How are traits inherited anyway?

Simple…

Mendelian Genetics

Qualitative Genetics

Population Genetics

Quantitative Genetics

Complex…

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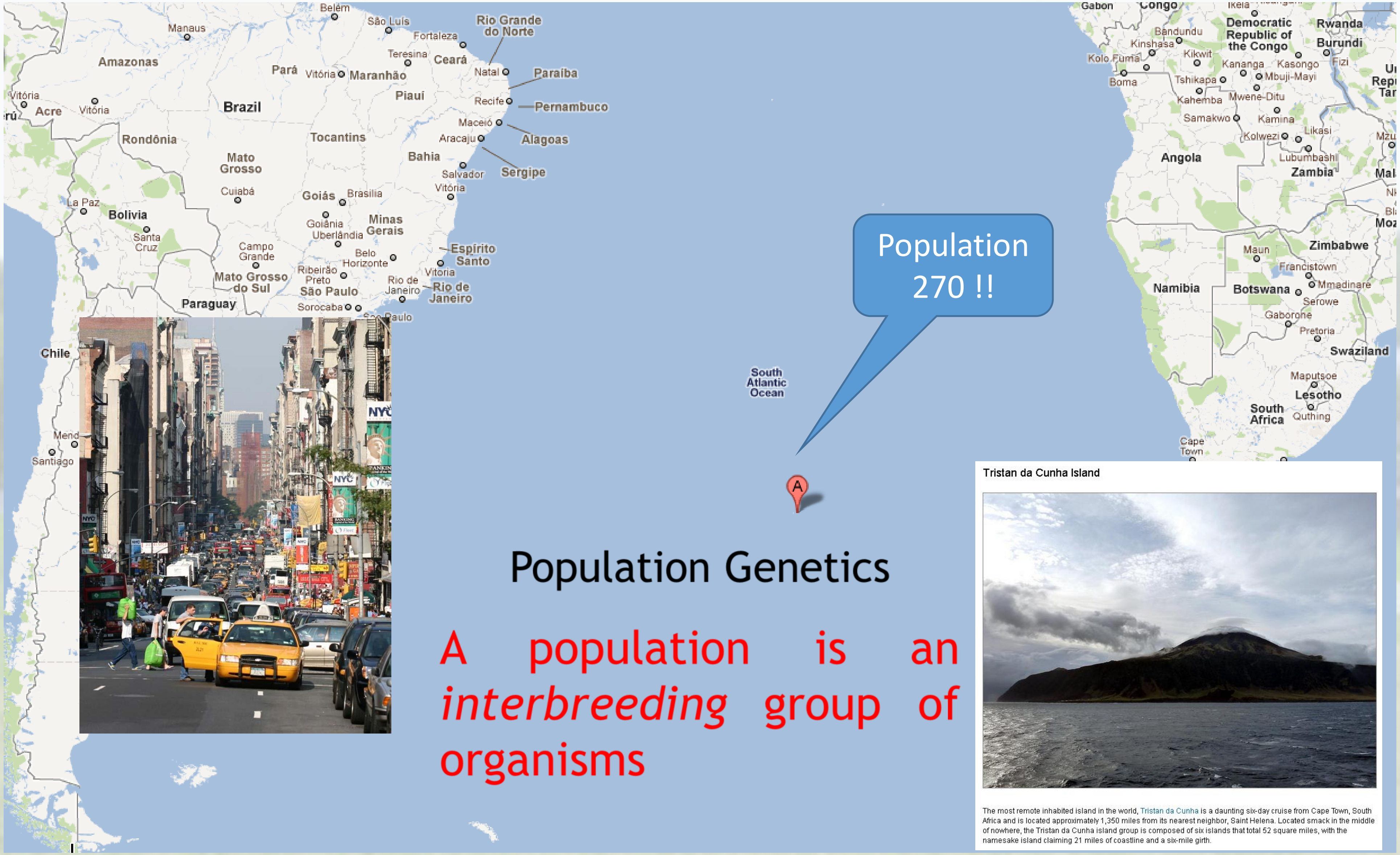
Large versus small “populations”



Population 270 !!

Tristan da Cunha Island

The most remote inhabited island in the world, Tristan da Cunha is a daunting six-day cruise from Cape Town, South Africa and is located approximately 1,350 miles from its nearest neighbor, Saint Helena. Located smack in the middle of nowhere, the Tristan da Cunha island group is composed of six islands that total 52 square miles, with the namesake island claiming 21 miles of coastline and a six-mile girth.

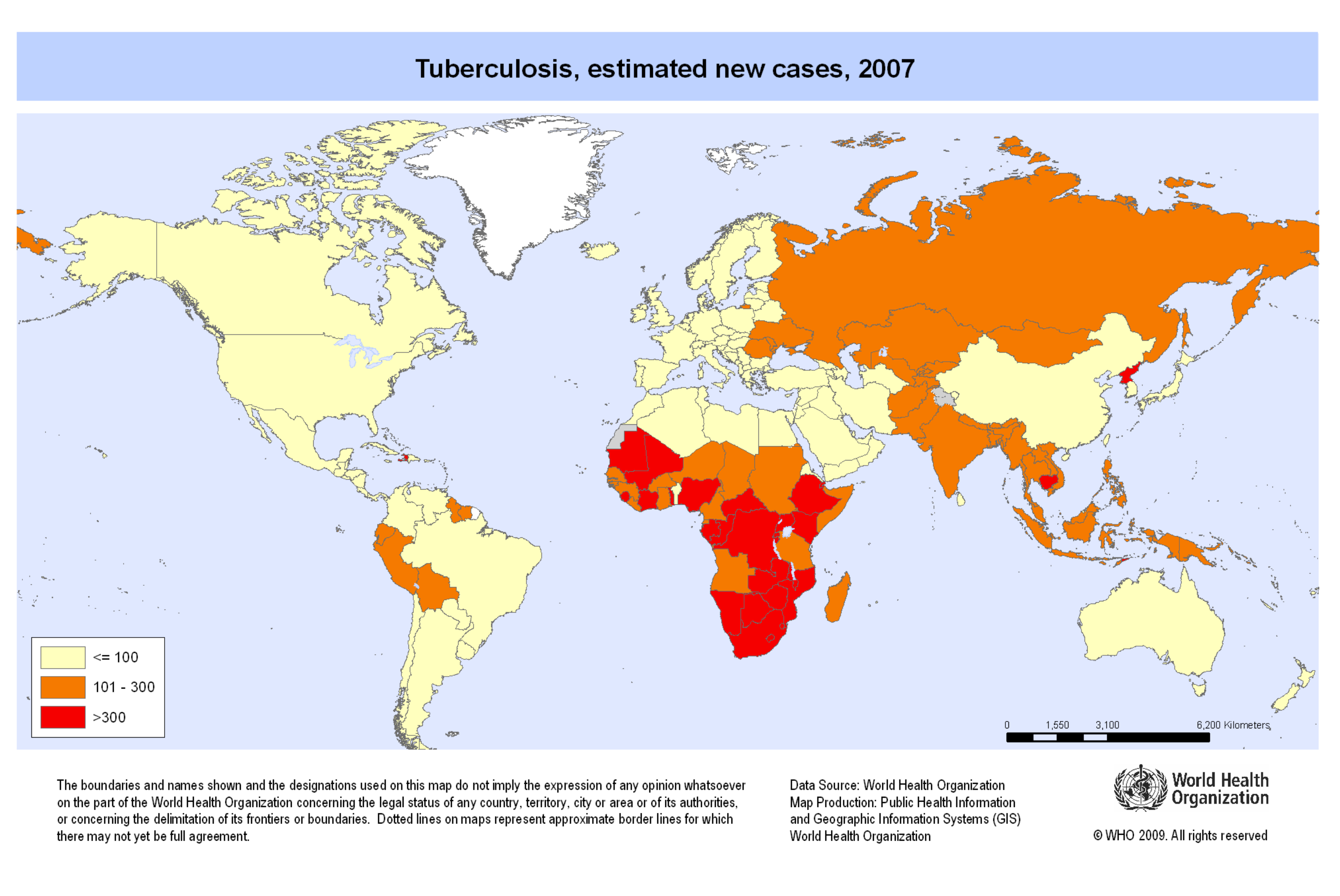
Population Genetics

A population is an *interbreeding* group of organisms

Incidence of Tuberculosis

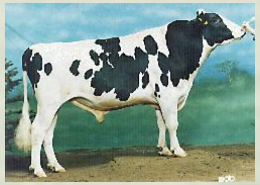
Tuberculosis, a chronic infectious disease caused by *Mycobacterium tuberculosis,* has reemerged as a leading public health problem. Approximately one-third of the world's population is infected with *M. tuberculosis,* and a recent World Health Organization report estimated that, in 1998, there were 8 million new cases of clinical tuberculosis and 1.9 million deaths from the disease. Interestingly, not all individuals exposed to *M. tuberculosis* become infected. Moreover, progression toward clinical tuberculosis is far from an inevitable consequence of infection with *M. tuberculosis,* since only ~10% of the vast number of infected individuals actually develop clinical disease (Bloom and Small 1998). Both *M. tuberculosis* infection and clinical tuberculosis result from complex interactions between the infectious agent, environmental factors, and the host.

Laurent Abel and Jean-Laurent Casanova, Am. J. Hum. Gen. 2000



Populations of animals...

Macdonald Campus Farm ??



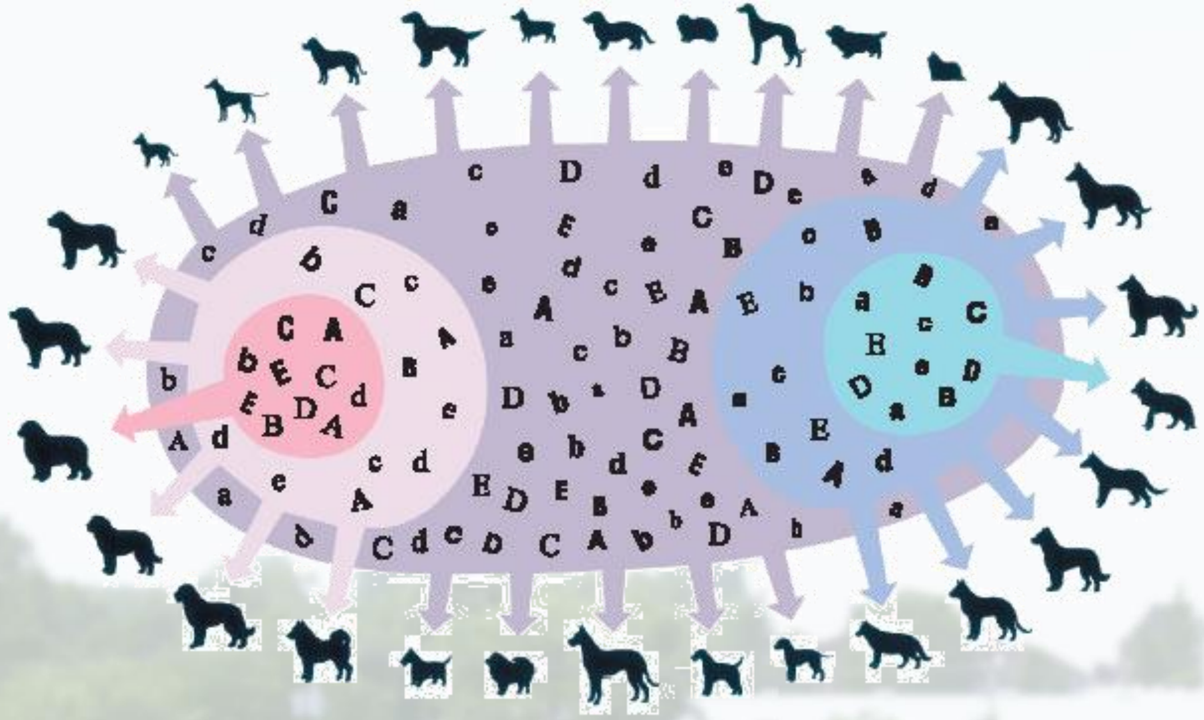
In the case of Population Genetics we're interested in the <u>frequency</u> of certain genes in a population

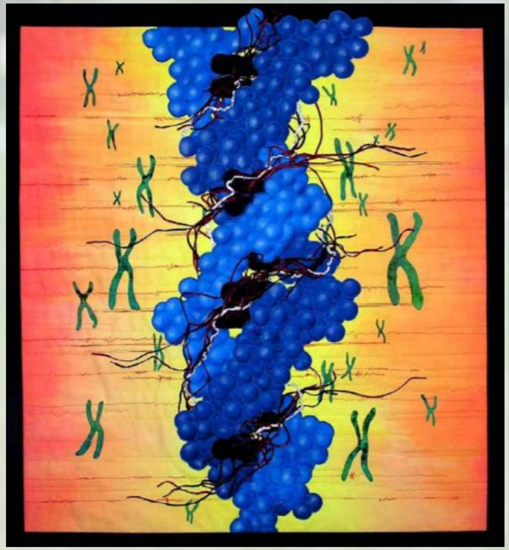
Notation:
Frequency of A = f(A)

The number of individuals with an AA genotype in dependent on the frequency of the "A" gene in the population

The number of individuals with an "aa" genotype in dependent on the frequency of the "a" gene in the population

The number of individuals with an "Aa" genotype in dependent on the frequency of both the "A" and the "a" genes in the population





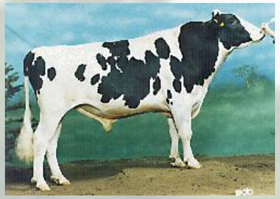
Gene Pool

all of the alleles on all of the genes in all of the individuals *for a given population*

Gene Frequency (*f*)

- incidence of a gene in a population
- fraction of loci occupied by a specific allele
- defined as being between 0 and 1 (or 100%)

How common is the red/white allele ?



Genes for Coat Colour in Shorthorn Cattle

	# of Animals	# Red Alleles	# White Alleles
RR 	600	1200	0
Rr 	200	200	200
rr 	200	0	400
		1400/2000	600/2000
Frequencies?		$f(R) = 0.7$	$f(r) = 0.3$

Godfrey Hardy
(1877 – 1947)

Wilhelm Weinberg
(1862 – 1937)

Allele and Genotype frequencies in a population remain constant (in equilibrium) over time (generations) unless external affects are introduced which disturb this state…

What are the expected frequencies of the genotypes ?

- the frequency of the RR genotype
  = the frequency of the R allele squared
  = $[f(R)]^2 = p^2$

- the frequency of the rr genotype
  = the frequency of the r allele squared
  = $[f(r)]^2 = q^2$

- the frequency of the Rr genotype = 2 x $f(R)$ x $f(r)$
  $= 2pq$
  Why?

Because of Mendel's First Law...

Alleles at each locus are <u>independent</u> events

The frequency of the Rr combination is equal to the frequency of the rR combination

So, f(Rr) = 2pq

	♂ R	♂ r
♀ R	RR p^2	Rr pq
♀ r	rR pq	rr q^2

$$p + q = 1$$

$$p^2 + 2pq + q^2 = 1 \text{ or } (p+q) \times (p+q) = 1$$

Godfrey Hardy
(1877 – 1947)

Think of Multiple Alleles
Versus
Two Loci

Wilhelm Weinberg
(1862 – 1937)

Results of the random union of the two gametes produced by *two individuals*, *each heterozygous for a given trait*. As a result of meiosis, half the gametes produced by each parent will carry the **B** allele; the other half the **b** allele.

	0.5 **B**	0.5 **b**
0.5 **B**	0.25 **BB**	0.25 **Bb**
0.5 **b**	0.25 **Bb**	0.25 **bb**

Results of the random union of the gametes produced by *an entire population* with a gene pool containing 80% **B** and 20% **b**.

	0.8 **B**	0.2 **b**
0.8 **B**	0.64 **BB**	0.16 **Bb**
0.2 **b**	0.16 **Bb**	0.04 **bb**

Note:

0.64
+ 0.16 + 0.16
+ 0.04
= 1.00 or 100%

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Incidence of colour blindness worldwide…

1 in 200
or
0.5%

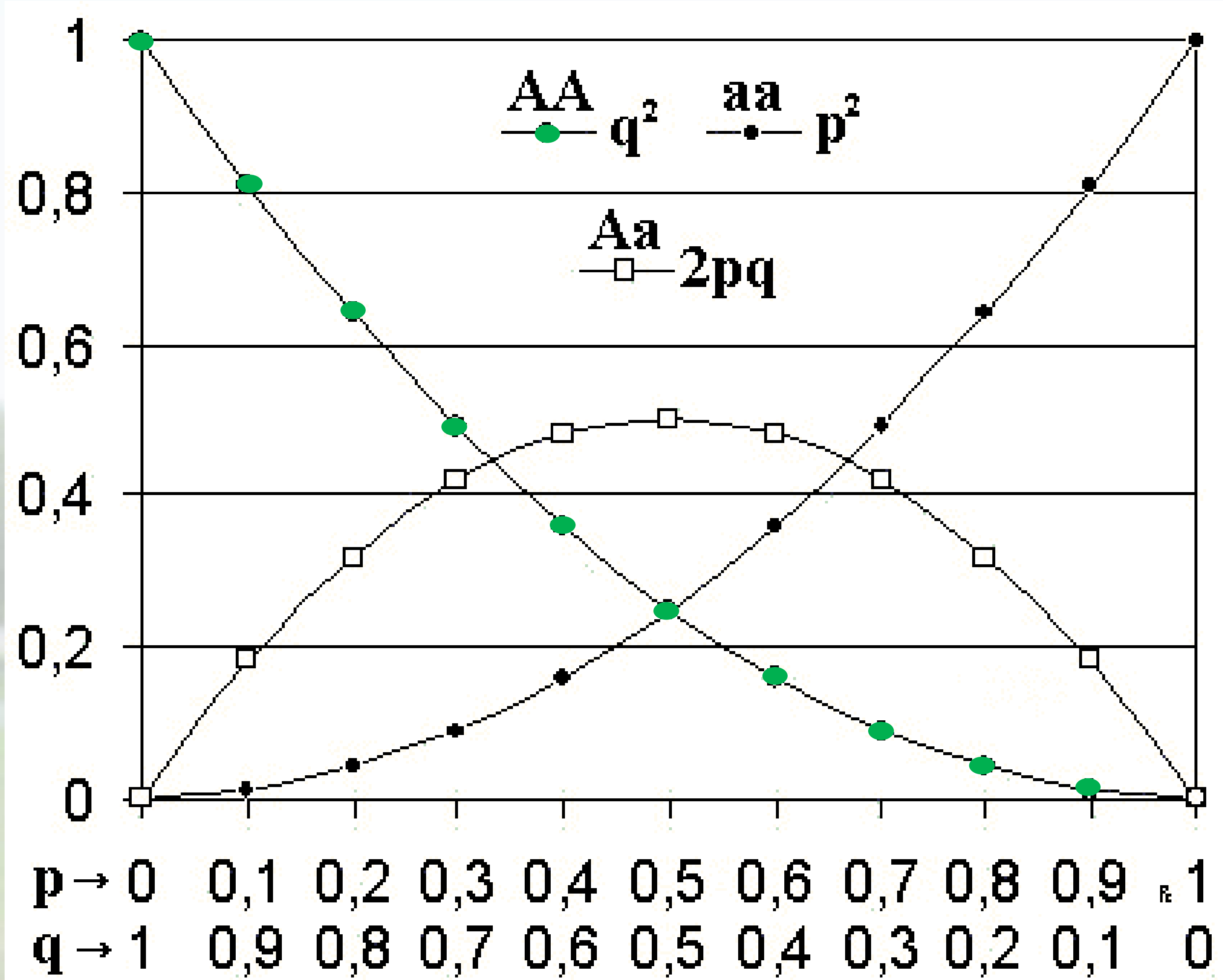
around 20m

1 in 12
or
8%

around 300m

Hardy-Weinberg Requirements

- the population is very (infinitely) large;
- all individuals can mate at random;
- all individuals produce the same number of offspring;
- there is no selection of certain alleles;
- no gene migration occurs; and
- no mutations take place.



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Genes for Coat Colour in Shorthorn Cattle

		# of Animals	# Red Alleles	# White Alleles
			f(R) = 0.7	f(r) = 0.3
RR		600	1200	0
Rr		200	200	200
rr		200	0	400

But is this population in Hardy-Weinberg Equilibrium?

- the frequency of the RR genotype [f(RR)] *is expected to be* [f(R)]^2 = p^2 = $(0.7)^2$ = 0.49 => 1000 x 0.49 = 490 “Red” Animals
- the frequency of the rr genotype [f(rr)] *is expected to be* [f(r)]^2 = q^2 = $(0.3)^2$ = 0.09 => 1000 x 0.09 = 90 “White” Animals
- the frequency of the Rr genotype [f(Rr)] *is expected to be* 2 x f(R) x f(r) = 2 x (0.7) x (0.3) = 0.42 => 1000 x 0.42 = 420 “Roan” Animals

Genes for Coat Colour in Shorthorn Cattle
in Hardy-Weinberg Equilibrium

		# of Animals	# Red Genes Alleles	# White Genes Alleles
RR		490	980	0
Rr		420	420	420
rr		90	0	180
			1400/2000	600/2000
Frequencies?			$f(R) = 0.7$	$f(r) = 0.3$

How to make use of Hardy Weinberg Theory: an example of Mulefoot in Cattle…

- If the incidence of mulefoot is one in ten thousand, how many individuals in a population are <u>*expected*</u> to be <u>*carriers*</u> (i.e., Mm) of the mulefoot gene?

- 1/10000 = 0.0001 = what ??

- Frequency of m? of q? of mm? of q^2 ?

- $q^2 = \sqrt{0.0001}$ => q = 0.01 => p = (1 – q) = 0.99

- So… Expected number of "carriers" = ?

- 2pq = 2 * 0.99 * 0.01 = 0.0198
- (i.e., almost 2%)

Figure 7. Mulefoot (syndactyly). Notice single toe as compared to the normal front foot. Beef Cattle Handbook Iowa Beef Centre

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Increasing the frequency of a gene...

Selection for coat colour in Shorthorn Cattle

RR

rr

Rr

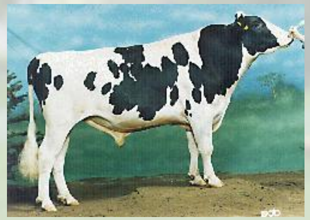
- Selection for RED...
- Selection for WHITE...
- Selection for ROAN!!

Increasing the frequency of a gene...

Selection for coat colour in Holstein Cattle

bb

Bb



BB

- Selection for RED & WHITE...
- Selection for BLACK & WHITE...

Selection for a *dominant* allele...

Selection for Black & White in Holstein Cattle

f(B) = 0.8 f(b) = 0.2

f(BB) = 0.64 f(Bb) = 0.32 f(bb) = 0.04

Selection for B_ for one generation means the frequencies will change...

$$p^* = [f(BB) + ½f(Bb)] / [f(BB) + f(Bb)]$$

$$= [0.64 + 0.16] / [0.64 + 0.32] = .833$$

$$q^* = 1 - p^* = .167$$

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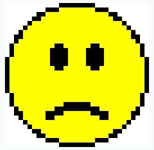
Selection for Qualitative Traits...

- Traits have relatively easily distinguishable phenotypes
- They are determined by observation (or simple tests)
- They have little or no environmental influence

In most cases, they have a non-additive mode of action

However, Most Economic Traits are ***Quantitative***



This means...

- We have to use more “complicated” methods to understand, identify, estimate and select these traits
- Changing frequencies is generally slow (unlike the “B” allele in Black & White)
- Unfavorable genes are sometimes linked with economically important traits

Examples of Quantitative Traits...

Not so easy !!

??

Milk Yield in Dairy Cattle

Meat Quality in Beef Cattle

Fertility

Egg Quality/Size in Chickens

Litter Size in Pigs

Wool Quality in Sheep

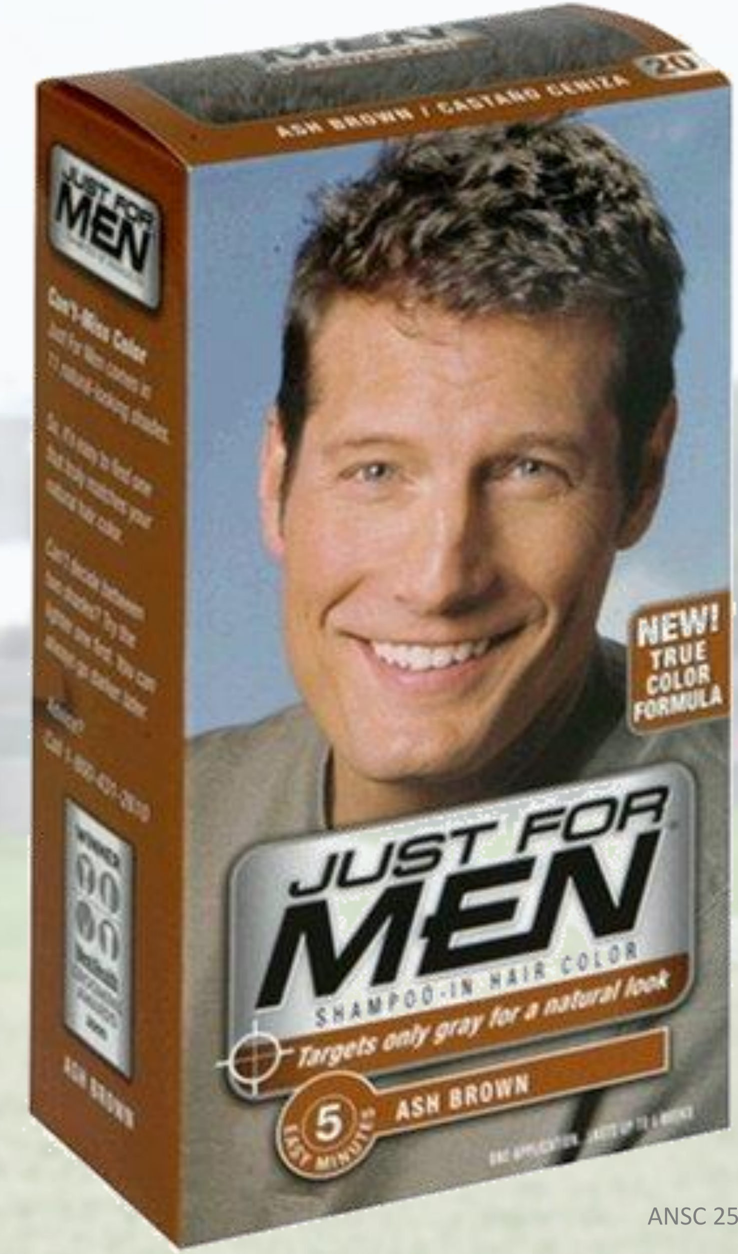
Speed in Race Horses

Survival !

Quantitative Inheritance

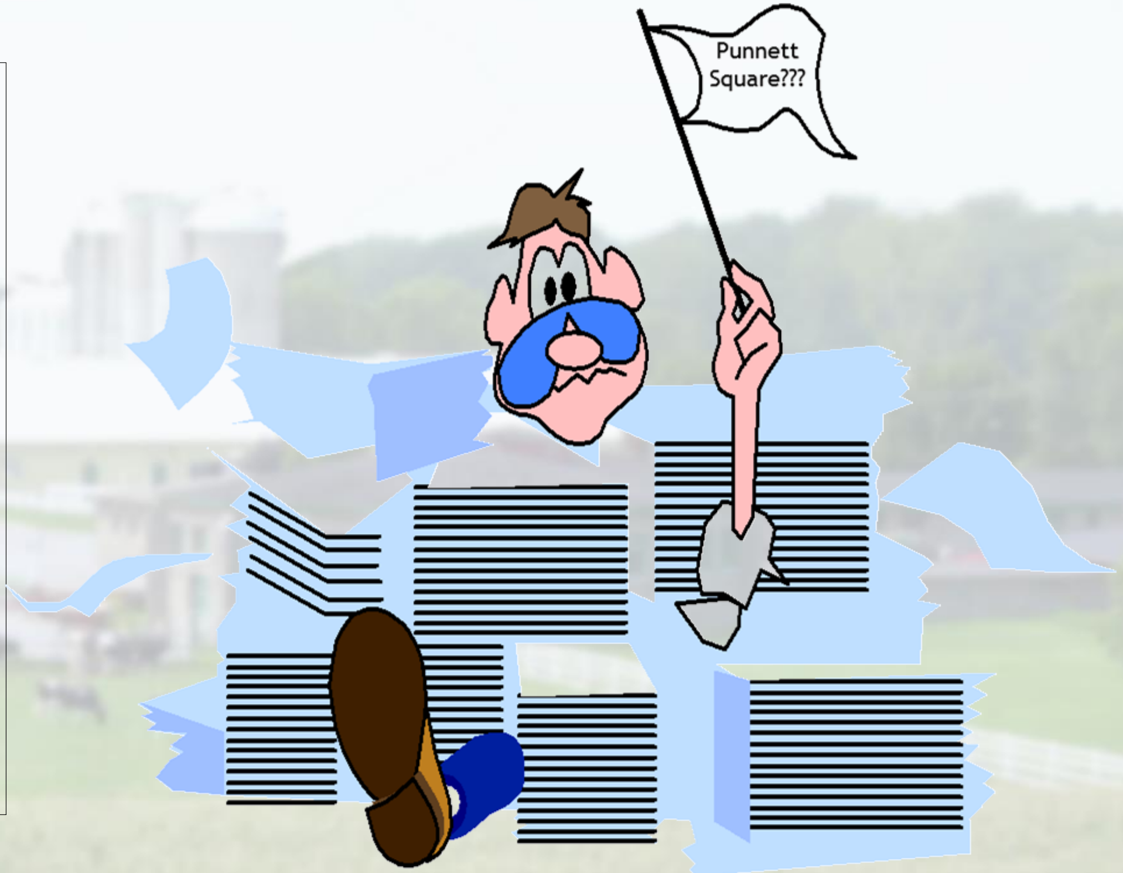
- Traits involve a large number of genes
- Each gene has a small but cumulative effect on the overall trait (i.e., there is an additive mode of action)
- There is continuous variation in the phenotypes
- There is a different method of measurement
- The environment has an influence on the expression of the trait

Hair Colour with an environmental modification…



No. of Gametes and Genetic Combinations

Pairs of genes	Genetically different gametes	Genetic Combinations (i.e., “size of the box”)
1	2	4
2	4	16
n	2^n	$(2^n)^2$
…		
20	approx 1 million	>1 trillion!



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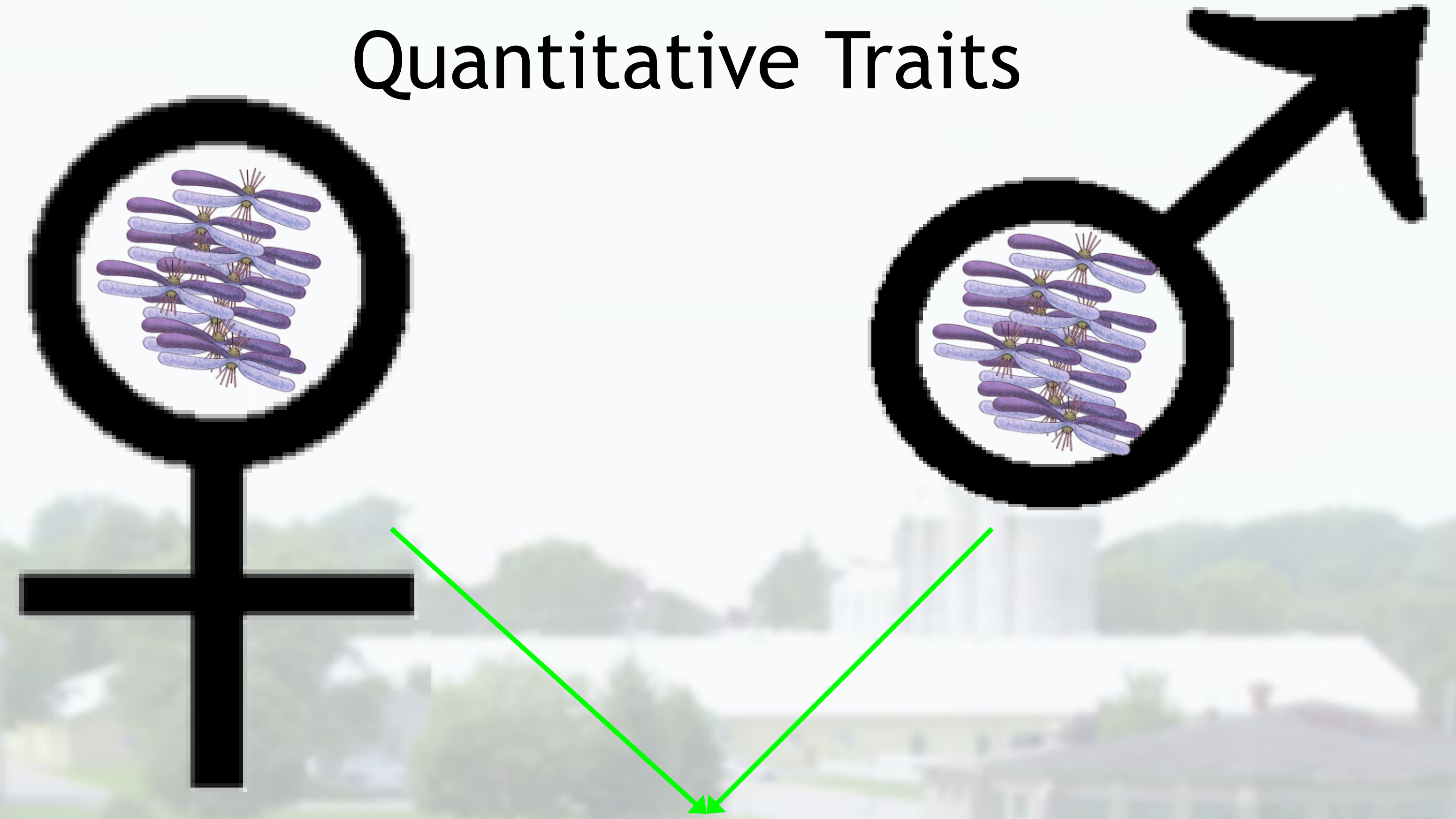
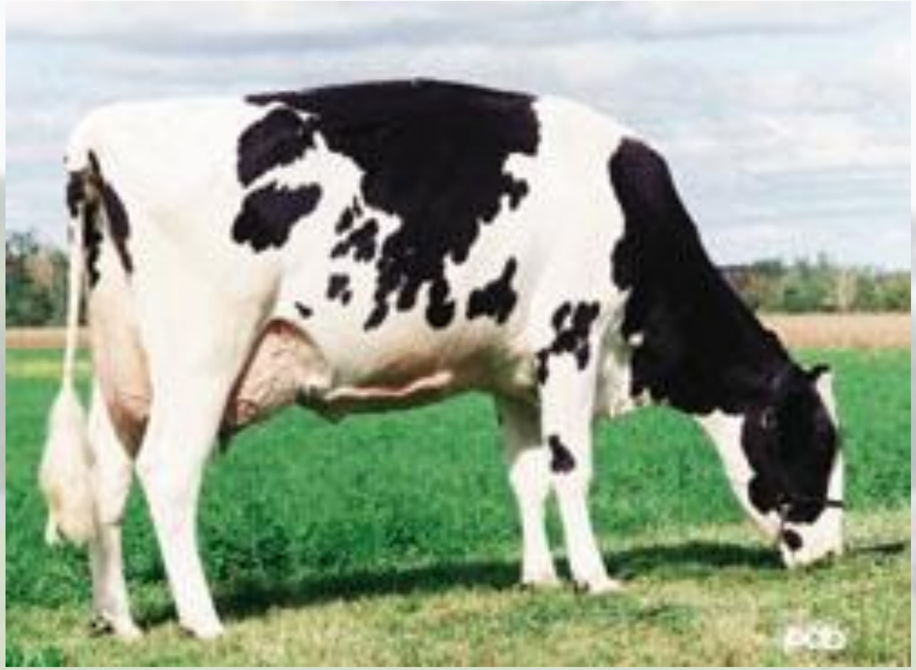
Quantitative Traits



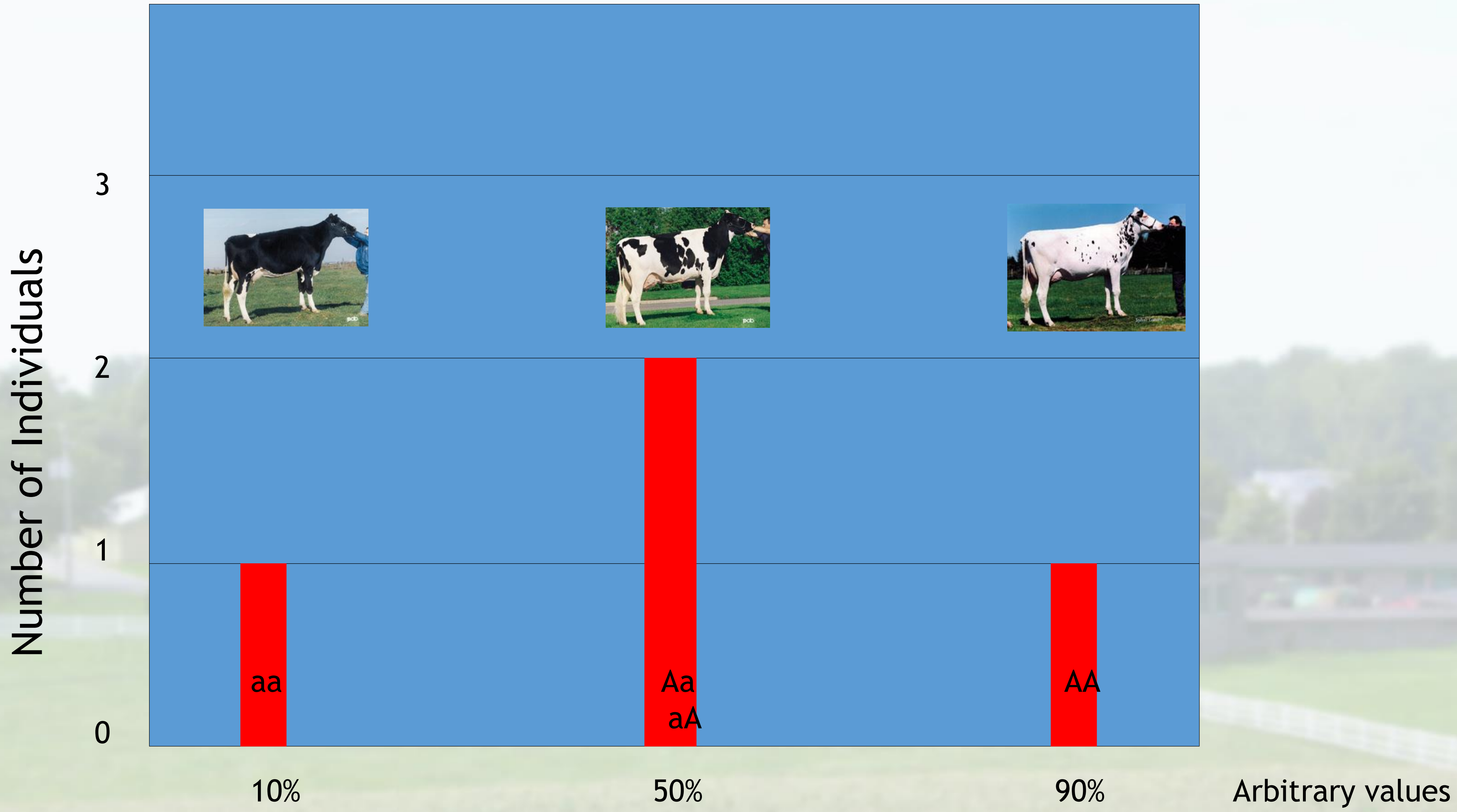
- Each partner contributes half of the genetic material to its progeny
- We don't know how many genes are involved, where they are, or what effect each one has
- Even if we did, there are simply too many of them involved!!

Additive Genes – An Example

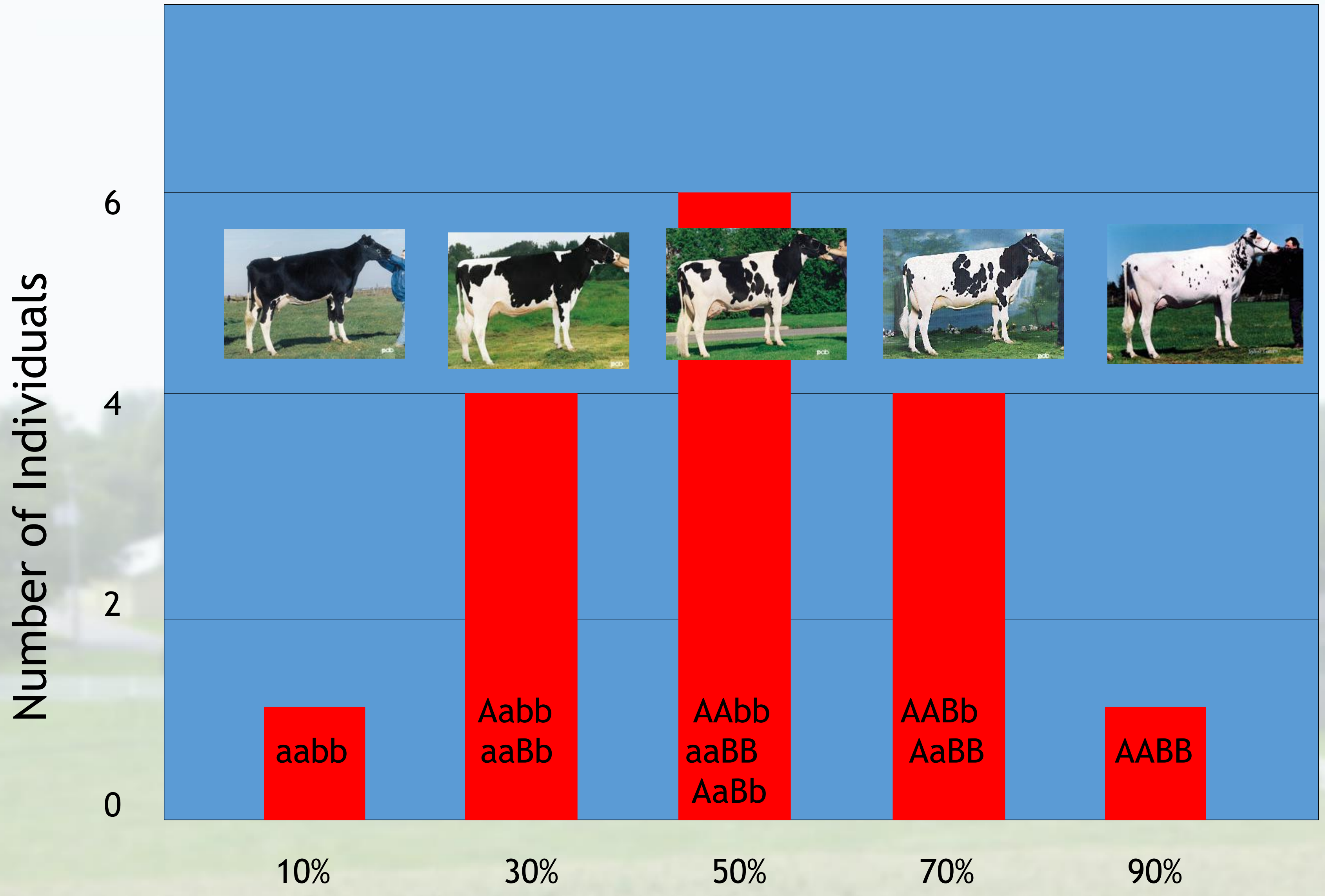
An Example using "Spotting" or "Black-to-White *ratio*" in Holsteins



Each DOMINANT allele adds *more* white



Percentage White
(**<u>if</u>** “spotting” were controlled by one gene)



Percentage White
(**if** "spotting" were controlled by **two** genes)

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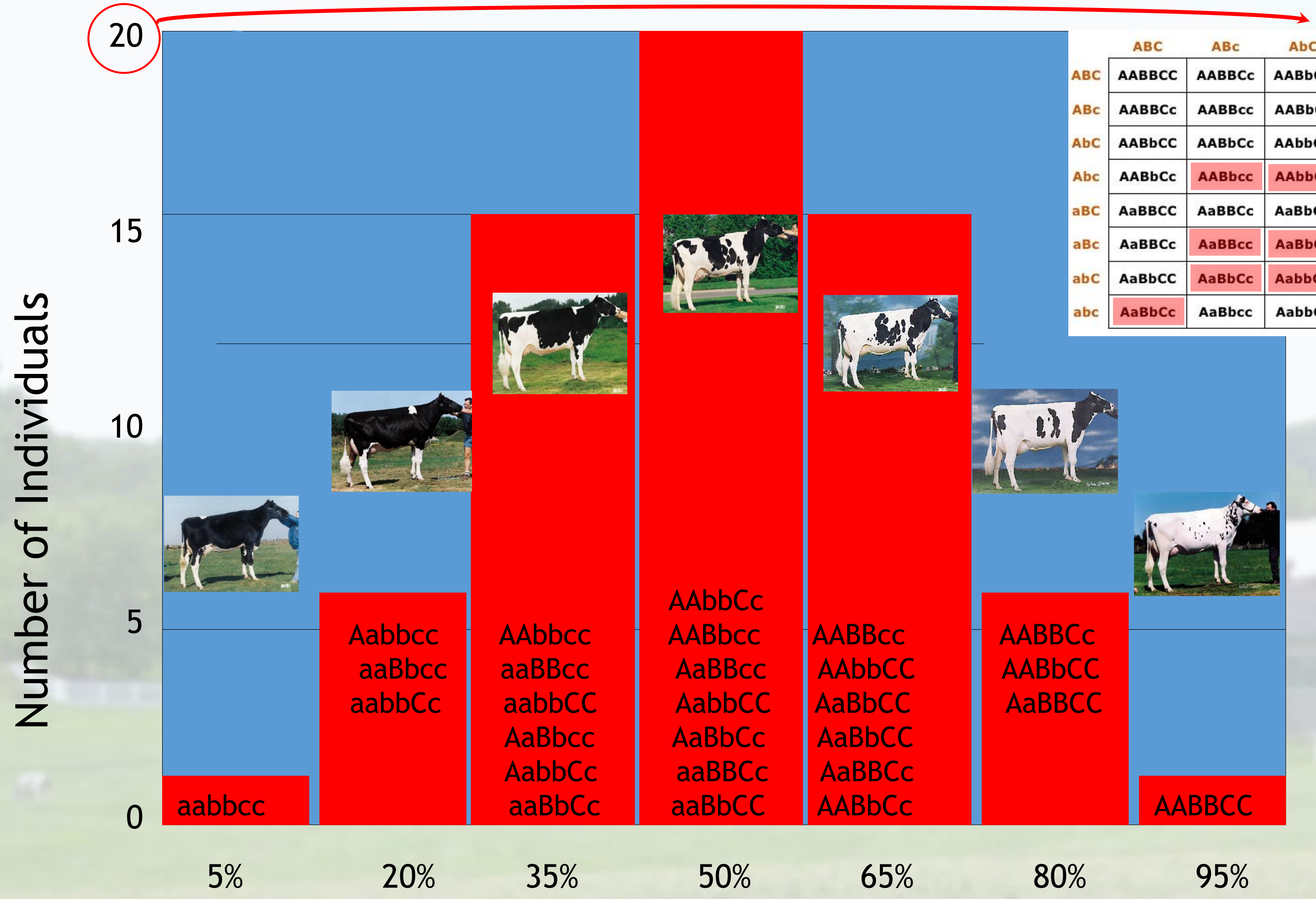
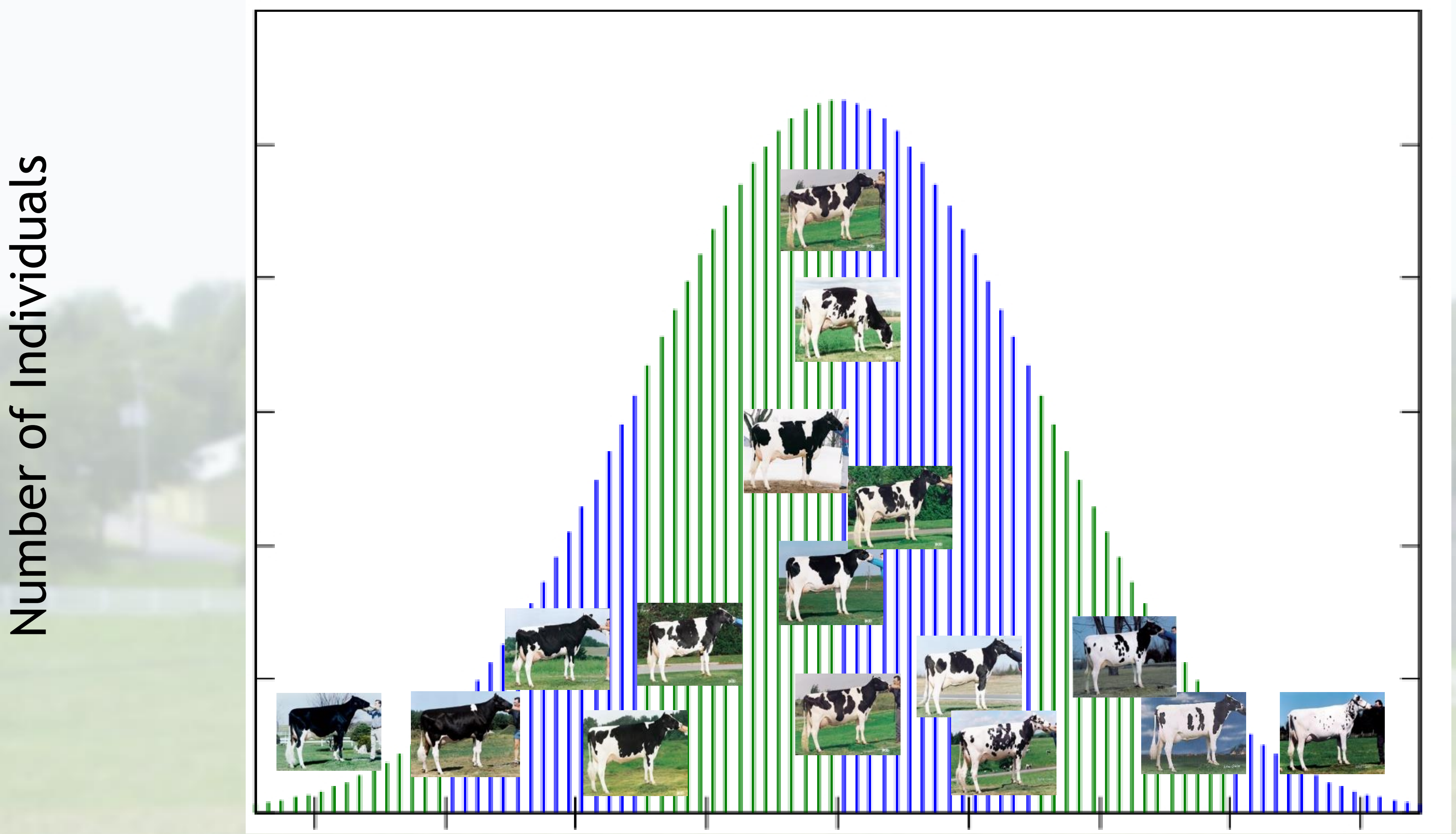


	ABC	ABc	AbC	Abc	aBC	aBc	abC	abc
ABC	AABBCC	AABBCc	AABbCC	AABbCc	AaBBCC	AaBBCc	AaBbCC	AaBbCc
ABc	AABBCc	AABBcc	AABbCc	AABbcc	AaBBCc	AaBBcc	AaBbCc	AaBbcc
AbC	AABbCC	AABbCc	AAbbCC	AAbbCc	AaBbCC	AaBbCc	AabbCC	AabbCc
Abc	AABbCc	AABbcc	AAbbCc	AAbbcc	AaBbCc	AaBbcc	AabbCc	Aabbcc
aBC	AaBBCC	AaBBCc	AaBbCC	AaBbCc	aaBBCC	aaBBCc	aaBbCC	aaBbCc
aBc	AaBBCc	AaBBcc	AaBbCc	AaBbcc	aaBBCc	aaBBcc	aaBbCc	aaBbcc
abC	AaBbCC	AaBbCc	AabbCC	AabbCc	aaBbCC	aaBbCc	aabbCC	aabbCc
abc	AaBbCc	AaBbcc	AabbCc	Aabbcc	aaBbCc	aaBbcc	aabbCc	aabbcc

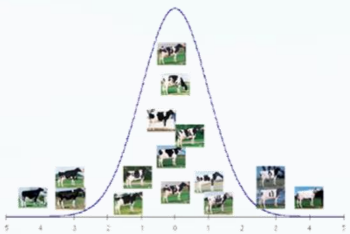
Percentage White
(**if** "spotting" were controlled by **three** genes)



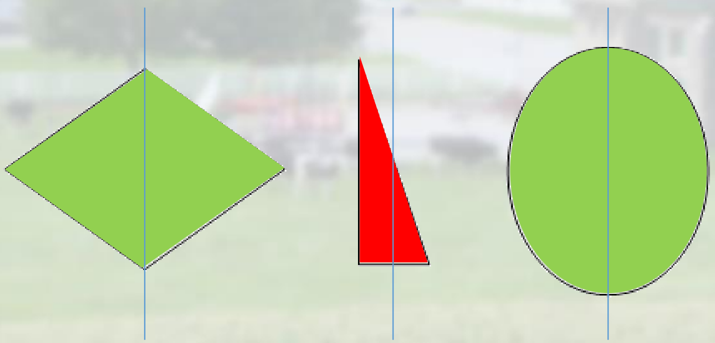
Percentage White

(**if** “spotting” were controlled by “hundreds” of genes)

The Normal Distribution

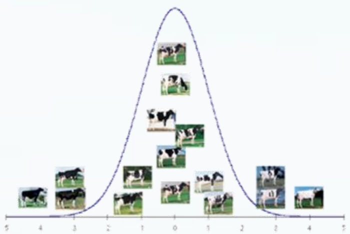


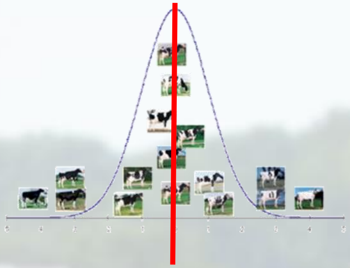
- A statistical method of describing how the members of a certain population behave
- It tells us how many individuals we expect to find in each category
- It allows us to make assumptions about the population without observing all the individuals in that population
- It is symmetric



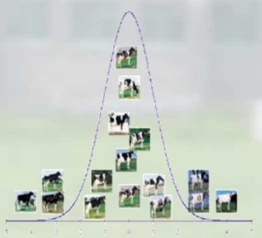
- It has two parameters that describes it completely...

Normal Distribution Parameters





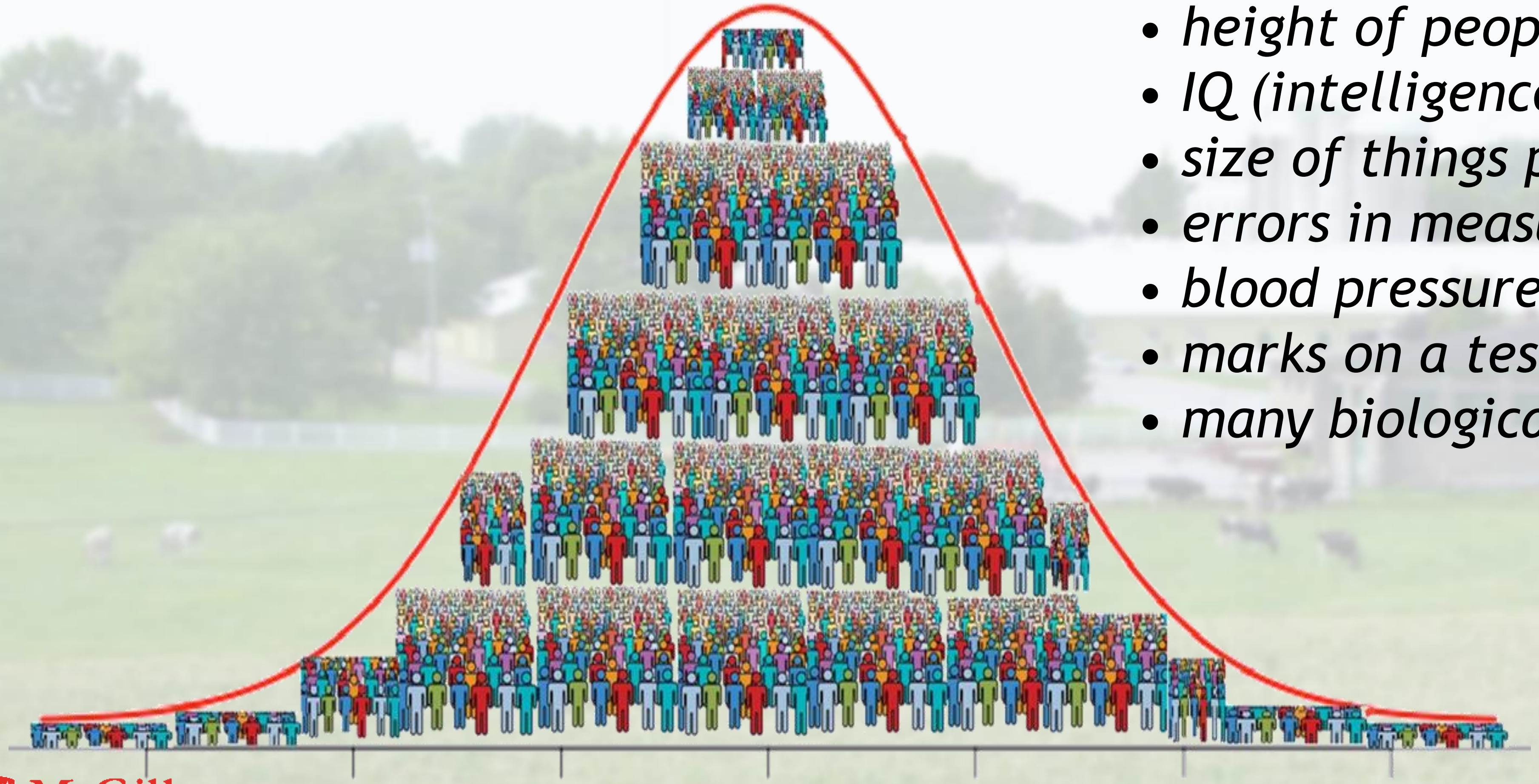
1. MEAN (or AVERAGE) = centre of the distribution



2. VARIANCE = “spread” of the distribution

2a. The STANDARD DEVIATION = $\sqrt{\text{variance}}$

Observations that follow a Bell Curve / Normal Distribution…



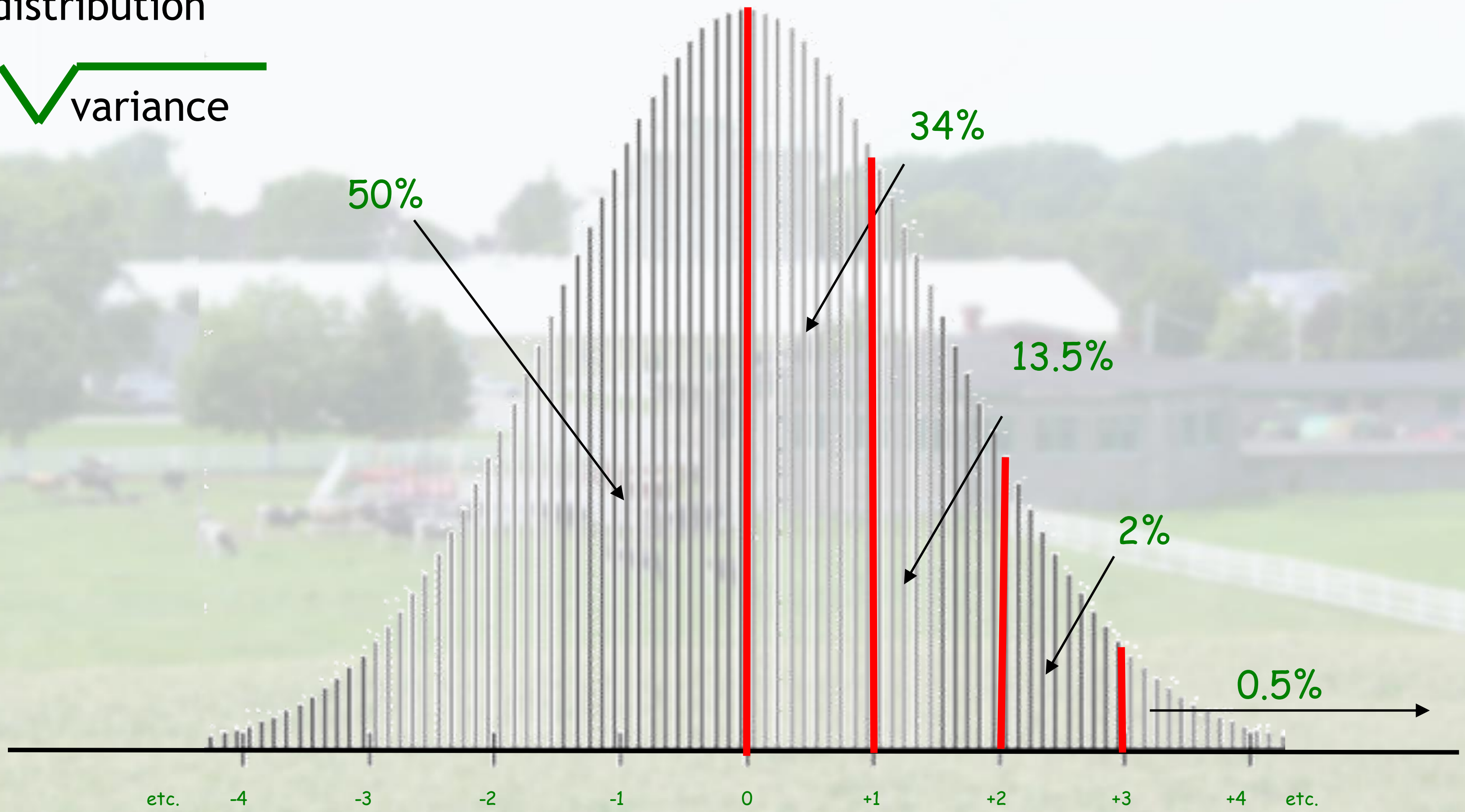
- *height of people*
- *IQ (intelligence quotient)*
- *size of things produced by machines*
- *errors in measurements*
- *blood pressure*
- *marks on a test…*
- *many biological traits*

How to make use of the Normal Distribution…

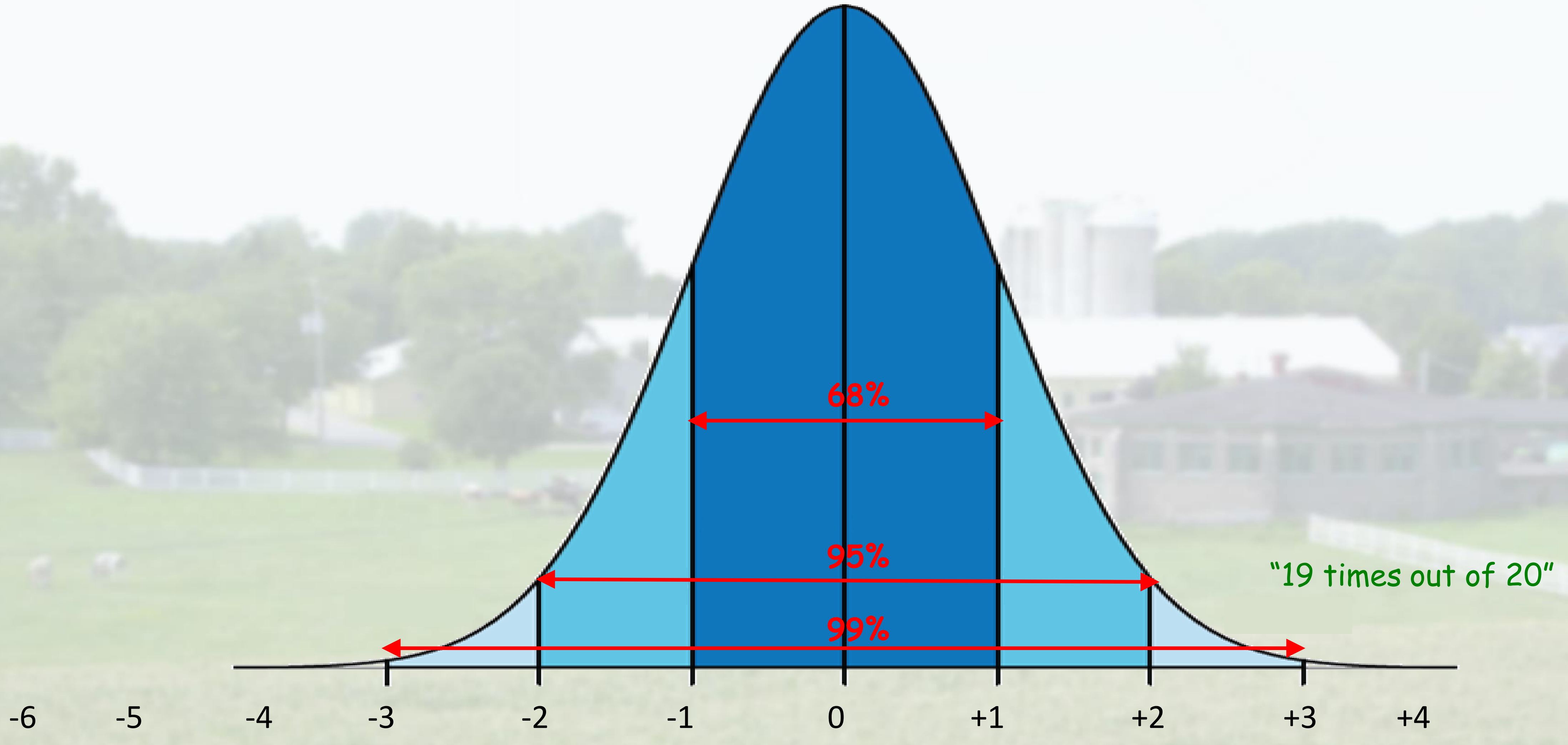
1. MEAN (or AVERAGE) = centre of the distribution

2. VARIANCE = "spread" of the distribution

2a. The STANDARD DEVIATION = $\sqrt{\text{variance}}$



How to make use of the Normal Distribution...



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Which Herd would you prefer?

1. Herd 1 = Yes
2. Herd 2 = No

	kg of milk	
Cow Numbers	Herd 1	Herd 2
1 & 7	8000kg	7200kg
2 & 8	9500kg	8300kg
3 & 9	9200kg	10500kg
4 & 10	8800kg	9000kg
5 & 11	8500kg	10200kg
6 & 12	9400kg	8200kg
Average	8,900kg	8,900kg
Variance	280,000kg²	1,333,333kg²
Std. Deviation	529kg	1154kg

	kg of milk	
Cow Numbers	Herd 1	Herd 2
1 & 7	8000kg	7200kg
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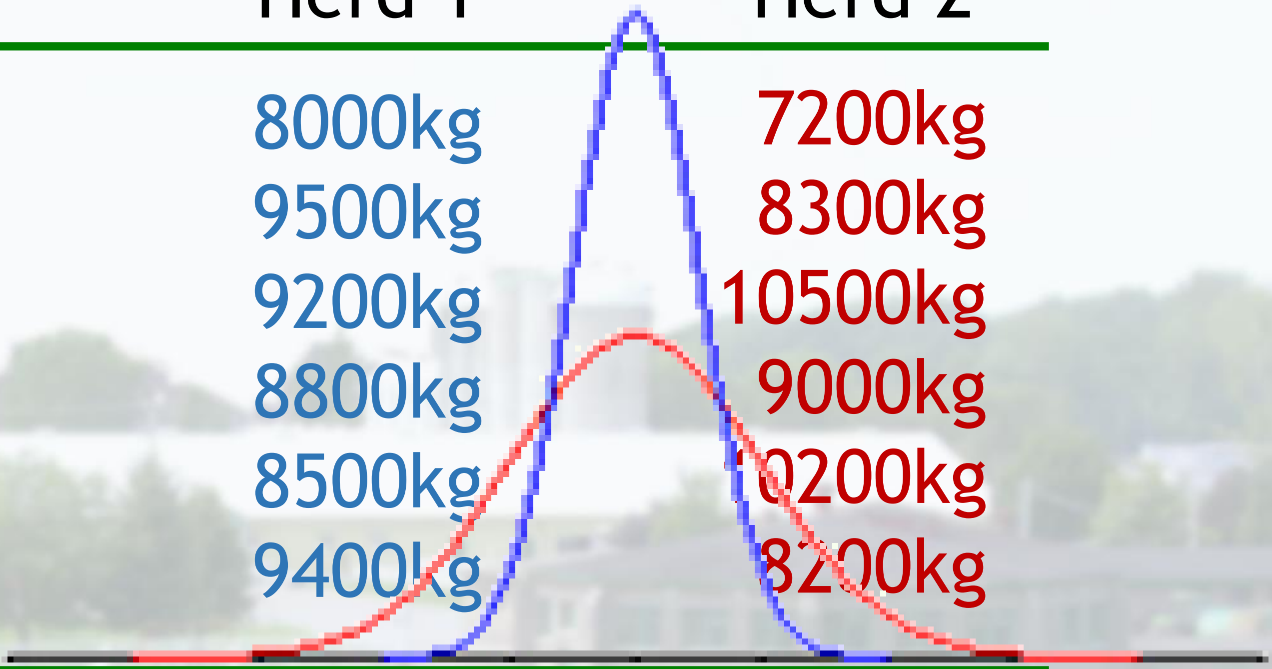

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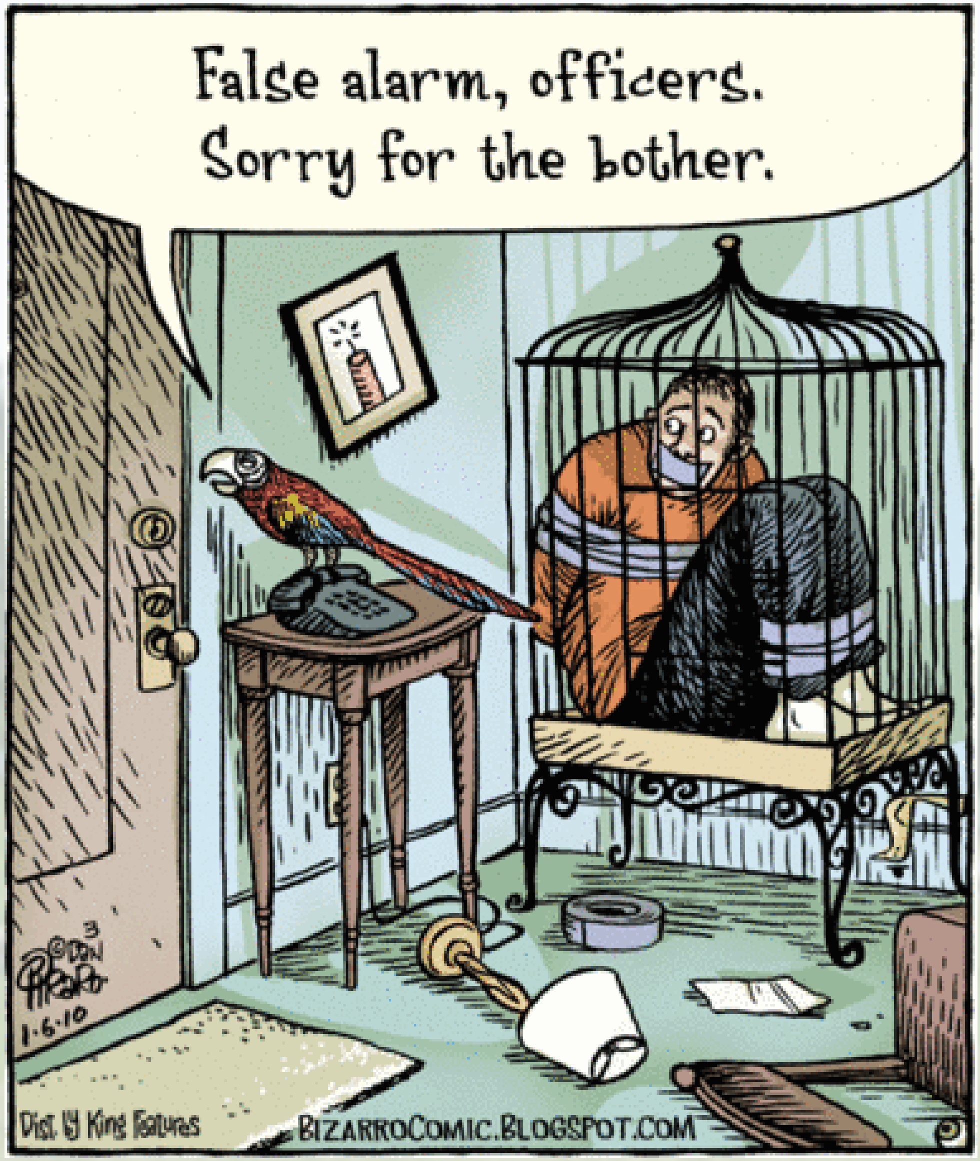
Another example…

Sow #		Herd 1	Herd 2
1		12	9
2		8	8
3	# of Piglets	10	10
4		6	10
5		7	8
6		11	9

	Herd 1	Herd 2
Mean	9 piglets	9 piglets
Variance	5.6 piglets^2	0.8 piglets^2
Std. Deviation	2.4 piglets	0.9 piglets



Question 5e…

(e) Consider the following mating between two parrots and speculate as to i) the genotypes of both parents and ii) the mode of inheritance for the trait(s) involved.

A **Red** male parrot is mated many times to a **Green** female parrot. Over a period of many years their offspring consist of the following numbers and phenotypes;

31 Red males; 48 Green females; 14 Green males; 15 Light Green females; 11 Light Red males; and 5 Light Green males.

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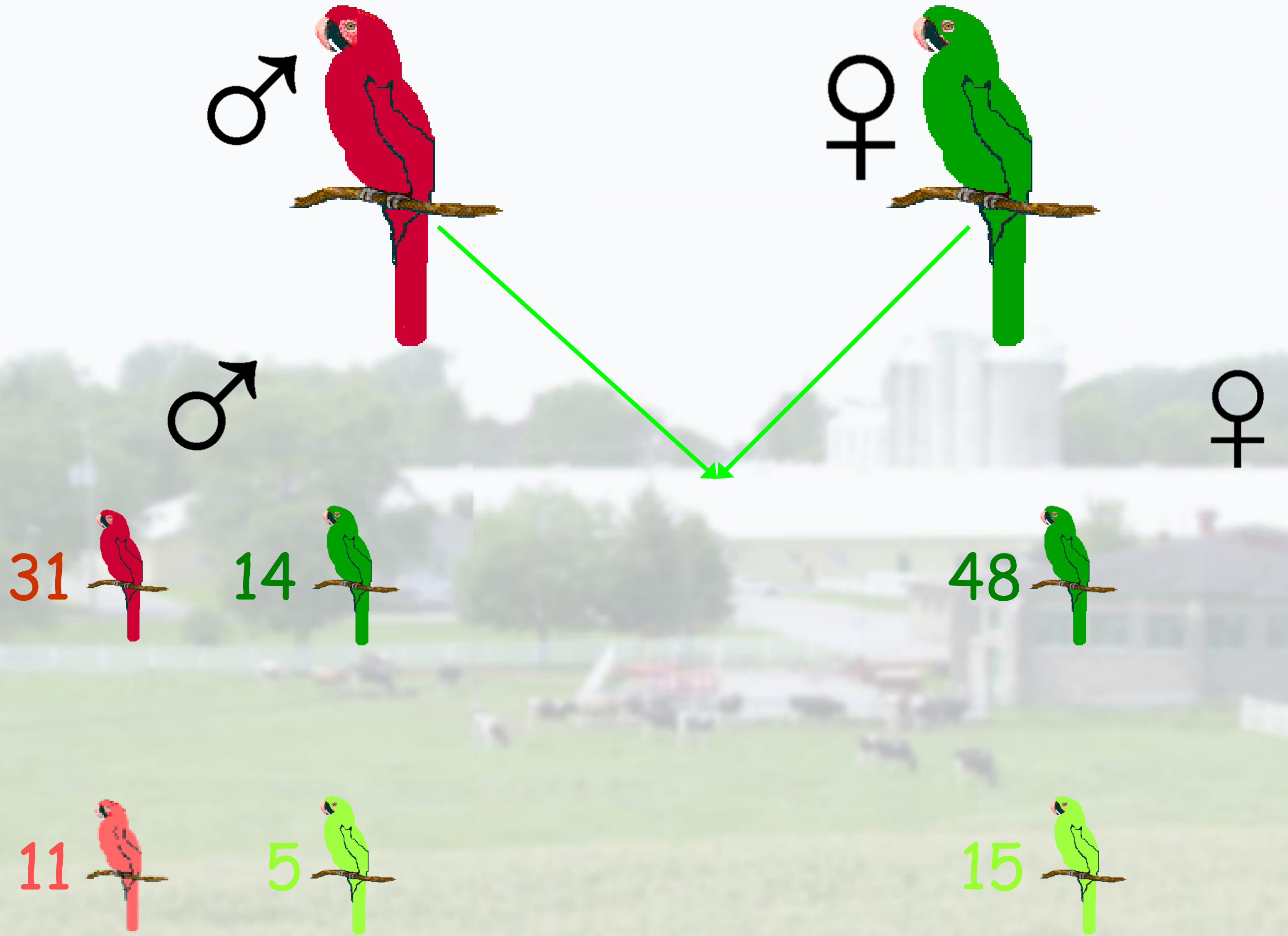
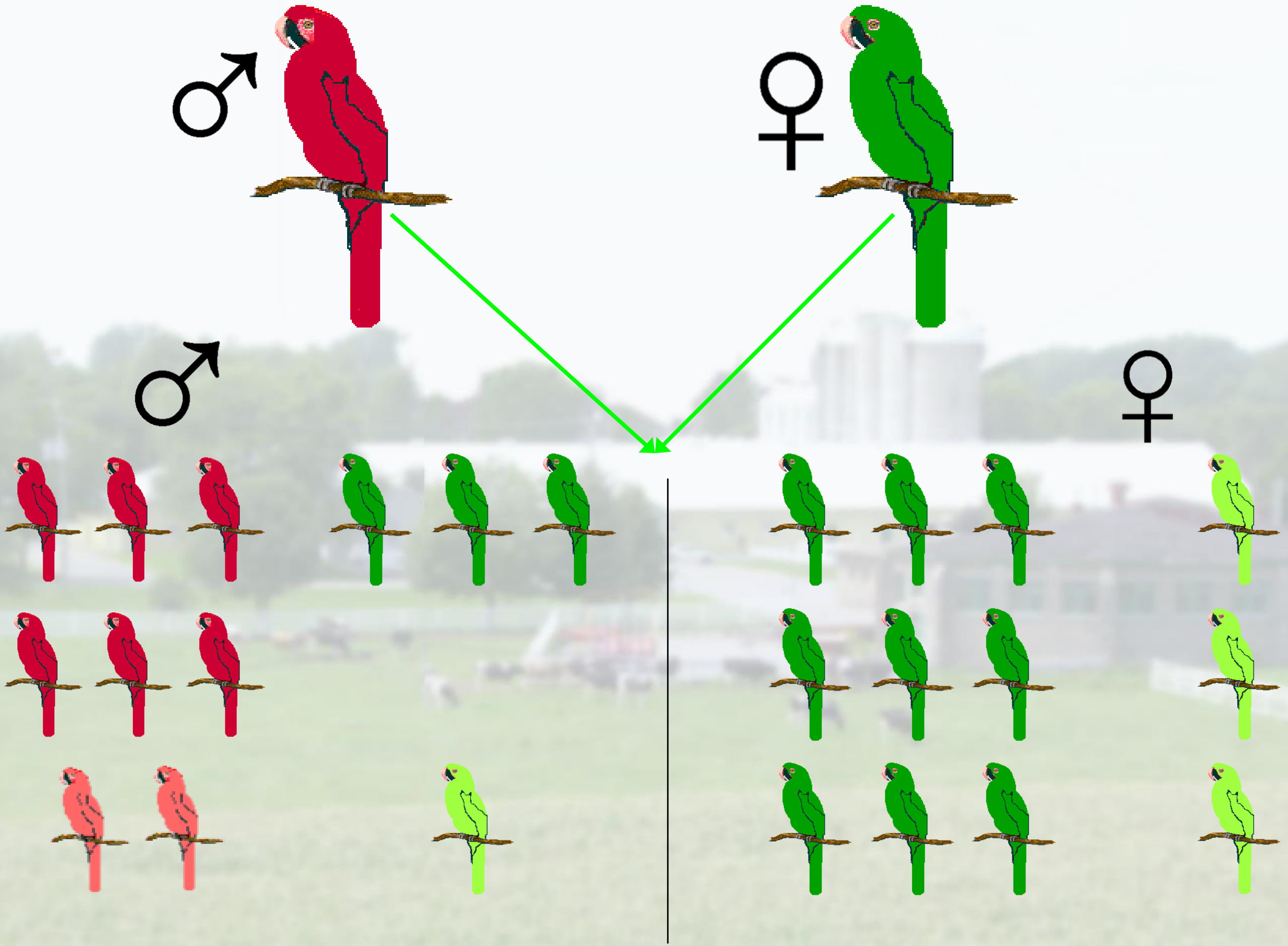
(e) Consider the following mating between two parrots and speculate as to i) the genotypes of both parents and ii) the mode of inheritance for the trait(s) involved.
A **Red** male parrot is mated many times to a **Green** female parrot. Over a period of many years their offspring consist of the following numbers and phenotypes;

31 Red males; 48 Green females; 14 Green males; 15 Light Green females; 11 Light Red males; and 5 Light Green males.

	Red	Light Red	Green	Light Green
Male	31	11	14	5
Female			48	15
Total				

	Red	Light Red	Green	Light Green
Male	6	2	3	1
Female			9	3
Total				


♂
♀
♂
♀
31
14
48
11
5
15

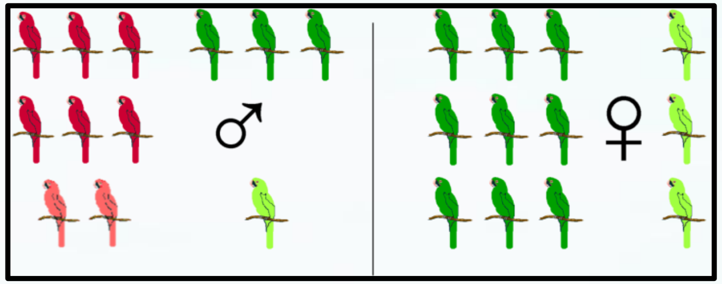


RR = 

rr = 

Rr = ♂  ♀ 

dd = or 



RrDd ♂ X RrDd ♀

		♂	♀
~~RR DD~~	~~1~~		
~~RR Dd~~	~~2~~		
~~RR dd~~	~~1~~		
Rr DD	2		
Rr Dd	4		
Rr dd	2		
rr DD	1		
rr Dd	2		
rr dd	1		

Red and Green are sex-influenced (the heterozygous condition is red in males and green in females).

Dilution is caused by a recessive epistasis from a second gene (the homozygous recessive condition causes *red* to become *light red* and *green* to become *light green*.

Finally, the RR (Red) condition is a lethal, meaning that no red females exist (since the heterozygous condition is *green*).