

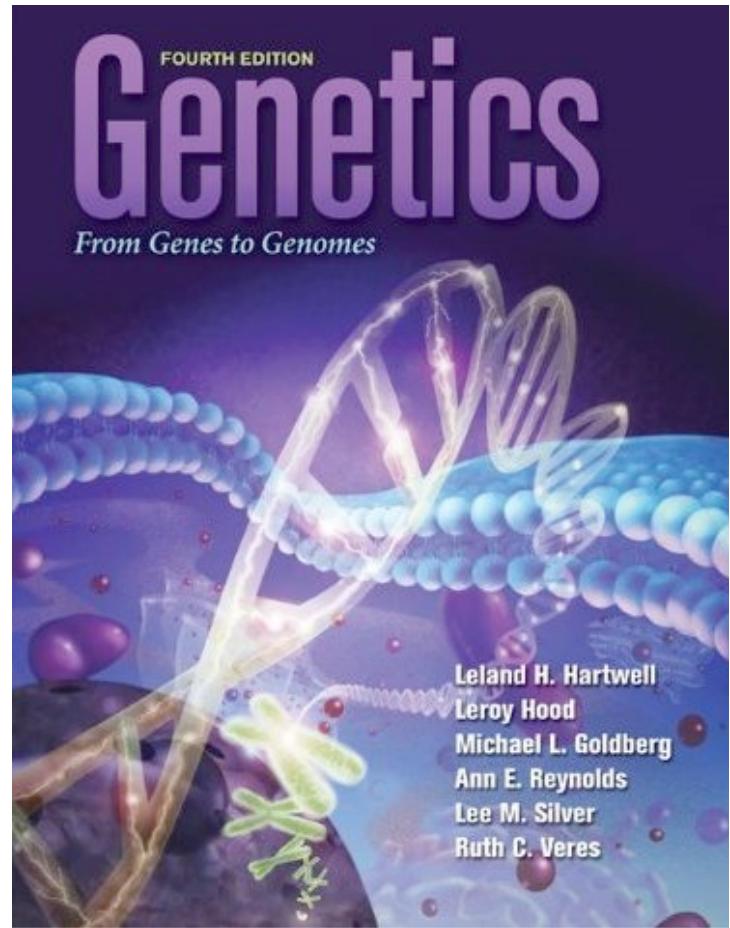
PowerPoint to accompany

Genetics: From Genes to Genomes

Fourth Edition

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Gregor Johann Mendel

(1882-1884)



Mendel's Principles of Heredity



CHAPTER OUTLINE

- **Mendel's Principles of Heredity**
- 2.1 Background: The Historical Puzzle of Inheritance
- 2.2 Genetic Analysis According to Mendel
- 2.3 Mendelian Inheritance in Humans

A family portrait with members of four generations

Why do some of the children look like only one of the parents, while some of the other children look more like the great, great grandparents?

What causes the similarities and differences of appearance and the skipping of generations?



Fig. 2.1

Gregor Mendel discovered the basic principles of genetics

Mendel was the first scientist to combine data collection, analysis, and theory to understand heredity

He inferred genetic laws about the appearance and disappearance of traits during different generations



Fig. 2.2

Genetics explains the mechanisms that determine the inheritance of traits

Genes are the basic units of heredity

- Heredity is the way that genes transmit traits from parents to offspring
- Genes are passed from one generation to the next

**Genes underlie the formation of every heritable trait,
e.g. cleft chin, hair loss, color of hair, skin, and eyes**

- Some traits are caused by a single change in a single gene, e.g. sickle-cell anemia
- Some traits are caused by complex interactions between many genes, e.g. facial features

Four general themes of Mendel's work

- 1. Variation is widespread in nature and provides for continuously evolving diversity**
- 2. Observable variation is essential for following genes from one generation to another**
- 3. Variation is inherited by genetic laws, which can explain why like begets like and unlike (e.g. Fig 2.3)**
- 4. Mendel's laws apply to all sexually reproducing organisms**

Genetic variation exists even within dog breeds

Mendel's laws explain why two black Labradors could have a litter of black, brown, and golden puppies



Fig. 2.3

Background to Mendel's work: The historical puzzle of inheritance

Artificial selection was the first applied genetic technique

- Purposeful control of mating by choice of parents for the next generation

Domestication of plants and animals was a key transition in human civilization

- Domestication of dogs from wolves
- Domestication of rice, wheat, barley, and lentils from weed like plants

Critical questions about selective breeding before Mendel's studies

**Concluding remarks by Abbot Cyril Napp at 1837
annual meeting of the Moravian Sheep Breeders Society:**

Three basic questions must be answered

- **What is inherited?**
- **How is it inherited?**
- **What is the role of chance in heredity?**

**Abbot Napp presided over the monastery where
Mendel began his seminal genetic experiments in 1864**

Two other theories of inheritance at the time of Mendel's studies

Inherited features of offspring are contributed mainly by only one parent (e.g. a "homunculus" inside the sperm, Fig 2.6)

Parental traits become mixed and changed in the offspring (i.e. "blended inheritance")

Neither theory could explain why some traits would appear, disappear, and then reappear

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Mendel studied the inheritance of alternative traits in pea plants

Mendel inferred laws of genetics that allowed predictions about which traits would appear, disappear, and then reappear

- This work was done in his garden at a monastery

Mendel's paper "Experiments in plant hybrids" was published in 1866 and became the cornerstone of modern genetics



Fig. 2.5

Keys to the success of Mendel's experiments

Pure-breeding lines of peas (*Pisum sativum*)

- Breeding could be done by cross-fertilization or selfing
- Large numbers of progeny produced within a short time
- Traits remained constant in crosses within a line

Inheritance of alternative forms of traits

- Antagonistic pairs of "either-or" traits: e.g. purple or white, yellow or green

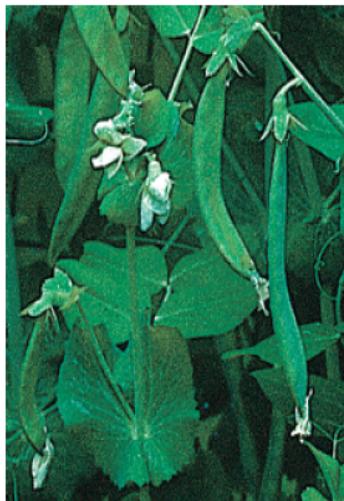
Brilliant experimentalist

- Planned experiments carefully
- Controlled the plant breeding
- Analyzed results mathematically

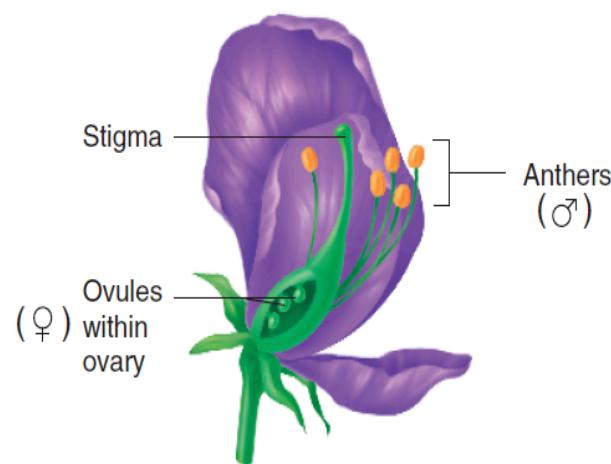
Pea Traits Studied by Mendel

Pea trait	Dominant trait	Recessive trait
Seeds		
Seed shape	Round	
		
Seed colour	Yellow	
		
Whole plants		
Flower colour	Purple	
		
Flower position	Axial	
		
Plant height	Tall	
		
Pod shape	Inflated	
		
Pod colour	Green	
		

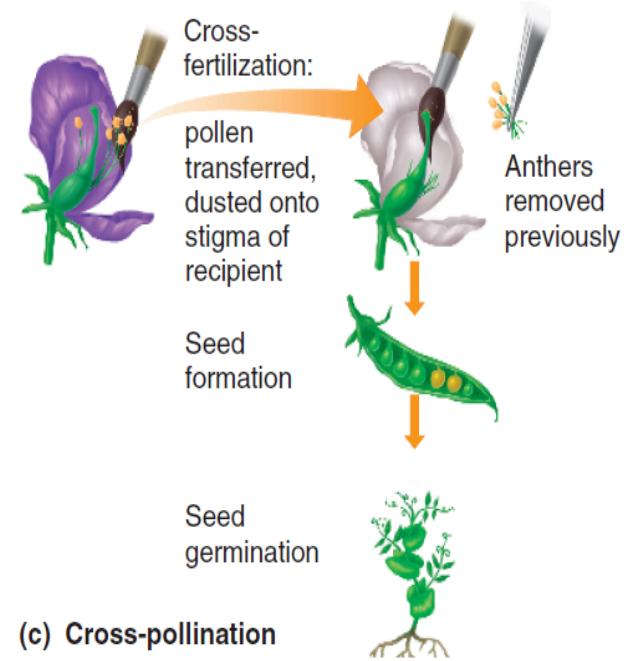
Mendel's experimental organism: The garden pea



(a) *Pisum sativum*



(b) Pea flower anatomy



(c) Cross-pollination

Fig. 2.7

Mendel studied seven antagonistic pairs of traits in peas

Three antagonistic pairs of traits are shown at right

Note that each hybrid resembles only one of the parents:
the dominant trait

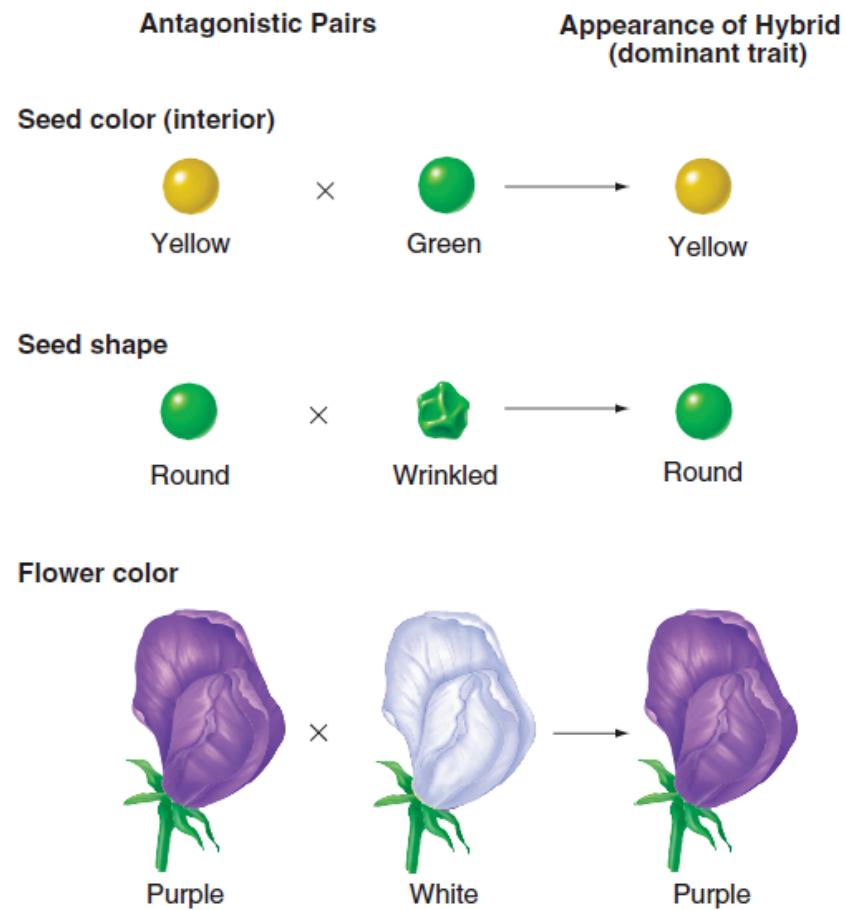


Fig. 2.8

Monohybrid crosses revealed units of inheritance and the law of segregation

Mendel crossed pure-breeding lines that differed in only one trait, e.g. seed color

Examined phenotypes of F₁ progeny and F₂ progeny

- F₁ progeny have only one of the parental traits
- Both parental traits reappear in F₂ progeny in a 3:1 ratio

These results disproved the blending hypothesis

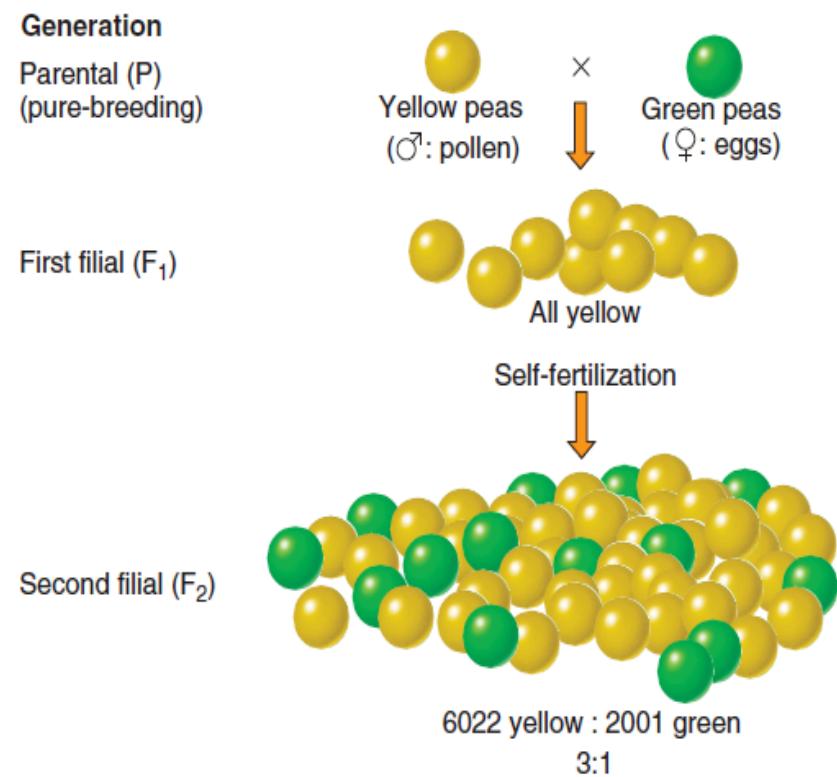


Fig. 2.9

Mendel proposed that each plant carries two copies of a unit of inheritance

Traits have two forms that can each breed true

- Trait that appears in F_1 progeny is the **dominant** form
- Trait that is hidden in the F_1 progeny is the **recessive** form
- Progeny inherit one unit from the maternal parent and the other unit from the paternal parent

Units of inheritance are now known as "**genes**"

- Alternative forms of a single gene are "**alleles**"
- Individuals with two different alleles for a single trait are "**monohybrids**"

Mendel's law of segregation

The two alleles for each trait separate during gamete formation

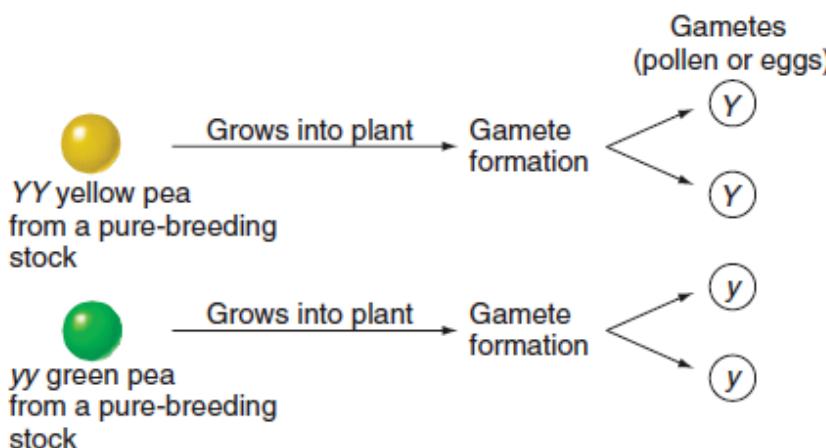


Fig. 2.10a

Two gametes, one from each parent, unite at random at fertilization

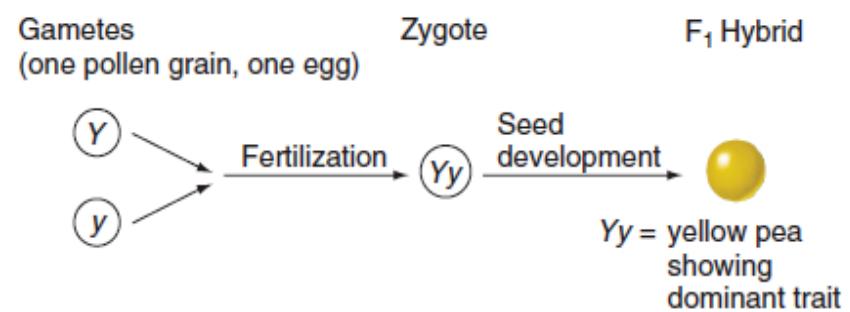


Fig. 2.10b

The Punnett square is a simple way to visualize the segregation and random union of alleles

Each F_1 hybrid produces two kinds of gametes in a 1:1 ratio

F_2 progeny

- 3:1 ratio of phenotypes
- 1/4 will breed true for the dominant trait
- 1/2 will be hybrids
- 1/4 will breed true for the recessive trait

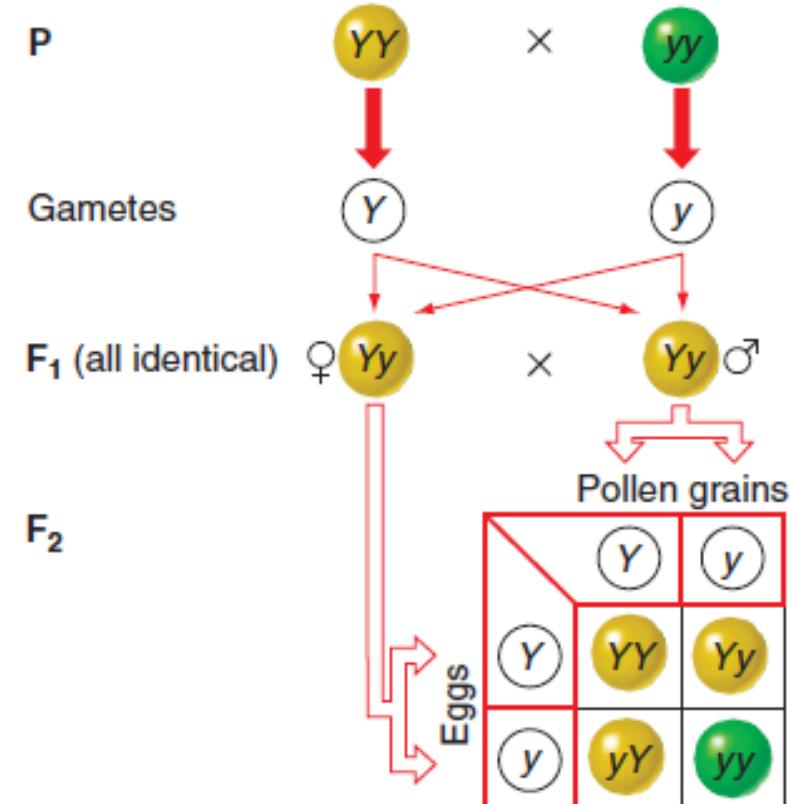


Fig. 2.11

Mendel's results and the Punnett square reflect the basic rules of probability

Product rule: probability of two independent events occurring together is the product of their individual probabilities

- What is the probability that event 1 AND event 2 will occur?

P(1 and 2) = probability of event 1 X probability of event 2

Sum rule: probability of either of two mutually exclusive events occurring is the sum of their individual probabilities

- What is the probability that event 1 OR event 2 will occur?

P(1 or 2) = probability of event 1 + probability of event 2

Applying probability to Mendel's crosses

From a cross of $Yy \times Yy$ peas

- What is the chance of getting YY offspring?
 - Chance of Y pollen is $1/2$
 - Chance of Y ovule is $1/2$
 - Chance of Y pollen and Y ovule uniting is $1/2 \times 1/2 = 1/4$
- What is the chance of getting Yy offspring?
 - Chance of Y pollen uniting with y ovule is $1/2 \times 1/2 = 1/4$
 - Chance of y pollen uniting with Y ovule is $1/2 \times 1/2 = 1/4$
 - Chance of either event happening is $1/4 + 1/4 = 1/2$

Mendel did further crosses to verify the law of segregation

F_2 plants were selfed to produce F_3 progeny

- All of the green F_2 peas were pure breeding
- 1/3 of the yellow F_2 peas were pure breeding
- 2/3 of the yellow F_2 peas were hybrids

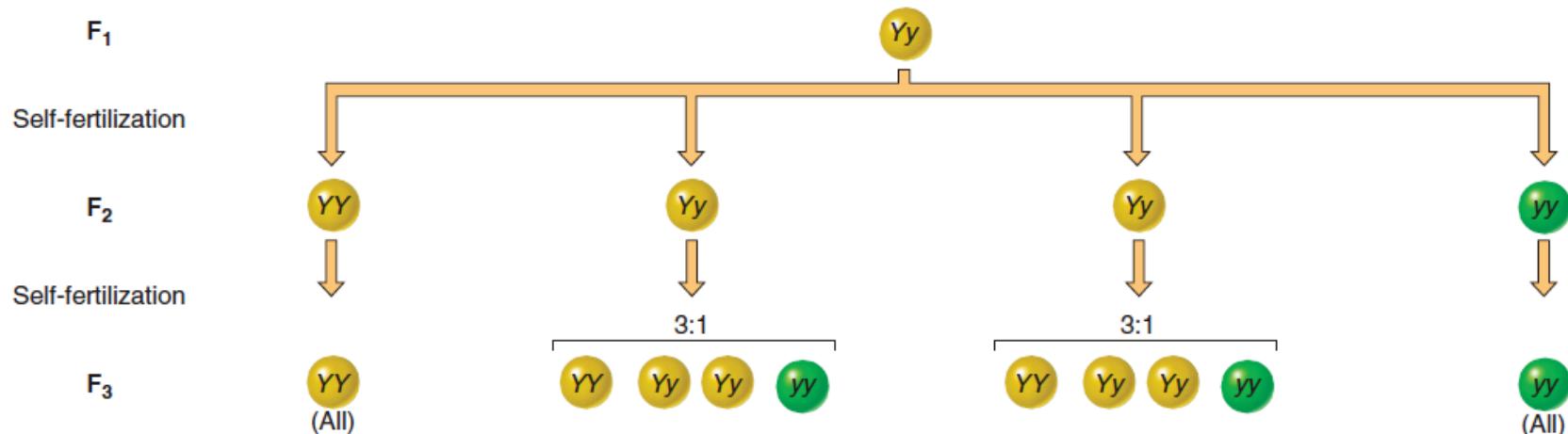


Fig. 2.12

Definitions of commonly used terms

Phenotype is an observable characteristic (e.g. yellow or green pea seeds)

Genotype is a pair of alleles in an individual (e.g. YY or Yy)

Homozygote has two identical alleles (e.g. YY or yy)

Heterozygote has two different alleles (e.g. Yy)

- The heterozygous phenotype defines the dominant allele (e.g. Yy peas are yellow, so the yellow Y allele is dominant to the green y allele)
- A dominant allele with a dash represents an unknown genotype (e.g. Y- stands for either YY or Yy)

Genotype vs phenotype in homozygotes and heterozygotes

From a cross of $Yy \times Yy$ peas

**Genotypes in F_2 progeny are
in 1:2:1 ratio (1/4 YY, 1/2 Yy,
1/4 yy)**

Phenotypes in F_2 progeny
are in 3:1 ratio (3/4 yellow,
1/4 green)

Genotype for the Seed Color Gene	Phenotype
YY Homozygous dominant	 Yellow
Dominant allele	
Yy	
Heterozygous	 Yellow
yy Homozygous recessive	 Green

Fig. 2.13

A testcross can reveal an unknown genotype

Is the genotype of an individual with a dominant phenotype (e.g. $Y-$) heterozygous (Yy) or homozygous (YY)?

- Solution: Testcross to homozygous recessive (yy) and examine progeny

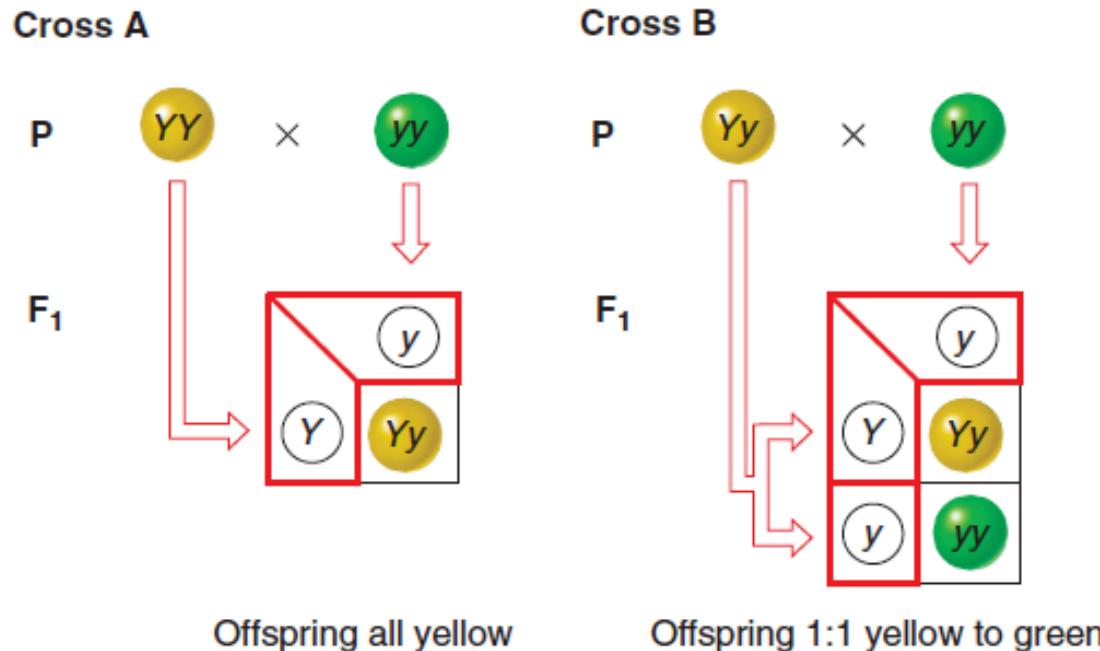


Fig. 2.14

Mendel's dihybrid crosses revealed the law of independent assortment

Mendel tested whether two genes in dihybrids would segregate independently

First, he crossed true-breeding yellow round peas with true-breeding green wrinkled peas to obtain dihybrid F₁ plants:

$$YY\ RR \times yy\ rr \rightarrow F_1\ Yy\ Rr$$

Then, the dihybrid F₁ plants were selfed to obtain F₂ plants:

$$F_1\ Yy\ Rr \times F_1\ Yy\ Rr \rightarrow F_2$$

Mendel asked whether all the F₂ progeny would be **parental types** (yellow round and green wrinkled) or would some be **recombinant types** (yellow wrinkled and green round)?

A dihybrid cross produces parental types and recombinant types

Each F₁ dihybrid produces four possible gametes in a 1:1:1:1 ratio

$$Yy Rr \rightarrow 1/4 YR, 1/4 Yr, \\ 1/4 yR, 1/4 yr$$

Four phenotypic classes occurred in the F₂ progeny:

- Two are like parents
- Two are recombinant

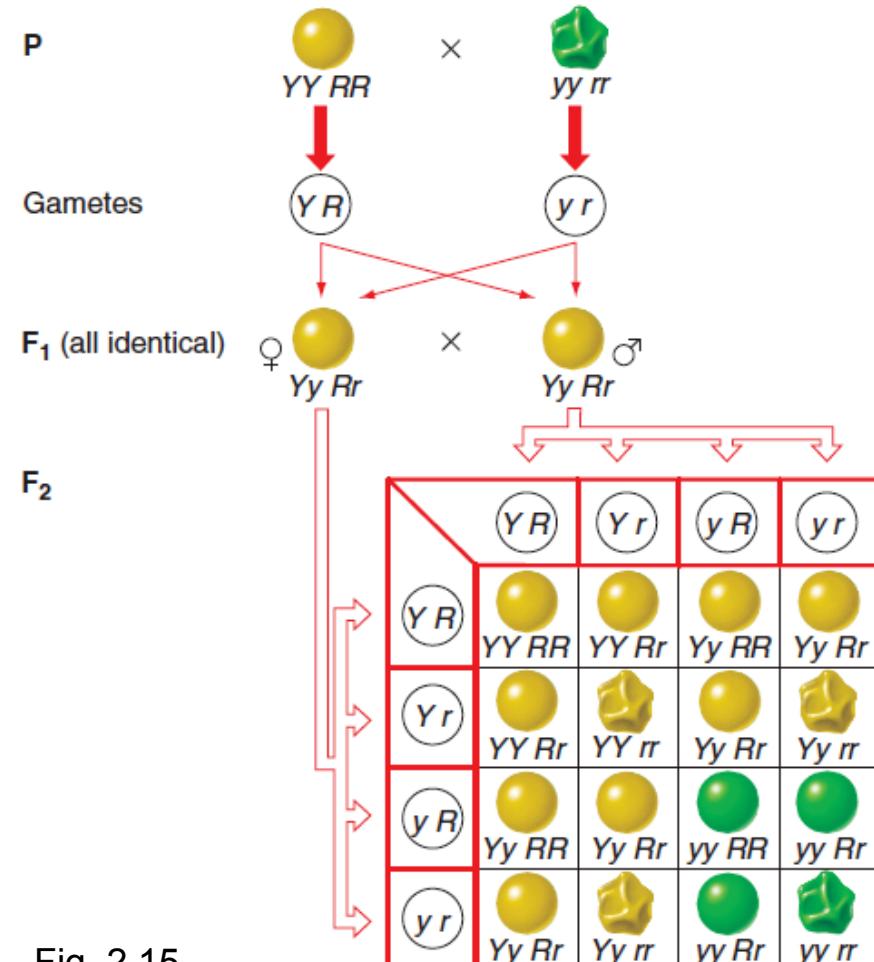


Fig. 2.15

Independent assortment in crosses of F₁ dihybrids produces a 9:3:3:1 phenotype ratio

Note that in these F₂ progeny, there is a 3:1 phenotype ratio of dominant to recessive forms

Type	Genotype	Phenotype	Number	Phenotypic Ratio
Parental	Y- R-	yellow round	315	9/16
Recombinant	yy R-	green round	108	3/16
Recombinant	Y- rr	yellow wrinkled	101	3/16
Parental	yy rr	green wrinkled	32	1/16

Ratio of yellow (dominant) to green (recessive) = 12:4 or 3:1

Ratio of round (dominant) to wrinkled (recessive) = 12:4 or 3:1

Fig. 2.15

Mendel's law of independent assortment

During gamete formation, different pairs of alleles segregate independently of each other

- **Y is just as likely to assort with R as it is with r**
- **y is just as likely to assort with R as it is with r**

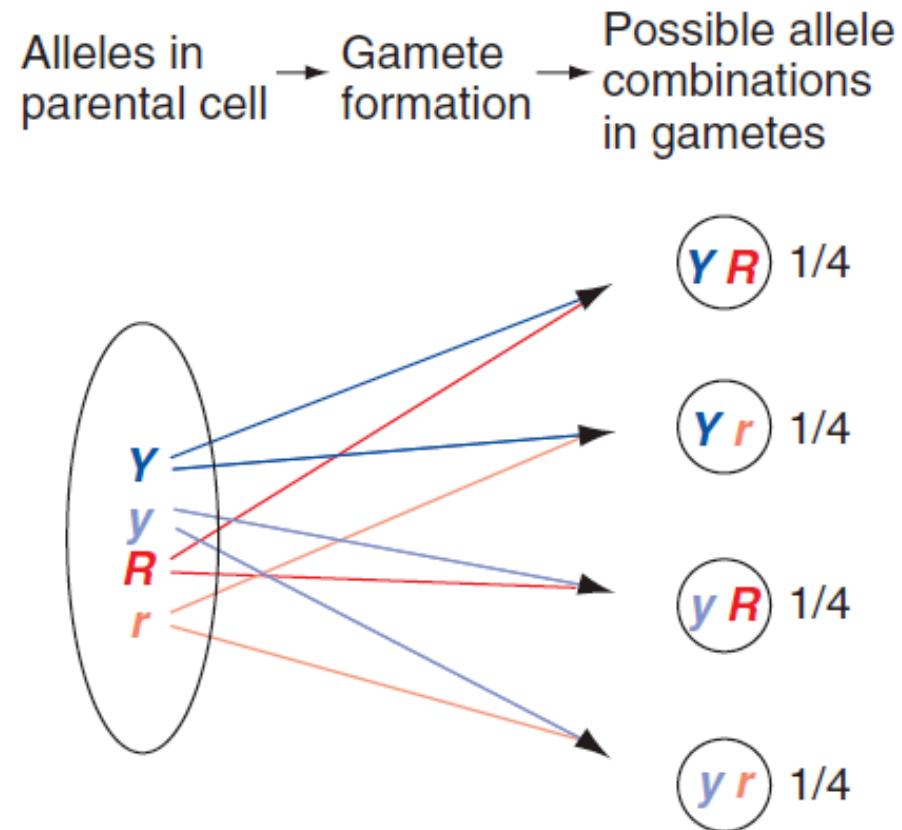


Fig. 2.16

Following crosses with branched-line diagrams

Progeny phenotypes for each gene are shown in different columns

This gives the same ratios as seen in the Punnett square in Fig 2.15

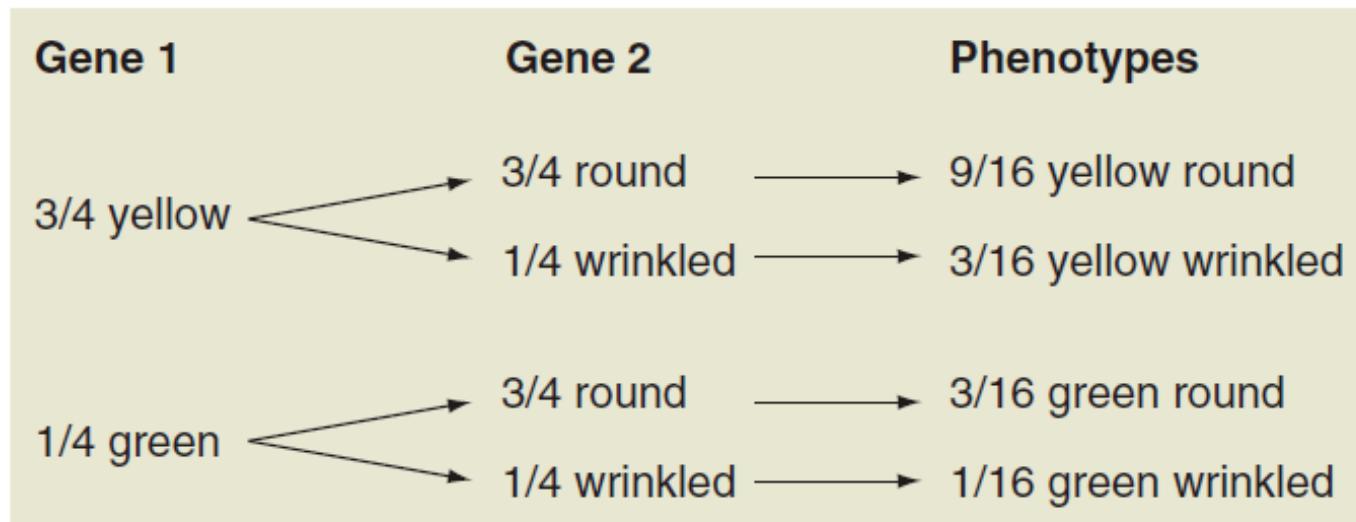
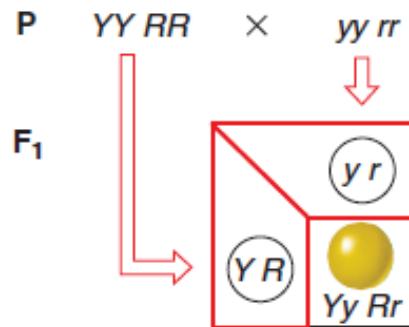


Fig. 2.17

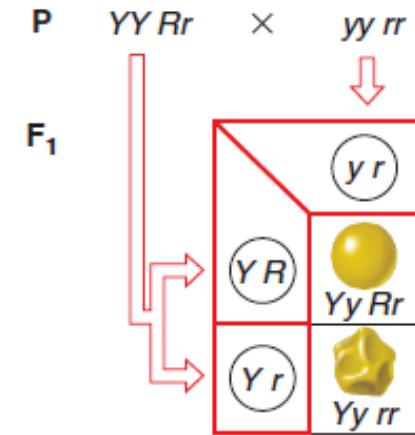
Testcrosses on dihybrids

Testcross dihybrids to individuals that are homozygous for both recessive traits

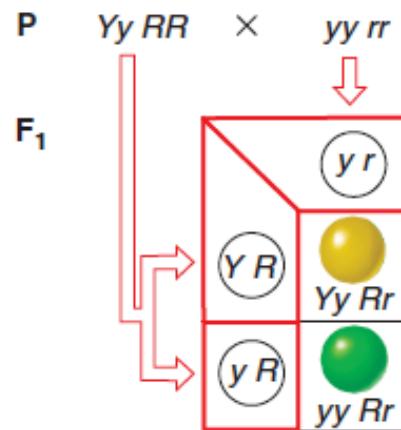
Cross A



Cross B



Cross C



Cross D

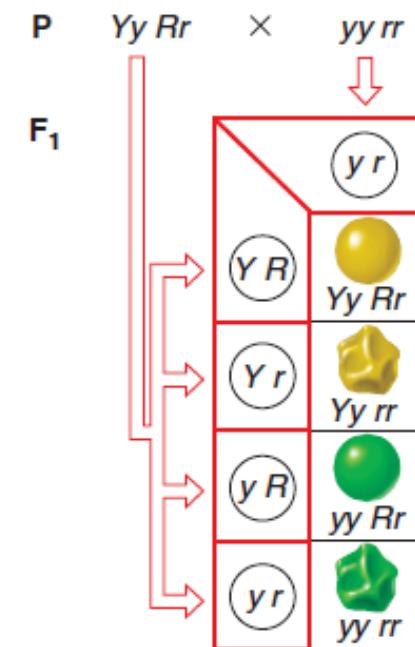


Fig. 2.18

Mendel's laws can be used to predict offspring from complicated crosses

To calculate the possible number of gamete genotypes from a hybrid, raise 2 to the power of the number of different traits

- $Aa\ Bb\ Cc\ Dd \rightarrow 2^4 = 16$ kinds of gametes
- $Aa\ Bb\ Cc\ Dd \times Aa\ Bb\ Cc\ Dd \rightarrow 16 \times 16 = 256$ genotypes
- To do a Punnett square with this cross involving four genes, you would need 16 columns and 16 rows
- An easier way is to break down a multihybrid cross into independently assorting monohybrid crosses

Predicting proportions of progeny from multi-hybrid crosses – example 1

Cross **Aa Bb Cc Dd x Aa Bb Cc Dd**

What proportion of progeny will be **AA bb Cc Dd**?

- **Aa x Aa → 1/4 AA**
- **Bb x Bb → 1/4 bb**
- **Cc x Cc → 1/2 Cc**
- **Dd x Dd → 1/2 Dd**

So, the expected proportion of **AA bb Cc DD** progeny is:

$$1/4 \times 1/4 \times 1/2 \times 1/2 = 1/64$$

Predicting proportions of progeny from multi-hybrid crosses – example 2

Cross **Aa Bb Cc Dd x Aa Bb Cc Dd**

How many progeny will show the dominant traits for **A, C, and D** and the recessive trait for **B**?

- **Aa x Aa → 3/4 A-**
- **Bb x Bb → 1/4 bb**
- **Cc x Cc → 3/4 C-**
- **Dd x Dd → 3/4 D-**

So, expected proportion of **A- bb C- D- progeny is:**

$$3/4 \times 1/4 \times 3/4 \times 3/4 = 27/256$$

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The science of genetics began with the rediscovery of Mendel's work

Mendel published his monumental breakthrough in understanding heredity in 1866, but hardly anyone paid attention to his work!

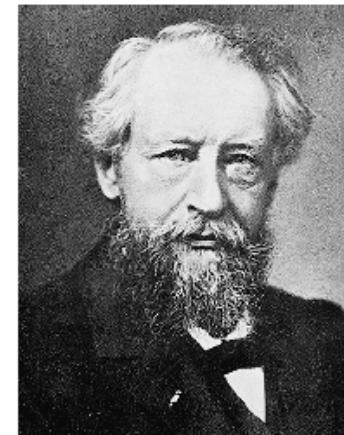
In 1900, three scientists independently rediscovered and acknowledged Mendel's work



(a) Gregor Mendel



(b) Carl Correns



(c) Hugo de Vries



(d) Erich von Tschermak

Fig. 2.19

Mendelian inheritance in humans

Many heritable traits in humans are caused by interaction of multiple genes and so don't show simple Mendelian inheritance patterns

In 2009, there were ~ 4300 single-gene traits known in humans

- See Table 2.1 for some of the common single-gene traits

Even with single-gene traits, determining inheritance pattern in humans can be tricky

- Long generation time
- Small numbers of progeny
- No controlled matings
- No pure-breeding lines

Some of the most common single-gene traits caused by recessive alleles in humans

Disease	Effect	Incidence of Disease
Thalassemia (chromosome 16 or 11)	Reduced amounts of hemoglobin; anemia, bone, and spleen enlargement	1/10 in parts of Italy
Sickle-cell anemia (chromosome 11)	Abnormal hemoglobin; sickle-shaped red cells, anemia, blocked circulation; increased resistance to malaria	1/625 African-Americans
Cystic fibrosis (chromosome 7)	Defective cell membrane protein; excessive mucus production; digestive and respiratory failure	1/2000 Caucasians
Tay-Sachs disease (chromosome 15)	Missing enzyme; buildup of fatty deposit in brain; buildup disrupts mental development	1/3000 Eastern European Jews
Phenylketonuria (PKU) (chromosome 12)	Missing enzyme; mental deficiency	1/10,000 Caucasians

Table 2.1

Some of the most common single-gene traits caused by dominant alleles in humans

Disease	Effect	Incidence of Disease
Hypercholesterolemia (chromosome 19)	Missing protein that removes cholesterol from the blood; heart attack by age 50	1/122 French Canadians
Huntington disease (chromosome 4)	Progressive mental and neurological damage; neurologic disorders by ages 40 - 70	1/25,000 Caucasians

Table 2.1

In humans, pedigrees can be used to study inheritance

Pedigrees are orderly diagrams of a family's relevant genetic features

Includes as many generations as possible (ideally, at least both sets of grandparents of an affected person)

Pedigrees can be analyzed using Mendel's laws

- **Is a trait determined by alternate alleles of a single gene?**
- **Is a trait dominant or recessive?**

Symbols used in pedigree analysis

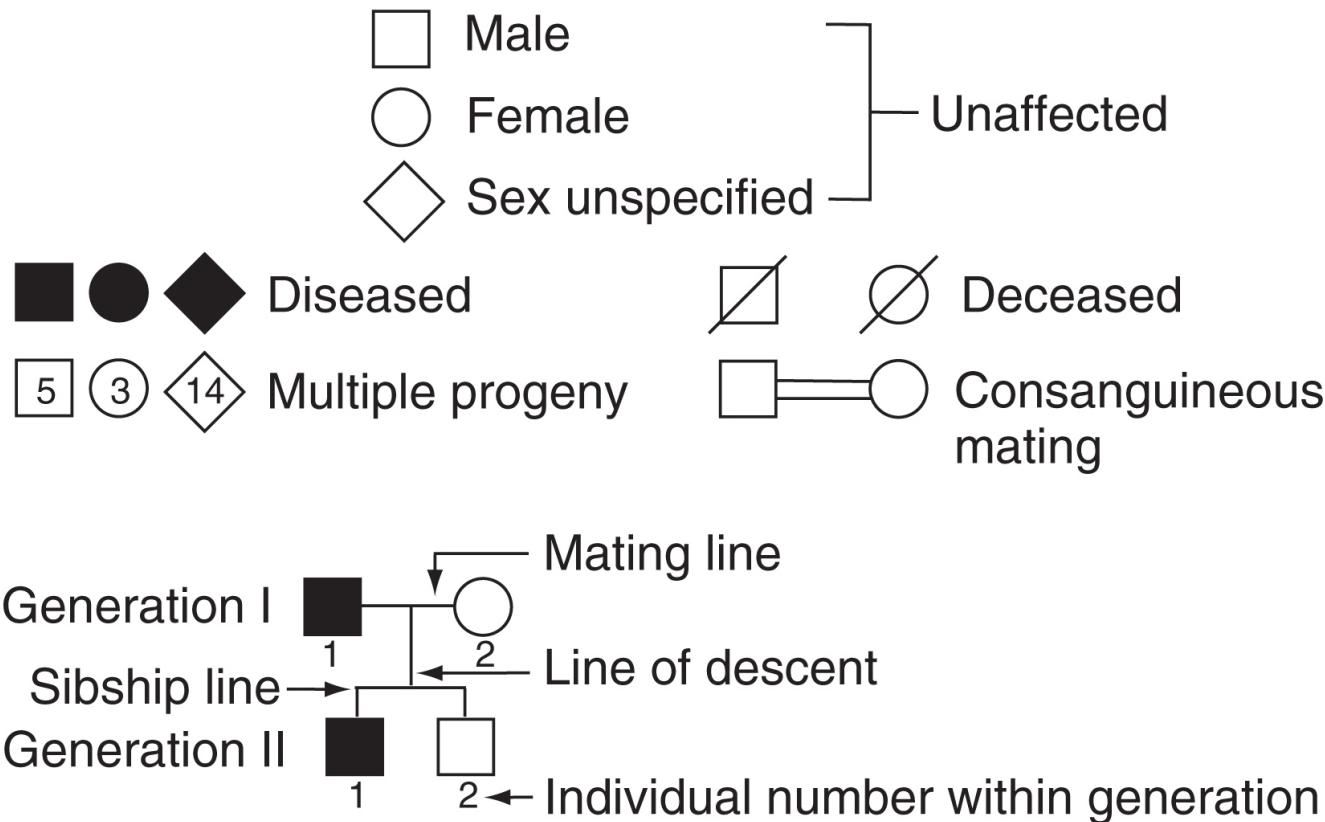


Fig. 2.20

A vertical pattern of inheritance indicates a rare dominant trait; e.g Huntington disease

Every affected person has at least one affected parent

Mating between affected person and unaffected person is effectively a testcross

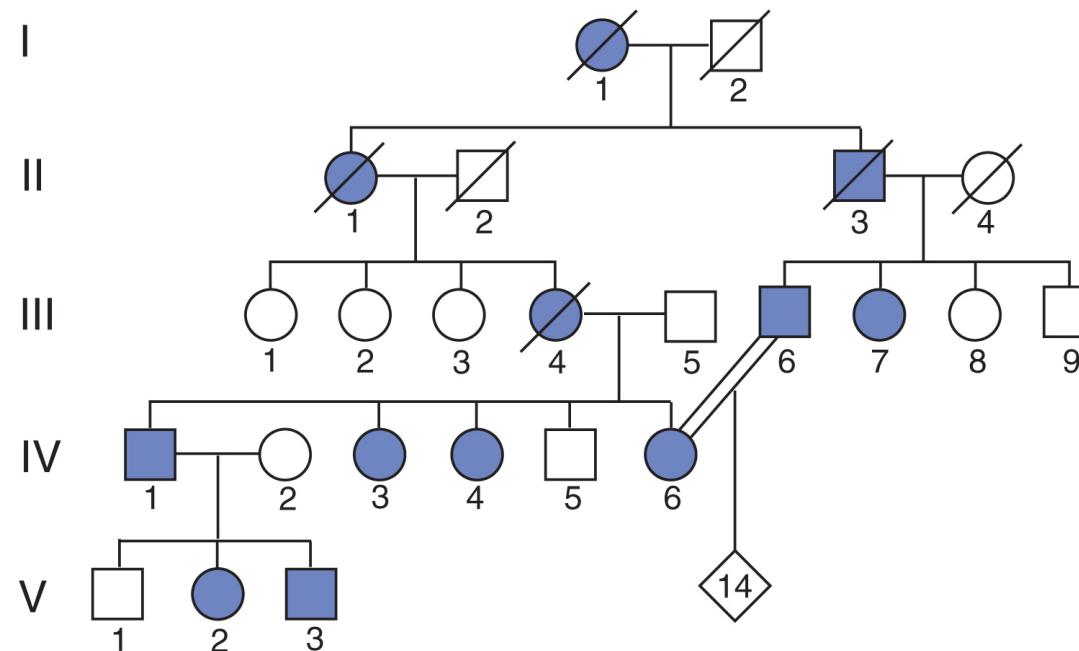


Fig. 2.21

A horizontal pattern of inheritance indicates a rare recessive trait; e.g. cystic fibrosis

Parents of affected individuals are unaffected but are heterozygous (carriers) for the recessive allele

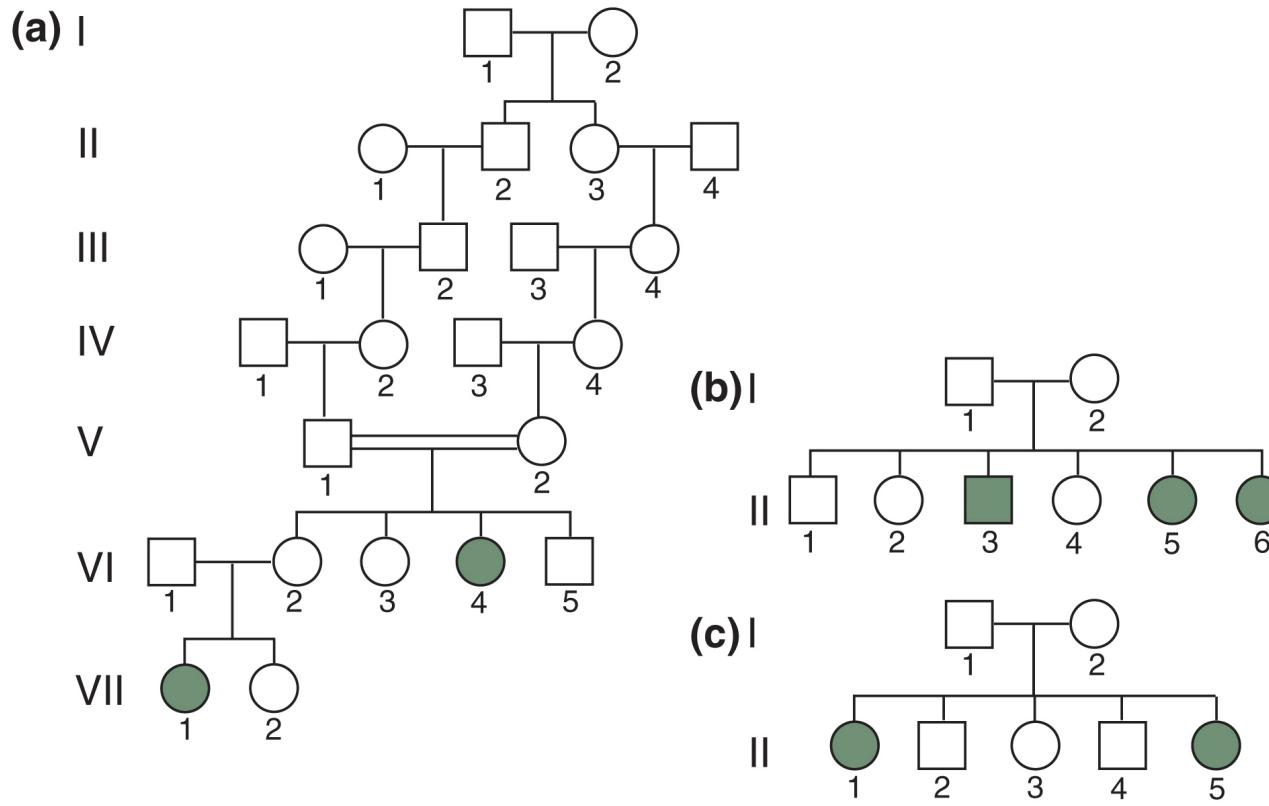


Fig. 2.22

How to recognize dominant traits in pedigrees

Three key aspects of pedigrees with dominant traits:

- 1. Affected children always have at least one affected parent**
- 2. As a result, dominant traits show a **vertical pattern** of inheritance**
- 3. Two affected parents can produce unaffected children, if both parents are heterozygotes**

Table 2.2

How to recognize recessive traits in pedigrees

Four keys aspects of pedigrees with recessive traits:

1. **Affected individuals can be the children of two unaffected carriers, particularly as a result of consanguineous matings**
2. **All the children of two affected parents should be affected**
3. **Rare recessive traits show a **horizontal pattern** of inheritance**
4. **Recessive traits may show a **vertical pattern** of inheritance if the trait is extremely common in the population [END]**

Table 2.2

Chapter 2 Review Questions