

Topic 3 and 10 Genetics and Meiosis

Topic 3.4 and 10.2 Inheritance

Essential idea: The inheritance of genes follows patterns
AND Genes may be linked or unlinked and are inherited
accordingly.

Understandings

- 3.4.U1 Mendel discovered the principles of inheritance with experiments in which large numbers of pea plants were crossed.
- 3.4.U2 Gametes are haploid so contain only one allele of each gene.
- 3.4.U3 The two alleles of each gene separate into different haploid daughter nuclei during meiosis.
- 3.4.U4 Fusion of gametes results in diploid zygotes with two alleles of each gene that may be the same allele or different alleles.
- 3.4.U5 Dominant alleles mask the effects of recessive alleles but co-dominant alleles have joint effects.

Understandings

- 3.4.U6 Many genetic diseases in humans are due to recessive alleles of autosomal genes, although some genetic diseases are due to dominant or co-dominant alleles.
- 3.4.U7 Some genetic diseases are sex-linked. The pattern of inheritance is different with sex-linked genes due to their location on sex chromosomes.
- 3.4.U8 Many genetic diseases have been identified in humans but most are very rare.
- 3.4.U9 Radiation and mutagenic chemicals increase the mutation rate and can cause genetic diseases and cancer.

Understandings

- 10.2.U1 Gene loci are said to be linked if on the same chromosome.
- 10.2.U2 Unlinked genes segregate independently as a result of meiosis.
- 10.2.U3 Variation can be discrete or continuous.
- 10.2.U4 The phenotypes of polygenic characteristics tend to show continuous variation.
- 10.2.U5 Chi-squared tests are used to determine whether the difference between an observed and expected frequency distribution is statistically significant.

Applications

- 3.4.A1 Inheritance of ABO blood groups. The expected notation for ABO blood group alleles: O = i, A=IA, B = IB.
- 3.4.A2 Red-green colour blindness and hemophilia as examples of sex-linked inheritance.
- 3.4.A3 Inheritance of cystic fibrosis and Huntington’s disease.
- 3.4.A4 Consequences of radiation after nuclear bombing of Hiroshima and accident at Chernobyl.
- 10.2.A1 Morgan’s discovery of non-Mendelian ratios in Drosophila.
- 10.2.A2 Completion and analysis of Punnett squares for dihybrid traits.
- 10.2.A3 Polygenic traits such as human height may also be influenced by environmental factors.

Skills


- 3.4.S1 Construction of Punnett grids for predicting the outcomes of monohybrid genetic crosses.
- 3.4.S2 Comparison of predicted and actual outcomes of genetic crosses using real data.
- 3.4.S3 Analysis of pedigree charts to deduce the pattern of inheritance of genetic diseases.
- 10.2.S1 Calculation of the predicted genotypic and phenotypic ratio of offspring of dihybrid crosses involving unlinked autosomal genes.
- 10.2.S2 Identification of recombinants in crosses involving two linked genes.
- 10.2.S3 Use of a chi-squared test on data from dihybrid crosses.

I. Mendel and the principles of inheritance

A. Mendel discovered the principles of inheritance with experiments in which large numbers of pea plants were crossed-

Johann Gregor Mendel (1822-1884)

- A. Because of his work with pea plants Mendel is considered the father of modern genetics.
- B. He planted 1000s of seeds per trial and carried out many trials to be sure of his results.
- C. His published work (1865) is now considered important, but at the time was ignored for 30 years.



unknown

II. Nature of Science: Making quantitative measurements with replicates to ensure reliability

A. Mendel’s genetic crosses with pea plants generated numerical data.

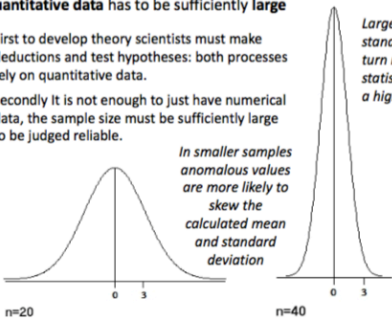
To use **statistical tests** correctly and reach **valid conclusions** samples of **quantitative data** has to be sufficiently large

First to develop theory scientists must make deductions and test hypotheses: both processes rely on quantitative data.

Secondly it is not enough to just have numerical data, the sample size must be sufficiently large to be judged reliable.

In smaller samples anomalous values are more likely to skew the calculated mean and standard deviation

Larger samples give smaller standard deviation, this in turn makes it easier to find a statistically significant result at a higher confidence level*



The sample size required varies:

- The larger the natural variation the larger the sample
- Depends on the type of statistical test used

*The standard deviation of the population is constant: (small) samples have a higher standard deviation than the population the sample comes from.

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<http://www.conceptstew.co.uk/796/ES/rsamplesize.html>

III. Basic Mendelian Genetics

Definitions This image shows a pair of homologous chromosomes. Name and annotate the labeled features.

Genotype
The combination of alleles of a gene carried by an organism

Phenotype
The expression of alleles of a gene carried by an organism

Centromere
Joins chromatids in cell division

Alleles
Different versions of a gene
Dominant alleles = capital letter
Recessive alleles = lower-case letter

Carrier
Heterozygous carrier of a recessive disease-causing allele

Homozygous dominant
Having two copies of the same dominant allele

Homozygous recessive
Having two copies of the same recessive allele. Recessive alleles are only expressed when homozygous.

Codominant
Pairs of alleles which are both expressed when present.

Heterozygous
Having two different alleles. The dominant allele is expressed.

Gene loci
Specific positions of genes on a chromosome

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IV. Dominant, Recessive and Co-dominant alleles

A. Inheritance of ABO blood groups.

- The ABO blood type classification system uses the presence or absence of certain antigens on red blood cells to categorize blood into four types.
- Distinct molecules called agglutinogens (a type of antigen) are attached to the surface of red blood cells.
- There are two different types of agglutinogens, type "A" and type "B".

	Group A	Group B	Group AB	Group O
Red blood cell type				
Antibodies in Plasma			None	
Antigens in Red Blood Cell				None

InvictaHOG

IV. Dominant, Recessive and Co-dominant alleles

- Antibodies (immunoglobulins) are specific to antigens and are used by the immune system to recognize 'foreign' antigens. If you are given the wrong blood type your body might react fatally as the antibodies cause the blood to clot!
- Blood type O is known as the universal donor, as it has no antigens against which the recipient immune system can react. Type AB is the universal recipient, as the blood has no antibodies which will react to AB antigens.

nobelprize.org

IV. Dominant, Recessive and Co-dominant alleles

B. The ABO blood type is controlled by a single gene, the ABO gene. This gene has three different alleles:

- i O allele (no antigen is produced)
- I^A A allele (type "A" antigen is produced)
- I^B B allele (type "B" antigen is produced)

I^A — Allele variant
i — Gene (lower case for "recessive" alleles)

Genotype	Phenotype	Antigen Produced
ii	O	none
I ^A I ^A or I ^A i	A	Type A antigen
I ^B I ^B or I ^B i	B	Type B antigen
I ^A I ^B	AB	Both A & B antigen

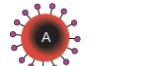
IV. Dominant, Recessive and Co-dominant alleles

C. Dominant alleles mask the effects of recessive alleles but co-dominant alleles have joint effects-

1. Dominant alleles have the same effect on the phenotype whether it is present in the homozygous or heterozygous state
2. Recessive alleles only have an effect on the phenotype when present in the homozygous state
3. Codominant alleles are pairs of different alleles that both affect the phenotype when present in a heterozygote

Type "A" allele is present and is dominant to type "O" allele


$I^A i$



Type "O" allele is present but is recessive to type "A" allele

Type "A" allele is present and is codominant to type "B" allele

$I^A I^B$

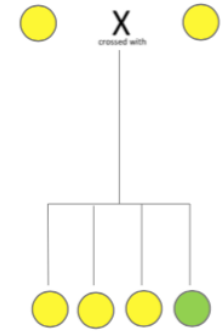


Type "B" allele is present and is codominant to type "A" allele

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V. Punnett Grids AND Segregation of Alleles

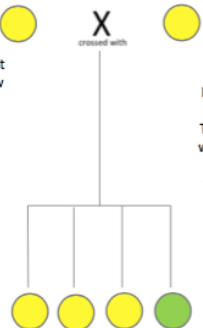
Explain this Mendel crossed some yellow peas with some yellow peas. Most offspring were yellow but some were green!



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V. Punnett Grids AND Segregation of Alleles

Segregation "alleles of each gene separate into different gametes when the individual produces gametes"



The yellow parent peas must be **heterozygous**. The yellow phenotype is expressed.

Through meiosis and fertilisation, some offspring peas are **homozygous recessive** – they express a green colour.

Mendel did not know about DNA, chromosomes or meiosis.

Through his experiments he did work out that 'heritable factors' (genes) were passed on and that these could have different versions (alleles).

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V. Punnett Grids AND Segregation of Alleles

Segregation "alleles of each gene separate into different gametes when the individual produces gametes"

F₀

Genotype: ♀ Yy X ♂ Yy

Gametes: Y or y Y or y

Punnett Grid:

gametes	♂		
♀			

F₁

Genotypes:

Phenotypes:

Phenotype ratio:

Key to alleles:
 Y = yellow
 y = green

Alleles segregate during meiosis (anaphase I) and end up in different haploid gametes.

Simplified notation of using upper case for dominant and lower case for recessive is acceptable in the case of two alleles without co-dominance.

Mendel from: http://history.nih.gov/exhibits/herberg/popul_30u/02_mendel.htm



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V. Punnett Grids AND Segregation of Alleles

Monohybrid Cross

Crossing a single trait.

F₀

♀  X  ♂

Genotype: Yy X Yy

Gametes: Y or y Y or y

Key to alleles:
 Y = yellow
 y = green

Alleles segregate during meiosis (anaphase I) and end up in different haploid gametes.

Fertilisation results in diploid zygotes.

A Punnett grid can be used to deduce the potential outcomes of the cross and to calculate the expected ratio of phenotypes in the next generation (F₁).

gametes		♂	
		Y	y
♀	Y	YY	Yy
	y	Yy	yy

F₁

Genotypes:

Phenotypes:

Phenotype ratio:

Mendel from: http://history.mh.gov/wh/bib/henrberg/papuz_3m102_mendel.htm



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gametes		♂	
		Y	y
♀	Y	YY	Yy
	y	Yy	yy

F₁

Genotypes:

Phenotypes:

Phenotype ratio:

Mendel from: http://history.mh.gov/wh/bib/henrberg/papuz_3m102_mendel.htm



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V. Punnett Grids AND Segregation of Alleles

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Crossing a single trait.

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Genotype: Yy X Yy

Gametes: Y or y Y or y

Key to alleles:
 Y = yellow
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Alleles segregate during meiosis (anaphase I) and end up in different haploid gametes.





Fertilisation results in diploid zygotes.

A Punnett grid can be used to deduce the potential outcomes of the cross and to calculate the expected ratio of phenotypes in the next generation (F₁).

gametes		♂	
		Y	y
♀	Y	YY	Yy
	y	Yy	yy

F₁

Genotypes: YY Yy Yy yy

Phenotypes:    

Phenotype ratio: **3 : 1**

Mendel from: http://history.mh.gov/wh/bib/henrberg/papuz_3m102_mendel.htm



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V. Punnett Grids AND Segregation of Alleles

Monohybrid Cross

What is the expected ratio of phenotypes in this monohybrid cross?

F₀

Phenotype: ♀  X  ♂

Genotype: yy X yy

Key to alleles:
 Y = yellow
 y = green

Homozygous recessive Homozygous recessive

Fertilisation results in diploid zygotes.

A Punnett grid can be used to deduce the potential outcomes of the cross and to calculate the expected ratio of phenotypes in the next generation (F₁).

gametes		♂	
		y	y
♀	y	yy	yy
	y	yy	yy

F₁

Genotypes:

Phenotypes:

Phenotype ratio:

Mendel from: http://history.mh.gov/wh/bib/henrberg/papuz_3m102_mendel.htm

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V. Punnett Grids AND Segregation of Alleles

Monoybrid Cross

What is the expected ratio of phenotypes in this monoybrid cross?

F₀ Phenotype: ♀ X ♂
 Genotype: **YY** crossed with **Yy**
Homozygous dominant *Heterozygous*

Key to alleles:
Y = yellow
y = green

Punnett Grid:

		gametes	
		Y ♂	y
Y ♀	Y	YY	Yy
	y	Yy	yy

F₁
 Genotypes:
 Phenotypes:
 Phenotype ratio:
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VI. Chi-squared Tests Are Used to Determine Whether the Difference Between an Observed and Expected Frequency Distribution is Statistically Significant

A. Used to test whether an observed frequency is significantly different to an expected frequency.

- Null Hypothesis (H₀) = there is no significant difference between the observed and expected results
- Alternate Hypothesis (H₁) = there is a significant difference between the observed and expected results

First calculate the value of χ^2

Collected data	Calculating χ^2			Total (χ^2) =
	Observed (O)	Expected (E)	$(O-E)^2/E$	
yellow				
green				
Total:				

And then compare it with the **critical value** at the desired level of certainty

D.F. (n-1)	p (certainty) (how sure do you want to be?)		
	0.1 (90%)	0.05 (95%)	0.01 (99%)
1	2.70554	3.84146	6.6349
2	4.60517	5.99146	9.21034
3	6.25139	7.81473	11.34487
4	7.77944	9.48773	13.2767
5	9.23636	11.0705	15.08627
6	10.64464	12.59159	16.81189
7	12.01704	14.06714	18.47531
8	13.36157	15.50731	20.09024
9	14.68366	16.91898	21.66599
10	15.98718	18.30704	23.20925

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VI. Chi-squared Tests Are Used to Determine Whether the Difference Between an Observed and Expected Frequency Distribution is Statistically Significant

Calculating χ^2

probability x sample size
 e.g. $0.75 \times 50 = 37.5$

actual number recorded expected number squaring (O-E) factors out any negatives

possible phenotypes	Collected data		Calculating χ^2		$(O-E)^2/E$
	Observed (O)	Expected (E)	(O-E)	$(O-E)^2$	
yellow					
green					
Total:	50	50			

add them up!

These must be the same (represent total sample size)

keep this value to compare to the critical values table

$\chi^2 =$ _____

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VI. Chi-squared Tests Are Used to Determine Whether the Difference Between an Observed and Expected Frequency Distribution is Statistically Significant

Do we accept or reject H₀?

$\chi^2 =$ _____

Degrees of Freedom = no. possible outcomes - 1

2 possibilities (yellow or green)
 \therefore d.f. = 1

In Biology, we normally aim for $p=0.05$ (95% confident)

Compare χ^2 with the critical value:

D.F. (n-1)	p (certainty) (how sure do you want to be?)		
	0.1 (90%)	0.05 (95%)	0.01 (99%)
1	2.70554	3.84146	6.6349
2	4.60517	5.99146	9.21034
3	6.25139	7.81473	11.34487
4	7.77944	9.48773	13.2767
5	9.23636	11.0705	15.08627

If $\chi^2 > C.V.$ we **reject** the null hypothesis (we are 95% sure that the observed results are different from the expected results)

If $\chi^2 < C.V.$ we **accept** the null hypothesis (we are 95% sure that the observed results are the same as the expected results)

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VI. Chi-squared Tests Are Used to Determine Whether the Difference Between an Observed and Expected Frequency Distribution is Statistically Significant

Worked Example: Mendel's Peas

In a cross between two heterozygous peas, we expect a 3:1 yellow:green ratio in the offspring, as shown in the punnet grid.

We can test this experimentally and use the results collected to determine whether the results collected differ significantly from the expected ratio.

Null hypothesis (H₀):
 "there is no significant difference between observed and expected results"

Sample size = 50 (50 offspring will be collected - modeled as coin flips)

A ratio of 3:1 can also be expressed in terms of probability:
 There is a **0.75 chance** of the offspring being **yellow**
 0.25 chance of the offspring being **green**.

F₀ phenotype: yellow yellow
 genotype: Yy Yy
 gametes: Y y Y y
 Punnet grid:
 YY Yy Yy yy
F₁ genotypes: 1 YY : 2 Yy : 1 yy
 phenotypes: yellow yellow green
 Ratio 3:1

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VI. Chi-squared Tests Are Used to Determine Whether the Difference Between an Observed and Expected Frequency Distribution is Statistically Significant

Results:

Total Observed: 35 15

Calculating χ^2

	Collected data		Calculating χ^2		$\frac{(O-E)^2}{E}$
	Observed (O)	Expected (E)	(O - E)	$(O - E)^2$	
yellow	35	37.5*			
green	15	12.5 [#]			
Total:	50	50			Total (χ^2) =

* Expected result for Yellow = 0.75 x 50 = 37.5
[#] Expected result for green = 0.25 x 50 = 12.5

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VI. Chi-squared Tests Are Used to Determine Whether the Difference Between an Observed and Expected Frequency Distribution is Statistically Significant

Results:

Total Observed: 35 15

Calculating χ^2

	Collected data		Calculating χ^2		$\frac{(O-E)^2}{E}$
	Observed (O)	Expected (E)	(O - E)	$(O - E)^2$	
yellow	35	37.5*	-2.5	6.25	0.1667
green	15	12.5 [#]	2.5	6.25	0.5
Total:	50	50			Total (χ^2) = 0.6667

* Expect
[#] Expect

squaring (O-E) factors out negative values

$\chi^2 = 0.6667$

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VI. Chi-squared Tests Are Used to Determine Whether the Difference Between an Observed and Expected Frequency Distribution is Statistically Significant

Do we accept or reject H₀?

$\chi^2 = 0.6667$

2 possibilities (yellow or green)
 \therefore d.f. = 1

D.F. (n-1)	p (certainty) (how sure do you want to be?)		
	0.1 (90%)	0.05 (95%)	0.01 (99%)
1	2.70554	3.84146	6.6349
2	4.60517	5.99146	9.21034
3	6.25139	7.81473	11.34487
4	7.77944	9.48773	13.2767
5	9.23636	11.0705	15.08627

Compare χ^2 with the critical value:
 0.6667 < 3.84146

we accept the null hypothesis
 (we are 95% sure that the observed results are the same as the expected results)

The data collected in this example **DO** fit the ration 3:1 yellow:green.

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VII. Test Cross

Test Cross *Used to determine the genotype of an unknown individual. The unknown is crossed with a known homozygous recessive.*

F₀ Phenotype: ♀ X ♂
 Genotype: **R ?** crossed with **r r**
unknown *Homozygous recessive*

Key to alleles:
R = Red flower
r = white

Possible outcomes:

F₁ Phenotypes:
Unknown parent = RR *Unknown parent = Rr*

gametes	♂	
♀		

gametes	♂	
♀		

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VII. Test Cross

Test Cross *Used to determine the genotype of an unknown individual. The unknown is crossed with a known homozygous recessive.*

F₀ Phenotype: ♀ X ♂
 Genotype: **R ?** crossed with **r r**
unknown *Homozygous recessive*

Key to alleles:
R = Red flower
r = white

Possible outcomes:

F₁ Phenotypes: **All red** **Some white, some red**
Unknown parent = RR *Unknown parent = Rr*

gametes	♂	
♀		

gametes	♂	
♀		

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VIII. Punnett Squares for Dihybrid Traits (10.2)

Review: 10.1.U7 Independent assortment of genes is due to the random orientation of pairs of homologous chromosomes in meiosis I.

Mendel's Law of Independent Assortment

"The presence of an allele of one of the genes in a gamete has no influence over which allele of another gene is present."

This only holds true for **unlinked genes** (genes on different chromosomes).

A and B are different genes on different chromosomes.
 A is dominant over a.
 B is dominant over b.

meiosis

All four genotypes are possible therefore 10.2.U2 Unlinked genes segregate independently as a result of meiosis.

genotype: AB genotype: Ab genotype: aB genotype: ab

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VIII. Punnett Squares for Dihybrid Traits (10.2)

Dihybrid Crosses

Consider two traits, each carried on separate chromosomes (the genes are unlinked).

In this example of *Lathyrus odoratus* (sweet pea), we consider two traits: **pea colour** and **pea surface**.

Key to alleles:
Y = yellow
y = green
S = smooth
s = rough

What is the predicted phenotype ratio for a cross between two pea plants which are heterozygous at both loci?

F₀ Phenotype: *Heterozygous at both loci* X *Heterozygous at both loci*
 Genotype: *Heterozygous at both loci* X *Heterozygous at both loci*

Punnet Grid:

gametes				

F₁

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VIII. Punnett Squares for Dihybrid Traits (10.2)

Dihybrid Crosses

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Key to alleles:
 Y = yellow
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 S = smooth
 s = rough

F₀ Phenotype: Smooth, yellow  X Smooth, yellow 
 Heterozygous at both loci Heterozygous at both loci

Genotype: SsYy SsYy

Punnett Grid:

gametes				

F₁

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VIII. Punnett Squares for Dihybrid Traits (10.2)

Dihybrid Crosses

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 Y = yellow
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F₀ Phenotype: Smooth, yellow  X Smooth, yellow 
 Heterozygous at both loci Heterozygous at both loci

Genotype: SsYy SsYy

Punnett Grid:

gametes	SY	Sy	sY	sy
SY	SSYY	SSYy	SsYY	SsYy
Sy	SSYy	SSyy	SsYy	Ssyy
sY	SsYY	SsYy	ssYY	ssYy
sy	SsYy	Ssyy	ssYy	ssyy

F₁

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VIII. Punnett Squares for Dihybrid Traits (10.2)

Dihybrid Crosses

Consider two traits, each carried on separate chromosomes (the genes are unlinked).

In this example of *Lathyrus odoratus* (sweet pea), we consider two traits: pea colour and pea surface. What is the predicted phenotype ratio for a cross between two pea plants which are heterozygous at both loci?





Key to alleles:
 Y = yellow
 y = green
 S = smooth
 s = rough

F₀ Phenotype: Smooth, yellow  X Smooth, yellow 
 Heterozygous at both loci Heterozygous at both loci

Genotype: SsYy SsYy

Punnett Grid:

gametes	SY	Sy	sY	sy
SY	SSYY	SSYy	SsYY	SsYy
Sy	SSYy	SSyy	SsYy	Ssyy
sY	SsYY	SsYy	ssYY	ssYy
sy	SsYy	Ssyy	ssYy	ssyy

F₁ Phenotypes: 9 Smooth, yellow  : 3 Smooth, green  : 3 Rough, yellow  : 1 Rough, green 

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VIII. Punnett Squares for Dihybrid Traits (10.2)

Dihybrid Crosses

Consider two traits, each carried on separate chromosomes (the genes are unlinked).

In this example of *Lathyrus odoratus* (sweet pea), we consider two traits: pea colour and pea surface. Calculate the predicted phenotype ratio for:



Key to alleles:
 Y = yellow
 y = green
 S = smooth
 s = rough

F₀ Phenotype: Smooth, yellow  X Smooth, yellow 
 Heterozygous at both loci Heterozygous for S, homozygous dominant for Y

Genotype: SsYy SsYY

Punnett Grid:

gametes	SY	sY
SY		
Sy		
sY		
sy		

F₁ Phenotypes: 6 Smooth, yellow  → 2 Rough, yellow 
 Present the ratio in the simplest mathematical form.

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VIII. Punnett Squares for Dihybrid Traits (10.2)

Dihybrid Crosses

Common expected ratios of dihybrid crosses.

SsYy X **SsYy**
Heterozygous at both loci X Heterozygous at both loci

	SY	Sy	sY	sy
SY	SSYY	SSYy	SsYY	SsYy
Sy	SSYy	Ssyy	SsYY	SsYy
sY	SsYY	SsYy	ssYY	ssYy
sy	SsYy	SsYy	ssYy	ssyy

9 : 3 : 3 : 1

SsYy X **SsYY**
Heterozygous at both loci X Heterozygous at one locus, homozygous dominant at the other

	SY	sY
SY	SSYY	SsYY
sY	SsYY	SsYY
sy	SsYY	ssYY

3 : 2

SsYy X **Ssyy**
Heterozygous at both loci X Heterozygous/Homozygous recessive

	SY	sy
SY	SSYy	Ssyy
Sy	SsYy	Ssyy
sY	SsYy	ssyy
sy	Ssyy	ssyy

4 : 3 : 1

Ssyy X **ssYY** = All SsYy


SSYY X **ssyy** = all SsYy

Ssyy X **ssYy** = 1 : 1 : 1 : 1

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VIII. Punnett Squares for Dihybrid Traits (10.2)

A. Completion and analysis of Punnett squares for dihybrid traits AND Calculation of the predicted genotypic and phenotypic ratio of offspring of dihybrid crosses involving unlinked autosomal genes-



Pen pal: Sooty after his one-night stand
Funny Shit

Guinea pig harem says 'hello Sooty'

A GUINEA pig called Sooty had a night to remember after escaping from his pen and tunnelling into a cage of 24 females. He romanced each of them in turn and was yesterday the proud father of 43 offspring. Staff at Little Friend's Farm in Pontypridd, South Wales, have now secured Sooty's pen — and begun looking for homes for the guinea pigs.

His owner, Carol Feehan, 42, said: "I'm sure a lot of men will be looking at Sooty with envy. We knew that he had gone missing after wriggling through the bars of his cage. We looked for him every where but never thought of checking the pen where we keep 24 females. We did a head count and found 25 guinea pigs — Sooty was fast asleep in the corner. He was absolutely shattered. We put him back in his cage and he slept for two days."

Key to alleles*:
C = color c = albino
A = agouti a = black
R = round ears
r = pointy ears
L = long whiskers
l = short whiskers
S = soft fur
s = rough fur
N = sharp nails n = smooth nails

* C and A genes are real. The rest are made up for this story.

VIII. Punnett Squares for Dihybrid Traits (10.2)

Sooty has soft fur and sharp nails.
In one of his matings with a rough-furred, smooth-nailed female, the following guinea piglets are produced:
6 x rough fur, sharp nails; 3 x soft fur sharp nails.

Deduce Sooty's Genotype

F₀ Phenotype: *Rough fur, smooth nails* ♀ X *Soft fur, sharp nails* ♂

Genotype:

Punnet Grid:

F₁ Phenotypes:

Key to alleles*:
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Genotype: ssn

Punnet Grid:

Possible Gametes				
All sn				

F₁ Phenotypes:

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Deduce Sooty's Genotype

F₀ Phenotype: *Rough fur, smooth nails* ♀ X *Soft fur, sharp nails* ♂
 Genotype: *ssnn* X *SSNn or SsNn or SsNn*

Punnett Grid:

Possible Gametes	SN	Sn	sN	sn
All sn	SsNn Soft fur Sharp nails	Ssnn Soft fur Smooth nails	ssNn Rough fur Sharp nails	ssnn Rough fur Smooth nails

F₁ Phenotypes:

Key to alleles*:
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Punnett Grid:

Possible Gametes	SN	Sn	sN	sn
All sn	SsNn Soft fur Sharp nails	Ssnn Soft fur Smooth nails	ssNn Rough fur Sharp nails	ssnn Rough fur Smooth nails

F₁ Phenotypes:

Only these two phenotypes have been produced.
 Sooty has only produced **SN** and **sN** gametes.
 It is most likely that his genotype is **SsNn**.

Key to alleles*:
 C = color c = albino
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VIII. Punnett Squares for Dihybrid Traits (10.2)

DBQ: Using the Chi-Square Test
 Warren and Hutt (1936) test-crossed a double heterozygote for two pairs of alleles in hens: one for the presence (Cr) or absence (cr) of a crest and one for white (I) or non-white (i) plumage.

For their F₁ cross, there were a total of 754 offspring:
 337 were white, crested;
 337 were non-white, non-crested;
 34 were non-white, crested;
 46 were white, non-crested

1. Construct a contingency table of observed values.
2. Calculate the expected values assuming independent assortment.
3. Determine the number of degrees of freedom.
4. Find the critical region for chi-square at a significance level of 5%.
5. Calculate chi-squared.
6. State the two hypotheses H₀ and H₁ and evaluate them using the calculated value for chi-squared.

VIII. Punnett Squares for Dihybrid Traits (10.2)

- A total of 754 offspring: 337 were white, crested; 337 were non-white, non-crested; 34 were non-white, crested; 46 were white, non-crested
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	O	E	O - E	(O - E) ²	$\frac{(O - E)^2}{E}$
white, crested					
non-white, non-crested					
non-white, crested					
white, non-crested					
Total				X ² =	

VIII. Punnett Squares for Dihybrid Traits (10.2)

- Determine the number of degrees of freedom.
 $df = \text{categories} - n =$
- Find the critical region for chi-square at a significance level of 5%.
 $p =$
- Calculate chi-squared.
 $\chi^2 = 468.3$
- State the two hypotheses H_0 and H_1 and evaluate them using the calculated value for chi-squared.

df	0.05	0.01
1	3.84	6.64
2	5.99	9.21
3	7.82	11.34
4	9.49	13.28
5	11.07	15.09
6	12.59	16.81
7	14.07	18.48
8	15.51	20.09
9	16.92	21.67
10	18.31	23.21
11	19.68	24.72
12	21.03	26.22
13	22.36	27.69
14	23.68	29.14
15	25.00	30.58