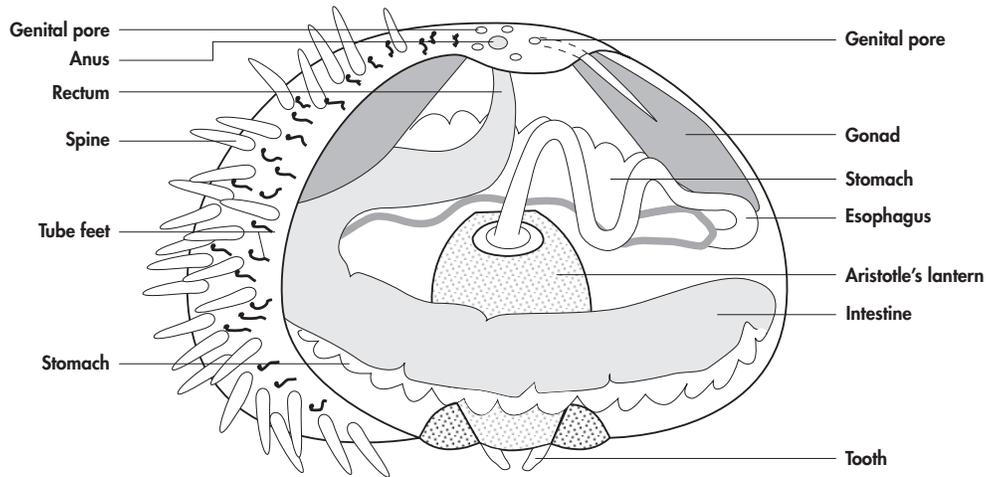


Very little of this new knowledge has come from studying human embryos themselves. Detailed studies of human embryos are impractical for both technical and ethical reasons. Therefore, most of what we now know about how human genes control human development has been derived by studying simpler organisms, such as yeast, fruit flies, sea urchins, frogs, and mice. Such organisms are frequently called **model systems**, because each of them has features that makes it the most suitable organism for studying certain particular aspects of heredity and/or development. But because none of them is equally suitable for studying all interesting aspects of heredity and development, they continue to be studied in parallel.

The most astonishing thing about such studies of model systems is the extent to which they provide information that is applicable to human beings. For example, as soon as it was discovered that one particular gene is essential for initiating eye development in fruit flies, it was quickly shown that the human version of that gene plays a very similar role in the development of our eyes. Moreover, certain serious abnormalities in human eye development and function have now been traced to defects in the DNA sequence of that very gene. Had it not been for the earlier studies of eye development in flies, however, we might never have discovered the important role of this gene in human eye development.

We will encounter several model systems, including some that are mentioned above, in the next few exercises. As we do, the qualities that make each of them useful for particular kinds of studies of heredity and development will be outlined.

Starting a New Generation: Sea Urchin Fertilization



A cut-away view of a sea urchin

INTRODUCTION

Sea urchins have long been the favorite model organism for studying **fertilization**, the process by which a sperm fuses with an egg. Fertilization converts the egg into what is called a **zygote** and triggers the changes that will transform it into a developing **embryo**. Sea urchins are favored for such studies for several reasons. First, a single female sea urchin may produce as many as 100,000 eggs at one time. Second, both eggs and sperm are released into the sea water, so fertilization occurs outside the body, where it is easily observed. Third, sea urchin eggs and embryos are translucent and just the right size to be easily studied with a microscope. And fourth, all of the embryos from a batch of fertilized eggs develop on the same schedule. As a result, it is easy to get enough embryos to perform chemical analyses at each stage of early development. Many of the things that have been learned by studying fertilization of sea urchin eggs have been useful in developing methods for *in vitro* fertilization of human eggs, to produce what journalists call “test tube babies.”

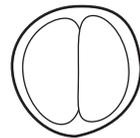
Sea urchins are members of the phylum Echinodermata (which means “spiny-skinned”); this phylum also includes the starfish and sand dollars. Sea urchins live in shallow near-shore waters in all the oceans of the world. The nearly round shell of an urchin, which is called its **test**, is covered with movable, protective spines. Between the spines are small, muscular **tube feet**, each of which has a suction cup on the end. The urchin uses the tube feet on the bottom of its test to walk about slowly on the ocean floor. But it can also use the ones on the top and sides to right itself if it happens to get flipped on its back by a wave or a potential predator.

With your teacher's assistance, pick up a sea urchin. The spines will not hurt you. On the top, locate the anus in the center and the genital pores around it. Then locate the mouth on the bottom. Notice the soft ring of skin (the oral membrane) around the five white teeth. The five-sided jaw apparatus, called Aristotle's lantern, is a complicated chewing organ consisting of five jaws and teeth that are adapted for scraping algae off rocks. Sea urchins are well adapted to life on the ocean bottom. They feed by moving on top of their food, holding it down with their spines and tube feet, and then tearing it to bits with their teeth. A sea urchin's diet, in addition to algae, may include coral, sponges, mussels, sand dollars, and kelp.

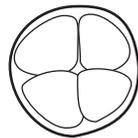
LIFE CYCLE

Like other animals, sea urchins pass their DNA on to their offspring in the nuclei of eggs and sperm that fuse during sexual reproduction. As you might have guessed, eggs are produced by female urchins and sperm by males. But to human beings, male and female urchins look identical. So there is no

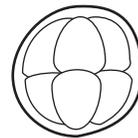
way of knowing which is which until they have been stimulated to **spawn** or release their **gametes**, which depending on their sex, are either eggs or sperm. As a result, your class may have to stimulate several urchins to spawn in order to get gametes of both types. Then you will fertilize some eggs with sperm and watch them as they divide to form multicell embryos.



2-cell stage
(~ 1 hour after fertilization)



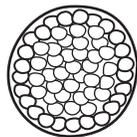
4-cell stage
(~1 1/2 hours)



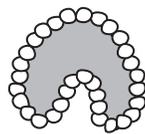
8-cell stage
(~2 hours)



16-cell stage
(cells are unequal in size; ~2 1/2 hours)



Blastula – a hollow ball of cells. Cleavage is over; blastula will break out of fertilization membrane and begin to grow. (~ 6-12 hours)



Gastrula – the ball gets a dimple, which deepens into a tube – the gut. (~ 1 day)

A sea urchin embryo develops into a swimming **larva**, a juvenile stage that bears no resemblance to an adult. In the ocean, the larvae swim about for many weeks or months, feeding on various tiny prey organisms and growing. Then (like caterpillars turning into butterflies) the larvae eventually undergo **metamorphosis** and transform into small adult sea urchins. Because urchin larvae and adults grow rather slowly and require particular kinds of algae and tiny animals as food at each stage of growth, it is extremely difficult to get them to go through a complete life cycle in captivity. Therefore, although sea urchins

provide a useful model system for studying fertilization and the genes that are expressed during the early stages of development, they are not very useful for studying other aspects of heredity and development.

MATERIALS

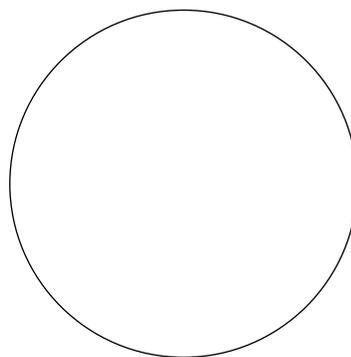
For each group of four students:

- 1 or 2 glass depression slides
- 2 or 3 dropping pipettes
- a compound microscope
- an egg suspension
- a sperm suspension
- a sample of previously fertilized eggs

PROCEDURE

Collecting Sea Urchin Gametes

1. Your teacher will demonstrate the technique used to get the sea urchins to spawn. It involves injecting a bit of a KCl solution into the body cavity. This creates a mild stress that (like many other mild stresses) causes the urchins to release their gametes. The eggs will be collected in a beaker of sea water. The sperm will be collected in a dry tube, and diluted with sea water later.
2. When your teacher informs you that the eggs are ready, use a pipette to pick up a drop of an egg suspension and place it on a clean glass depression slide. Examine the slide in your microscope with a 4X or 10X objective. The eggs are small and round. Draw a picture of their appearance in the microscope.

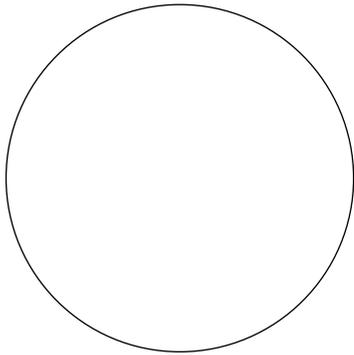


Sea urchin eggs

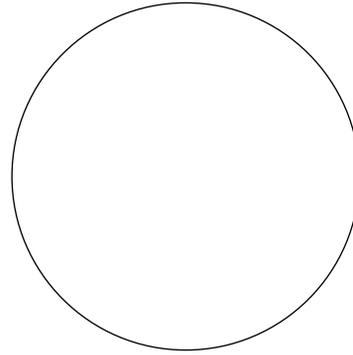
3. You will have the best chance of being able to view the fertilization process if you have 10-20 eggs in your depression slide. If you have more than that, remove part of the sample and replace it with sea water.

Fertilization

4. Your teacher will inform you when a sperm suspension is ready. Using a clean pipette, add a drop of this sperm suspension to the egg suspension on your slide. It is very important not to add too many sperm. If you do, the water will become too cloudy to see the eggs clearly, and excess sperm will cause abnormal development of the embryos. The correct amount is when 10-100 sperm can be seen around each egg.
5. Observe the sperm-egg mixture with a 4X or 10X objective. Draw what you observe. Fertilization will be evident when a fertilization membrane forms around the egg. Draw what this looks like.

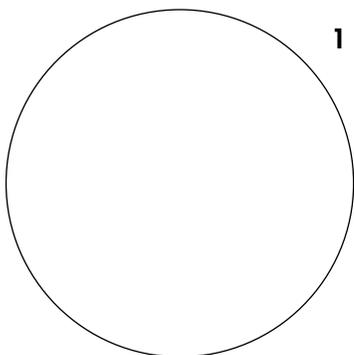


**Sperm and
egg mixture**

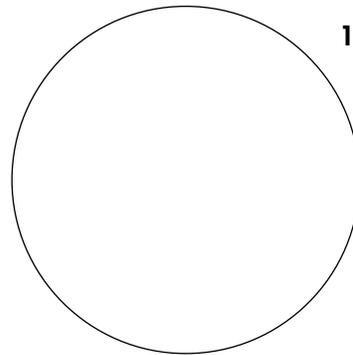


**Fertilized
sea urchin egg**

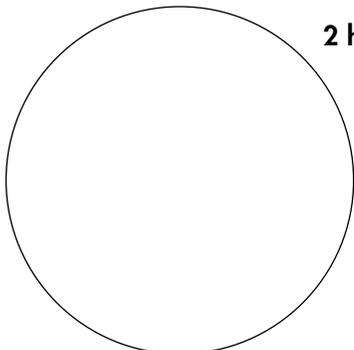
6. The eggs that you fertilized in the depression slide probably will not continue to develop normally while being viewed with the microscope; the light source will heat them up too much. Your teacher will prepare a mixture of sperm and eggs in a beaker and leave it on the bench top. You should examine a drop of this suspension every 15 minutes or so to monitor development. The first division should occur about an hour after fertilization. Draw pictures of the divisions. Your teacher may also have samples of eggs that were fertilized some time before your class began that you can examine to see more advanced stages of development.



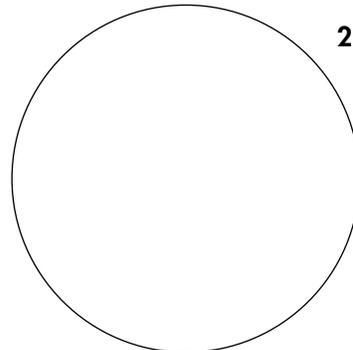
1 hour



1 1/2 hours



2 hours



2 1/2 hours

POSTLAB QUESTIONS

1. If the body cells found in one particular species of an adult sea urchin have 14 chromosomes, how many chromosomes would an egg or sperm of that species have?

2. What do you think would happen if one of the gametes (either the egg or the sperm) had the wrong number of chromosomes? Why?

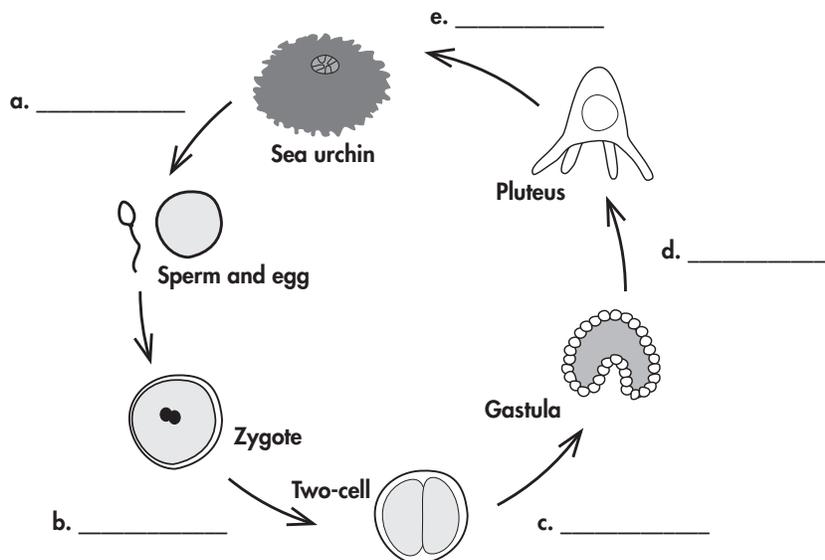
3. What are some differences between a fertilized and unfertilized egg?

4. What is the function of the fertilization membrane? Why would that be important?

5. What happens to the fertilized egg about an hour after fertilization?

6. When a cell of an embryo divides, how are each of the newly formed cells similar to one another and to the original fertilized egg but different from the unfertilized egg?

7. Mitosis and meiosis are essential aspects of the cycle of life and development. Complete the diagram below by writing mitosis or meiosis on the correct lines.



The Miracle of Life

WITH ANY LUCK, IN the preceding exercise you saw male and female sea urchins release sperm and eggs and then you watched those cells fuse and initiate the development of a new generation. Now, through the wonders of modern technology, you will be able to follow this up with extraordinary views of the equivalent processes in human beings. The exceptional photography in the video *The Miracle of Life* will take you on a journey through the reproductive tracts of both the human female and the human male and will allow you to observe the numerous stages of the human reproductive process- from the early stages of gamete development, through the moment of conception, and to the moment of birth.

Read the questions on the work sheet below and on the next page before the video begins. As you watch the video, take notes to help you answer the questions later. Then write your answers on the work sheet in complete sentences.

THE MIRACLE OF LIFE QUESTIONS

1. Describe the journey of the egg as it becomes mature and travels toward the sperm.

2. Describe the journey of the sperm as they leave their site of origin and travel toward the exterior.

3. About how many sperm does a man produce in his lifetime?

4. About how many sperm are released in a single ejaculation?

5. After sperm are released into the vagina, how long are they viable?



Name _____

Date _____ Hour _____

6. Describe the barriers that the sperm face as they travel up the female reproductive tract toward the egg.

7. Where is the egg when the sperm reach it?

8. About how many sperm reach the egg?

9. What happens to the sperm after it enters the egg?

10. When does the fertilized egg begin dividing?

11. What is the fertilized egg called after it divides?

12. How long after fertilization does the embryo implant itself in the uterine wall?

13. Describe the human embryo at the following stages:

Example: 4 weeks: It has arm buds and the beginnings of eyes.

5 weeks: _____

6 weeks: _____

7 weeks: _____

8 weeks: _____

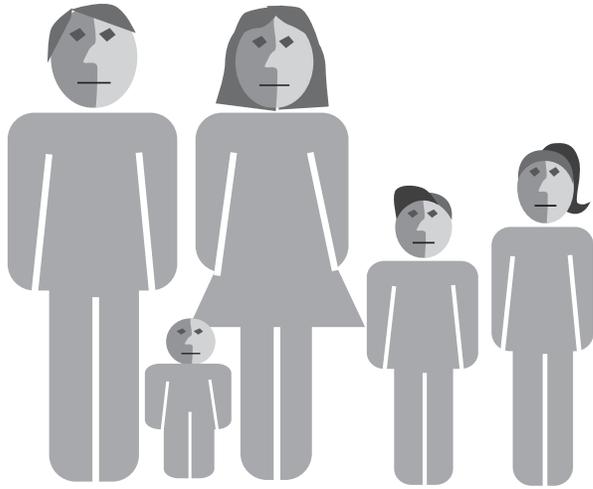
10 weeks: _____

14 weeks: _____

18 weeks: _____

CHAPTER 2

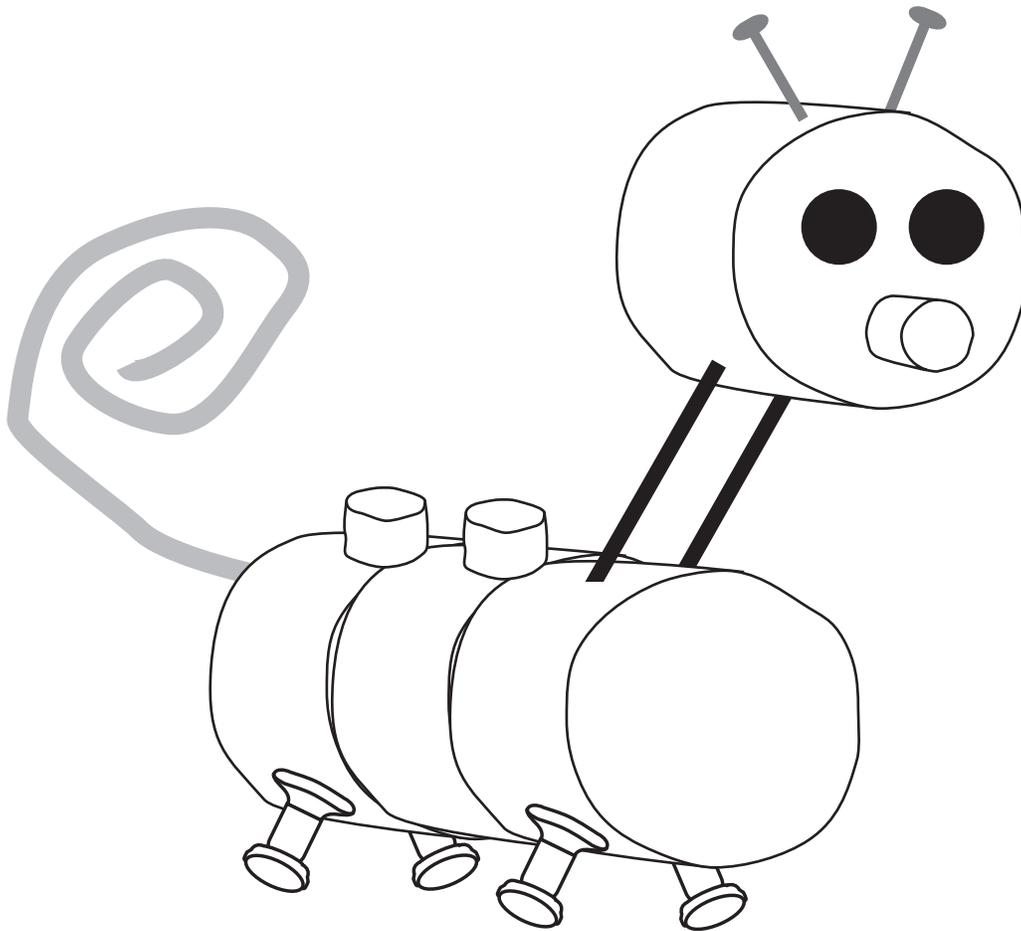
**Passing Traits from
One Generation
to the Next**



SECTION C

**If All the Kids
Have Mom and
Dad's Genes,
Why Don't They
All Look Alike?**

Really Relating to Reebops



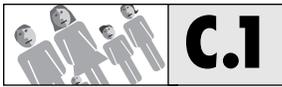
INTRODUCTION

NOW FOLKS, HERE WE REALLY DO have a model system for studying heredity. (A model system in the same sense that the term “model” was used in Chapter 1.) Reebops are imaginary creatures that were invented by Patti Soderberg at the University of Wisconsin. As you create baby Reebops from marshmallows and other objects, they can help you see how the visible traits of a baby are related to the combination of genes that it inherited from its mom and dad (and why all the kids in the family don’t always look alike) Have fun Reebopping!

MATERIALS

An envelope containing one set of red chromosomes and one set of green chromosomes

Boxes at the front of the room containing Reebop body parts, such as marshmallows, toothpicks, nails, etc.



Name _____

Date _____ Hour _____

PROCEDURE

If you find any words in the instructions below that you do not understand, check out the Genetic Glossary (page S 93).

1. You and your lab partner will receive an envelope that contains 14 red chromosomes that belong to Mom Reebop and 14 green chromosomes that belong to Dad Reebop. Decide which of you will act as Mom and which will act as Dad. Place your chromosomes on the table in front of you, letter side down. Your lab partner should do the same with the other set of chromosomes.
2. Arrange your 14 chromosomes into pairs by length and width. Select one chromosome from each of your seven pairs and place all seven in a special “gamete” (egg or sperm) pile. Your lab partner should do the same. The leftover chromosomes should now be returned to the envelope.

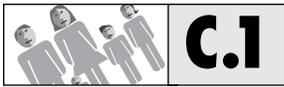
What type of cell division has just occurred? _____

3. Combine the seven red and seven green chromosomes from the two gamete piles to form a “baby” pile. Now each Reebop baby will have 14 chromosomes just like Mom and Dad did. But half will be red and half green, indicating that half came from Mom and half from Dad.
4. Line up the chromosomes contributed to the baby by Mom and Dad in pairs of similar size, letter side up. You will see that each chromosome in a pair carries a gene of similar type (same letter of the alphabet).

Some chromosome pairs might carry the same allele (either both capital letters or both lower case), indicating that the baby is homozygous (has two alleles of the same type) for the kind of gene carried on that chromosome.

Other chromosome pairs might carry one dominant (capital letter) allele and one recessive (lower-case) allele, indicating that the baby is heterozygous (has two alleles of different type) for the kind of gene carried on that chromosome.

The combination of genes carried on these seven chromosome pairs defines your Reebop baby’s genotype (genetic constitution). Record this genotype on the lines below.

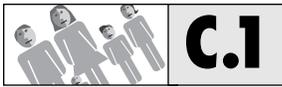


Name _____

Date _____ Hour _____

5. Refer to the Reebop Genotype-Phenotype Conversion Table on page S94 to determine your baby's phenotype. Record the phenotype on the lines below, keeping the phenotypic traits in the same order as the genes you listed in step 4.

6. You are now ready to construct your Baby Reebop. Collect the body parts that you will need and return to your desk to build your baby.



GENETIC GLOSSARY

allele: one of two or more forms of a gene that can exist at a single locus.

chromosome: a structure in the nucleus of a eukaryotic cell that contains a linear array of many genes. A chromosome is composed of a single DNA double helix molecule wound around many protein molecules that stabilize it and regulate its function.

codominant: refers to a pair of alleles, both of which exert an effect on the phenotype when they are present together. In codominance, the heterozygote has a phenotype different from that of either homozygote and sometimes (but not always) is intermediate in phenotype.

diploid: having two complete sets of chromosomes, one set derived from the mother and one from the father.

dominant: refers to an allele that has the same effect on the phenotype whether it is present in the homozygous or heterozygous condition. (Thus, if *A* is a dominant allele, individuals with the *AA* and *Aa* genotypes have the same phenotype.)

genotype: the specific combination of alleles that an individual possesses at one or more loci.

haploid: having only one set of chromosomes (as in a sperm or egg nucleus).

heterozygous: having two different alleles at a particular locus.

homozygous: having two identical alleles at a particular locus.

incomplete dominance: a form of codominance in which the heterozygote is about halfway between the two homozygotes in phenotype. (For example, if homozygous plants have red or white flowers and the heterozygous plant has pink flowers, the situation is sometimes called incomplete dominance. But it is just a special type of codominance.)

locus: a region of a chromosome or DNA molecule where a particular kind of gene, coding for a particular kind of protein, is located. Different variants at a single locus are known as alleles.

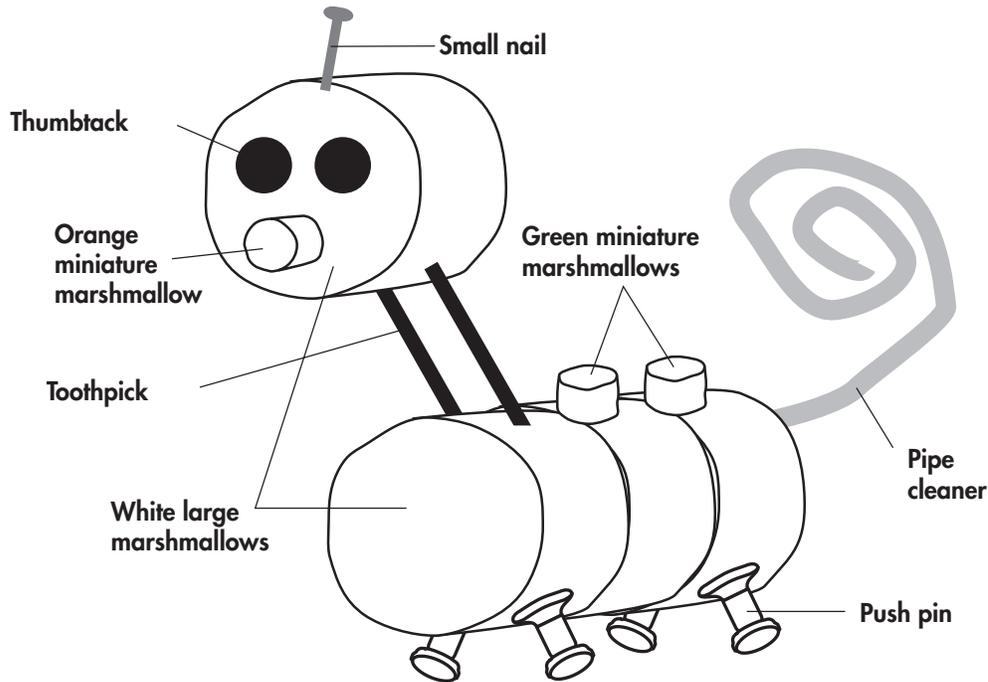
meiosis: the “reduction division” in which a diploid cell divides to produce haploid cells that will function as gametes (eggs or sperm).

phenotype: the outward appearance of an individual with respect to one or more traits that is associated with some particular genotype.

recessive: refers to an allele that has no effect on the phenotype unless it is present in the homozygous condition.

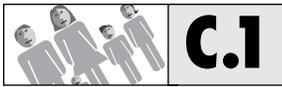
recombination: the process in which two haploid sets of chromosomes are brought together in a pair of gametes to produce a new diploid offspring. Usually this new diploid will be different in genotype from both of its parents.

REEBOP GENOTYPE-PHENOTYPE CONVERSION TABLE



GENOTYPE	PHENOTYPE
DD	Three body segments
Dd	Three body segments
dd	Two body segments
AA	Two antennae
Aa	One antenna
aa	No antennae
NN	Red nose
Nn	Orange nose
nn	Yellow nose
EE	Two eyes
Ee	Two eyes
ee	One eye
MM	Three green humps
Mm	Two green humps
mm	One green hump
TT	Curly tail
Tt	Curly tail
tt	Straight tail
LL	Blue legs
Ll	Blue legs
ll	Red legs

Note: Toothpicks function as the bones and ligaments that hold the Reebops together.



Name _____

Date _____ Hour _____

REEBOP REVIEW

1. Define the following terms and give an example of each from this activity. (You may refer to the Genetic Glossary.)

allele: _____

genotype: _____

phenotype: _____

homozygous: _____

heterozygous: _____

2. If a Reebop female with a red nose and a Reebop male with a yellow nose marry and have children, what genotype and phenotype for nose color will their children have? (You may refer back to the Reebop Genotype-Phenotype Conversion Table.)

genotype _____ phenotype _____

3. If a Reebop female with one antenna and a Reebop male with no antennae marry and have children, what genotypes and phenotypes might their children have with respect to number of antennae?

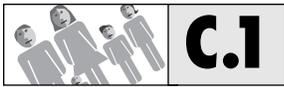
genotypes _____ phenotypes _____

4. If a Reebop female with one antenna and a Reebop male with one antenna marry and have children, what is the probability that they will have a baby with no antennae? (If you have a problem with this question, check out section C.2!)

5. If a Reebop female with two green humps and a Reebop male with two green humps marry and have children, what is the probability that their first baby will have two green humps?

6. If a Reebop female with three green humps and a Reebop male with three green humps marry and have children, what is the probability that they will have a baby with two green humps?

7. If a Reebop baby has a straight tail, but both of his parents have curly tails, what are genotypes of the two parents?



Name _____

Date _____ Hour _____

CLASS REEBOP DATA

FILL IN THE NUMBER of Reebops found in your class with the following heritable traits:

Antennae

One _____

Two _____

None _____

Nose color

Red _____

Orange _____

Yellow _____

Humps

One _____

Two _____

Three _____

Eyes

One _____

Two _____

Segments

Two _____

Three _____

Tail

Curly _____

Straight _____

Leg color

Blue _____

Red _____

ANALYSIS OF REEBOP FINDINGS

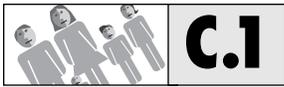
1. Describe the phenotypes of Mom and Dad Reebop.

2. Using the information in the Reebop Genotype-Phenotype Conversion Table, list all the possible genotypes that would produce the phenotypes exhibited by Mom and Dad.

3. How many of the Reebop babies in your class have the same phenotypes as Mom or Dad?

4. Do any two babies in your class have exactly the same phenotypes?

5. Why do some Reebop babies have traits that are not seen in either Mom or Dad?



Name _____

Date _____ Hour _____

6. Which Reebop traits are dominant?

7. Which Reebop traits exhibit codominance?

8. Use the information you have about the phenotypes of all of the Reebop babies in your class to figure out what the genotypes of Mom and Dad Reebop are. Write the answer below.

9. If you know the genotype of the parents, is it possible to predict all of the possible genotypes of babies that they might produce?

10. If you know the genotype of the parents, is it possible to predict the genotype of any particular baby, such as their first one?

11. The Reebops appear to have only one gene on each chromosome. Do you think this is true of real, living organisms?

Determining Genetic Probabilities With a Punnett Square

INTRODUCTION

Often someone would like to know how likely it is that two parents with a particular phenotype will have an offspring with the same or a different phenotype. For example, a cat breeder may want to know how likely it is that if a black cat and a white cat mate they will produce a white kitten. Or two people who both have parents with a heritable disease may want to know how likely it is that one of their children would have that same disease.

Many years ago a man by the name of Punnett figured out how to use a square diagram to answer such questions. Biologists have been using this method, a **Punnett square**, for similar purposes ever since. It works for any organisms – plants, animals, or Reebops – that reproduce sexually. There are only two requirements: (1) we must be able to figure out what the genotypes of both parents are with respect to the trait we are interested in, and (2) we must know what phenotype is associated with each possible combination of the alleles that are involved.

PROCEDURE

Here we will use a Punnett square to answer the following question: If a Reebop female with one antenna and a Reebop male with one antenna marry and have children, what is the probability that one of their children will have two antennae? But the following steps would be used for answering all such questions that involve one locus with two alleles.

1. Determine what the genotypes of the parents are with respect to the trait of interest. According to our Genotype-Phenotype Conversion Table in the previous lesson, a Reebop with one antenna has the genotype Aa. So both the female and the male have the genotype Aa.
2. Draw a larger square that contains as many smaller squares in each direction as there are alleles to be considered for each of the parents (fig. 1). In this case, two.

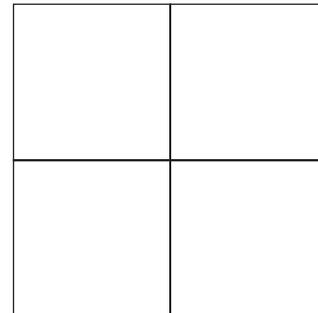
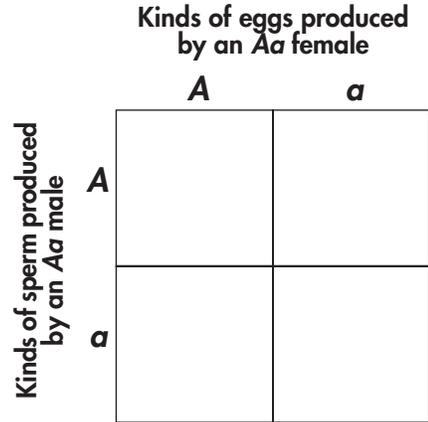
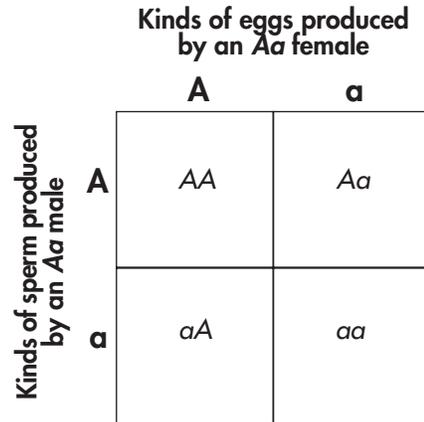


Figure 1

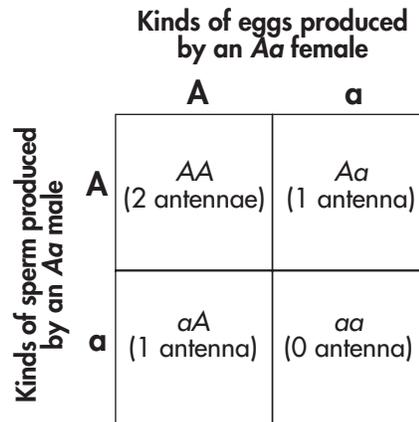
- Above the two boxes at the top place letters corresponding to the genotypes of the haploid eggs a female of the specified genotype (in this case, Aa) would produce following meiosis (fig. 2).
- Beside the two boxes on the left place letters corresponding to the genotypes of sperm a male of the specified genotype (Aa) would produce following meiosis (fig. 2).


Figure 2

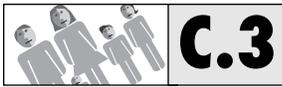
- Next, place letters in each of the smaller boxes indicating the genotype that would be produced if an egg of the type indicated above were combined with a sperm of the type indicated to the left (fig. 3). These are the four genotypes that would be formed with equal likelihood when an egg is selected at random and combined with a sperm that is also selected at random.


Figure 3

- Now in each box place words indicating the phenotype that is associated with the genotype specified in that box (fig. 4).


Figure 4

- Now determine how many of the four equally likely genotypes will result in the phenotype that the question asked about. In this case we get the answer that the probability of having a baby with two antennae is 1 in 4.



Exploring Human Traits: Create-a-Baby

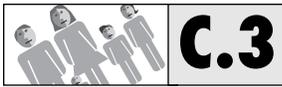
INTRODUCTION

Our imaginary friends, the Reebops, helped us understand how it is possible for two parents who look very similar to one another to have a family of children that all look different from their parents and from one another. The secret lies in the processes of meiosis and recombination. These two processes work in sequence, first to select various parental alleles at random and then to bring them together to form combinations that are entirely new and different.

In this exercise, you and a partner will simulate human meiosis and recombination to produce an imaginary baby that will have some features that resemble your features and some that do not. In the process, you will learn that heredity is often a bit more complicated than in the simple examples we encountered with the Reebops, in which each trait was controlled by a single pair of alleles at one locus. In real life, most of the features that we recognize in ourselves and others are controlled by alleles at more than one locus. In fact, most of them have a more complex genetic basis than any that you will encounter in this exercise.

PROCEDURE

You and your partner will work together to determine your own phenotypes and estimate your genotypes for each of 22 traits. These genotypes will be recorded in the Create-a-Baby Table. Then you will each simulate meiosis to select one of your alleles at each locus that is to be passed on to your baby. In each case where a heterozygous locus is involved, you will use a coin toss to determine which allele is to be passed on. When all of these alleles have been recorded, you will be able to predict the phenotype of your imaginary baby. Then you will each draw a baby with this phenotype.



DETERMINING GENDER

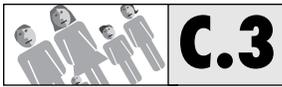
To begin, you and your partner must decide which of you will be Parent 1 (the mom) and which will be Parent 2 (the dad). In humans and many other animals, gender is determined by the **X** and **Y chromosomes**, or **sex chromosomes**. Females have two X chromosomes, so they always pass an X on to each of their babies. Males have an X and a Y, so a father may pass on to his baby either an X chromosome (in which case a girl will be produced) or a Y (in which case a boy will be produced).

Find the Create-a-Baby Table on page 105. Under the Baby's Genotype, record an X to represent the sex chromosome contribution of Parent 1. Now Parent 2 should flip the coin to determine which sex chromosome "he" will contribute (heads = Y and tails = X). Record this under Baby's Genotype and then record the gender of the baby under Baby's Phenotype.

DOMINANT/RECESSIVE TRAITS

On the next page you will find pictures of human phenotypic traits related to facial features. For the purposes of this exercise, we are going to pretend that each of the traits in the top six rows of the diagram is determined by a pair of alleles at a single locus that exhibit a simple dominant/recessive relationship.

1. Where necessary, you and your partner should help each other determine what your own phenotypes are with respect to each of the above traits.
2. Next, each partner needs to determine what genotype corresponds to his/her phenotype for each of these traits. This is easy if you have the homozygous-recessive phenotype: just record the homozygous-recessive genotype in the correct box of the Create-a-Baby Table on page 105. But in each case where you have a dominant phenotype, you will need to flip a coin to determine whether you will record the homozygous-dominant or heterozygous genotype (heads = homozygous-dominant; tails = heterozygous). For example, if you have a mole, you will need to flip the coin to determine whether to record MM or Mm as your genotype at that locus in the second line of the Create-a-Baby Table.
3. Next, each parent needs to determine which allele she or he will pass on to the baby at each locus. In each case where you are homozygous, this is easy: just record the appropriate allele in the correct Baby's Genotype box. But if you are heterozygous, you will need to use the coin again to determine which allele you will pass on (heads = the dominant allele; tails = the recessive allele). Be sure that both parents record the allele they are passing on, so that the baby will be diploid at all loci.
4. Once you have recorded the baby's genotype for all 12 of these features, record the baby's corresponding phenotype.



CODOMINANT TRAITS

In some cases a pair of alleles exhibit a **codominant** relationship, in which the phenotype of the heterozygote is different from (sometimes intermediate between) that of either homozygote. For the purposes of this exercise, we are going to pretend that the six phenotypic traits that are pictured in the bottom three rows of the diagram are each controlled by a pair of codominant alleles at a single locus.

1. You should proceed in a similar manner with each of these codominant traits as you did with the dominant/recessive traits above. That is, first you should determine your own phenotype, then your genotype, and finally which allele you will pass on to the baby. When in doubt about your own phenotype, choose the one corresponding to the heterozygous genotype.
2. After you have determined the baby's genotype for these six codominant traits, record the corresponding phenotype.

DOMINANT/RECESSIVE TRAITS

Trait	Genotype	Phenotype	Trait	Genotype	Phenotype
Mole	<i>MM</i>	mole	Cheeks	<i>FF</i>	freckles
	<i>Mm</i>	mole		<i>Ff</i>	freckles
	<i>mm</i>	no mole		<i>ff</i>	no freckles
Eyebrows (size)	<i>EE</i>	meet	Cheeks	<i>DD</i>	dimples
	<i>Ee</i>	meet		<i>Dd</i>	dimples
	<i>ee</i>	do not		<i>dd</i>	no dimples
Eyebrows (texture)	<i>KK</i>	bushy	Chin	<i>PP</i>	dimple
	<i>Kk</i>	bushy		<i>Pp</i>	dimple
	<i>kk</i>	fine		<i>pp</i>	no dimple
Eyebrows (shape)	<i>BB</i>	arched	Chin (shape)	<i>ZZ</i>	round
	<i>Bb</i>	arched		<i>Zz</i>	round
	<i>bb</i>	straight		<i>zz</i>	square
Eyes (shape)	<i>OO</i>	oval	Mouth (shape)	<i>CC</i>	bowed
	<i>Oo</i>	oval		<i>Cc</i>	bowed
	<i>oo</i>	almond		<i>cc</i>	straight
Earlobes (shape)	<i>LL</i>	free	Hairline	<i>QQ</i>	widow's peak
	<i>Ll</i>	free		<i>Qq</i>	widow's peak
	<i>ll</i>	attached		<i>qq</i>	straight

CODOMINANT TRAITS

Face (shape)	<i>AA</i>	round	Hair (curliness)	<i>HH</i>	curly
	<i>Aa</i>	oval		<i>Hh</i>	wavy
	<i>aa</i>	square		<i>hh</i>	straight
Nose (size)	<i>NN</i>	large	Eyes (separation)	<i>ll</i>	far apart
	<i>Nn</i>	medium		<i>li</i>	medium
	<i>nn</i>	small		<i>ii</i>	close set
Lips (size)	<i>GG</i>	full	Eyelashes (length)	<i>JJ</i>	long
	<i>Gg</i>	medium		<i>Jj</i>	medium
	<i>gg</i>	thin		<i>jj</i>	short

MULTIGENIC TRAITS

In actuality, most human heritable traits are determined not by a pair of alleles at a single locus but by a combination of alleles at two or more loci. Such traits are said to be **multi-genic**. For example, it is believed that human skin color is determined by the combination of alleles present at seven or more different loci. Thus, as we can see by looking around the world, enormous variation in skin color is present in the human population, even within what is usually considered to be a single ethnic group. Inheritance patterns for hair and eye color are only slightly less complex.

In this exercise, however, we will simplify the situation by pretending that each of these three color phenotypes is determined by only a pair of alleles at two loci, as follows:

Hair color			Eye color			Skin color		
Genotype	SS	Phenotype	Genotype	UU	Phenotype	Genotype	WW	Phenotype
RR	SS	Black	TT	UU	Deep brown	VV	WW	Black
RR	Ss	Black	TT	Uu	Deep brown	VV	Ww	Dark brown
RR	ss	Red	TT	uu	Brown	VV	ww	Light brown
Rr	SS	Brown	Tt	UU	Greenish brown	Vv	WW	Medium brown
Rr	Ss	Brown	Tt	Uu	Light brown	Vv	Ww	Beige
Rr	ss	Blond	Tt	uu	Gray blue	Vv	ww	Light beige
rr	SS	Dark blond	tt	UU	Green	vv	WW	Olive
rr	Ss	Blond	tt	Uu	Dark blue	vv	Ww	Fair
rr	ss	Light blond	tt	uu	Pale blue	vv	ww	Ivory

1. You should proceed with these traits in the same general way that you did with the dominant/recessive traits. If you are in doubt about which of the two combinations of alleles you should use to account for your own phenotype, flip a coin.
2. After you have determined your own genotype for each of these traits, determine which allele at each locus you will pass on to the baby. In every case where you are heterozygous, flip a coin to determine which allele you will pass on (heads = capital letter allele; tails = small letter allele).

Remember, like you, the baby should have four alleles for each of these traits, two different letters from each parent.

DRAWING ON YOUR GENETIC RESOURCES

When you and your partner have finished filling in the Create-A-Baby Table on the next page, name the baby. Then each of you should draw its face, incorporating as many aspects of its recorded phenotype as possible. Remember that it's supposed to be a baby, not an adult, that you are drawing. Do not look at your partner's drawing until both of you are finished. Then compare your two drawings and see how similar they look. If they look quite different, you can consider it evidence for a concept you will encounter shortly: namely, that the same genes can produce different phenotypes in different environments.



Name _____

Date _____ Hour _____

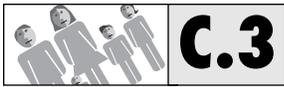
CREATE-A-BABY TABLE

Parent 1's name
(the Mom) _____

Parent 2's name
(the Dad) _____

Baby's name

Trait	Parent 1's Genotype	Parent 2's Genotype	Baby's Genotype	Baby's Phenotype
Gender				
Mole				
Eyebrows (size)				
Eyebrows (texture)				
Eyebrows (shape)				
Eyes (shape)				
Earlobes (shape)				
Cheeks (freckles)				
Cheeks (dimples)				
Chin (dimple)				
Chin (shape)				
Mouth (shape)				
Hairline				
Face (shape)				
Nose (size)				
Lips (size)				
Hair (curliness)				
Eye (separation)				
Eyelashes (length)				
Hair (color)				
Eyes (color)				
Skin (color)				



Name _____

Date _____ Hour _____

CREATE-A-BABY REVIEW

1. Define each of the following terms.

chromosome: _____

codominant: _____

diploid: _____

haploid: _____

meiosis: _____

multigenic: _____

recombination: _____

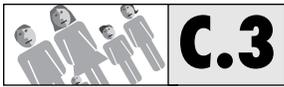
2. What was the probability that you and your partner would produce a boy? A girl? Explain.

3. Explain how it is possible for your baby to have a visible trait that neither you nor your partner have.

4. If you and your partner repeated this exercise and produced another imaginary baby, do you think it would look just the same as the one you produced already? Explain.

5. A woman who is heterozygous for the chin-dimple trait marries a man without a chin dimple. What are the possible genotypes and phenotypes of their children?

6. What is the probability that the man and woman discussed in the preceding question will have a baby with a chin dimple?



Name _____

Date _____ Hour _____

7. A man and a woman who are both heterozygous for two traits, the cheek-dimple and the chin-dimple traits, get married. What is the probability that they will have a baby that has cheek dimples but not a chin dimple? (If you have trouble answering this question, check out section C.4.)

8. What is the probability that a man with dark blonde hair and a woman with red hair will have a baby with brown hair?

Using a More Complicated Punnett Square

INTRODUCTION

In Exercise C.2 we learned how to use a Punnett square to figure out the probability that a baby would have a trait that was determined by alleles at a single locus. A Punnett square can also be used to determine the probability that a child will have a trait or combination of traits that involves alleles at two or more loci. It just gets a bit more complicated.

PROCEDURE

Let's see how to use a Punnett square to answer a question such as the following: When a man with an oval face and wavy hair marries a woman with an oval face and wavy hair and they have a baby, what is the probability that their baby will have a square face and curly hair? We follow a procedure that is similar to the one we followed before, except that our diagram must be larger to make room for alleles at two loci.

1. From the diagrams that illustrated the codominant traits, we find that the genotypes of the parents are as follows:

Man with oval face and wavy hair: *Aa Hh*

Woman with oval face and wavy hair: *Aa Hh*

2. Now we need to draw a diagram that has enough boxes along each edge to accommodate all of the different kinds of gametes each parent can produce. The rule for this is that each edge of the diagram should have 2^n boxes, where n is the number of loci being considered. In our first Punnett square, with only one locus being considered, we only needed 2^1 or two boxes on a side. But here, with two loci to be considered, we need 2^2 or 4 boxes along each edge of the large square.

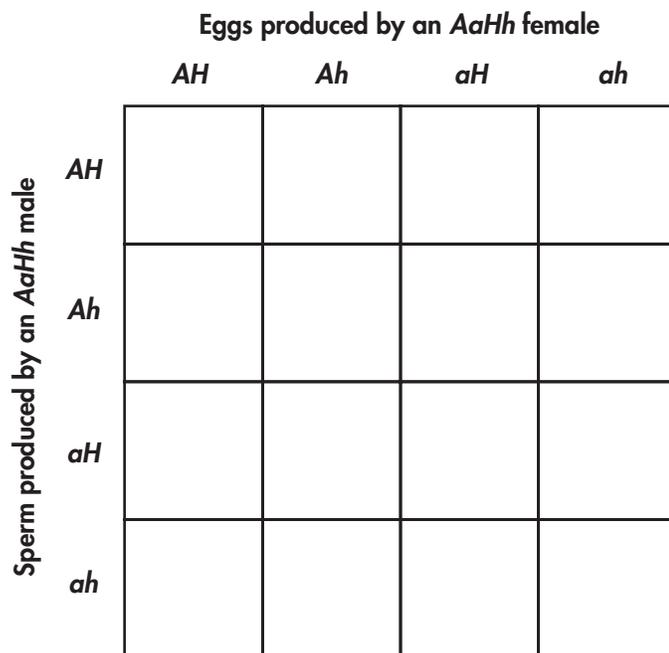


Figure 1

- Above the squares along the top row we write the genotypes of all the different kinds of eggs the woman can produce with respect to alleles at the *a* and *h* loci (*AH*, *Ah*, *aH*, and *ah*) as done in fig. 1.
- Beside the squares along the left side, we write the genotypes of the kinds of sperm the man will produce (fig. 1). (In this case, it happens to be the same combinations of alleles as for the eggs, because he happens to have the same genotype as his wife in this particular example. But this is not always the case, of course.)
- In each of the smaller boxes, we now write the genotype we will get when we combine an egg of the type shown above with a sperm of the type shown to the left (fig. 2).
- Below these genotypes, we write the corresponding phenotypes (fig. 2).
- Now we determine how many of the boxes contain the phenotype that the question asked about, namely, a square face and curly hair. We see that only one of the 16 boxes (shaded in the diagram) is labeled “square curly.” Thus we can conclude that the prospect of these two parents having a baby with a square face and curly hair is 1-in-16. From this same diagram we can also determine the probability that each of the other possible phenotypes would appear in the progeny. For example, the probability of a baby resembling both of the parents with respect to these two traits (oval face and wavy hair) is 4-in-16 (4/16) or 1-in-4 (1/4).

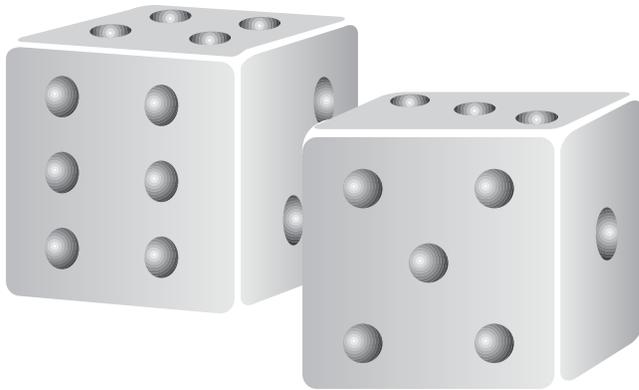
Eggs produced by an *Aa Hh* female

		<i>AH</i>	<i>Ah</i>	<i>aH</i>	<i>ah</i>
Sperm produced by an <i>Aa Hh</i> male	<i>AH</i>	<i>AA HH</i> Round Curly	<i>AA Hh</i> Round Wavy	<i>Aa HH</i> Oval Curly	<i>Aa Hh</i> Oval Wavy
	<i>Ah</i>	<i>AA Hh</i> Round Wavy	<i>AA hh</i> Round Straight	<i>Aa Hh</i> Oval Wavy	<i>Aa hh</i> Oval Straight
	<i>aH</i>	<i>Aa HH</i> Oval Curly	<i>Aa Hh</i> Oval Wavy	<i>aa HH</i> Square Curly	<i>aa Hh</i> Square Wavy
	<i>ah</i>	<i>Aa Hh</i> Oval Wavy	<i>Aa hh</i> Oval Straight	<i>aa Hh</i> Square Wavy	<i>aa hh</i> Square Straight

Figure 2

CHAPTER 2

**Passing Traits from
One Generation
to the Next**



SECTION D

**How Are
Genetic
Experiments
Actually
Performed?**



A Colorful Experiment in Yeast Genetics

INTRODUCTION

OK, FOLKS, ENOUGH IMAGINARY organisms for a while. Let's do a real genetic experiment, with a real, live model organism. The model organism we will use is baker's yeast. Yes, this is the same organism that the bakers of Bunny Bread use to make that spongy white stuff for your peanut butter and jelly sandwiches! Baker's yeast is a unicellular fungus with a life cycle that at first seems very different from that of the more familiar animals and plants (see page 113).

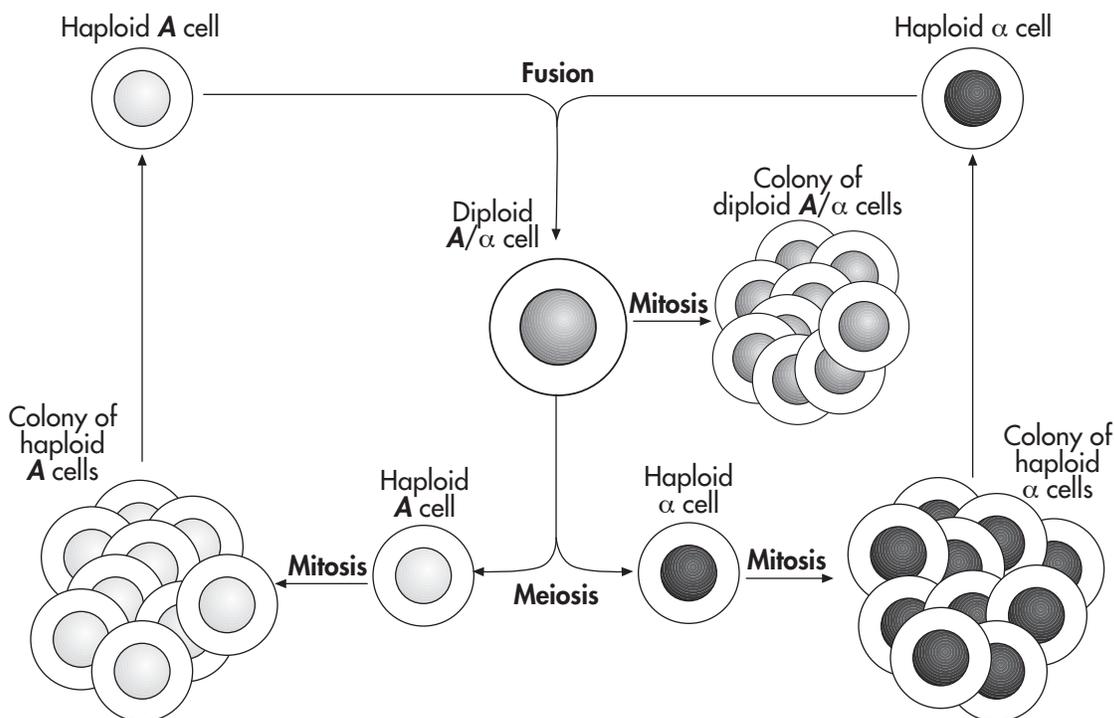
As different as it looks at first glance however, you will notice that the yeast life cycle does resemble the life cycle of animals and plants in several very important regards. It involves haploid and diploid cells and thus meiosis and recombination. Indeed, yeast follows the same basic rules of inheritance that we do, even though its haploid cells bear no resemblance to the sperm and egg cells of animals.

Because yeast can complete its life cycle in less than a day (under optimum conditions), it can be used to perform many different genetic experiments in a very short time. As a result, it is one of the most popular model organisms for geneticists who are interested in studying the basic principles of genetics that apply to all eukaryotic organisms.

In this exercise, we will use red and white strains of yeast to study a simple genotype-phenotype relationship that until now we had only encountered as a theoretical concept. In addition to strains that differ in color, we will also need strains that differ in mating type so that they will be able to fuse to make diploids. Yeast geneticists call the two mating types of yeast a (small a) and α (alpha). But to be sure that we do not confuse the two strains in our experiment, we will use the terms A (capital A) and α (alpha). In a sense, the two mating types, A and α , are to yeast as males and females are to animals.

Your job will be to formulate a hypothesis about the genetic basis for the color difference that you will observe between the haploid strains you will cross, use that hypothesis to make a prediction about what color the diploids will be, and then mate four strains of yeast to test your hypothesis.

THE LIFE CYCLE OF YEAST



Haploid and diploid yeast cells look similar, and both can divide mitotically to form large colonies. Haploid cells come in two mating types, which we will call *A* and α . As long as these two mating types are kept apart, they continue to grow and divide in the haploid state. But if they make contact, they fuse to form an *A*/ α diploid. Under most conditions, the *A*/ α diploids will grow and divide continuously, forming colonies.

Under certain nutritional conditions, however, *A*/ α diploids undergo meiosis to produce new *A* and α haploids. If the *A* and α cells are not separated at once, they fuse again to make new *A*/ α diploids. At first this might seem like a waste of effort, but it is not. Because various alleles will have been sorted out and recombined at random in the process, the new generation of *A*/ α diploids will include individuals that are genetically different from those in the earlier generation, and one or more of these new variants might be better adapted to the nutritional conditions that now exist.

MATERIALS

For each group of four student(s):

- 1 petri dish containing yeast growth medium
- marking pen
- a packet of sterile toothpicks
- culture of Red Mating type *A* yeast
- waste container
- culture of Red Mating type α yeast
- culture of White Mating type *A* yeast
- culture of White Mating type α yeast
- disinfectant

PROCEDURE

Day 1: Growing Your Haploid Yeast Cells

Do not open your petri dish until instructed to do so.

1. Leave your petri dish upside down. Draw four lines with the marking pen, as shown in the diagram. Write your name and class hour at the bottom. Write "Mating Type A" across the top and "Mating Type α " along the left side. Then write the letters indicating the colors of the yeast strains (R for red and W for white) in the spaces indicated (fig. 1).

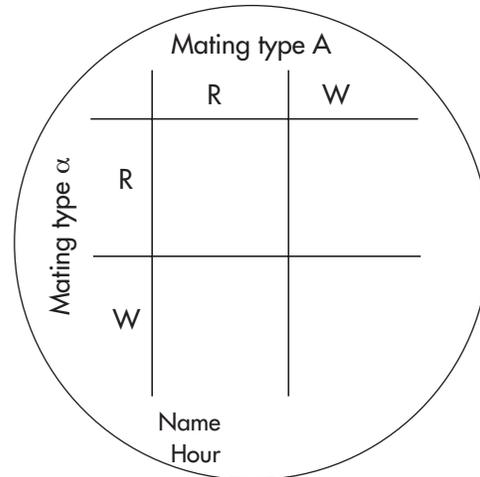


Figure 1

2. Shake your box of toothpicks gently so that a toothpick comes part way out of the corner hole. Remove the toothpick carefully, without touching the other end. If any toothpicks fall out of the box, ignore them and throw them away later.

3. Select the culture dish that has the Red Mating type A yeast strain on it. Leave it upside down. While holding your toothpick in one hand, use your other hand to lift the bottom half of the dish that contains the Red Mating type A culture. Do not turn it over. Now gently scrape the end of your toothpick across the culture to pick up a small quantity of yeast on the toothpick. Put the stock culture back on its lid.

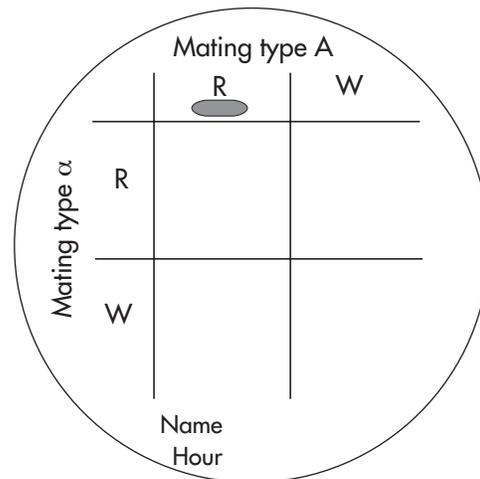


Figure 2

4. Lift the bottom of your experimental dish (the one you marked in step 1). Do not turn it over. Carefully transfer the yeast cells to your dish by rubbing your toothpick on the agar in the box that contains R under the Mating Type A (fig. 2). Put the plate back on its lid. Discard the toothpick.
5. Repeat steps 2-4 with each of the other three strains of yeast. Use a fresh toothpick for each strain, and place each kind of the yeast in the space indicated on fig. 2.
6. Put your stock cultures and your experimental culture dish in the places indicated by the teacher.
7. Wipe your work area with disinfectant and wash your hands.

Day 2: Making the Genetic Crosses

Do not open your petri dish until instructed to do so.

1. Examine your petri dish carefully. Have all four of your yeast colonies grown well? Record your observations on the Day 2 Work Sheet.
2. With the dish still closed, draw four circles and number them 1 to 4 (fig. 3).

3. Get a sterile toothpick. Lift the agar-containing part of the petri dish, and — while keeping the dish upside down — gently rub the Red Mating type *A* colony with the end of the toothpick. Now rub the toothpick on the agar lightly in the center of circle 1. You want to deposit only a small number of cells on the agar — barely enough to see. If you have more than this, try to scrape off the excess. Discard the toothpick in the waste jar.

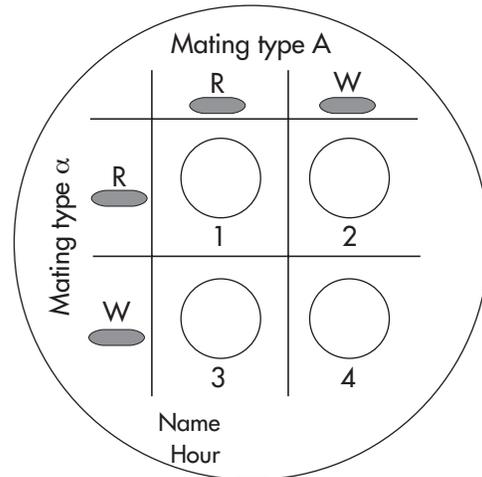


Figure 3

4. With a new sterile toothpick gently rub the Red Mating type α colony and then rub the toothpick in the same region of circle 1 where you rubbed with the Red Mating type *A* toothpick. Mix the two kinds of yeast cells together with the toothpick, but avoid stabbing the agar. Discard the toothpick in the waste jar.
5. Repeat steps 3 and 4 for the three empty circles, so as to cross the White Mating type *A* and Red Mating type α strains in circle 2, the Red Mating type *A* and White Mating type α strains in circle 3, and the two white strains in circle 4.
6. Place your petri dish in the incubator or where your teacher directs you.
7. Wipe your work area with disinfectant. Wash your hands.
8. Complete the Day 2 Work Sheet.



Name _____

Date _____ Hour _____

DAY 2 WORK SHEET

1. Describe the appearances of the four colonies of haploid yeast cells at the beginning of class on Day 2.

2. Formulate a hypothesis about the genetic difference that causes the difference in appearance of the red and white yeast strains.

3. Which color trait do you think will be dominant, or do you think that they will be codominant? Why?

4. Based on the above hypotheses, what do you predict the color phenotypes of the diploids will be in the following four crosses that you have set up?

Red Mating type *A* x Red Mating type α _____

Red Mating type *A* x White Mating type α _____

White Mating type *A* x Red Mating type α _____

White Mating type *A* x White Mating type α _____



Name _____

Date _____ Hour _____

Day 3: Observing Your F1 (A/ α Diploids)

1. Get your petri dish and observe your results.

Even though there are no sperm and eggs involved, a Punnett square diagram can be used to record and analyze the results of yeast crosses such as the ones you performed. Use your observed results to fill in the blanks on the Punnett square on the Day 3 Work sheet on the next page.

2. Are any of your results unclear? If so, indicate which ones, describe what you see, and provide a good explanation for these results.

3. If any of your test circles contain a mixture of red and white cells, incubate the dish for another day and see if things change. If they do, be sure to record this on your Day 3 Work Sheet.
4. When you are through working with your cultures, spray disinfectant in your dish, tape it shut, and dispose of it as instructed by your teacher. Wipe your work area with disinfectant. Wash your hands.
5. Finish filling out the Day 3 Work Sheet.

DAY 3 WORK SHEET

1. Use the results from your yeast crosses to fill in the blanks on the diagram below:

		Mating type A	
		R	W
Mating type α	R	Genotype _____ Phenotype _____	Genotype _____ Phenotype _____
	W	Genotype _____ Phenotype _____	Genotype _____ Phenotype _____

2. What ratio of phenotypes did you observe as a result of the four crosses you performed?

3. What does this indicate about which allele is dominant and which is recessive?

4. Is this what you predicted on your Day 2 Work Sheet?

5. In the table below, list what you predicted and what you observed for each of the four crosses.

Cross	Predicted Phenotype of Diploid	Observed Phenotype of Diploid
Red Mating type A by Red Mating type α		
Red Mating type A by White Mating type α		
White Mating type A by Red Mating type α		
White Mating type A by White Mating type α		



Name _____

Date _____ Hour _____

6. If your predicted and observed phenotypes do not agree, how can you account for that, and can you propose a good hypothesis to account for the results you actually observed?

7. If you have come up with a new hypothesis, can you think of a way to test it?



Experimenting with Wisconsin Fast Plants: Option 1, Phase 1

INTRODUCTION

MOST PLANTS ARE NOT suitable for use in classroom biology projects, because most plants grow slowly, take months or years to produce seeds that are ready to be planted, and get so large that there is not room for more than a few of them in a classroom.

Paul Williams, a plant biologist at the University of Wisconsin, set out to change all that and develop plants that would be convenient and fun for students to grow and study in the classroom. To achieve his goal, he selected the most rapidly flowering plants he could find, crossed them with one another, and continued this selective breeding for several plant generations. The resulting plants are the Wisconsin Fast Plants, some of which you will use in this exercise. These plants flower in two weeks, produce mature seed in five to six weeks, and are so small that it is possible to grow hundreds of them in a classroom.

Another name for Wisconsin Fast Plants is **rapid-cycling brassicas**. *Brassica* is the genus of plants that includes cabbage, broccoli, cauliflower, turnips, mustard greens, collards, and many other popular food plants. The Fast Plants are members of the species *B. rapa*, the *Brassica* species from which bok choy and Chinese cabbage were derived.

Initially you will use the Fast Plants just to study the plant life cycle. You will plant the seeds, watch the plants germinate and grow, and learn how to transfer pollen from one plant to another when the flowers appear. Then you will watch the seeds develop from the flowers you have pollinated and eventually collect the seeds. By the time your seeds are mature, however, you will find out that they are part of a more extensive and more interesting experiment. You will be given more information about that when the time comes. But for now, let's just get our seeds planted and watch our garden grow.



MATERIALS

For the class (Day 1):

- 1 container of potting mix
- 2 spoons
- 1 ruler
- 1 bottle of 1/8 X Peter's Professional Fertilizer
- masking tape
- felt-tip marking pens

For each group of four students (Day 1):

- 1 film-can growth system (Fig. 4)
- 1 water bottle
- Fast Plant seeds in a small envelope

For each set of four student groups (Day 1):

- 1 plant lighthouse
- 1 piece of foil-covered cardboard
- 6 pieces of 1 inch thick insulating foam

For each group of four students later on:

- 14 25-cm bamboo skewers to be used as plant stakes
- 14 split-ring ties to hold plants to stakes
- 4 dried bees
- 4 toothpicks
- Duco fast-drying cement
- 1 brown paper lunch bag
- 1 small envelope

PROCEDURE

You will grow your plants in a film-can growth system that consists of several parts (Fig. 1-4). The film cans will hold your plants and the soil in which they grow; the other pieces form an automatic watering system that will keep the soil moist and give your plants a constant supply of water and nutrients.

Put a piece of masking tape on the bottom chamber of your growth system (the nutrient reservoir) and with the marking pen write your group name and your class period on the tape. (Make sure that the tape does not overlap the clear stripe on the bottom chamber, because you will need to look through this stripe to monitor the fluid level.)

1. Preparing the growth system and planting the seeds (Day 1)

- a. Make sure that a wick is about half in and half out of the bottom of each can (Fig. 1).
- b. Hold your film-can cluster over the container of soil and fill each can loosely. Tap the film cans on the side to help the soil settle, but **DO NOT PRESS THE SOIL INTO THE CANS**.
- c. Use the ruler to scrape off any excess soil so that each can is filled up to but not over the top (Fig. 2).
- d. Make sure that both ends of the long wick hang out of your slotted tray so that they will hang freely into the nutrient reservoir (Figs. 3-4).
- e. Hold the film-can cluster over the slotted tray. Turn your water bottle upside down and squeeze gently to direct a stream of water at each film can. Water each can until water drips from its wick (Fig. 2). (This will cause the soil to settle somewhat.)
- f. Water the wick in the slotted tray until it is saturated and water runs freely into the nutrient reservoir.
- g. Place four seeds, evenly spaced, on the surface of the soil in each film can.

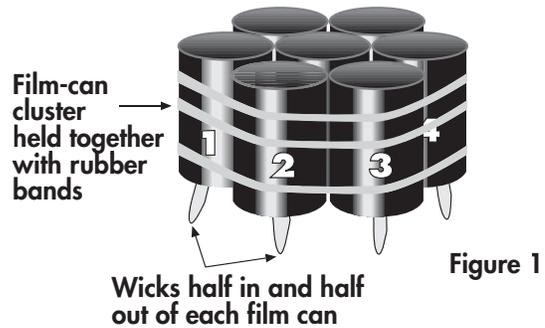


Figure 1

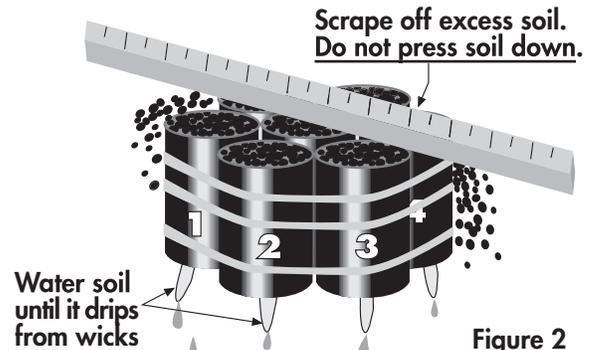


Figure 2

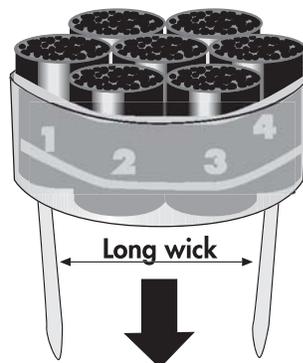


Figure 3

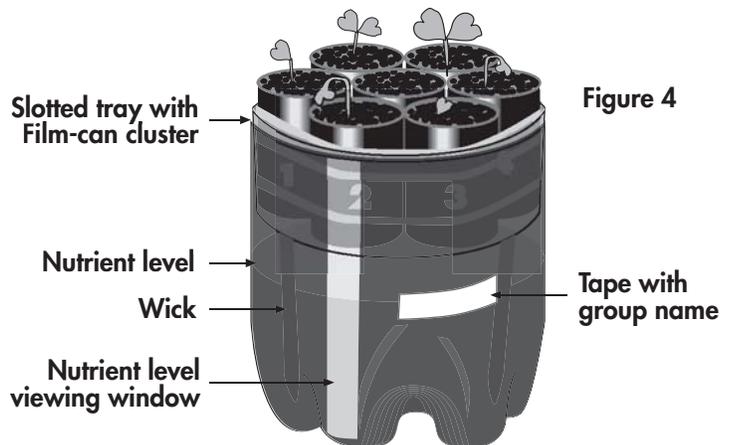


Figure 4

 **D.2**

- h. Take your film-can cluster back to the container of potting mix. Carefully sprinkle soil over the seeds to fill each can to the top. Level the soil with the ruler. **DO NOT PRESS THE SOIL INTO THE CANS.**
- i. Add 1/8 X Peter's Professional Fertilizer (as a nutrient solution) to the nutrient reservoir until the level is just below the bottom of the slotted tray.
- j. Place your film-can cluster in the slotted tray. Water each can gently until water begins to run out of it and through the slots into the nutrient reservoir.
- k. Your plants will be grown in a plant lighthouse (Fig. 5). Take your growth system to the plant lighthouse to which your teacher assigned you.
- l. If the following has not already been done, stack six foam blocks on the floor of the lighthouse and then place the foil-covered cardboard on top of the stack.
- m. Place your growth system on top of the foil-covered cardboard, toward one corner of the lighthouse.

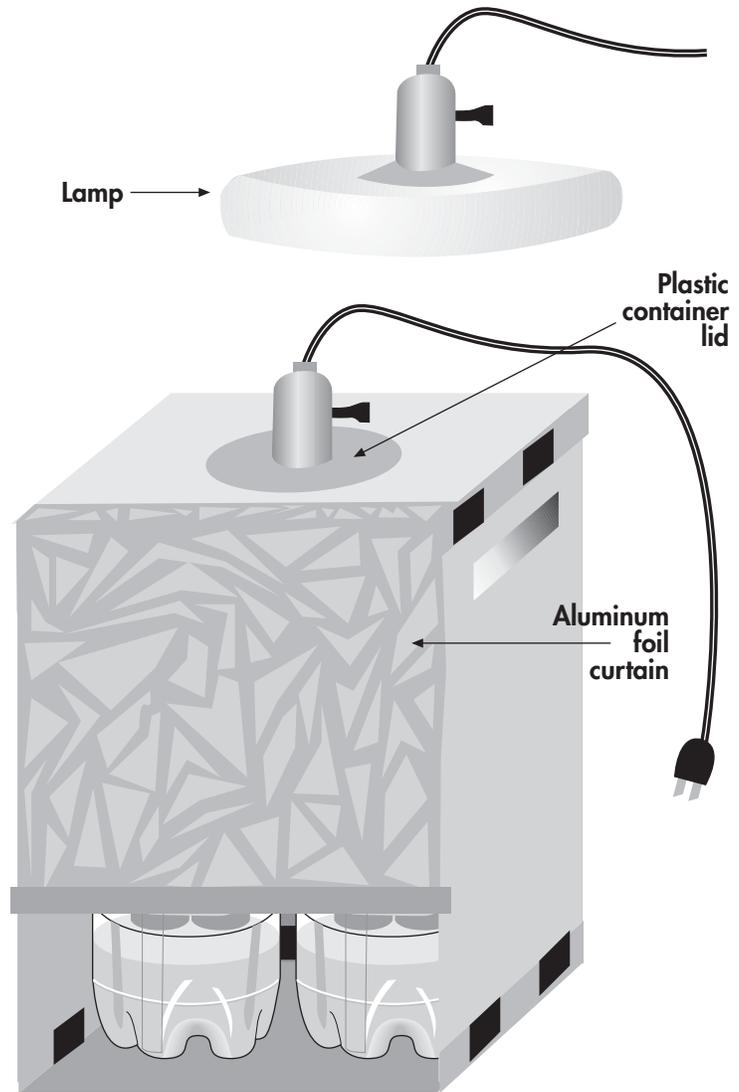


Figure 5

2. After Day 1

- a. **Days 2-4** Use your water bottle to sprinkle the surface of the soil in each film can. Record how many plants emerge in each can and when they emerge.
- b. **Every day after Day 4** Check the liquid level in your nutrient reservoir. Add 1/8 X Peter's nutrient as necessary to keep liquid level up near (but never above) the bottom of the upper chamber. A good way to do this is to move the film-can cluster to one side, slowly pour the Peter's nutrient into the upper chamber and let it run through to the bottom. This will keep all the wicks wet. It is particularly important to fill the reservoir just before a weekend or holiday.

Observe your plants regularly and keep a record of their progress. Record when they look like each of the stages pictured on your work sheets (see pages S121-S123). After most of your plants reach one of the pictured stages, fill in the date and the number of days that have passed since you planted the seeds. It would also be a good idea to keep a journal in which you describe what you see each time you observe the plants.

- c. **Day 4 or 5** If there are fewer than two seedlings in any of your film cans, you may transplant seedlings from cans that have more than two. To do this, use a pencil to make a depression in the spot to which you wish to move a seedling. Carefully lift a seedling using your fingers or a pair of forceps, and tuck its roots into the depression you have just made. Use the pencil to tuck soil around its roots, and sprinkle the soil lightly with water.
- d. **Day 7 or 8** Remove all but the two healthiest-looking seedlings from any film can that still has more than two. Use a pair of scissors to snip off each unwanted plant just above ground level.
- e. **Days 8-14** As your plants grow taller, use bamboo stakes to support them and prevent them from falling over. Insert a stake near a plant; then attach the plant to the stake with a split ring tie (Fig. 6).



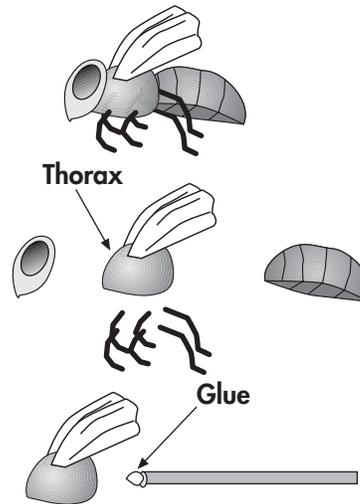
Figure 6

As the plants grow, remove foam sheets from the lighthouse as necessary to prevent the tips of the plants from getting closer than 10 cm to the light.

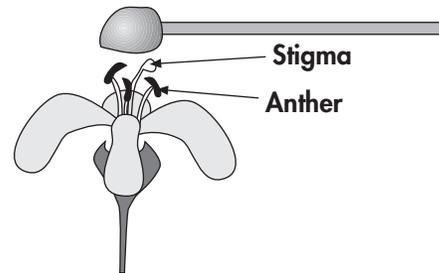
3. Making “bee sticks” and using them to pollinate plants

- a. **Day 11 or 12** Using a dry, dead bee and a toothpick, make a bee stick as follows:

Hold the bee by the wings while you remove the abdomen, the head, and the legs. (Don’t worry. This bee has long since lost the ability to sting you.) What you have left is the thorax with the wings attached.

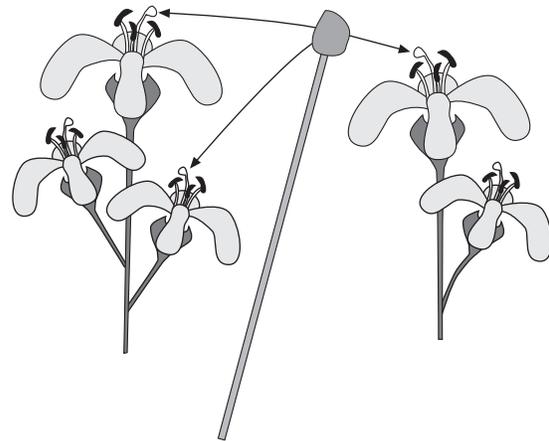


Place a small drop of fast-drying glue on the tip of the toothpick and stick it in the hole left by the removal of the abdomen or the head. Stick the other end of the toothpick into a foam sheet and leave your bee stick overnight to dry. The next day, after the glue is dry, remove the wings from the thorax.



- b. **Days 13 to 18** After flowers on your plants open, cross-pollinate the plants as follows:

Use the bee stick to pick up pollen from the anthers of one flower. (The anthers are the male parts of the flower that are arranged around the central stigma, which is the female part of the flower.) To pick up more pollen, rotate the beestick as you touch an anther.



Now transfer the pollen to the stigmas of flowers on several different plants; this is called cross-pollination. Brassica flowers are self-incompatible, which means that pollen from one plant is unable to fertilize flowers on that same plant but usually can fertilize flowers on another plant.

The more plants you involve in such cross-pollination, the more likely you are to obtain a lot of healthy seeds. (So all students in the group should take turns pollinating.)



Repeat the cross-pollination process on at least three successive days. Try to use a different cross-pollination pattern each day.

You will harvest your seeds 20 days after your last cross-pollination. Add a tape label to your nutrient reservoir that indicates what the date will be.

4. Harvesting seeds

Seedpods and seeds begin to develop and grow shortly after the flowers have been successfully pollinated, but it takes 20 days for the seeds to become mature.

- a. 20 days after the last day you pollinated, remove your film-can cluster from the watering system. Put the cluster first on a paper towel and then back in the light-house so that the plants can dry out.

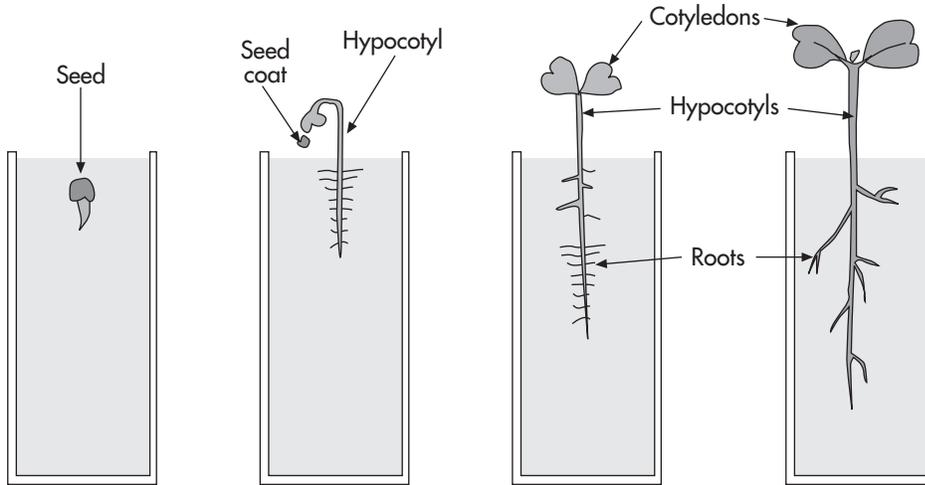
Rinse out both chambers of the watering system and let them dry out, so they will be ready for reuse.

- b. After the plants have dried for about five days, the seed pods should be crisp and brown. As soon as they are, cut the seed pods off the plants one at a time and put them in the paper bag. Seal the bag with staples or tape and then crush the pods.
- c. Unseal the bag and carefully dump its contents into a shallow container or onto a sheet of white paper. Pick off and discard large pieces of debris. Blow gently to blow off small pieces of debris.
- d. Transfer as many seeds as you can to a small envelope. Label the envelope with your names and your class hour. Store the seeds in a safe, dry place until your teacher announces that it is time to start Phase 2 of the Fast Plants experiment.
- e. Clean out your film-can cluster and prepare it for reuse. If you have lost any wicks, ask your teacher for a piece of capillary material to make new wicks.

D.2

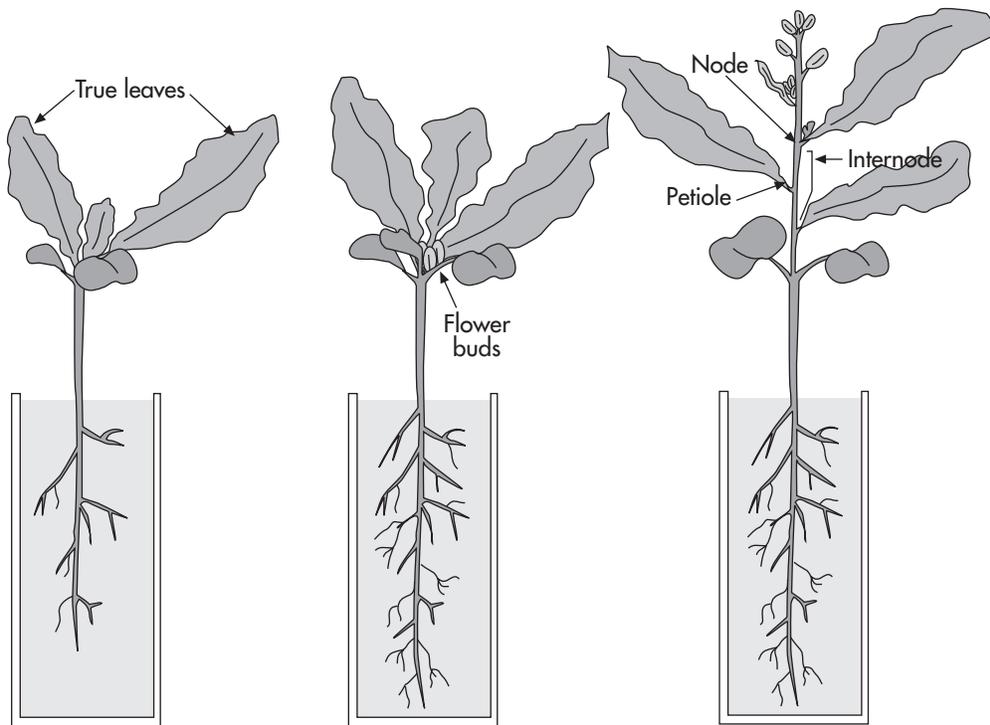
Name _____

Date _____ Hour _____



Calendar date _____

Days since planting _____



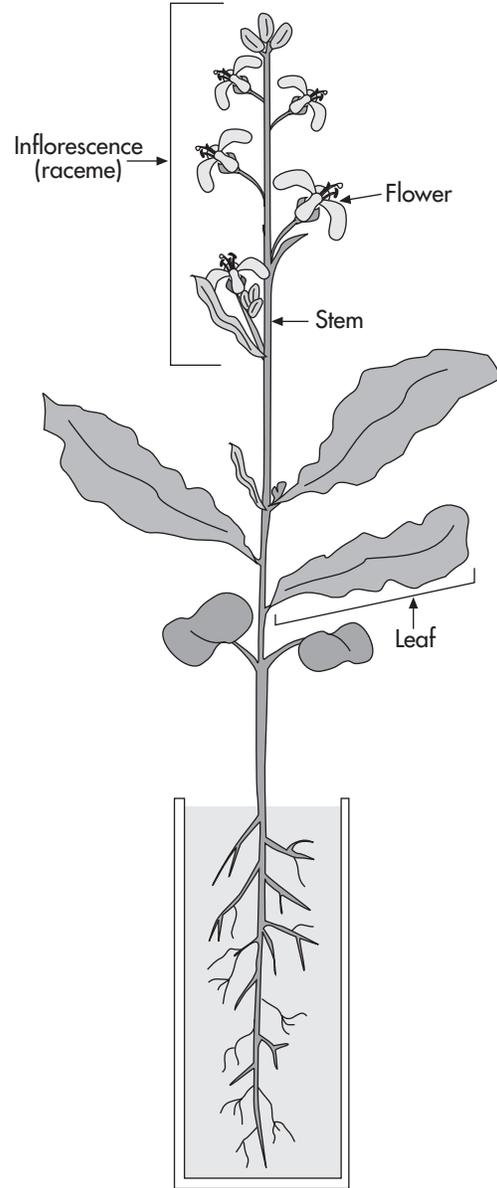
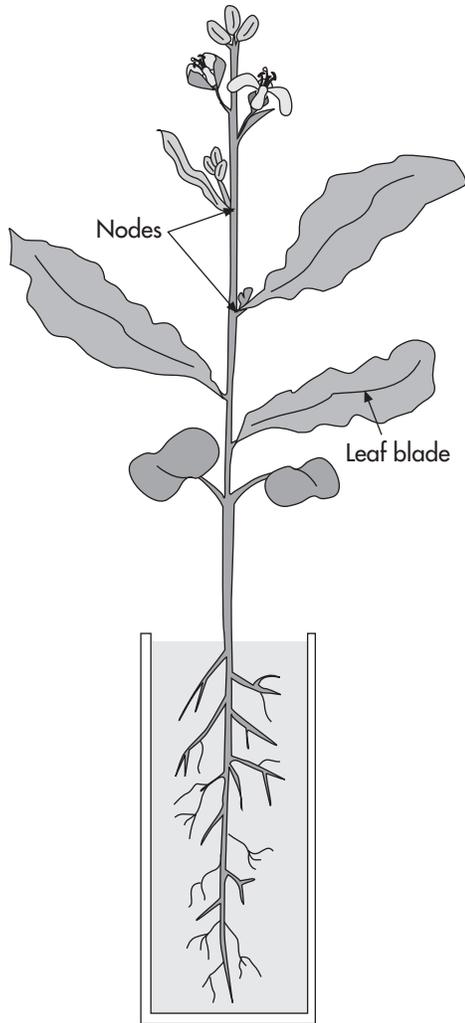
Calendar date _____

Days since planting _____

D.2

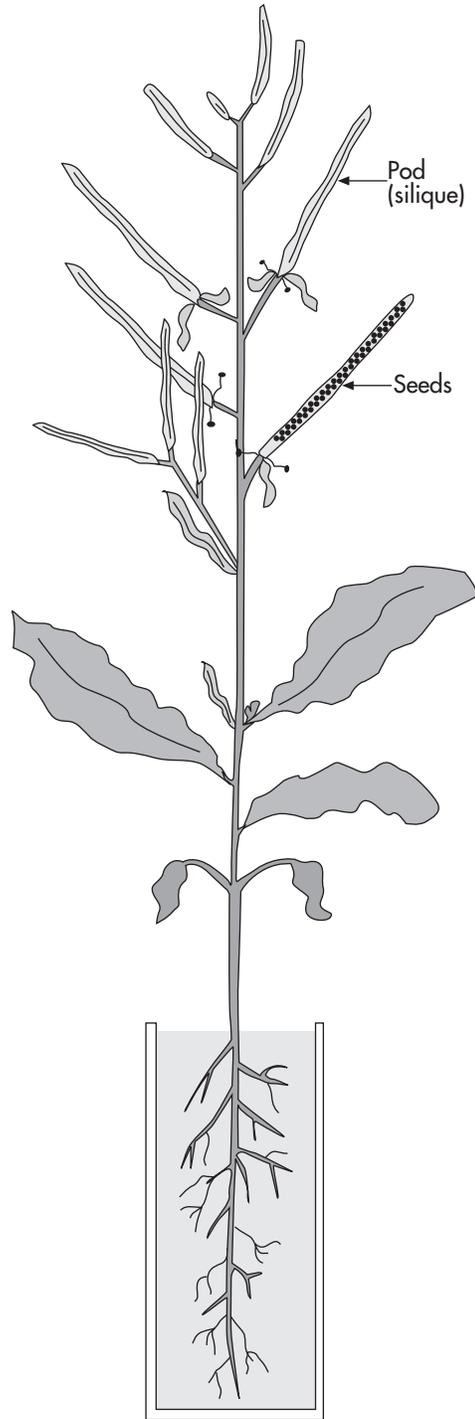
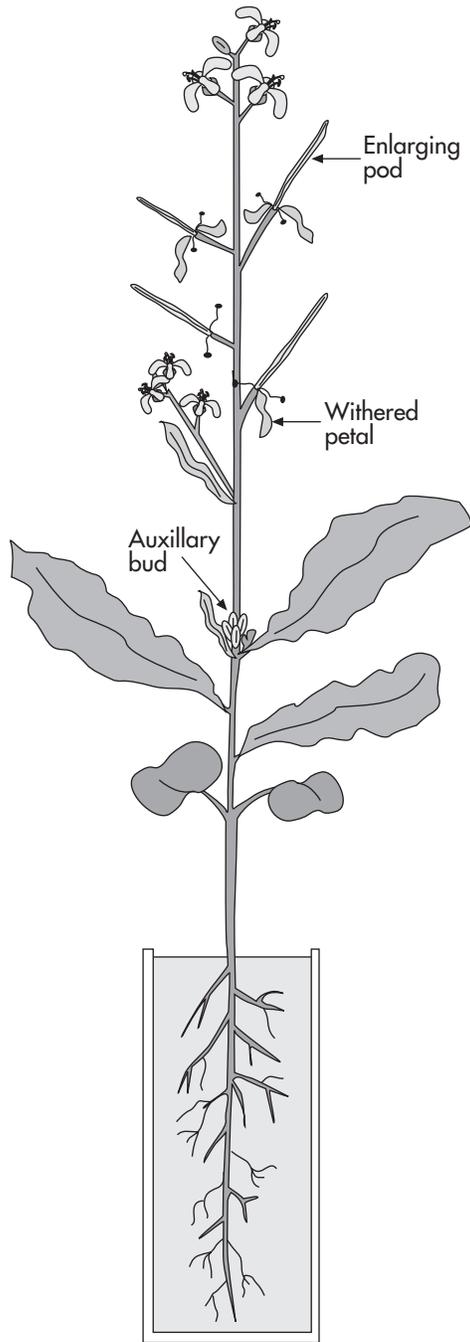
Name _____

Date _____ Hour _____



Calendar date _____

Days since planting _____



Calendar date _____

Days since planting _____

Experimenting with Wisconsin Fast Plants: Option 1, Phase 2

INTRODUCTION

NOW IT CAN BE TOLD! The seeds that you planted at the beginning of Phase 1 were not produced by just any Fast Plants. You were given seeds that had been produced by cross-pollinating two plants that differed from one another with respect to two conspicuous traits.

Organisms that are produced by a cross between genetically distinguishable parents are called **hybrids**. When those parents differ in two heritable traits, the cross between them is called a **dihybrid cross**. The seeds you received were the result of such a dihybrid cross.

The principal purpose of Phase 2 of the Fast Plants exercise is twofold. First you are to determine what distinguishing traits were present in the plants that generated the seeds you initially planted, and then you are to determine what sort of inheritance patterns those traits exhibit.

Biologists have a set of terms that they use to keep track of the generations in such genetic experiments. The plants with which the experiment begins are members of the **parental**, or **P**, generation. Their offspring are called the **first filial**, or **F₁**, generation. [The Latin words for *son* and *daughter* are *filius* and *filia*, respectively.] The progeny of the F₁ generation are called the **second filial**, or **F₂**, generation.

The seeds with which you began Phase 1 were produced by crossing two visibly different P-generation plants. We will call these two different P-generation plants P_A and P_B. The plants that you grew initially constituted the F₁ generation. You cross-pollinated your F₁ plants to produce the seeds that you will soon use to produce plants of the F₂ generation. The objective of this experiment is to determine which of the visible traits present in the P-generation plants (but not visible in your F₁ plants) will reappear in the F₂ plants. Because you may use a mathematical method to test certain genetic hypotheses, it is important to germinate a substantial number of F₂ seeds and to keep careful track of how many plants of each different phenotype you see.



MATERIALS

For the class:

- 1 container of potting mix
- 2 spoons
- 1 ruler
- 1 bottle of 1/8 X Peter's Professional Fertilizer

For each group of four students:

- 1 film-can growth system
- 1 water bottle
- 1 envelope with 6 P_A seeds
- 1 envelope with 6 P_B seeds
- 1 envelope with 6 double-mutant seeds
- the F₂ seeds collected in Phase 1

For each set of four groups of four students:

- 1 plant lighthouse
- 1 piece of foil-covered cardboard
- 6 pieces of 1 inch thick styrofoam

PROCEDURE

You will follow the same basic procedures as for Phase 1 for the first few days, except that you will plant different kinds of seeds in different film cans.

1. Preparing the growth system and planting the seeds (Day 1)

- Make sure that a wick is about half in and half out of the bottom of each can (Fig. 1).
- Hold your film-can cluster over the container of soil and fill each can loosely. Tap the film cans on the side to help the soil settle, but **DO NOT PRESS THE SOIL INTO THE CANS**.
- Use the ruler to scrape off any excess soil so that each can is filled up to, but not over the top (Fig. 2).
- Make sure that both ends of the long wick hang out of your slotted tray and hang freely into the nutrient reservoir.
- Hold the film-can cluster over the slotted tray. Turn your water bottle upside down and squeeze gently to direct a stream of water at each film can. Water each can until water drips from its wick (Fig. 2). (This will cause the soil to settle somewhat.)
- Water the wick in the slotted tray until it is saturated and water runs freely into the nutrient reservoir.

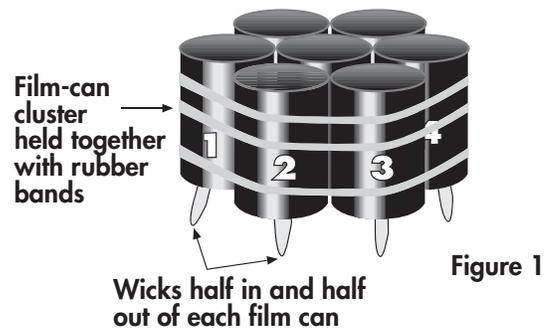


Figure 1

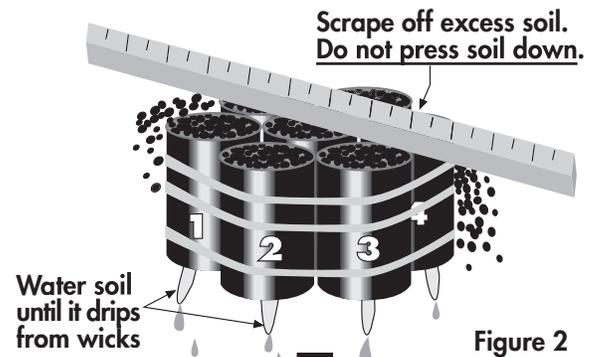


Figure 2

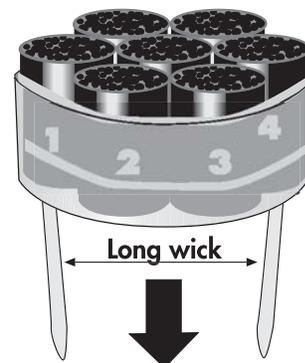


Figure 3

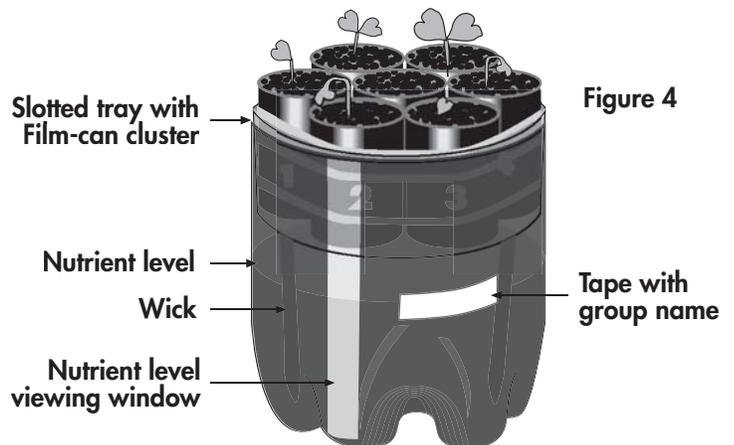


Figure 4



- g. Place the film-can cluster in the slotted tray. Paying attention to the numbers on your film cans, place six seeds, evenly spaced, on the surface of the soil in each film can, according to the following plan:

Can 1: six PA seeds.

Can 2: six PB seeds.

Can 3: six double-mutant seeds.

Cans 4-7: six of your F₂ seeds in each can. If you do not have enough F₂ seeds, try to get some from another group. If you have extra F₁ seeds, share with those who need more.

- h. Take your film-can cluster back to the container of potting mix. Carefully sprinkle soil over the seeds to fill each can to the top. Level the soil with the ruler. **DO NOT PRESS THE SOIL INTO THE CANS.**
- i. Add 1/8 X Peter's nutrient solution to the nutrient reservoir until the level is just below the bottom of the slotted tray.
- j. Place your film-can cluster in the slotted tray. Water each can gently until water begins to run out of it and through the slots into the nutrient reservoir.
- k. Take your growth system to your plant lighthouse. If the following has not already been done, stack six foam blocks on the floor of the lighthouse and then place the foil-covered cardboard on top of the stack.
- l. Place your growth system on top of the foil-covered cardboard, toward one corner of the lighthouse.

2. After Day 1

- a. **Days 2-4** Use your water bottle to sprinkle the surface of the soil in each film can.
- b. **Days 3-5** Observe your film cans daily and record what you see on the Observations pages. Record how many seedlings emerge in each can and when they emerge. Each day after that observe all seedlings carefully, looking for significant differences among them. Compare your plants to the photographs of mutant Fast Plants or to the live Fast Plant mutants that your teacher put on display. By Day 5, assign phenotypes to all the plants that are present in each can.
- c. **Day 8** Reexamine all of your plants carefully and record your observations. Do you think that all of the phenotypes that you assigned on Day 5 were correct? Or do you think that any of them should be changed? In which parts of the plant does it seem to be easiest to distinguish the various phenotypes? In the cotyledons? In the stems? Or in the first true leaves? Or are different traits distinguished more easily in different organs?



3. In conclusion

Fill out the Wisconsin Fast Plants Phase 2 Work Sheet.



Name _____

Date _____ Hour _____

WISCONSIN FAST PLANTS WORK SHEET

1. What are the two mutant traits that distinguished your PA and PB plants from one another and from wild-type Wisconsin Fast Plants?

The PA plants are _____ mutants.

The PB plants are _____ mutants.

2. If the mutant traits exhibited by the P₁ and P₂ generation are heritable, why didn't those two traits appear in their progeny in the F₁ generation?

3. Based on your explanation above, what would you predict that the ratio of wild-type to mutant individuals should have been for each of these two traits in the F₂ generation? Explain.

4. Above each of the tables below, record how many F₂ plants germinated and grew large enough that their phenotypes could be determined with confidence. Then in the right hand column of each table record how many of these F₂ plants had each of the indicated phenotypes.

Table 1.A. Data collected by our own group.

The number of plants analyzed was _____.

Phenotype	Number of F ₂ plants
Wild-type with respect to the PA trait:(_____)	
Mutant with respect to the PA trait: (_____)	
Ratio of wild-type to mutant: _____ to _____	
Wild-type with respect to the PB trait:(_____)	
Mutant with respect to the PB trait:(_____)	
Ratio of wild-type to mutant: _____ to _____	



Name _____

Date _____ Hour _____

Table 1.B. Combined data for the whole class.

The number of plants analyzed was _____.

Phenotype	Number of F ₂ plants
Wild-type with respect to the PA trait:(_____)	
Mutant with respect to the PA trait:(_____)	
Ratio of wild-type to mutant: _____ to _____	
Wild-type with respect to the PB trait:(_____)	
Mutant with respect to the PB trait:(_____)	
Ratio of wild-type to mutant: _____ to _____	

5. With respect to the PA trait, how does the ratio of wild-type to mutant individuals that you predicted in Question 3 compare to the ratios of wild-type to mutant individuals that you reported in tables 1A and B?

The predicted wild-type-to-mutant ratio was ____:1

The wild-type-to-mutant ratio we observed with our group's F₂ plants was ____:1

The wild-type-to-mutant ratio observed by the entire class was ____:1

In your opinion, are these differences between the predicted and the observed wild-type-to-mutant ratios significant?

Yes ____ No ____ Can't decide ____

Explain

6. How do the predicted and observed wild-type-to-mutant ratios for the PB trait compare?

The predicted wild-type-to-mutant ratio was ____:1

The wild-type-to-mutant ratio we observed with our group's F₂ plants was ____:1

The wild-type-to-mutant ratio observed by the entire class was ____:1

In your opinion, are these differences between the predicted and the observed wild-type-to-mutant ratios significant?

Yes ____ No ____ Can't decide ____

Explain



Name _____

Date _____ Hour _____

7. How confident are you of the validity of your answer to Question 6?
 Very confident ____ Fairly confident ____ Not at all confident ____
 Explain your answer:

8. Record the observed phenotypes of the F_2 plants with respect to combinations of P_1 and P_2 traits.

In tables 1A and B (Question 4) you recorded the number of F_2 plants that were wild-type or mutant with respect to the P_A and P_B traits individually. In the next two tables record the numbers of F_2 plants that had each of the four possible combinations of these two traits.

Table 2.A. Data collected by our own group.

The number of plants analyzed was _____.

Phenotype with respect to the P_A trait: (_____)	Phenotype with respect to the P_B trait: (_____)	Number of F_2 plants
Wild-type	Wild-type	
Mutant	Wild-type	
Wild-type	Mutant	
Mutant	Mutant	

Table 2.B. Combined data for the whole class.

The number of plants analyzed was _____.

Phenotype with respect to the P_A trait: (_____)	Phenotype with respect to the P_B trait: (_____)	Number of F_2 plants
Wild-type	Wild-type	
Mutant	Wild-type	
Wild-type	Mutant	
Mutant	Mutant	



Name _____

Date _____ Hour _____

9. In the table below, compare the ratios of the four possible combinations of P_A and P_B traits that you and your class observed with the ratios that are predicted for this kind of dihybrid cross. In each case, set the number of double mutants to one.

Phenotypic combinations	Predicted ratio for a dihybrid cross*	Ratio observed in our own plants‡	Ratio observed for entire class‡
Wild-type for the P _A trait and wild-type for the P _B trait			
Mutant for the P _A trait and wild-type for the P _B trait			
Wild-type for the P _A trait and mutant for the P _B trait			
Mutant for the P _A trait and mutant for the P _B trait	1	1	1

* You can obtain this ratio either by (a) using the product-of-probabilities method, (b) using a Punnett Square, or (c) reviewing similar calculations that you made for Exercise 2.C.3 (Create-a-Baby).

‡ To obtain the numbers for each of these blanks, divide the number of plants observed in that category by the number of double-mutant plants observed in the same data set.

10. Do you think that the differences between the predicted and the observed ratios in the above table are significant?

Yes ____ No ____ Can't decide ____

Explain

11. How confident are you of the validity of your answer to Question 10?

Very confident ____ Fairly confident ____ Not at all confident ____

Explain

Note: The next unit (2.E) illustrates a mathematical method that many biologists use to determine whether differences between predicted results and observed results in an experiment such as this one are significant. You may find it interesting to review this unit, even if your teacher does not make it a class assignment.



Experimenting with Wisconsin Fast Plants: Option 2

INTRODUCTION

MOST PLANTS ARE NOT suitable for use in classroom biology projects. That is because most plants grow slowly, take months or years to produce seeds that are ready to be planted, and get so large that there is not room for more than a few of them in a classroom.

Paul Williams, a plant biologist at the University of Wisconsin, set out to change all that, and to develop plants that would be convenient and fun for students to grow and study in the classroom. To achieve his goal, he selected the most rapidly flowering plants he could find, crossed them with one another, and continued this selective breeding for several plant generations. The resulting plants are the Wisconsin Fast Plants, some of which you will use in this exercise. These plants flower in two weeks, produce mature seed in five to six weeks, and are so small that it is possible to grow hundreds of them in a classroom.

Another name for Wisconsin Fast Plants is **rapid-cycling brassicas**. *Brassica* is the genus of plants that includes cabbage, broccoli, cauliflower, turnips, mustard greens, collards, and many other popular food plants. The Fast Plants are members of the species *B. rapa*, the *Brassica* species from which bok choy and Chinese cabbage were derived.

You will use the Fast Plants to study the inheritance patterns for two visible plant traits. Organisms that are produced by a cross between genetically distinguishable parents are called **hybrids**, and when those parents differ in two heritable traits, the cross between them is called a **dihybrid cross**. You will be analyzing the results of a dihybrid cross.

Biologists have a set of terms that they use to keep track of the generations in such genetic experiments. The plants with which the experiment begins are members of the **parental**, or **P**, generation. Their offspring are called the **first filial**, or **F₁**, generation. [The Latin words for *son* and *daughter* are *filius* and *filia*, respectively.] The progeny of the F₁ generation are called the **second filial**, or **F₂**, generation.

The seeds that you will be given will produce plants representing all three generations of plants in the dihybrid cross that you are to analyze. We will call the two different types of parental plants P_A and P_B to distinguish them. P_A and P_B plants were crossed to produce the F₁ seeds. Then F₁ plants were crossed to produce the F₂ seed. You will also be given some ‘double-mutant’ seeds, so that you will be able to see what plants will look like if they have a combination of the mutant traits of the P_A and P_B plants.



The objective of this experiment is to determine what sorts of visible traits that were present in the P-generation plants disappear in the F₁ generation, but then reappear in the F₂ generation, and in what combinations they reappear. Because you may want to use a mathematical method to test certain genetic hypotheses, it will be important to germinate a substantial number of F₂ seeds, and to keep careful track of how many plants of each different phenotype you see.

MATERIALS

For the class:

- 1 container of potting mix
- 2 spoons
- 1 ruler
- 1 bottle of 1/8 X Peter's Professional Fertilizer

For each group of four students:

- 1 film-can growth system
- 1 water bottle
- 1 envelope containing 6 P_A seeds
- 1 envelope containing 6 P_B seeds
- 1 envelope containing 6 F₁ seeds
- 1 envelope containing 18 F₂ seeds
- 1 envelope containing 6 double-mutant seeds

For each set of four groups of four students:

- 1 plant lighthouse
- 1 piece of foil-covered cardboard
- 6 pieces of 1 inch thick insulating foam

PROCEDURE

You will grow your plants in a film-can growth system that consists of several parts. The film cans (Fig. 1) will hold your plants and the soil in which they grow; The other pieces form an automatic watering system that will keep the soil moist and give your plants a constant supply of water and nutrients.

Put a piece of masking tape on the bottom chamber of your growth system, and with the marking pen write your group name and your class period. (Make sure that the tape does not overlap the clear stripe on the bottom chamber, because you will need to look through this stripe to monitor the fluid level.)

1. Preparing the growth system and planting the seeds (Day 1)

- a. Make sure that a wick is about half in and half out of each can (Fig. 1).
- b. Hold your film-can cluster over the container of soil and fill each can loosely. Tap the film cans on the side to help the soil settle, but **DO NOT PRESS THE SOIL INTO THE CANS**.
- c. Use the ruler to scrape off any excess soil so that each can is filled up to but not over the top (Fig. 2).
- d. Make sure that both ends of the long wick hang out of your slotted tray so that they will hang freely into the nutrient reservoir (Figs. 3-4).

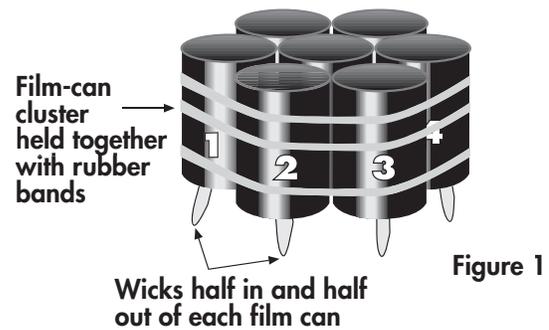


Figure 1

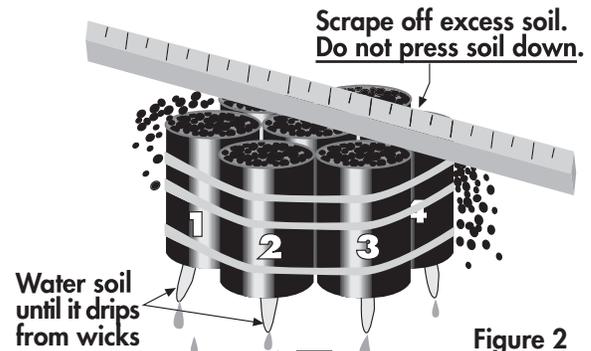


Figure 2

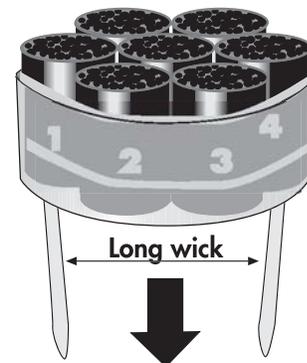


Figure 3

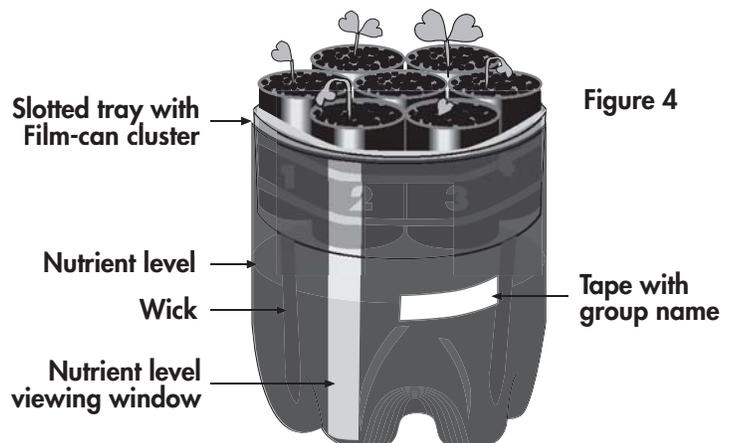


Figure 4

 **D.2**

e. Hold the film-can cluster over the slotted tray. Turn your water bottle upside down and squeeze gently to direct a stream of water at each film can. Water each can until water drips from its wick (Fig. 2). (This will cause the soil to settle somewhat.)

f. Water the wick in the slotted tray until it is saturated and water runs freely into the nutrient reservoir.

g. Place the film-can cluster in the slotted tray. Paying attention to the numbers on your film cans, place six evenly spaced seeds on the surface of the soil in each film can, according to the following plan:

- Can 1: six PA seeds.
- Can 2: six PB seeds.
- Can 3: six F₁ seeds.
- Cans 4-6: six F₂ seeds each.
- Can 7: six double-mutant seeds.

h. Take your film-can cluster back to the container of potting mix. Carefully sprinkle soil over the seeds to fill each can to the top. Level the soil with the ruler. **DO NOT PRESS THE SOIL INTO THE CANS.**

i. Add 1/8 X Peter's nutrient solution to the nutrient reservoir until the level is just below the bottom of the slotted tray.

j. Place your film-can cluster in the slotted tray. Water each can gently until water begins to run out of it and through the slots into the nutrient reservoir.

k. Your plants will be grown in a plant lighthouse (Fig. 5). Take your growth system to the plant lighthouse assigned to you by your teacher.

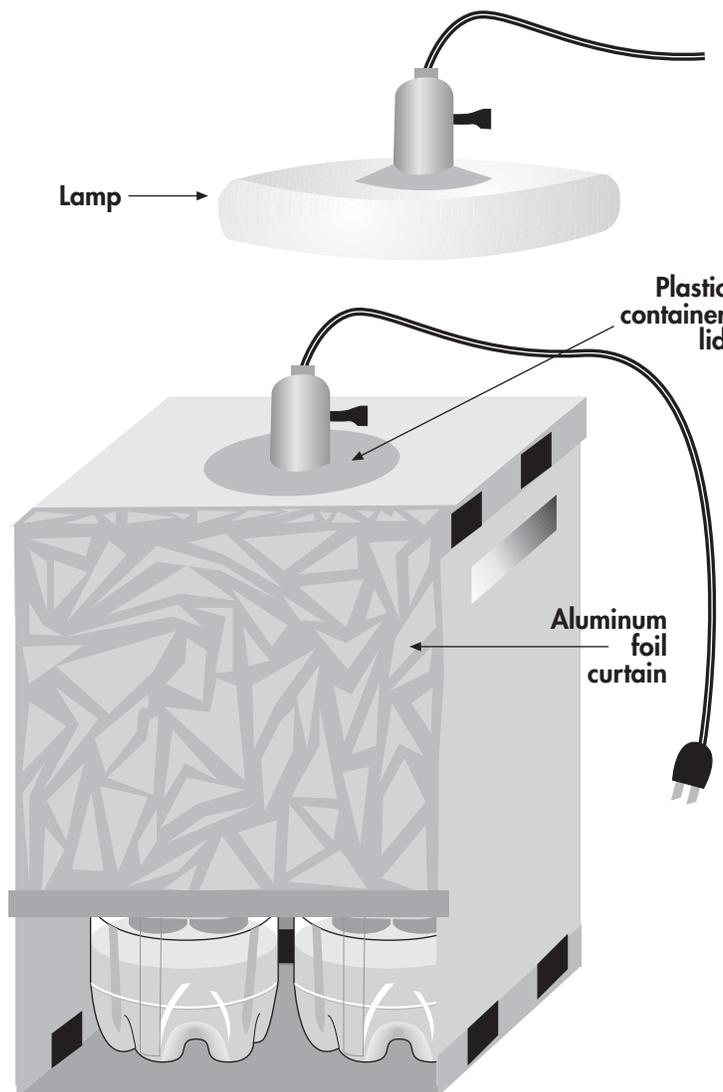


Figure 5



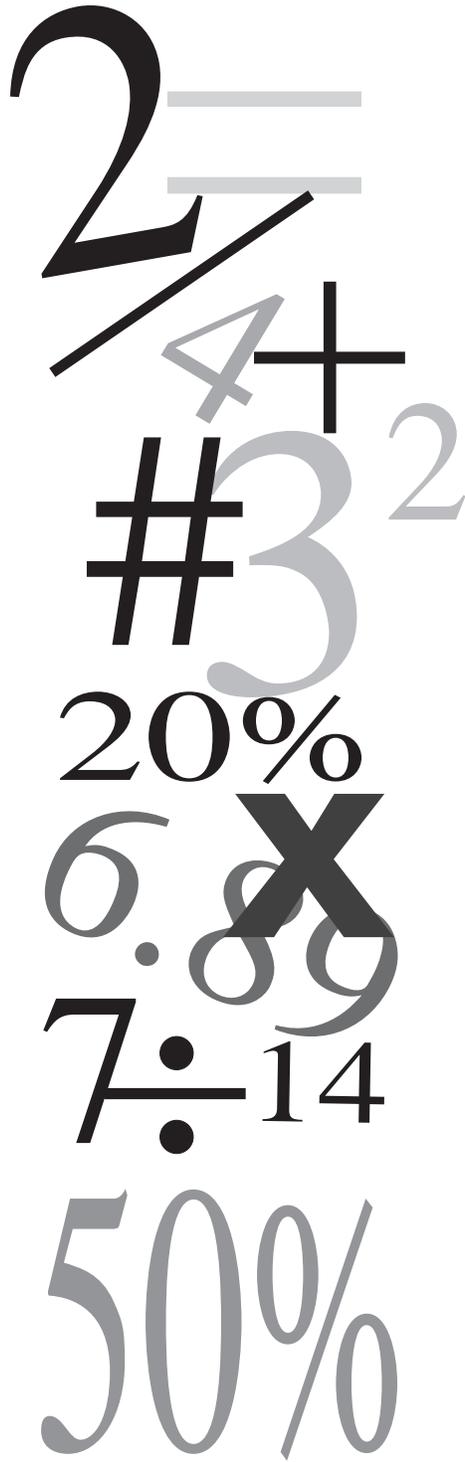
- l. If the following has not already been done, stack six foam blocks on the floor of the lighthouse and then place the foil-covered cardboard on top of the stack.
- m. Place your growth system on top of the foil-covered cardboard, toward one corner of the lighthouse.

2. After Day 1

- a. **Days 2-4** Use your water bottle to sprinkle the surface of the soil in each film can.
- b. **Days 3-5** Observe your film cans daily and record what you see on the Observations pages. Record how many seedlings emerge in each can and when they emerge. Each day after that observe all seedlings carefully, looking for significant differences among them. Compare your plants to the photographs of mutant Fast Plants or to the live Fast Plant mutants that your teacher put on display. By Day 5, assign phenotypes to all the plants that are present in each can.
- c. **Day 8** Reexamine all of your plants carefully and record your observations. Do you think that all of the phenotypes that you assigned on Day 5 were correct? Or do you think any of them should be changed? In which parts of the plant does it seem to be easiest to distinguish the various phenotypes? In the cotyledons? In the stems? Or in the first true leaves? Or are different traits distinguished more easily in different organs?

3. In conclusion

Fill out the Wisconsin Fast Plants Work Sheet.



CHAPTER 2

**Passing Traits from
One Generation
to the Next**

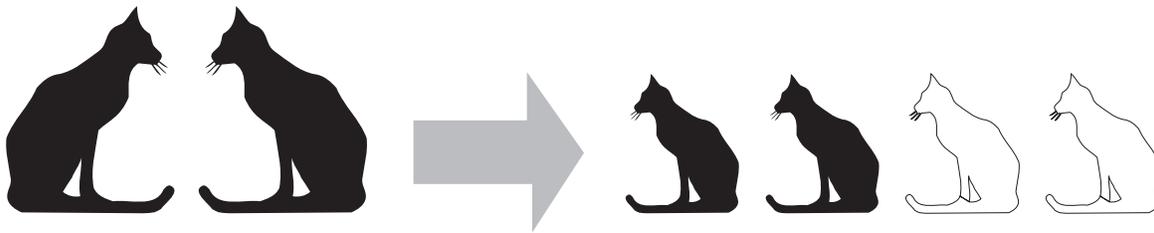
SECTION E

**How Are
Genetic
Results
Evaluated
Statistically?**

Introduction to Using Statistics to Evaluate Genetic Explanations

GENETICS IS ALL ABOUT using the seen (the visible phenotype) to infer the unseen (the invisible genotype). Sometimes, however, math can be used to determine whether or not the inference that you have drawn about the genotype-phenotype relationship is a reasonable one.

As an example of how this works, let's suppose that you have a pair of black cats at home that mated and produced a litter of two black kittens and two white ones. How would you explain this?



Well, because you've just learned all about dominant and recessive alleles while you were studying Reebops, Create-a-Baby, and red and white yeast cells, you'd probably suggest that both Momcat and Dadcat must be heterozygous with respect to coat-color alleles, each having one dominant "black" allele and one recessive "white" allele, and that kittens that happened to receive one white allele from each parent developed the white phenotype. In short, you'd use the visible phenotypes of the cats and kittens, together with your understanding of possible genotype-phenotype relationships, to make a reasonable inference about the genotypes of both the parent cats and the kittens.

REAL COOL, BABY!

However, when you show your kittens to your friend Katy, and tell her how you explain their coat colors, she disagrees strongly. She says, "Based on what we learned in class, if Momcat and Dadcat really were heterozygous for a pair of black/white coat-color alleles, they should have had three black kittens and one white one, not two of each!" You think about that for a minute and respond, "Well, 2-to-2 is not that far from 3-to-1, and the difference could be due just to chance. After all, Katy, you know you won't always get two heads and two tails if you flip a coin four times." Katy says, "Well that may be, but 1/2 white kittens doesn't seem to me to be very close to the 1/4 white kittens that your hypothesis predicts." After arguing about this for a while longer, you finally agree to discuss it with your teacher.



After you explain the problem to your teacher, he says, "The way to settle this is not by arguing about it, but by analyzing your results statistically to see whether Katy is correct in thinking that you need to think about some alternative explanation for the kittens. I recommend running a Chi square test, because Chi square is specifically designed to determine whether or not the difference between the results you observed and the results that were predicted by your genetic hypothesis are too great to be due to chance alone."

Too Many White Kittens? Using Chi Square (χ^2) to Find Out

THE INSTRUCTIONS YOUR TEACHER gave you for running a Chi square test on your black/white kitten data were as follows:

- The formula for determining the value of χ^2 (Chi square) is:

$$\chi^2 = \frac{(\text{Observed} - \text{Expected})^2}{\text{Expected}} \text{ summed for all classes}^*$$

- * In this formula the term “summed for all classes” refers to all classes of objects that were observed, not all classes of students who made such observations!

- The way you would apply this formula to your kittens, which fall into two classes (black and white) is:

$$\chi^2 = \frac{(\text{Obs. black} - \text{Exp. black})^2}{\text{Exp. black}} + \frac{(\text{Obs. white} - \text{Exp. white})^2}{\text{Exp. white}}$$

or, more specifically (since your hypothesis predicts that 3/4 of the kittens should be black and 1/4 should be white):

$$\chi^2 = \frac{(2 - 3)^2}{3} + \frac{(2 - 1)^2}{1} = \frac{1}{3} + \frac{1}{1} = 1.33$$

- Your χ^2 value is 1.33.
- To find out the meaning of this χ^2 value, you must look it up in a standard table like the one below. But before you can do this, you must decide how many **degrees of freedom** you have, so you will know which line to look in.
- The degrees of freedom in such an experiment is one less than the number of classes you distinguished. Since you distinguished two classes in this case (black and white kittens) you have one degree of freedom.

	p (The probability that the difference seen between the observed and the expected values could be due to chance alone.)								
Degrees of Freedom	90%	70%	50%	30%	20%	10%	5%	1%	0.5%
1	0.02	0.15	0.46	1.1	1.6	2.7	3.8	6.6	7.9
2	0.21	0.71	1.4	2.4	3.2	4.6	6.0	9.2	10.6
3	0.58	1.4	2.4	3.7	4.6	6.2	7.8	11.3	12.8

- When you search along the '1 degree of freedom' line, you find that a χ^2 value of 1.33 lies somewhere between the 20% and the 30% columns. This means that if the hypothesis on which you based your predictions is correct, the difference you observed between the predicted numbers and the actual numbers of black and white kittens can be expected to occur (in a litter of four) more than 20% of the time, due to chance alone.

By convention, scientists usually use a 5% cut-off value to decide whether or not to reject the hypothesis on which a set of predicted values is based. More specifically, if deviations as large as those observed could be expected to occur more than 5% of the time due to chance alone, then the deviations are not large enough to justify rejecting the hypothesis on which the predictions were based.

- What this result does not mean: The results of the Chi square test you just performed does not prove that your hypothesis about the inheritance of these coat colors is correct, only that it is possibly correct. [The results of a Chi square test can never prove that a hypothesis is correct, although they can indicate that a hypothesis is very unlikely to be correct.]
- What your Chi square result does mean, however, is that Katy's rejection of your hypothesis, based solely on the difference between the observed and expected number of black and white kittens in your litter, was not scientifically sound.

AN IMPORTANT POINT: A Chi square test is very sensitive to the size of the sample observed. Thus, although a black kitten:white kitten ratio of 2:2, instead of 3:1, is not adequate to cause rejection of your genetic hypothesis when only one litter of four kittens was observed, it would have been a very different matter if the same 2:2 ratio had been obtained after examining several litters containing a total of 40 kittens. We can see this very easily by calculating χ^2 for such a sample size:

$$\chi^2 = \frac{(20 - 30)^2}{30} + \frac{(20 - 10)^2}{10} = \frac{100}{30} + \frac{100}{10} = 13.3$$

If we look up this χ^2 value of 13.3 on the '1 degree of freedom' line, we find that it indicates that this large a deviation from the predicted 3:1 ratio would be expected to occur by chance much less than 0.5% of the time. This is a very different outcome than we obtained when we saw the same ratio of black to white kittens in a single litter of four kittens, and it would clearly indicate that your original hypothesis to explain black versus white coat color in kittens should be rejected, and a new hypothesis should be sought.

- Because χ^2 is so sensitive to sample size, it must always be calculated using the actual numbers observed, and never using fractions, decimal fractions or percentages instead of actual numbers!

How to Perform a Chi-Square Test on Any Data Set

THE PROCEDURE USED TO perform a Chi square test on the black/white kitten data can be generalized to analyze the results of any genetic experiment as follows:

- STEP 1.** State a simple genetic hypothesis that makes a precise prediction about how the offspring resulting from some particular mating should be distributed between various phenotypic classes.

[In the case of the kittens, the hypothesis was that Momcat and Dadcat were both heterozygous with respect to a pair of alleles that control coat color: the dominant black allele and the recessive white allele. The prediction made from this hypothesis is that Momcat and Dadcat should have three black kittens for every white one.]

- STEP 2.** Count the actual offspring to determine how they actually are distributed between those phenotypic classes.

[In the case of the kittens this was very simple: there were two black and two white kittens.]

- STEP 3.** Determine the number of offspring that are to be expected in each phenotypic class. To do this, multiple the total number of offspring that were actually produced by the frequency with which each phenotypic class is expected to occur.

When we did this for the kittens it was misleadingly simple, because there were exactly four kittens in the litter, and the two phenotypic classes (black and white) were expected with frequencies of 0.75 and 0.25, respectively. Thus when we multiplied 4×0.75 and 4×0.25 , we got integral numbers: 3 and 1, respectively.

But suppose there had been five in the litter of kittens Momcat gave birth to. In this case the expected number of black kittens would have been 5×0.75 , or 3.75, and the expected number of white kittens would have been 5×0.25 , or 1.25. Yes, you may – and indeed in most cases you will – get non-integral numbers of individuals expected in each class.



STEP 4. Calculate χ^2 according to the formula:

$$\chi^2 = \frac{(\text{Observed} - \text{Expected})^2}{\text{Expected}} \text{ summed for all classes}$$

STEP 5. Estimate your p value using the χ^2 table like the one shown in E.2. (This is a standardized table of values that can be found in all sorts of scientific textbooks and reference books.) Remember that the number of degrees of freedom you will use will be one less than the number of phenotypic classes predicted by your hypothesis.

STEP 6. Use the 5% rule to decide whether or not your data are consistent with your genetic hypothesis. That is, unless your χ^2 value is smaller than the one given in the 5% column (indicating that deviations from expected values as large as the ones that you obtained could occur more than 5% of the time by chance alone), you should search for a genetic hypothesis that is more consistent with your data.

Now let's use the chi square method to analyze your Wisconsin Fast Plant data.

WISCONSIN FAST PLANTS CHI SQUARE WORK SHEET B

The data necessary for performing the following Chi square tests should be recorded on your Fast Plants Phase 2 Work Sheet.

Part One: A Simple Trial Run

To become familiar with running the Chi square test, let's apply it to just one of the mutant traits that showed up in your F₂ plants.

One half of the class should calculate χ^2 and p values for the trait that was exhibited by the P_A plants, and the other half of the class should do this for the P_B trait. In both cases the pooled data from the entire class should be used for the analysis. And in both cases we will assume that the hypothesis to be tested is that the trait in question is controlled by a single gene with two alleles, with the mutant allele being recessive to the wild-type allele. Thus, in both cases the expected wild-type-to-mutant frequency will be 3:1.

The mutant trait I am analyzing by χ^2 is _____

Total number of F₂ plants obtained by the class: _____.

Phenotype	Expected #	Observed #	Difference	(Difference) ²
Wild-type				
Mutant				

Multiply the total number of F₂ plants by the expected frequencies (3/4 and 1/4) to get the expected numbers of plants in each category. You probably will get non-integral numbers.

$$\chi^2 = \frac{(\text{Observed} - \text{Expected})^2}{\text{Expected}} \text{ summed for all classes}$$

(Remember: in this formula “classes” refers to phenotypic classes of plants, not classes of students.)

χ^2 : _____ p: _____ Use the table on page S150 to determine the value of p.

Conclusion: _____

Part Two: Chi Square Analysis of the Two Phenotypes at Once

Now that you have performed a Chi square analysis for one phenotype (the PA or PB trait), it should be easy for you to modify the analysis to consider both phenotypes at once.

What you will be able to test this way is whether plants with the four possible combinations of mutant and wild-type traits are present in the F₂ generation in proportions that are not significantly different from the proportions that are predicted by either a Punnett Square diagram, or a product-of-probabilities calculation. If the observed ratios are not significantly different from the predicted ratios, this will indicate that alleles at the two different loci that are being considered exhibit what biologists call “independent assortment.” (That is to say, the allele an offspring receives from one of its parents at one locus is independent of the allele that it receives from that parent at the other locus.)

Independent assortment of alleles at two loci always occurs if those loci are on separate chromosomes. However, if the two loci are located close together on the same chromosome, they will exhibit “linkage,” which is the opposite of independent assortment. In such cases, an allele at one locus will travel from parent to offspring together with the allele at the second locus with which it is physically linked on a particular parental chromosome. This will result in the F₂ generation exhibiting an overabundance of individuals with the two allelic combinations that their grandparents had, and a deficiency of the other two possible combinations. In extreme cases of linkage, only two of the four possible combinations will be observed.

So, in short, what we will be asking with this next Chi square analysis is whether or not the relative abundance of F₂ plants with the four different phenotypic combinations is significantly different from the proportions predicted on the assumption of independent assortment of alleles at the two different loci we are studying.

COMBINED DATA FOR THE ENTIRE CLASS

 TOTAL NUMBER OF F₂ PLANTS: _____

PA phenotype	PB phenotype	Frequency expected*	Number expected	Number observed	Difference	Difference ²
Wild-type	Wild-type					
Mutant	Wild-type					
Wild-type	Mutant					
Mutant	Mutant					

*You can obtain these frequencies by either (a) using the product-of-probabilities method, (b) using a Punnett Square, or (c) reviewing similar calculations you made for previous exercises.

χ^2 : _____ p _____



Name _____

Date _____ Hour _____

Conclusion: _____
