What have we learned?

Whale vs virus-wow they show how evolution acts at different levels

Darwin’s contribution and wow all those other folks that he relied upon

History of life on earth…wow so many cool species.

Wow inheritance is a lot more complicated than I thought because there are single locus traits and multilocus traits…alleles interact, genes interact-eek!

Protein synthesis Transcription translation-its amazing t hat eukaryotes can make so many different proteins by tweaking the process adding bits and pieces

Going from genotype to phenotype or going from genes to traits-wow there are so many ways genes can be regulated (epigenetics, RNA interference)-turned off and on in different places in multicellular/eukaryotic animals

Where are we going?

Digging Deeper

This section of the course could be considered the core. Hopefully you have mastered the material in the previous two sections and are able to really start understanding deeply how we have ended up with the great diversity of populations and species we have today.

We will start with Chapter 6 which focuses on questions like, how do we see the frequencies of genes change in populations over time? What are the forces that can cause this change?

We will then jump to Chapter 10, a great chapter with lots of examples of Natural Selection.

We will read parts of Chapter 7 which focuses on how we approach and understand complex traits where phenotypes are a function of many genes as well as the environment.

We will only read parts of Chapter 8. Chapter 8 focuses on how we build phylogenetic trees and connects closely with our MEGA labs which we will tackle at the end of the semester in lab.

Chapter 6 The ways of change: drift and selection

Genetics of Populations
We are moving up to population level!
We will be focusing on a single locus with 2 alleles in a whole population!

Hang onto this definition of evolution ("Change in gene or allele frequencies over time.")

1. **Hardy-Weinberg-how do we use it?**

2. Genetic Drift (Drosophila example bottlenecks and founder events)

3. Landscape genetics (Gene Flow, is at end of chapter but I am moving forward)

4. Digging around in the field of Population Genetics (we will see what we get through)

If you are a fruit fly (or *Drosophila*) geneticist observing odd looking at two different eye colors, or looking at very a specific trait in a pea plant or tracking a nasty little base change or point mutation in humans that causes a particular condition, Punnett Squares might be the approach you need!

But to understand POPULATIONS we need to go beyond thinking about individuals and their individual genotypes and phenotypes.

But what happens when you get to a whole population?
Are you going to sit and create Punnett squares for each individual cross, see who the offspring are over and over again??
No!

Things get too complicated!

In early 1900‘s geneticists extended Mendel’s model from parents and their offspring to entire populations across generations using mathematical models.

They imagined (mathematically) a situation where the population...

- Was really big
- Was mating randomly
- Was not experience selection at the locus of interest (meaning in their imagined locus with only two alleles both those alleles were equally “successful”)

We have two copies of each chromosome…

The black allele at the gumball locus

The white allele at the gumball locus

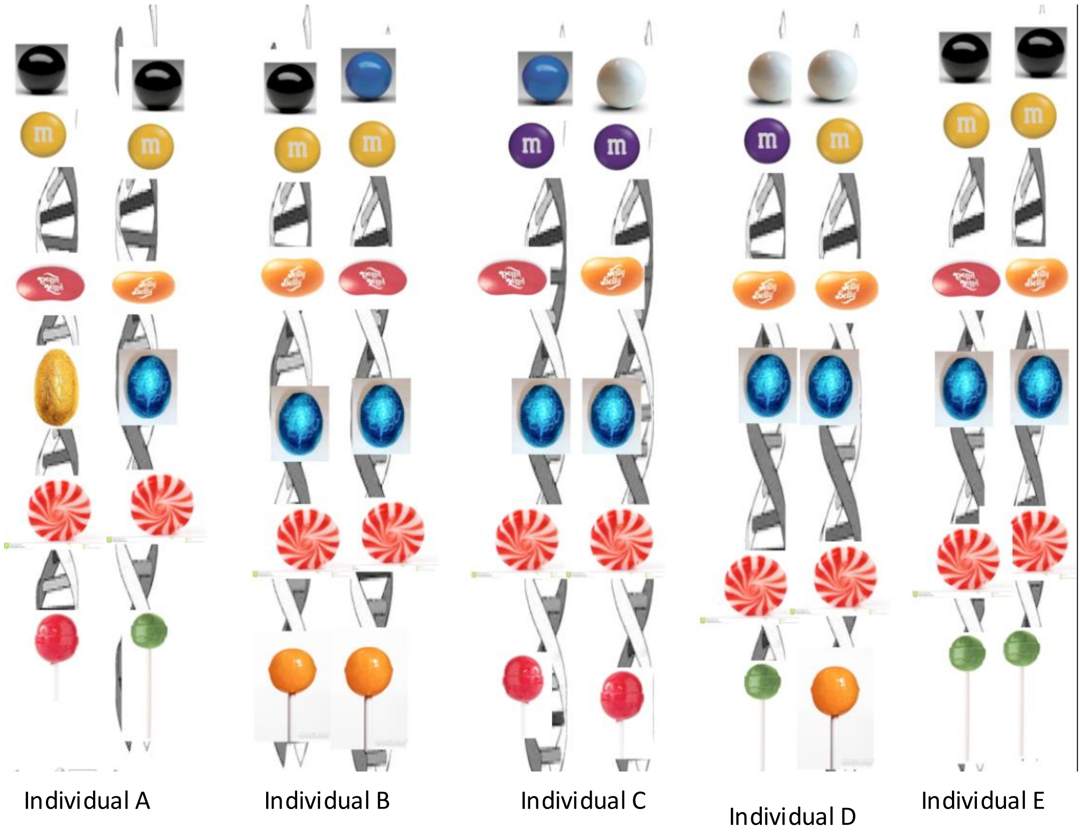
At the gumball locus you are heterozygous…

At the m+m locus you are homozygous…

There might be other individuals in the population that are homozygous at this locus.

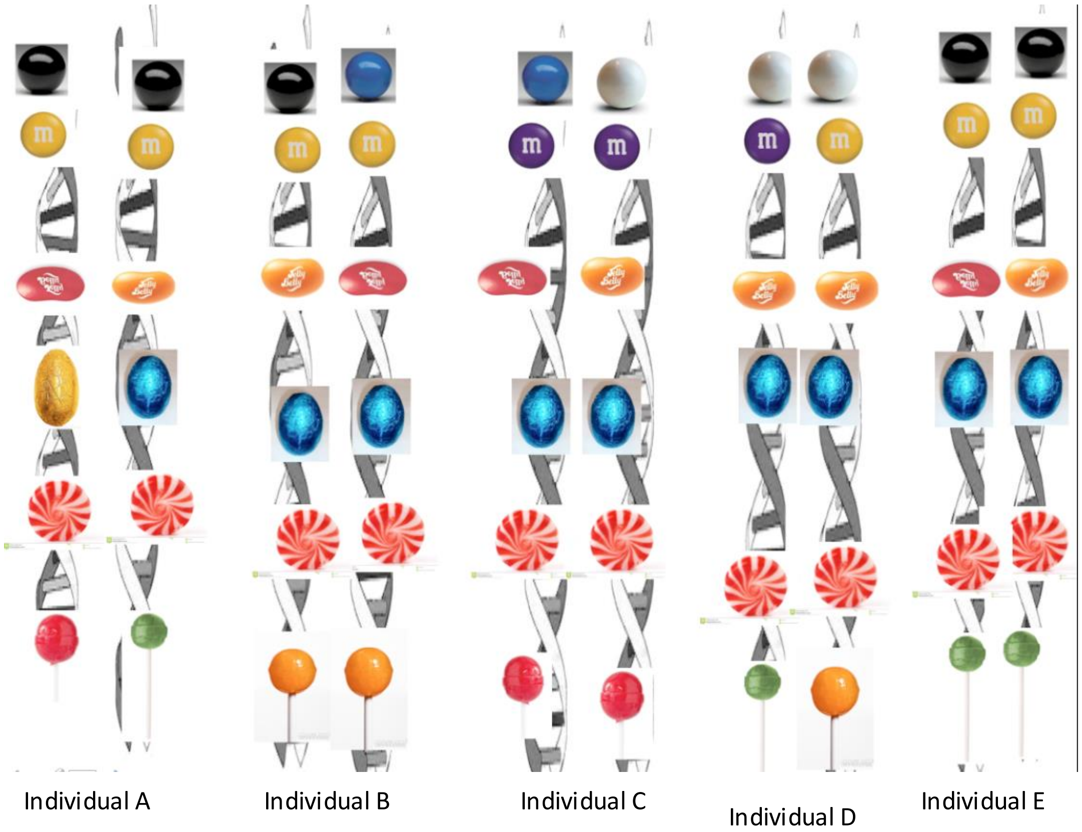
Shown here are two homologous chromosomes of the 23 pairs of chromosomes you have.

Here we have 5 pairs of homologous chromosomes in 5 different individuals (A-E) (imagine that we pulled out chromosome #1 from their bodies and lined them up).



1. *Which individuals are heterozygous at the gumball locus?*
2. *How many different alleles are there at the gumball locus in this* ***population*** *(of 5 individuals)?*
3. *Which locus has the least amount of genetic variation?*
4. *Which locus has the greatest heterozygosity? (Which locus has the largest proportion of heterozygous individuals.)*

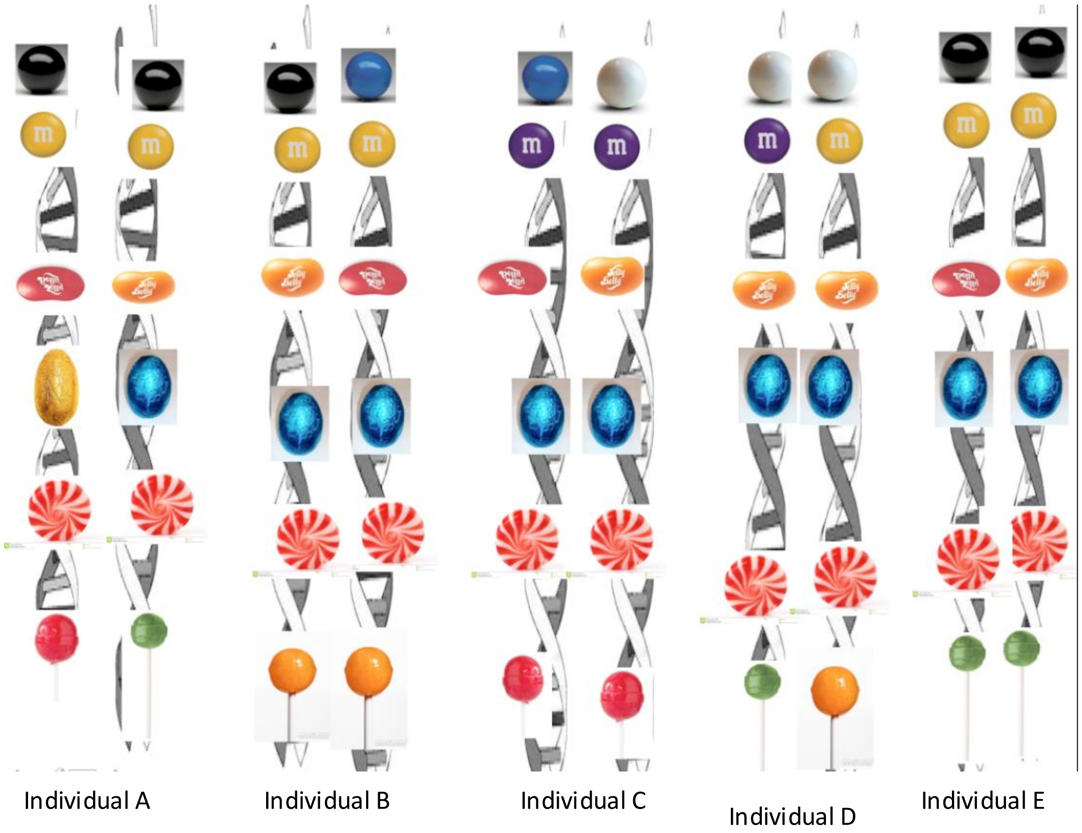
Here we have 5 pairs of homologous chromosomes in 5 different individuals (A-E).



In this population, what are the ***allele*** *frequencies of the two alleles at the m+m locus?*

5. Freq of the yellow allele=
6. Freq of the purple allele=

Here we have 5 pairs of homologous chromosomes in 5 different individuals (A-E)



What are the ***genotype*** *frequencies at this m+m locus?*

7. Freq of YY individuals is=

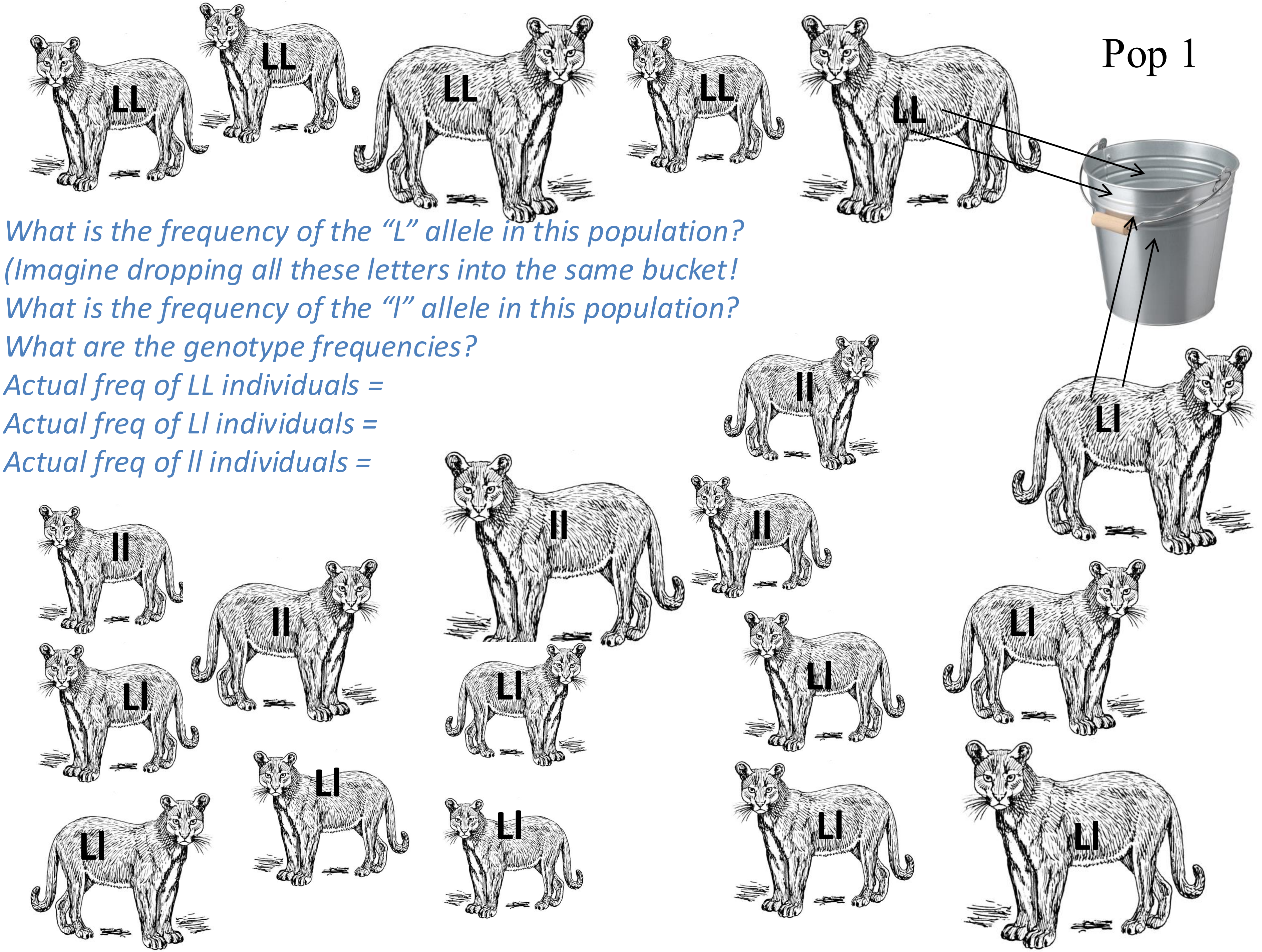
8. Freq of YP individuals is=

9. Freq of PP individuals is=

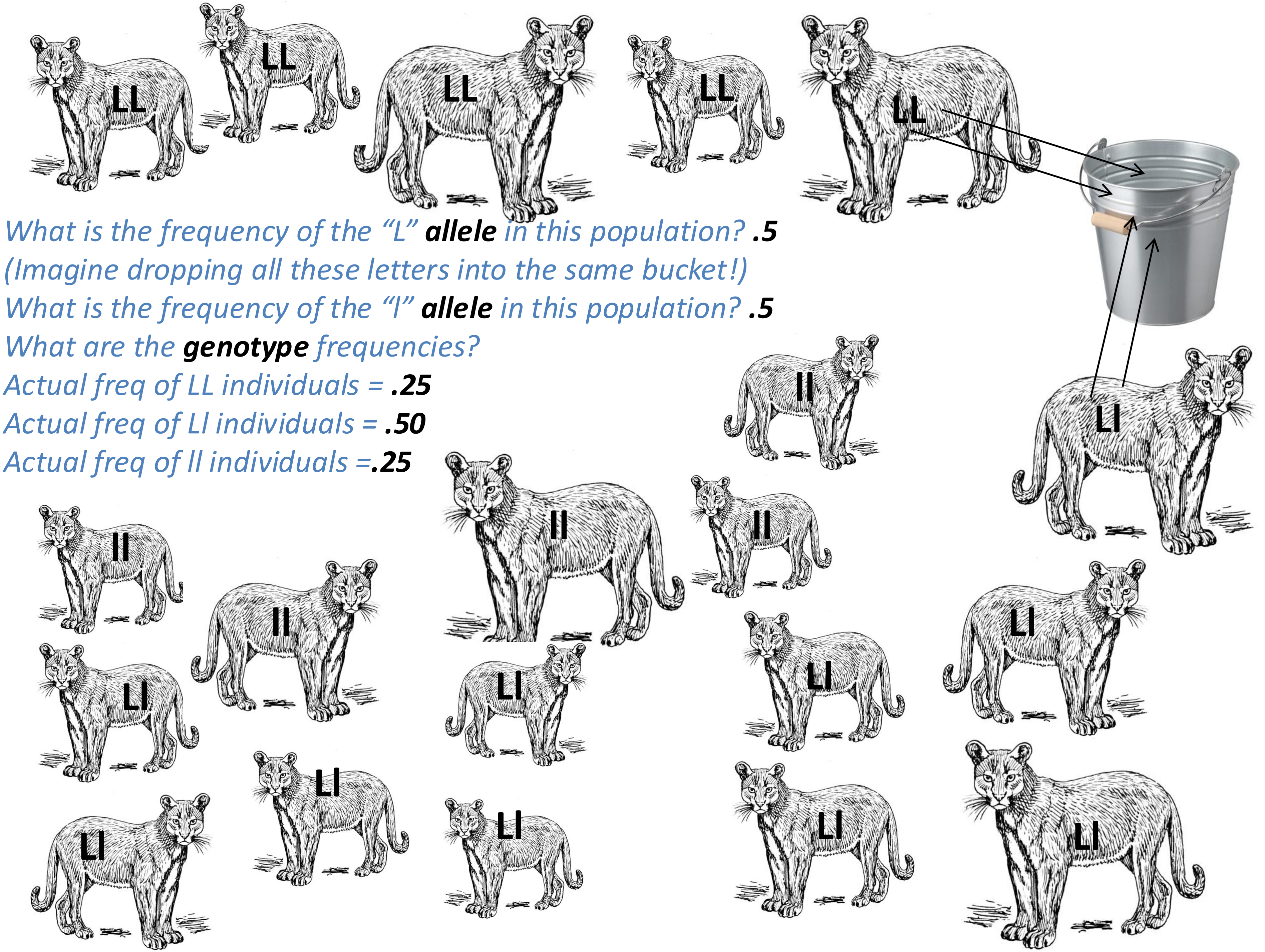
Now lets turn to a bigger population and display only one locus at a time…..

Look at your handout and answer the questions!

Pop 1



What is the frequency of the “L” allele in this population?
(Imagine dropping all these letters into the same bucket!
What is the frequency of the “l” allele in this population?
What are the genotype frequencies?
Actual freq of LL individuals =
Actual freq of Ll individuals =
Actual freq of ll individuals =



What is the frequency of the "L" ***allele*** *in this population?* **.5**
(Imagine dropping all these letters into the same bucket!)
What is the frequency of the "l" ***allele*** *in this population?* **.5**
What are the ***genotype*** *frequencies?*
Actual freq of LL individuals = **.25**
Actual freq of Ll individuals = **.50**
*Actual freq of ll individuals =***.25**

Lets take that bucket of alleles with half “L” and half “l” alleles.

<u>Next we will ask..Is this population in Hardy Weinberg Equilibrium?</u>
Notice how I use the calculations below to answer this question.

You answer this by calculating what you would **expect** the genotype frequencies to be.
Imagine mixing around all those alleles in the bucket and pulling alleles out.
What is the chance of pulling out an L allele?
What is the chance of pulling out another L allele?
(imagine the population size is really large so you don’t have to worry about replacement)

Go back to your middle school math class on probability...if you are interested in the chance of pulling out two “L” alleles, what do you do?

You multiply the chance of pulling out one with the chance of pulling out the other.
So your chance of getting an **“LL”** individual is ____ x ____ right? =____ (p^2)

Lets do the same for your ll individual.
What is the chance of an **“ll”** individual?
It will also be ____x _____ right? = ___   (q^2)

Lets take that bucket of alleles with half “L” and half “l” alleles.

Next we will ask..Is this population in Hardy Weinberg Equilibrium?
Notice how I use the calculations below to answer this question.

You answer this by calculating what you would **expect** the genotype frequencies to be.
Imagine mixing around all those alleles in the bucket and pulling alleles out.
What is the chance of pulling out an L allele? (.5 right?)
What is the chance of pulling out another L allele? (.5 right?)
(imagine the population size is really large so you don’t have to worry about replacement)

Go back to your middle school math class on probability...if you are interested in the chance of pulling out two “L” alleles, what do you do?

You multiply the chance of pulling out one with the chance of pulling out the other.
So your chance of getting an “LL” individual is .5 x .5 right? =.25 (p^2)

Lets do the same for your ll individual.
What is the chance of an “ll” individual?
It will also be .5 x .5 right? =.25 (q^2)

Now lets work on those heterozygotes!

I completed this one for you on handout!

The chance of getting an “L” is .5, the chance of an “l” is .5 too.
So this would =.25 again for an “Ll” individual

BUT there are actually TWO ways of getting a heterozygote!

Biologists do not care about the ORDER of the two alleles. Both Ll and lL are in the category heterozygote so in addition to the Ll way we need to add the other way which is lL.

When we do this we find the chance of getting an lL individual is also .25

So we add these two ways (.25 + .25) to get .5 =(2pq)

So how do the actual and expected genotype frequencies compare?
Is this population in HW? (How close are the actual and expected frequencies?)

Well, yeah it is so it is kind of a boring example!
If it was NOT we would want to dig deeper and think about what might be going on in this population to push it out of HW Equilibrium. There are a number of factors that might push populations out of HW-you will learn about these in the coming slides.

Review
We asked is the cougar population in Hardy Weinberg Equilibrium?

To answer this we ask… do the expected or predicted genotype frequencies match the actual?

We calculated the actual as…
*Actual freq of LL individuals = **.25***
*Actual freq of Ll individuals = **.50***
*Actual freq of ll individuals = **.25***

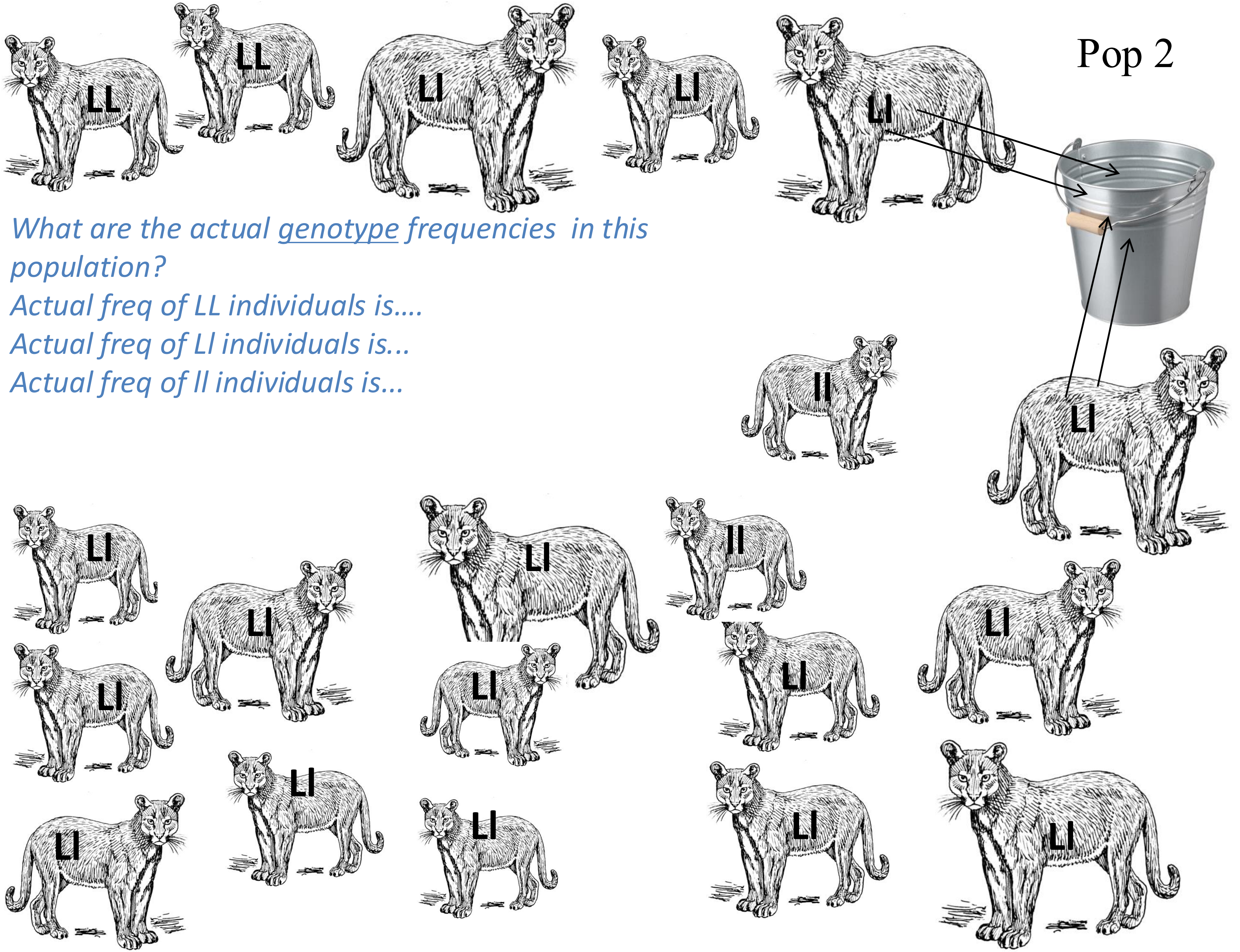
We calculated the expected as…
Expected freq of LL is (.5) (.5) =.25 = (p^2)
Expected freq of Ll is (.25 + .25)=.5 =(2pq)
Expected freq of ll (.5) (.5) =.25 = (q^2)

Yay they are the same! SO yes it is in HW equilibrium.

Now lets change our population!

See the back of the handout!

Pop 2

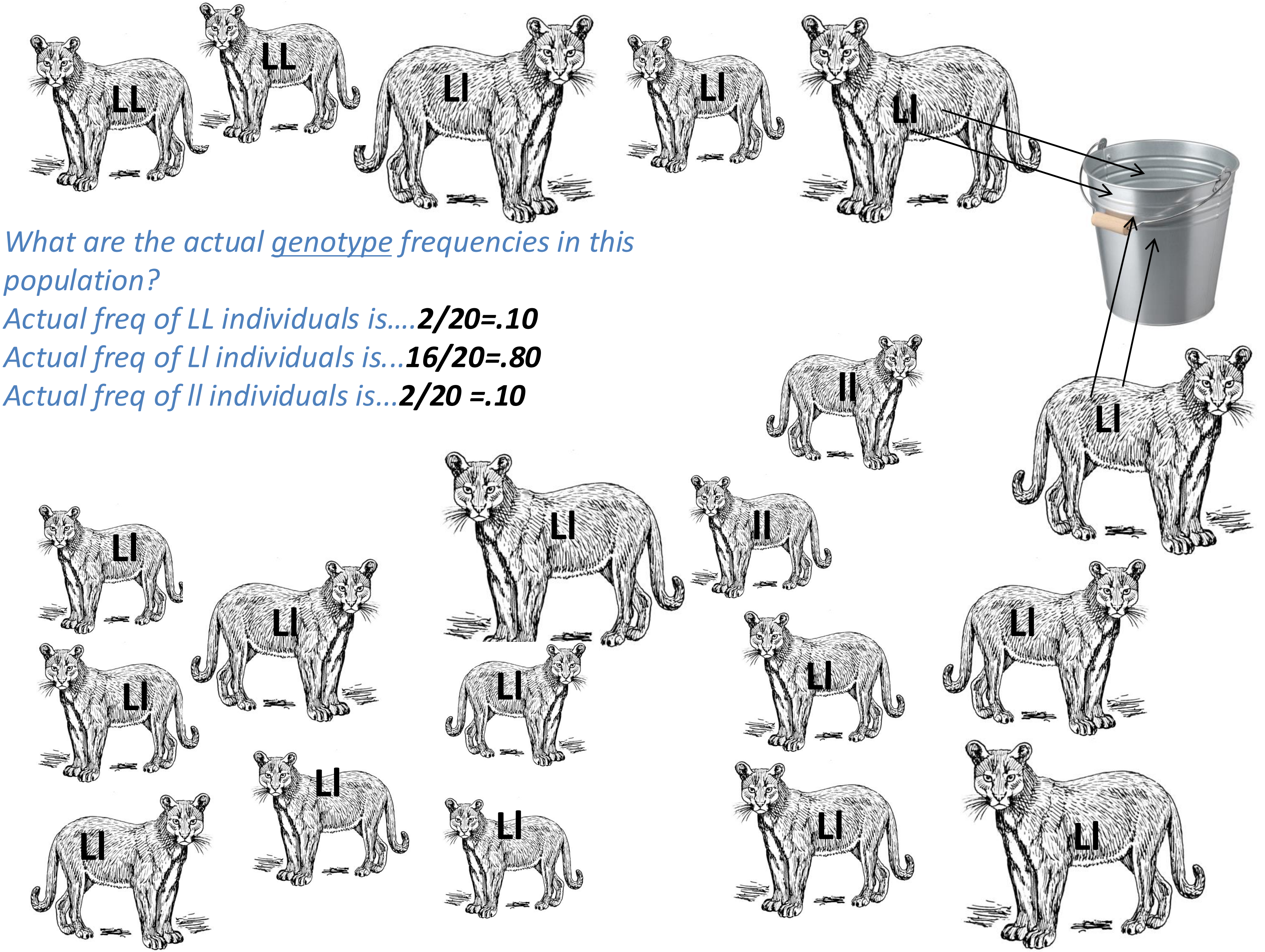


What are the actual *__genotype__* *frequencies in this population?*

Actual freq of LL individuals is….

Actual freq of Ll individuals is...

Actual freq of ll individuals is...



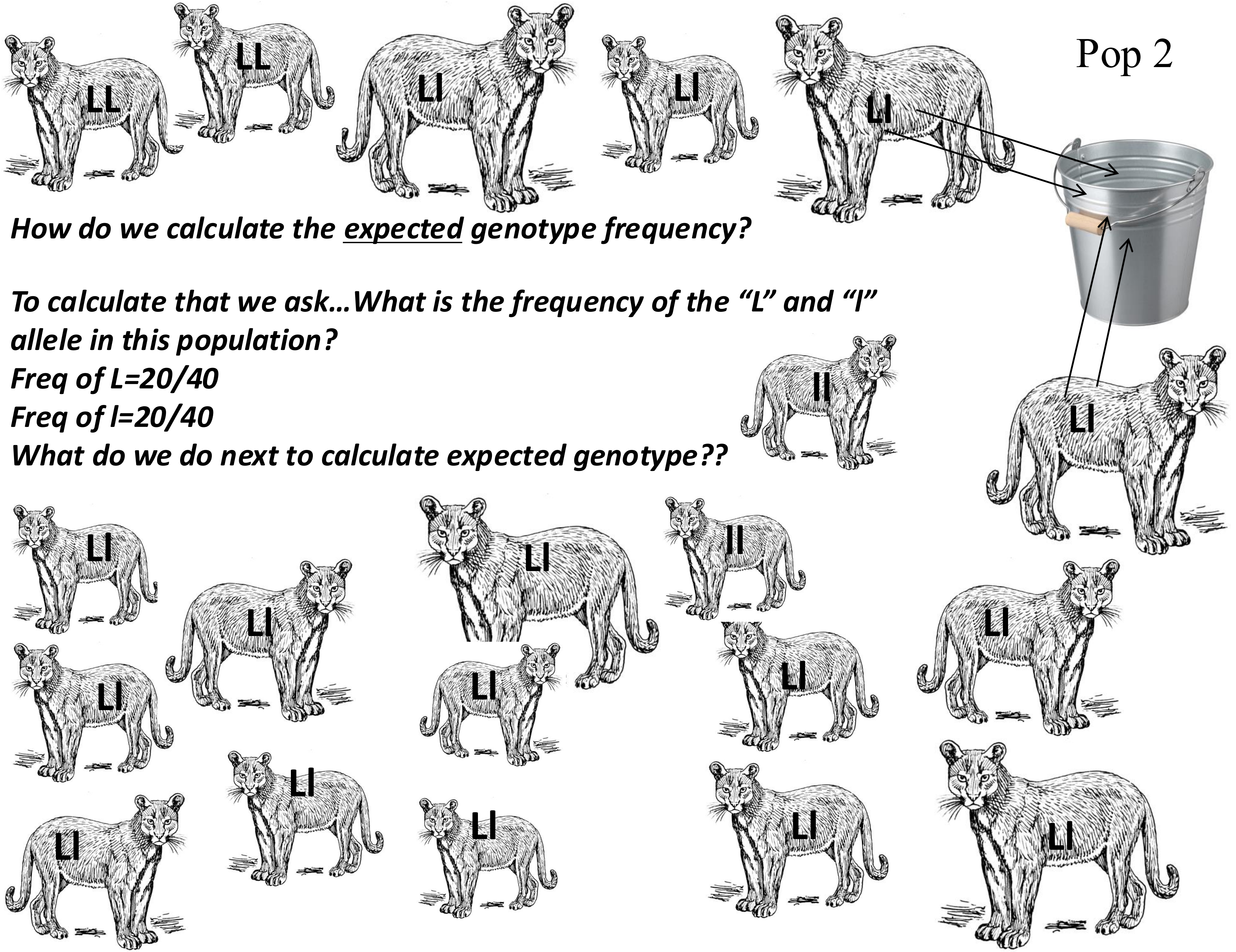
What are the actual *__genotype__* *frequencies in this population?*

*Actual freq of LL individuals is….****2/20=.10***

*Actual freq of Ll individuals is...****16/20=.80***

*Actual freq of ll individuals is...****2/20 =.10***

Pop 2

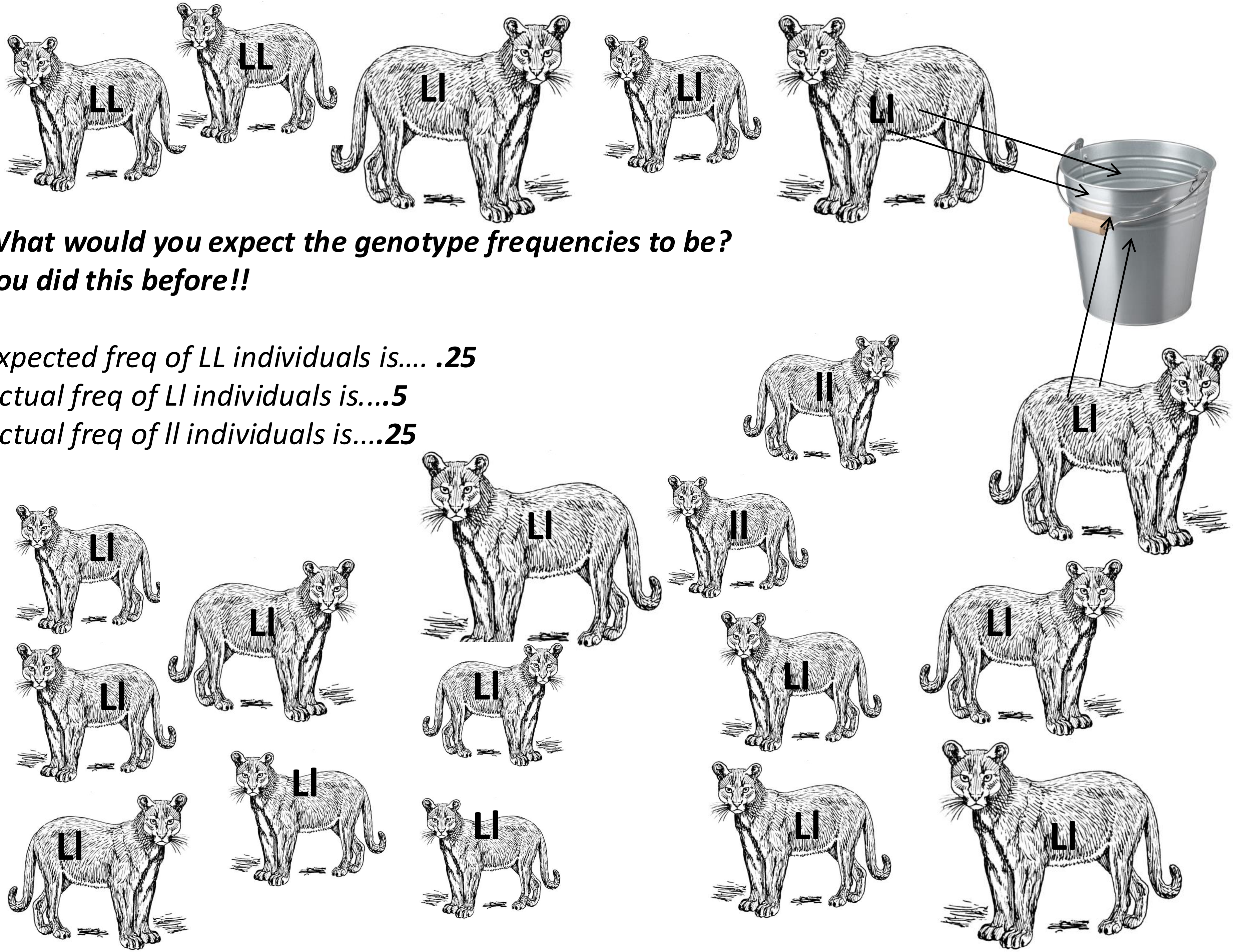


How do we calculate the <u>expected</u> genotype frequency?

To calculate that we ask…What is the frequency of the "L" and "l" allele in this population?
Freq of L=20/40
Freq of l=20/40
What do we do next to calculate expected genotype??

What would you expect the genotype frequencies to be?
You did this before!!

Expected freq of LL individuals is…. **.25**
*Actual freq of Ll individuals is....***5**
*Actual freq of ll individuals is....***25**



Is <u>this</u> population in Hardy Weinberg Equilibrium?
Lets formally compare!

What are the actual genotype frequencies?
*Actual freq of LL individuals is….**2/20=.10***
*Actual freq of Ll individuals is…**16/20=.80***
*Actual freq of ll individuals is…**2/20 =.10***

Now take that L= .5 to generate your expected values.

What are the expected? (same as before...)
Expected freq of LL is (.5) (.5) =**.25** = (p^2)
Expected freq of Ll is (.25 + .25)=**.5** =(2pq)
Expected freq of ll (.5) (.5) =**.25** = (q^2)

Is the actual different from the expected?
YES so the population is NOT in HW
Which genotype is overrepresented?
Our next question would be why?
How did they end up not in HW? (A couple possible explanations.)

Ok so we just dove into actually using something called the HW Theorem, but notice that it really just requires you to use some basic logic.

Review

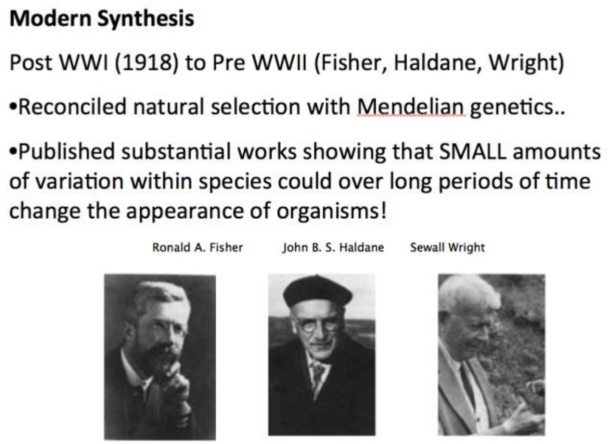
The Hardy-Weinberg principle serves as a null hypothesis for determining whether something interesting is happening in a population.

When genotype frequencies do not conform to Hardy-Weinberg proportions (are not “in HW”), something interesting like genetic drift, natural selection or nonrandom mating (like inbreeding!) may be occurring in that population (these are the topics in this chapter)!

If we find a population that is not in HW-we might investigate further to see which of these might be taking place.

The HW Theorem is the main tool of Population Geneticists!

(Modern Synthesis)



Modern Synthesis

Post WWI (1918) to Pre WWII (Fisher, Haldane, Wright)

- •Reconciled natural selection with Mendelian genetics..
- •Published substantial works showing that SMALL amounts of variation within species could over long periods of time change the appearance of organisms!

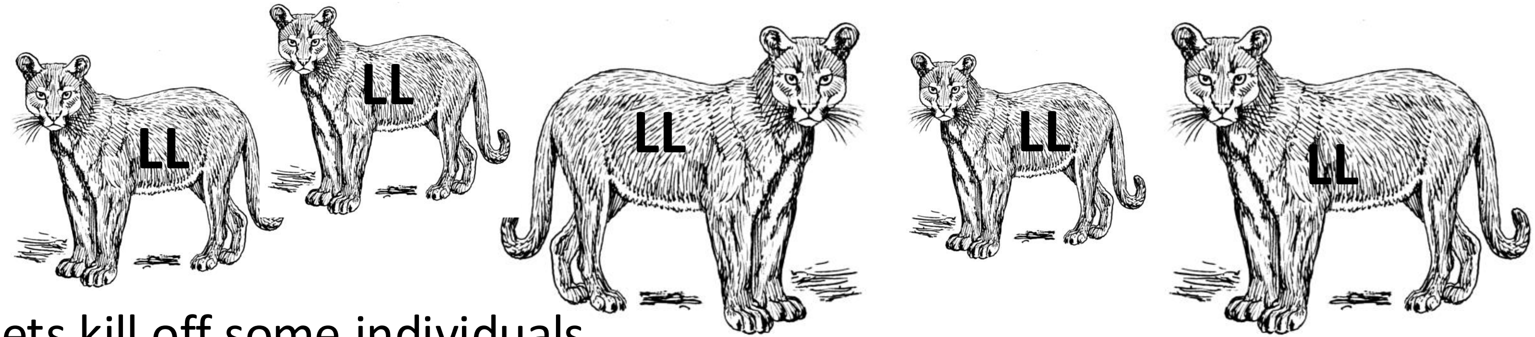
Ronald A. Fisher John B. S. Haldane Sewall Wright

Our emphasis will be on **Using** Hardy-Weinberg…

TYPE 1 Questions - We will use it as a clue indicating whether selection (or drift or something else) is taking (or has taken) place in a population by asking “Is this population in HW?” *(You just did this with the cougars.)*

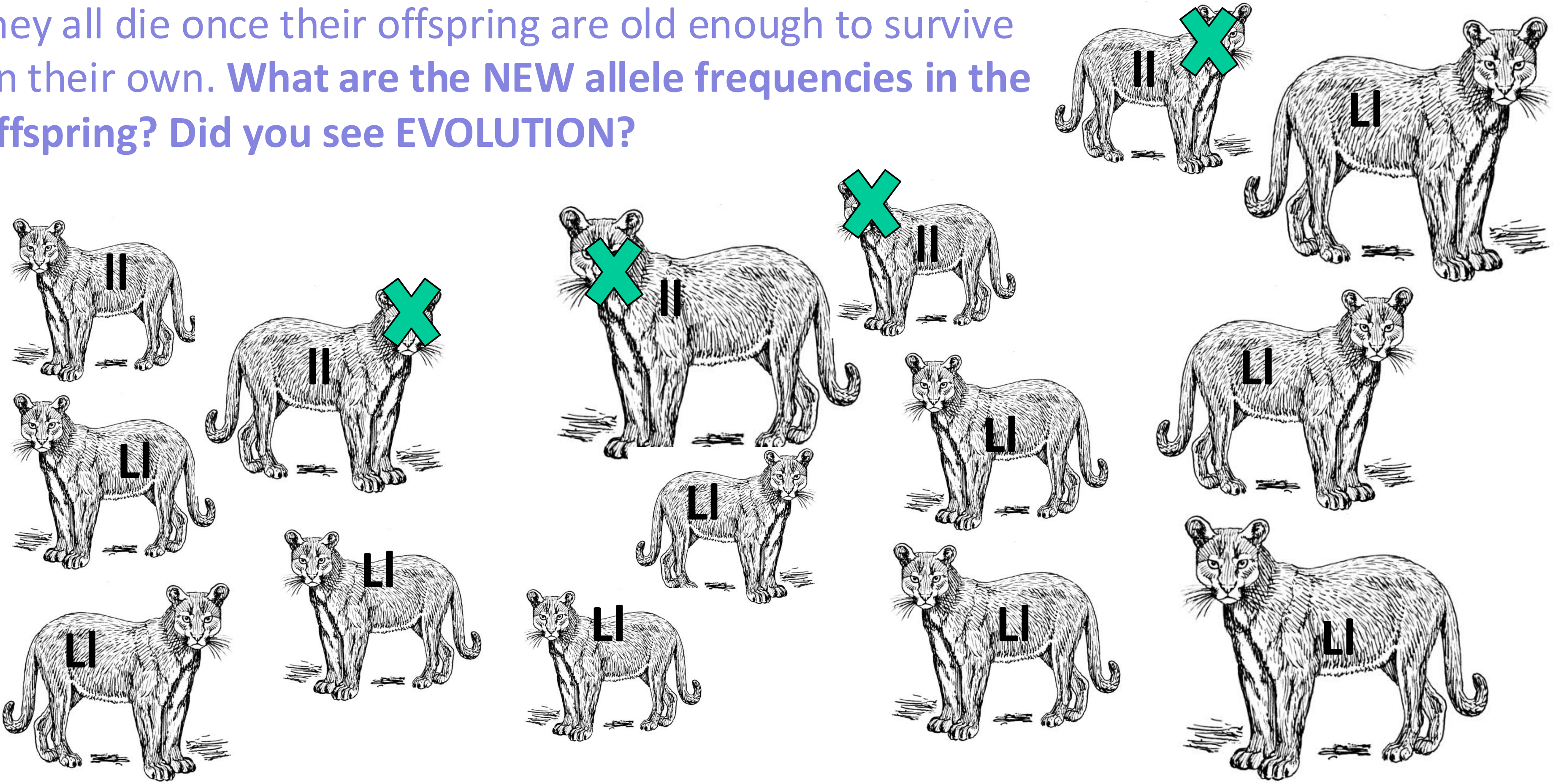
TYPE 2 Questions - We will use it to predict genotype frequencies in next generation (for example when natural selection has taken place or when there are only a subset if individuals survivors due to random chance).

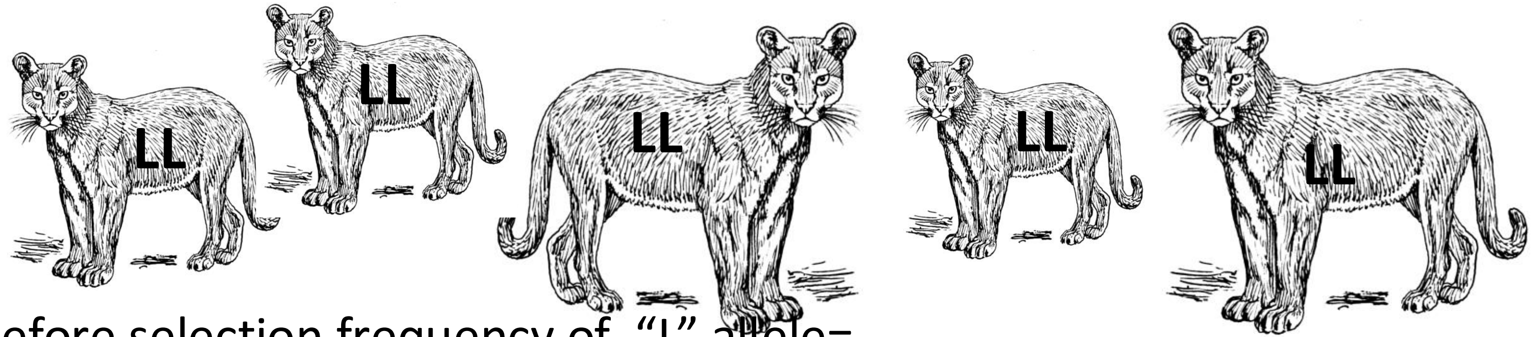
So you just did a TYPE 1 question with the Pumas…
We will do a TYPE 2 question in the next class and kill some Pumas off ☹



Lets kill off some individuals…

Imagine all the surviving pumas mate randomly and then they all die once their offspring are old enough to survive on their own. **What are the NEW allele frequencies in the offspring? Did you see EVOLUTION?**





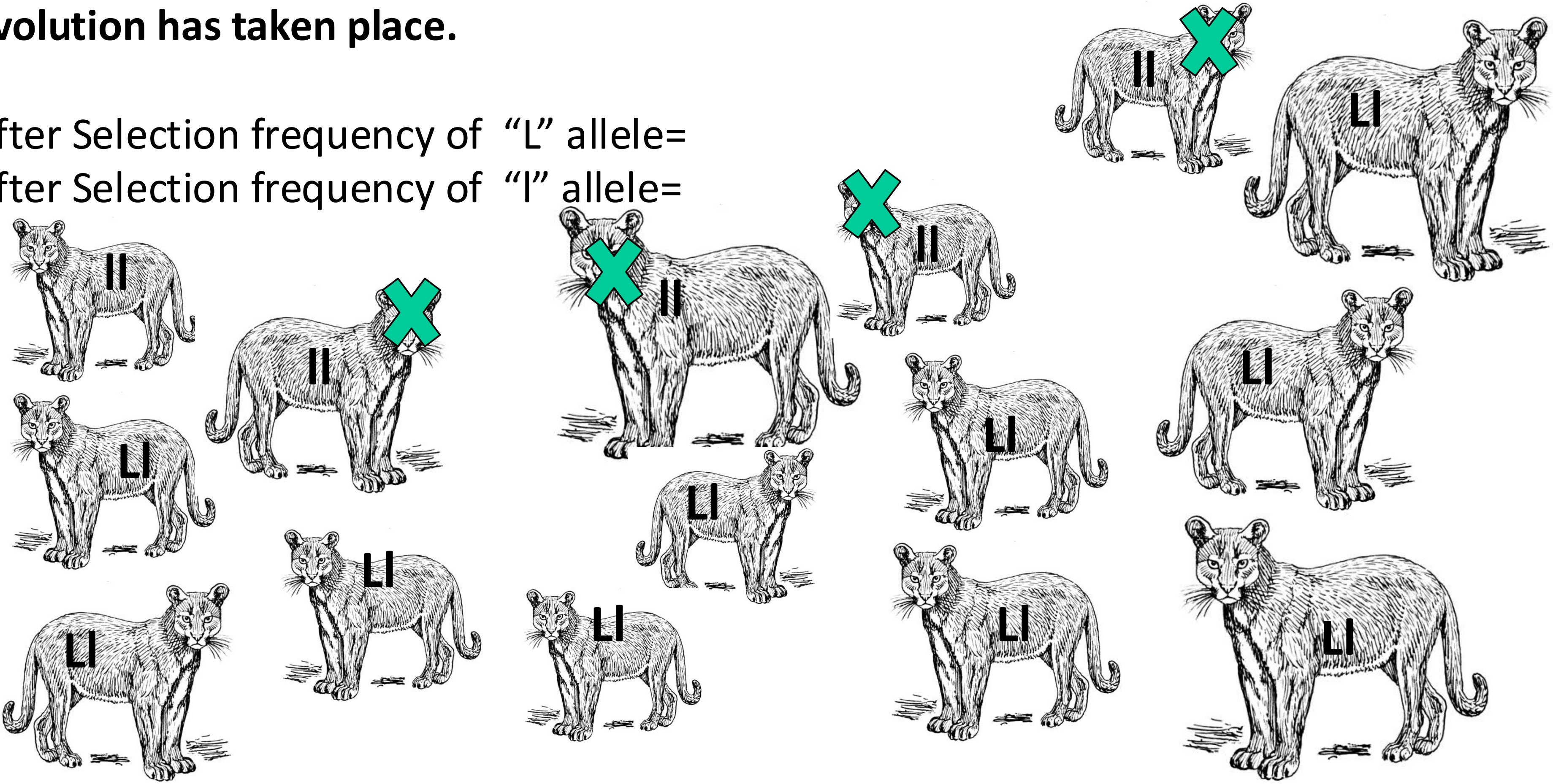
Before selection frequency of "L" allele=

Before selection frequency of "l" allele=

Lets kill off some individuals…to determine whether evolution has taken place.

After Selection frequency of "L" allele=

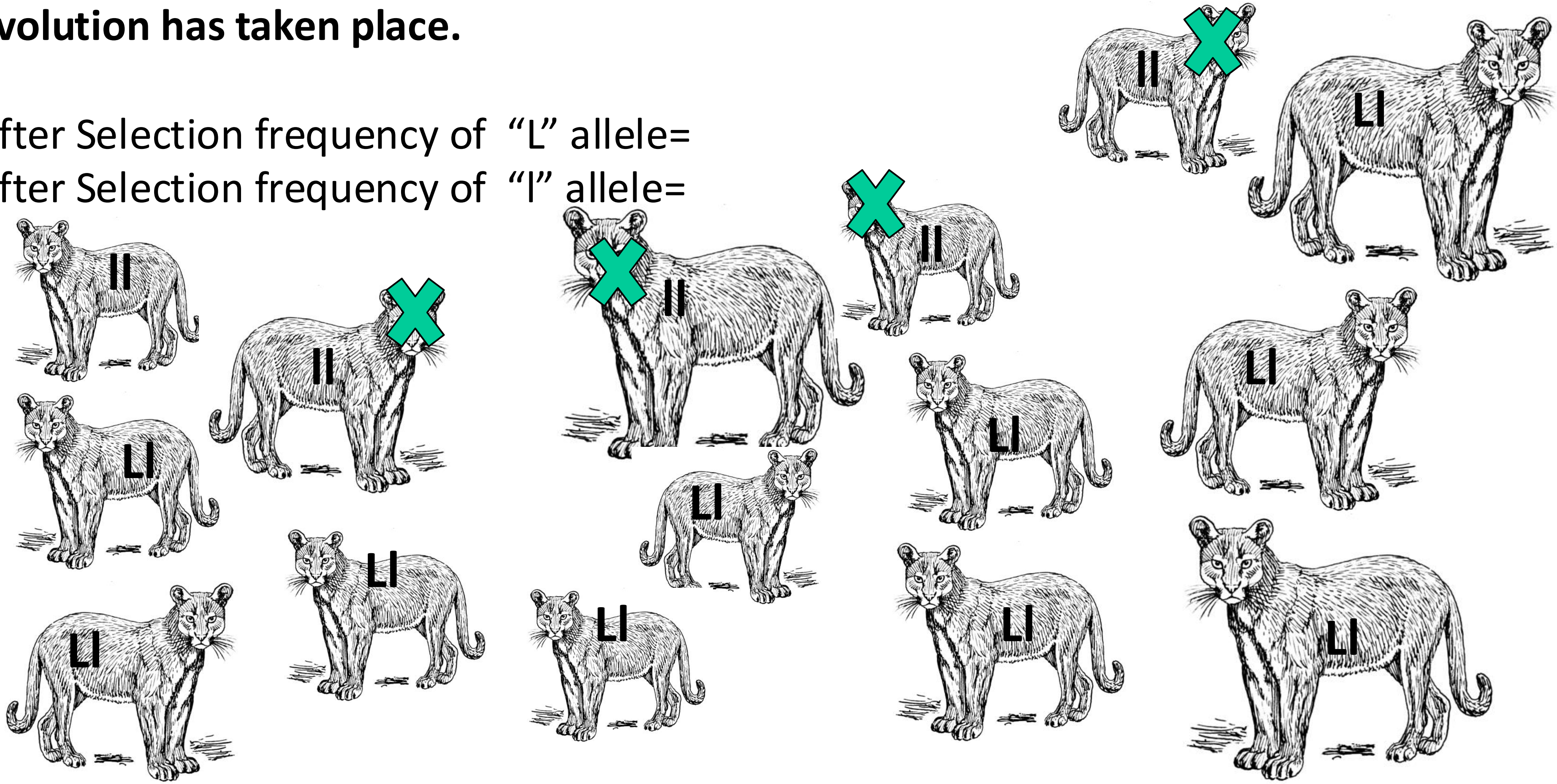
After Selection frequency of "l" allele=

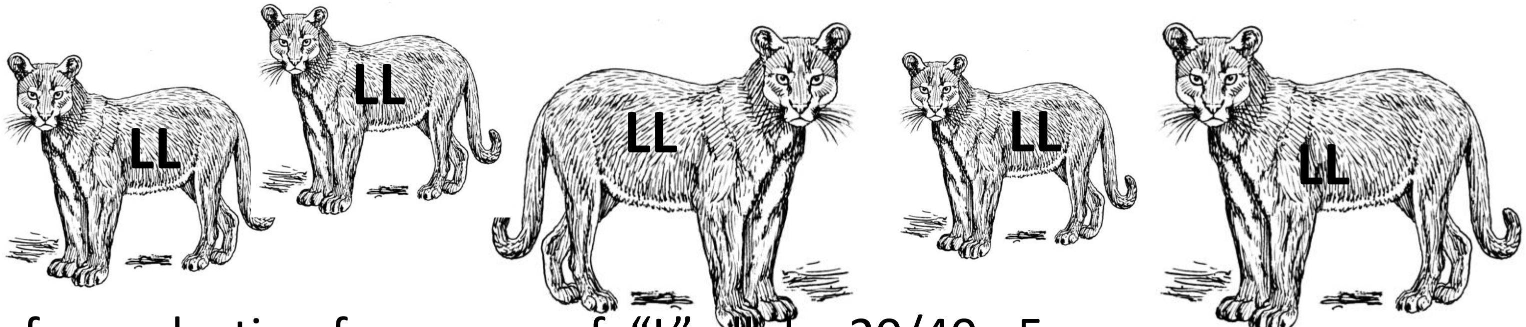


Before selection frequency of “L” allele=20/40=.5
Before selection frequency of “l” allele=20/40=.5

Lets kill off some individuals…to determine whether evolution has taken place.

After Selection frequency of “L” allele=
After Selection frequency of “l” allele=

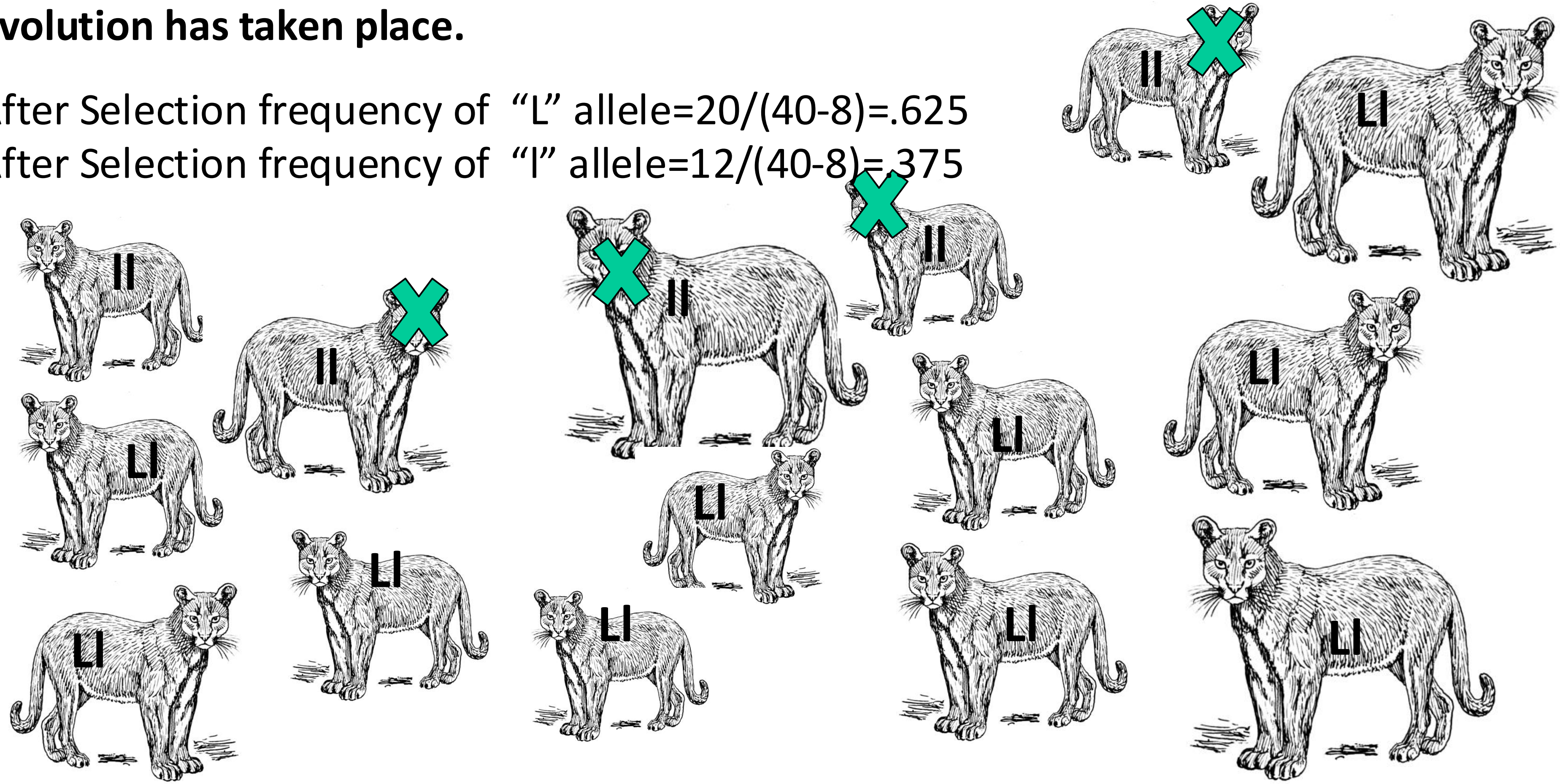


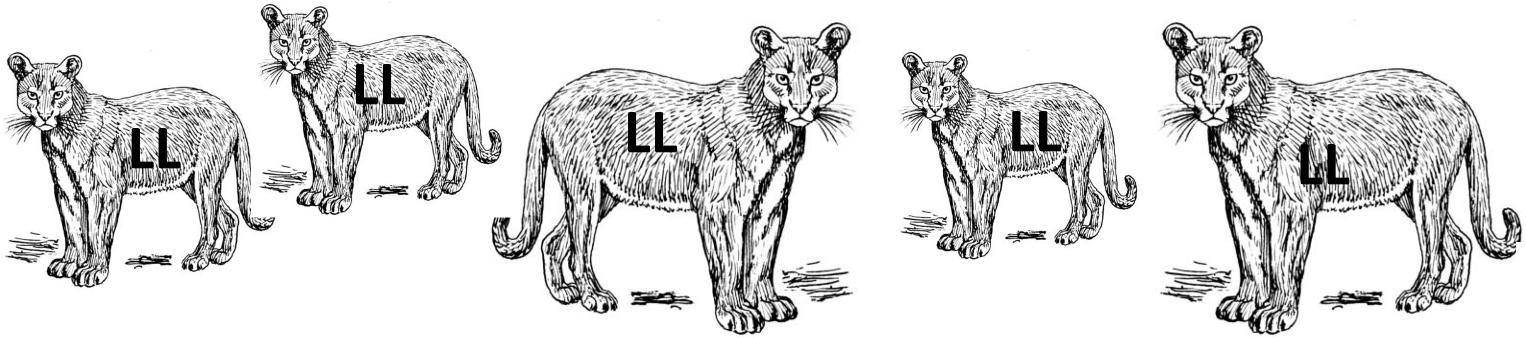


Before selection frequency of "L" allele=20/40=.5
Before selection frequency of "l" allele=20/40=.5

Lets kill off some individuals…to determine whether evolution has taken place.

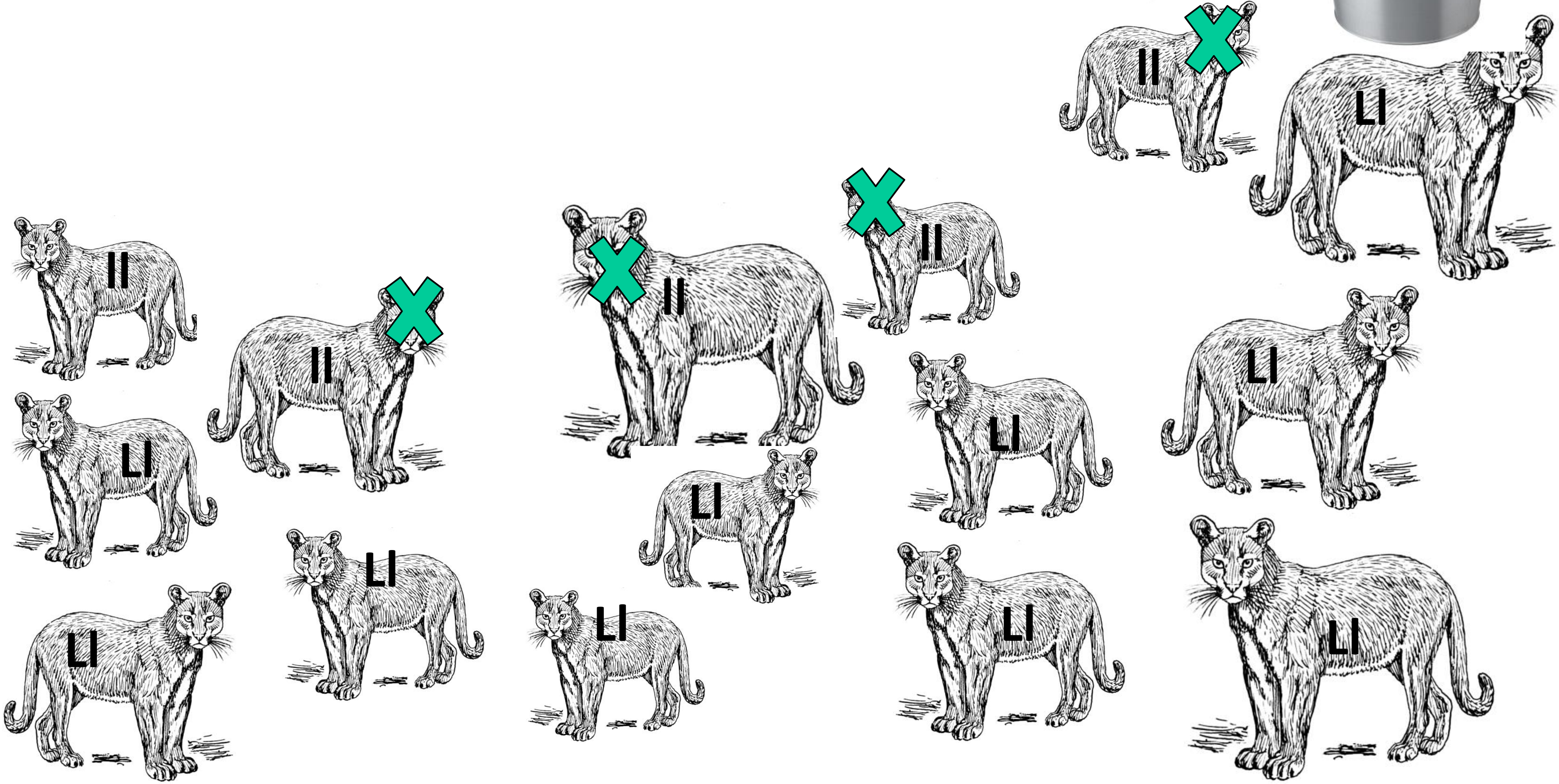
After Selection frequency of "L" allele=20/(40-8)=.625
After Selection frequency of "l" allele=12/(40-8)=.375





Put surviving alleles in bucket.

After Selection frequency of “L” allele=20/(40-8)=.625
After Selection frequency of “l” allele=12/(40-8)=.375



Before selection frequency of “L” allele=20/40=.5
Before selection frequency of “l” allele=20/40=.5

After Selection frequency of “L” allele=20/(40-8)=.625
After Selection frequency of “l” allele=12/(40-8)=.375

Did the population evolve?

Put surviving alleles in bucket.

We could also calculate what the genotypes of individuals would be **in the next generation of Cougars after this selection event by assuming random mating** (and assuming all adults die off that year).

Take your “pool“ or bucket of gametes and simulate mating by pulling random gametes out and combining them to make new diploid individuals.

What are the different genotypes you expect to see in the next generation? HINT: Use HW Theorem!

What are the different genotypes you expect to see in the next generation? HINT: Use HW Theorem!

You do this by taking L= .625 and l=.375 to generate your expected values.

Expected freq of LL is.... (.625)(.625) = _____ = (p^2)
Expected freq of Ll is.... 2(.625)(.375) =_____=(2pq)
Expected freq of ll.... (.375)(.375) =____ = (q^2)

Chapter 6 The ways of change: drift and selection

Genetics of Populations
We are moving up to population level!
We will be focusing on a single locus with 2 alleles in a whole population!

Hang onto this definition of evolution ("Change in gene or allele frequencies over time.")

1. Hardy-Weinberg-how do we use it?

2. Genetic Drift (Drosophila example bottlenecks and founder events)

3. Landscape genetics (Gene Flow, is at end of chapter but I am moving forward)

4. Digging around in the field of Population Genetics (we will see what we get through)

2. Genetic Drift

What is it?

Which of the following two scenarios would be more likely to happen..

A. Your friend flips a coin 5 times and gets 5 heads in a row.

B. Your friend flips a coin 100 times and gets 100 heads in a row.

Most of you probably chose A… 5 heads in a row is probably less surprising because it can happen quite often, just by **chance**.

Flipping a coin 5 times is really not very many times and so is essentially a small sample.

Genetic drift is basically a “sampling error” problem.

In genetic drift the “sample” is the number of individuals in the population.

Genetic drift happens more often when populations get small.

There are two classic ways populations end up small

A. When a large population declines dramatically in size (**bottlenecking event**).

B. When a large population has dispersing individuals that establish new populations (**founder event**).

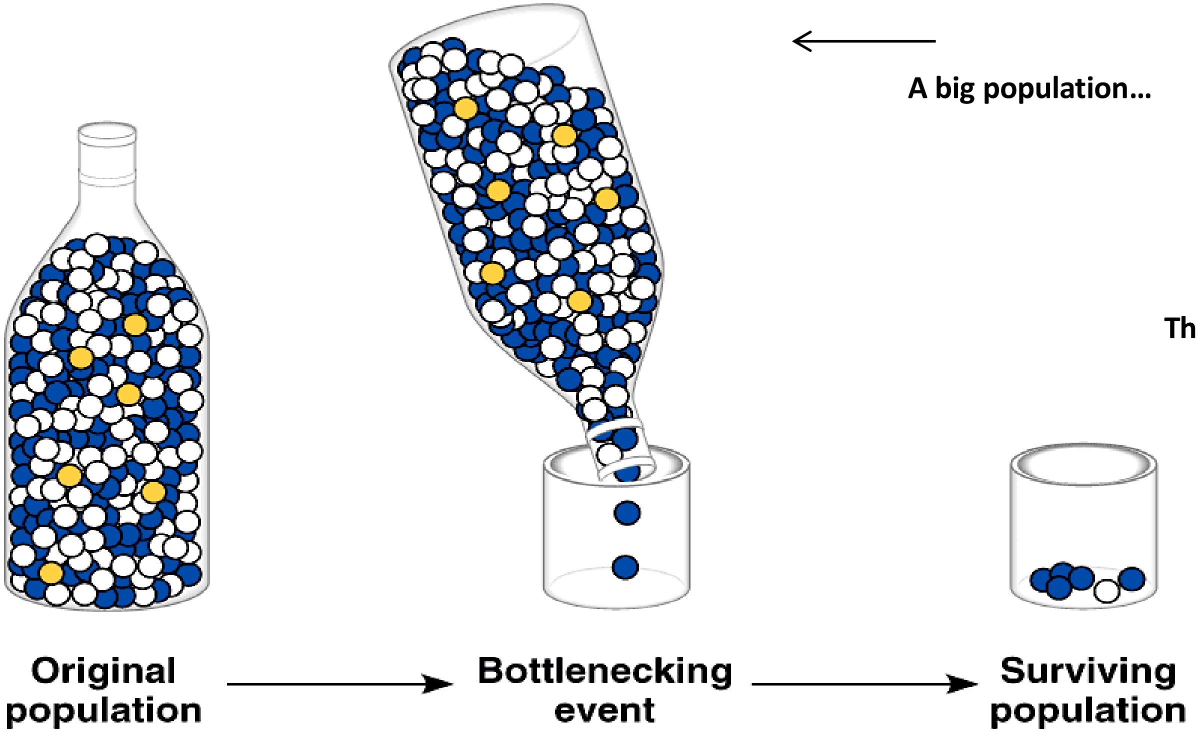
FYI…your text talks about founder events being special cases of bottlenecks! (I just find it easier to divide them)

HINT: Whenever you are asked a question and it seems to be about a small population…the answer will likely have something to do with genetic drift!

Genetic Drift - Population Bottleneck Event

Imagine you have all the **alleles** from a single locus of a single population in a bottle…

(How many alleles are there at this locus in the original population? What are the allele frequencies in the surviving population?)



A big population…

That is suddenly reduced in size…

Is the surviving population a representative sample?

Genetic Drift - Population Bottleneck Event

What happens during population bottlenecks?

- Was genetic variation lost?

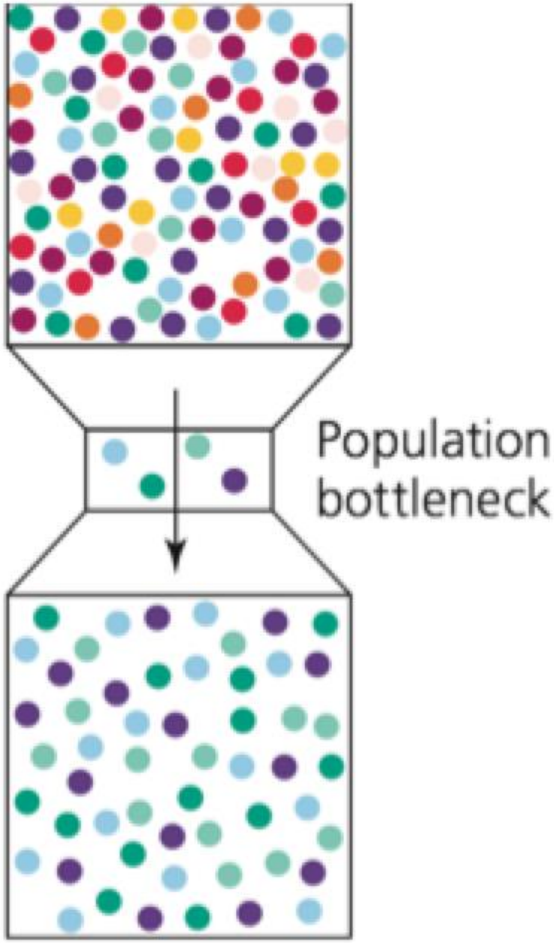
(What would be your evidence?)

- Did allele frequencies change?

(Calculate before and after)

- Did you see evolution?

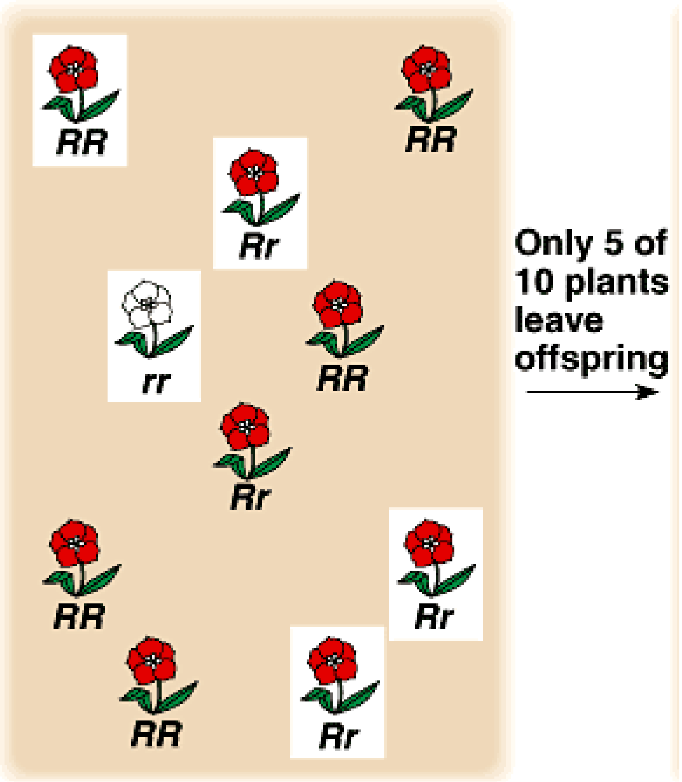
(yes because, no because…?)



A population of flowering plants going through a bottleneck. Instead of alleles (represented as marbles, m+m's or jelly beans) here you see **individuals** in a population that is going through a bottleneck along with their **genotypes**.

Freq of R=

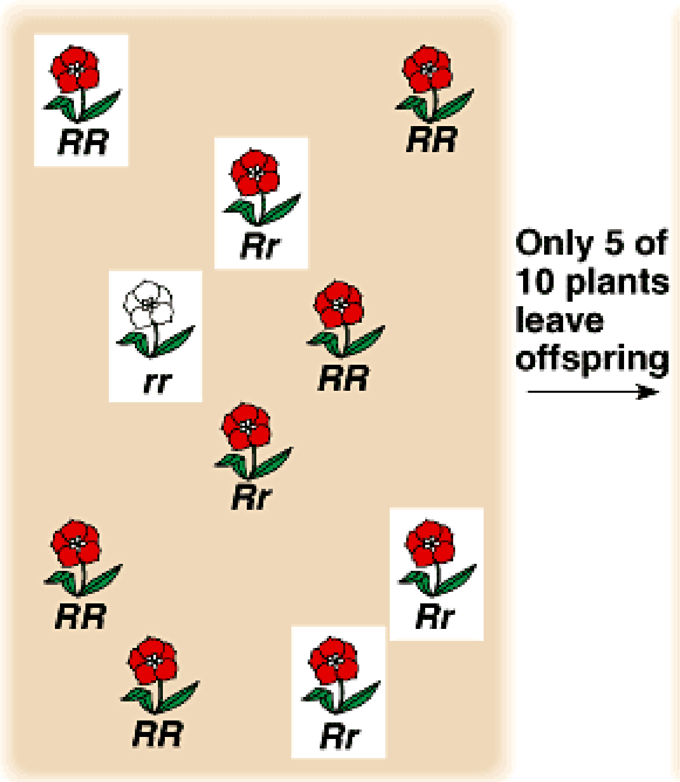
Freq of r=



A population of flowering plants going through a bottleneck.

Freq of R=

Freq of r=



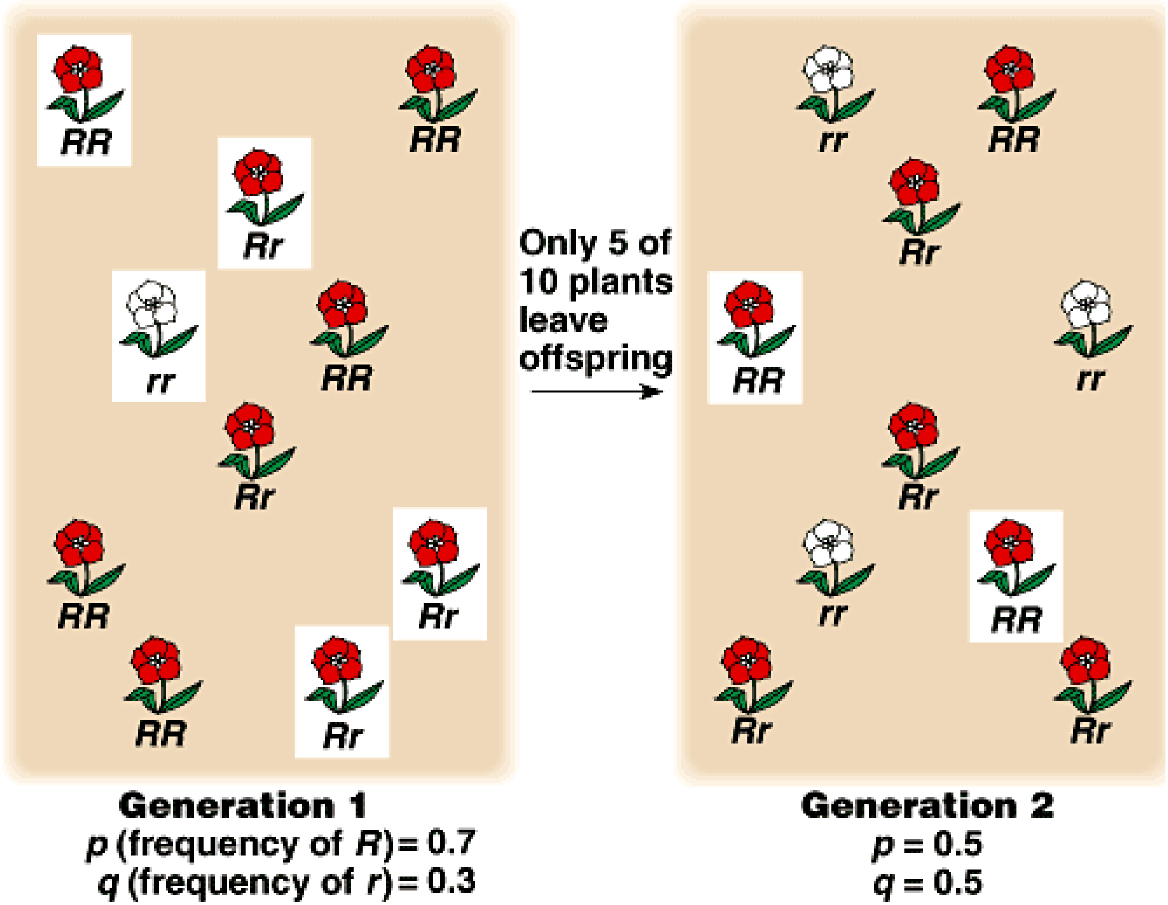
Generation 1
p (frequency of R) = 0.7
q (frequency of r) = 0.3

If only those in white box survive by chance and they mate randomly to create the next generation, what will the new freq of R and r be in this population?

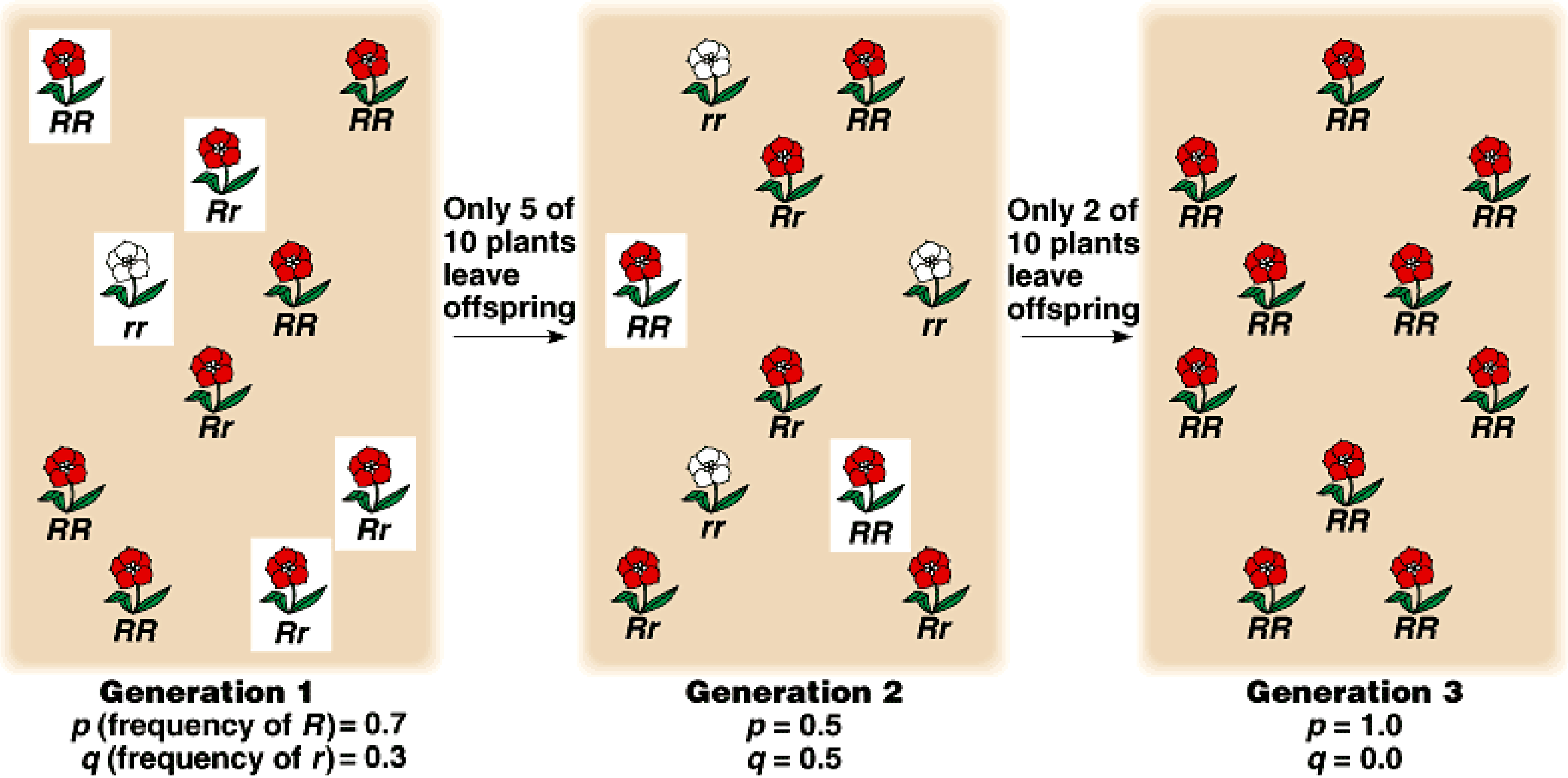
Freq of R=

Freq of r=

A population of flowering plants going through a bottleneck.



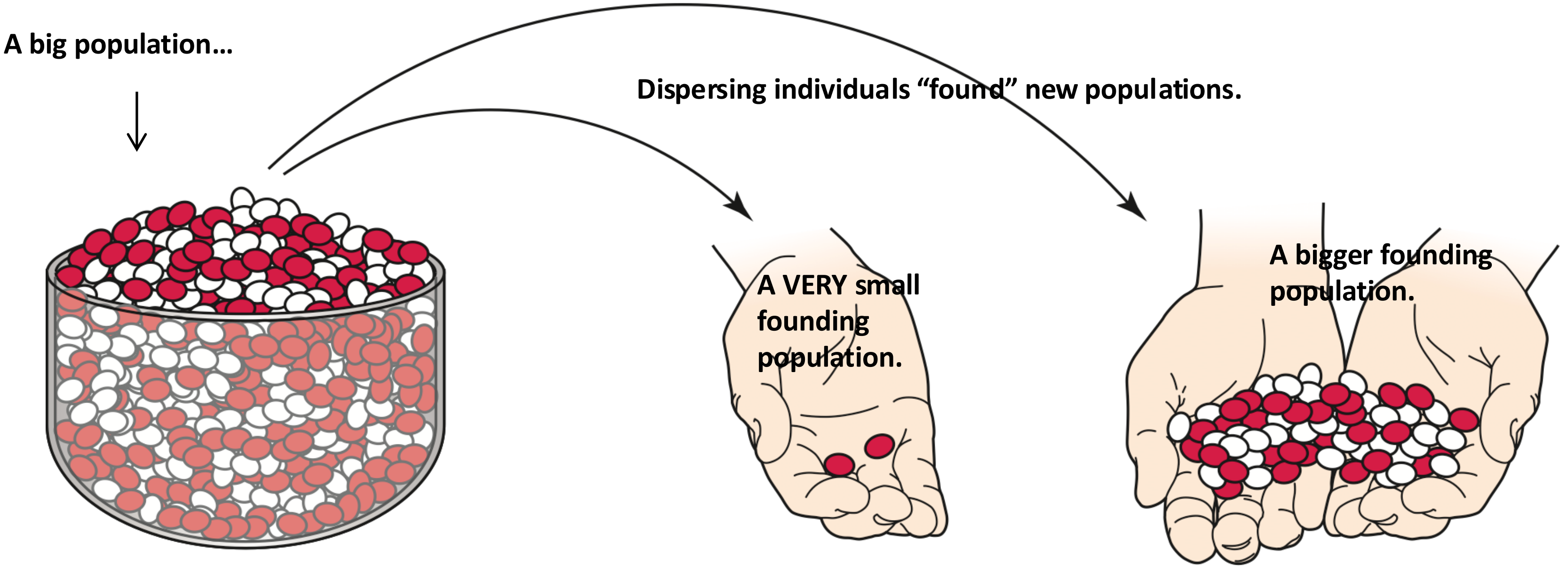
A population of flowering plants going through a bottleneck.



Genetic Drift - Founder Event

Small populations being established in a new place.

(Here…the "m+m"s in the bowl are all the alleles from a single locus of a single population…How many alleles are there at this locus?)



A big population…

Dispersing individuals "found" new populations.

A VERY small founding population.

A bigger founding population.

50% red
50% white

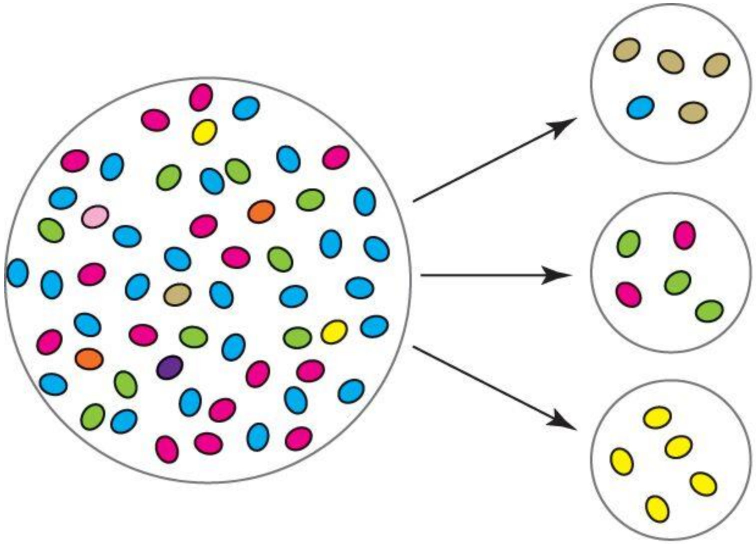
100% red
0% white

51% red
49% white

Which of the two founding populations is more representative of the allele frequency of the parent population in the bowl?

Genetic Drift - Founder Event

Imagine these colored jelly beans are alleles.



New populations started by a small number of individuals

What happens during founder events?

- Was genetic variation lost in each of these founding populations?

(What would be your evidence?)

- Did allele frequencies change?

(Calculate before and after)

- Did you see evolution?

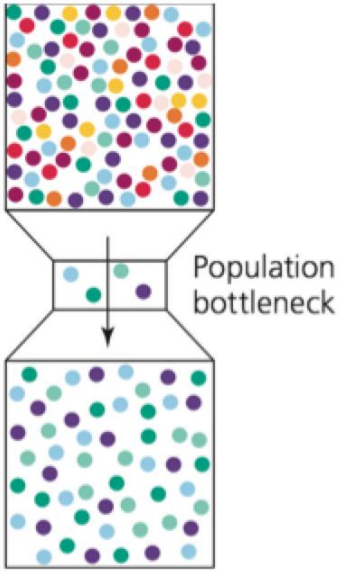
(yes because, no because…?)

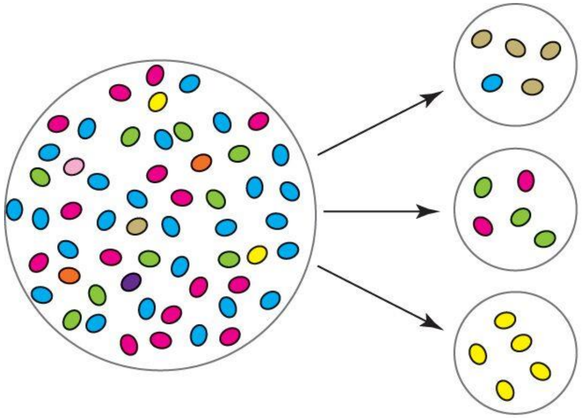
Review!

There are two classic ways populations end up small

A. When a large population declines dramatically in size (**bottlenecking event**).

B. When a large population has dispersing individuals that establish new populations (**founder event**).





New populations started
by a small number of individuals

Real examples!

When do populations end up small?

1. Founder events……

Ex. Humans mutineers! (in your text)

(27 individuals lived in isolation for decades on Pitcairn Island)

2. Bottlenecking events…..

Ex. Elephant seals (in your text)

Northern elephant seals reduced to about 30 in the 1890s.

300 base pair stretch of ***mt*DNA** which typically has around 30 variable regions within it had only 2.

Southern pop had 23 variable regions in same segment!

Ex. Florida Panther=Puma=Cougar=Mountain lion

https://www.fws.gov/refuge/florida_panther/wah/panther.html

With Fresh Blood, Inbred Florida Panthers Rebound
By Robert Roy Britt
posted: 18 August 2005

A controversial breeding program has improved the genetic diversity of inbred Florida panthers and the endangered animals are on the rebound, scientists announced today.

As few as 30 wild panthers roamed the Florida Everglades in the early 1990s. Abnormalities such as low sperm counts and heart defects were becoming common, studies found, and the kittens had low survival rates.

In 1995, researchers outfitted some female Texas panthers with radio collars and introduced them into four sections of the Florida Everglades. Some Florida panthers were also tagged.

Researchers monitored the cats and kittens and found that the hybrids had better survival rates, presumably because they were more genetically diverse. By 2003, three of the Texas panthers were still alive, and they were removed -- scientists figured enough fresh blood had been injected into the Florida population and they wanted to keep outside genetic exposure to a minimum.

Today, there are at least 87 wild panthers in Florida.

"More than three times as many hybrid kittens appear to reach adulthood as do purebred ones," Pimm and his colleagues write in a paper that will be published early next year in the British journal Animal Conservation.

And the hybrids are on the move. The purebred panthers rarely ventured beyond protected areas north of interstate 75 and west of State Highway 29. Hybrid offspring have moved south and east into new sections of the Everglades National Park and Big Cypress National Preserve. They're pushing into places that are less hospitable, but they're doing so with success, the scientists said.

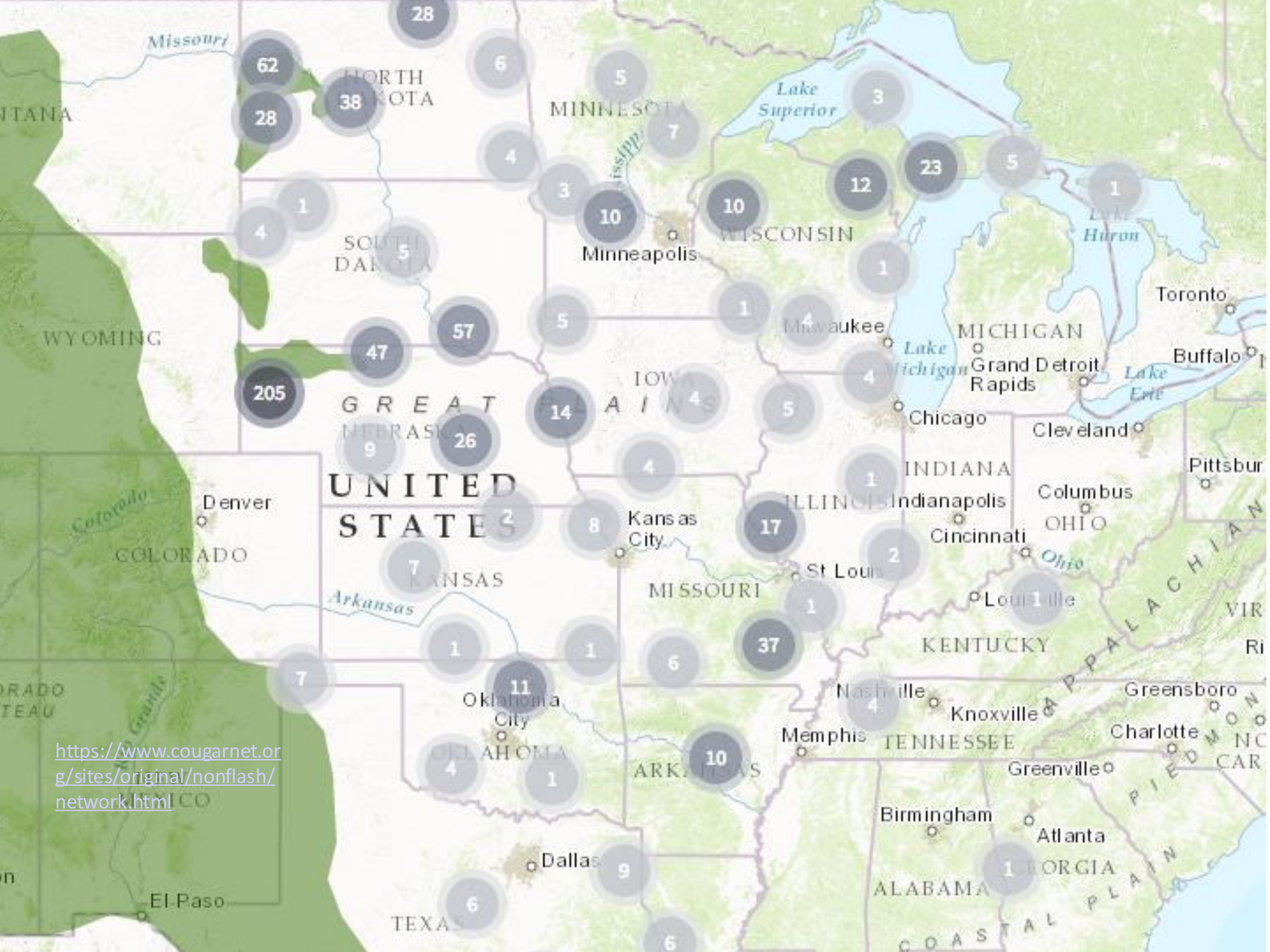
The federal government has decided that the hybrids will be called Florida panthers for purposes of determining their endangered species status.

→Estimates today are 160???

Questions you should be able to answer based on the article on the previous slide.

- How many were left in the wild?
- What kinds of health problems did they have?
- How many panthers were brought in from what other location?
- What were some of the risks associated with moving panthers?
- They use the word trade-offs. What point do they make?
- Consider checking out this other article!

https://www.sciencedaily.com/releases/2019/10/191003111755.htm



https://www.cougarnet.org/sites/original/nonflash/network.html

Exciting Florida panther encounter…

Ok this one should work! (or google scary Florida panther encounter on youtube and it should come up)
https://www.youtube.com/watch?v=xcSyZbhvZwY

Cougar caught on trail cam recently…
https://www.mprnews.org/story/2022/11/03/wolf-researchers-record-rare-video-of-a-mountain-lion-in-northern-minnesota

Map of MN DNR Confirmed Cougar Sightings
https://www.dnr.state.mn.us/mammals/cougar/cougar_verifications.html

Ex. Mongolian Wild Horse or Przewalski's Horse

Foals captured in Mongolia in 1800s and shipped to Europe

(After 1945 only two captive populations in zoos remained, in Munich and Prague. The most valuable group, in the Ukraine, was shot by German soldiers during WWII. ….By the end of the 1950s, only 12 individual Przewalski's horses were left in the world From Wikipedia)

- Went extinct in wild in 1960s
- 9 individuals used to start a new pop.
- Reintroduced to Mongolia
- Currently reproducing in wild!

Watch this if you have time…

How did they capture the foals? ☹

https://www.amnh.org/explore/videos/biodiversity/wild-horse-mongolia

Ex. Dairy cows

https://www.scientificamerican.com/article/from-two-bulls-nine-million-dairy-cows/

BIOLOGY

From Two Bulls, Nine Million Dairy Cows

Just two Y chromosomes exist in a huge population of U.S. Holsteins; researchers want to know what traits have been lost

By Maureen O'Hagan, Undark on June 20, 2019

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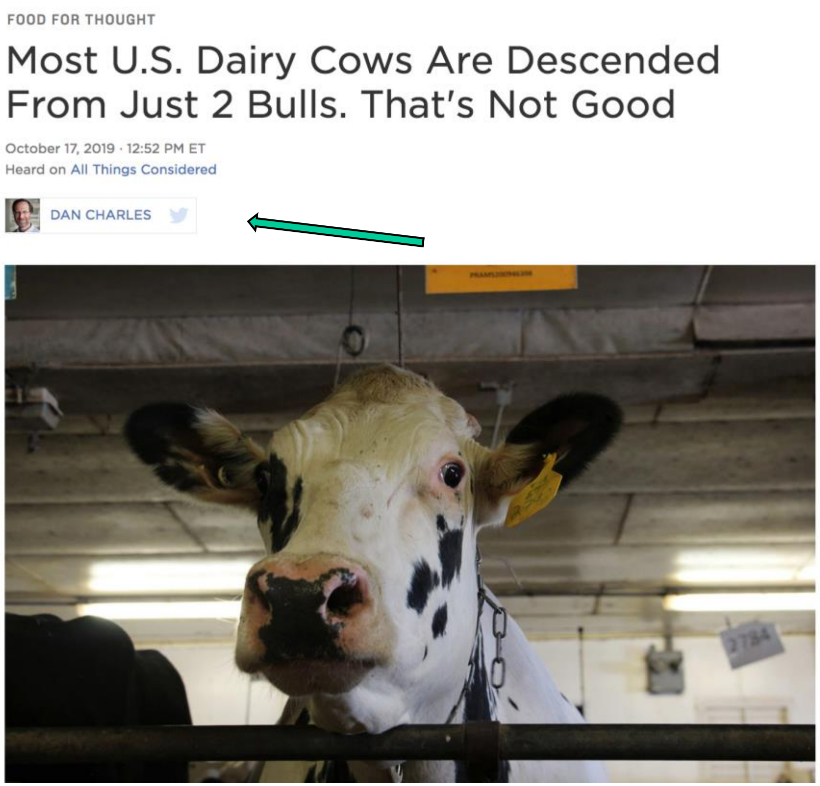


FOOD FOR THOUGHT

Most U.S. Dairy Cows Are Descended From Just 2 Bulls. That's Not Good

October 17, 2019 · 12:52 PM ET
Heard on All Things Considered

DAN CHARLES

https://www.npr.org/sections/thesalt/2019/10/17/770696476/most-u-s-dairy-cows-are-descended-from-just-2-bulls-thats-not-good

Ex. from laboratory setting-Drosophila

What did these researchers do and what does this show?

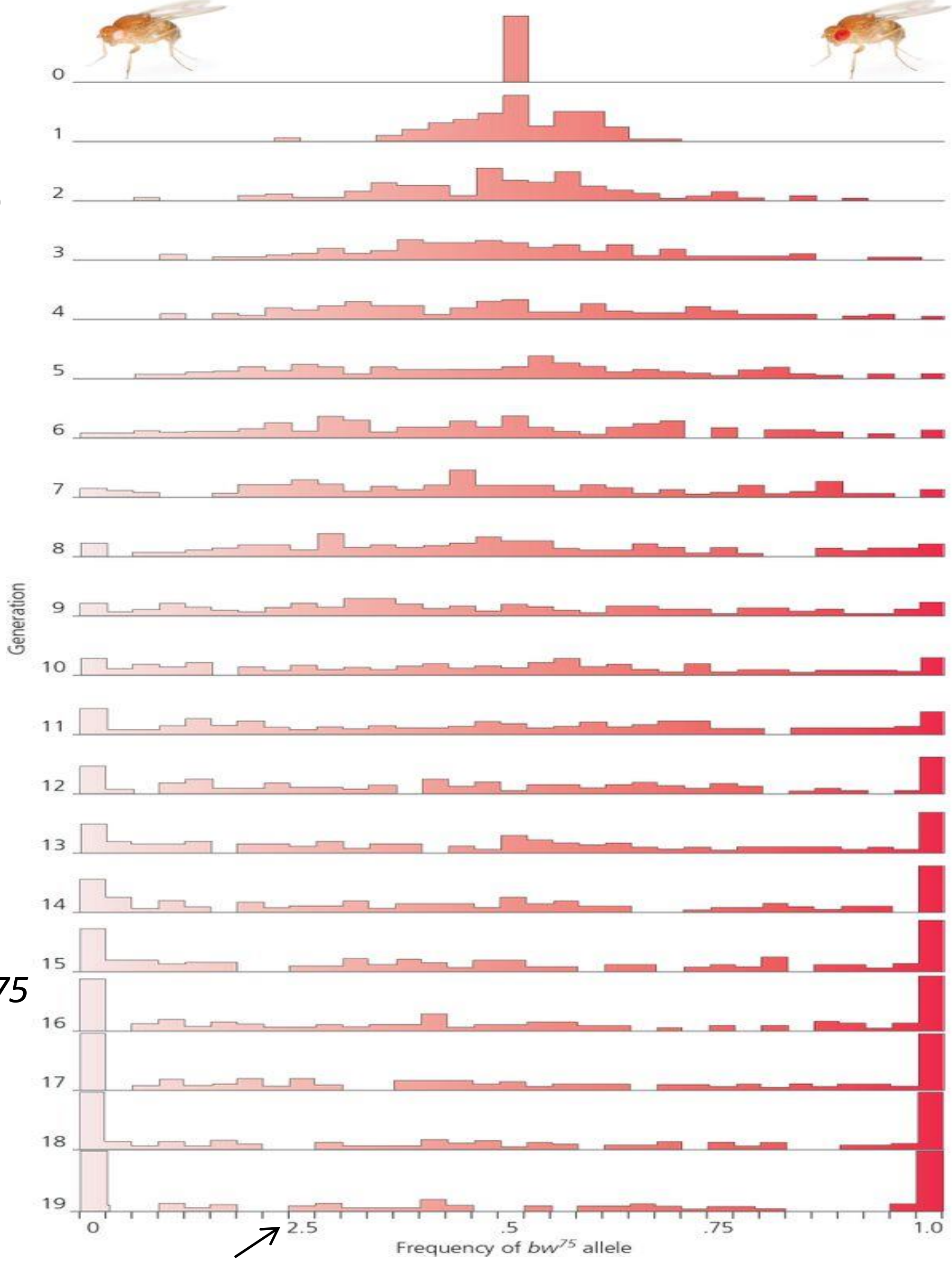
Which generation shows the first flies with the *bw*^{75} allele **fixed** in the population?

Which generation shows the first flies with the *bw*^{75} allele **lost** in the population?

What color are the eyes of *bw*^{75} *bw*^{75} flies?

How about *bw bw flies?*

(107 populations of 8 heterozygous flies- *bw bw*^{75})



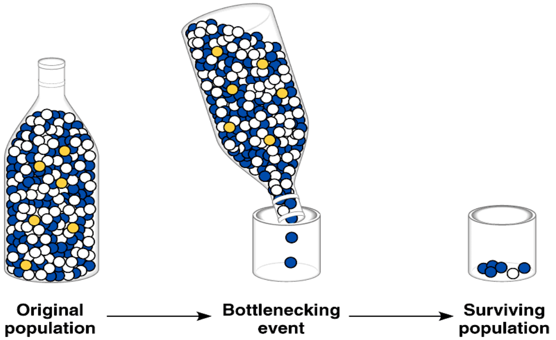
Mistake in graphic should be .25!

Review

In very small populations (bottlenecks, founder events)

1. variation is lost (alleles are lost)

AND



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2. rare alleles can become common

3. common alleles might become less common

Evolution occurs DUE TO random changes in gene frequencies-not a result of selection!

(FYI..In reality not always a big difference between bottleneck and founder)