

Genetic Variation:
What is it and why is it important?

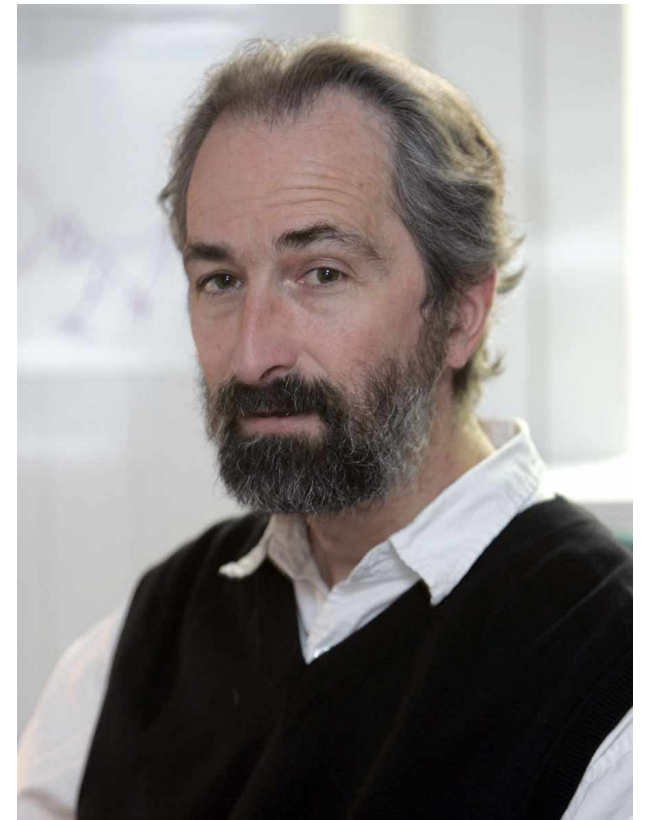
“Nothing in biology makes sense except in light of evolution”

Theodosius Dobzhansky 1973



“Nothing in evolution makes sense
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genetics”

Michael Lynch 2007



Population genetics

- The study of distribution and change in allele frequencies and genotype frequencies over time

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 - ❖ Influenced by:
 - Natural Selection
 - Random Genetic Drift
 - Mutation
 - Gene Flow
 - Recombination
 - Population structure

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- Goal: To determine the genetic basis of evolution

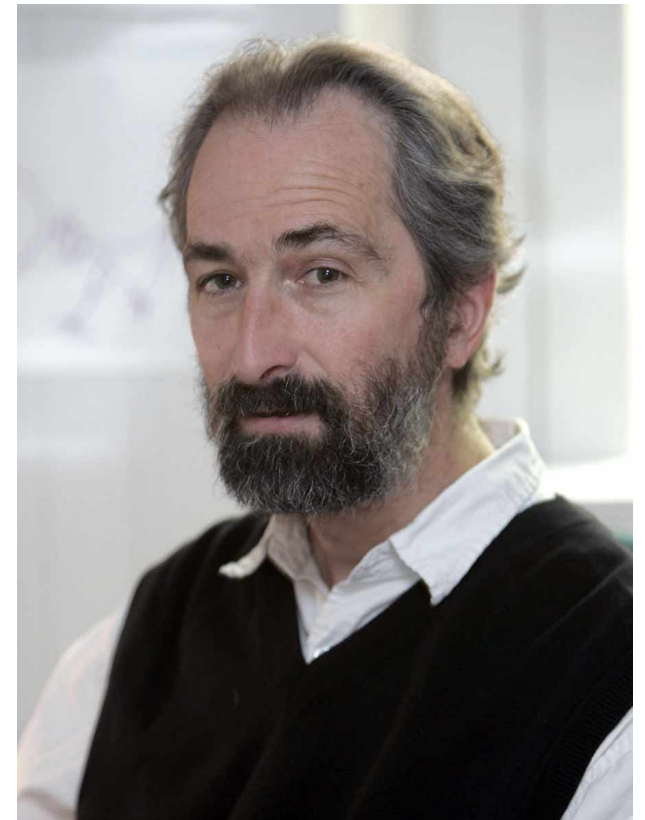
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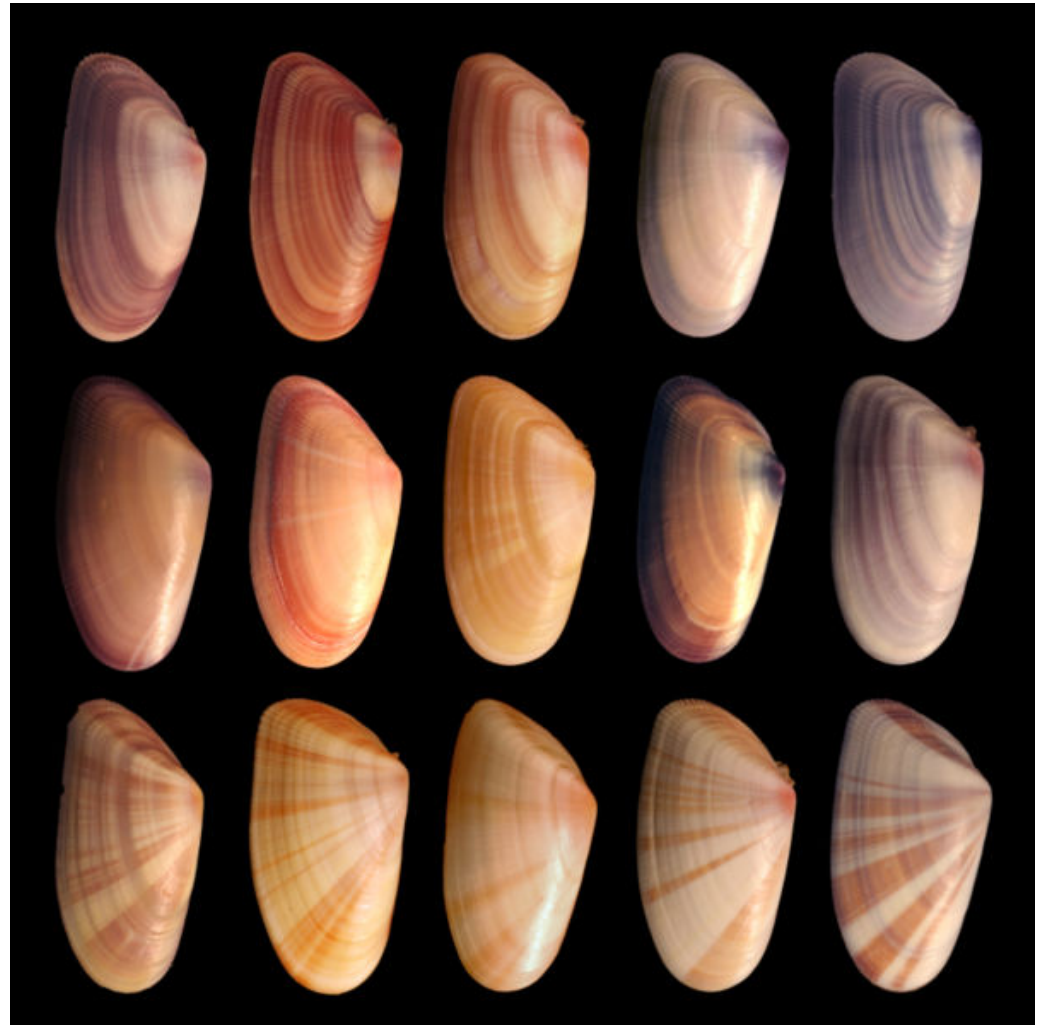


Types of Variation

- Continuous variation: Complete range of measurements from one extreme to the other
 - Color

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Donax variabilis

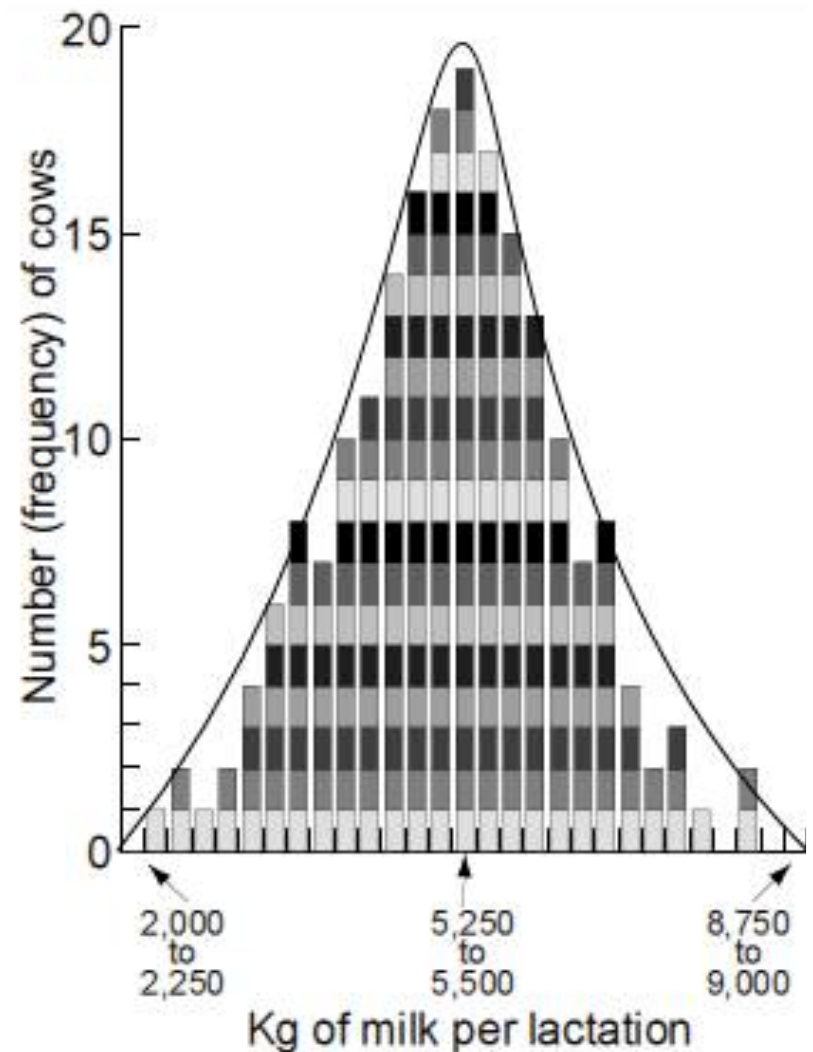
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 - Color
 - Height



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 - Milk production in cows



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Types of Variation

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- Discrete variation: Individuals fall into a number of distinct classes or categories

Types of Variation

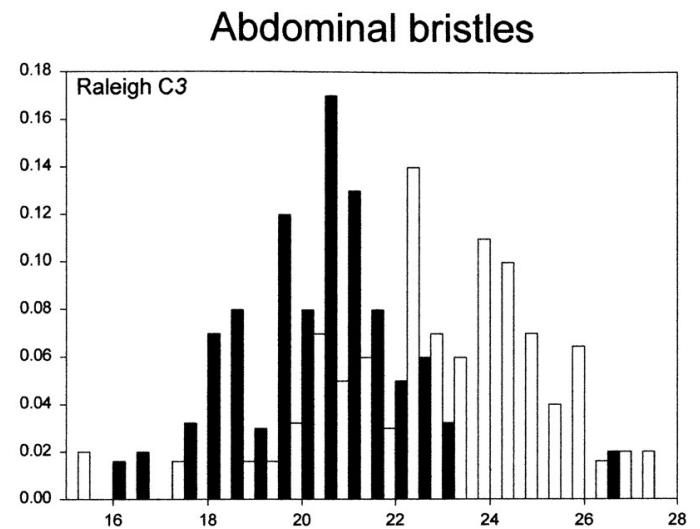
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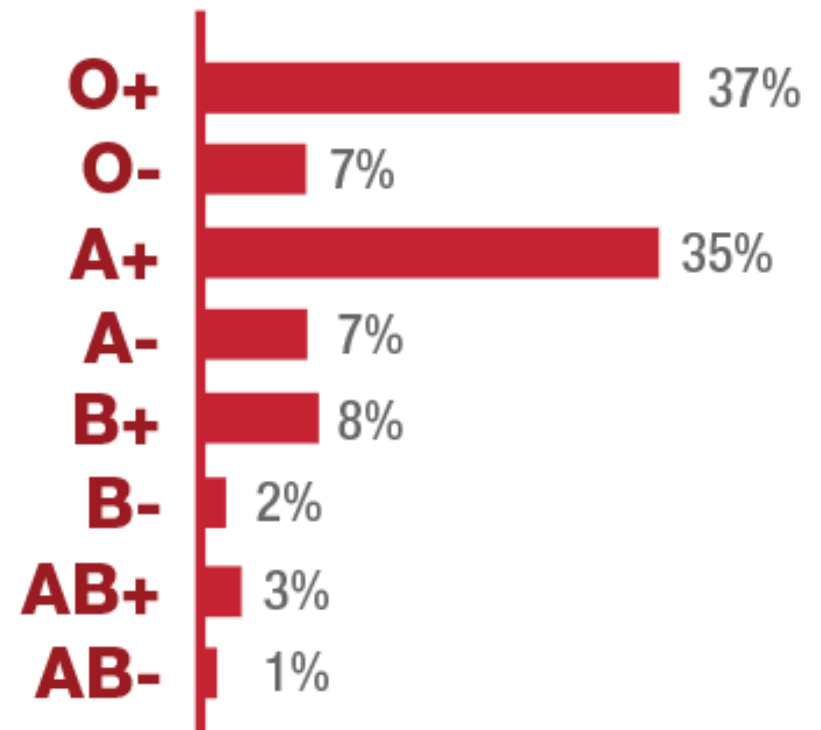
Tilney L G & DeRosier D J 2005



Lyman & Mackay 1998

Types of Variation

- Continuous variation: Complete range of measurements from one extreme to the other
- Discrete variation: Individuals fall into a number of distinct classes or categories
 - Bristle number in *D. melanogaster*
 - Human blood groups



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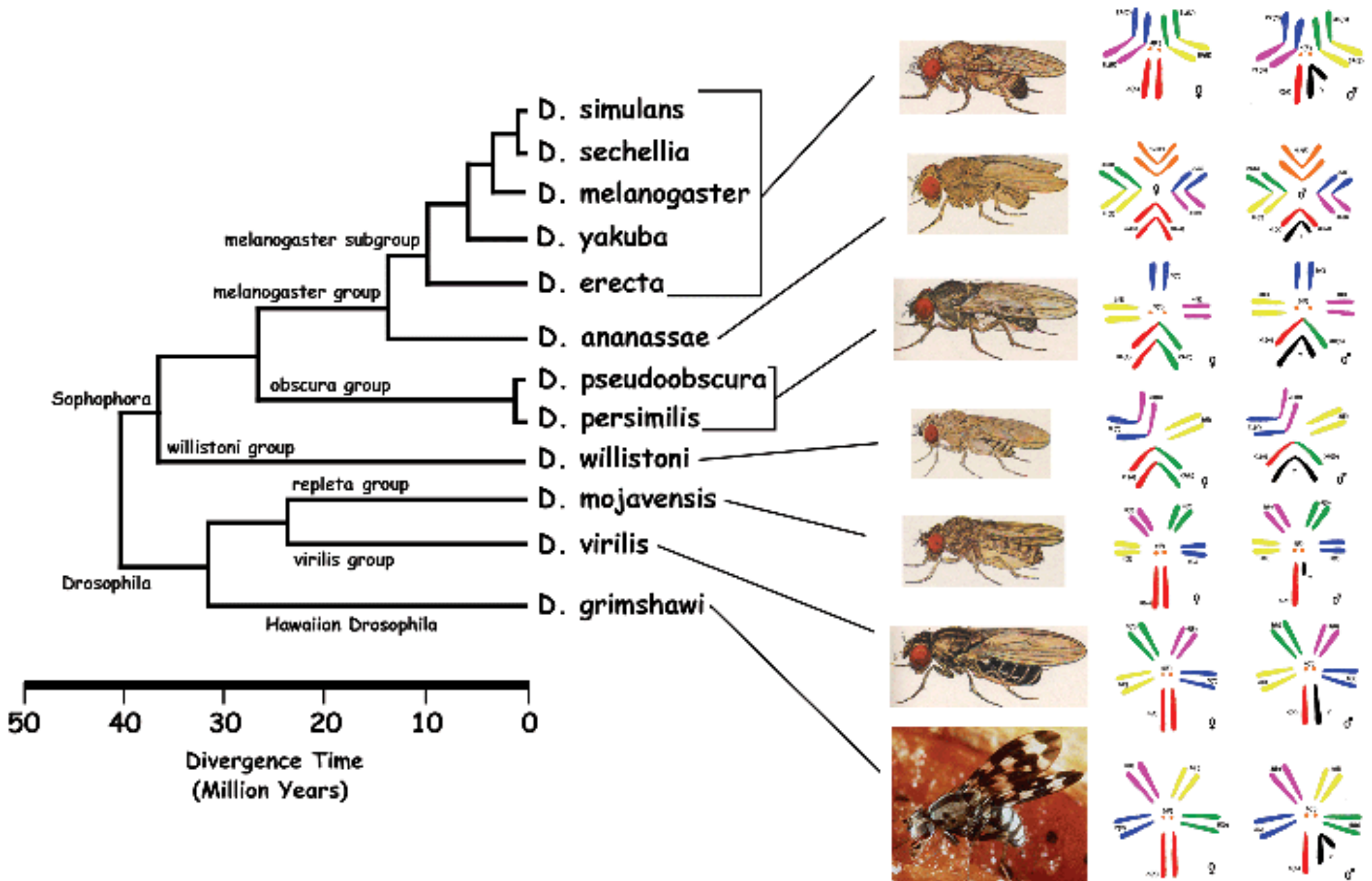
Discrete Genetic Variation

- Chromosomal variation
- Protein variation
- DNA variation

Chromosomal Variation

- Variation in chromosome number, gene number, gene order etc.

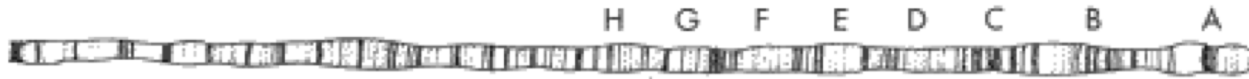
Chromosomal Variation



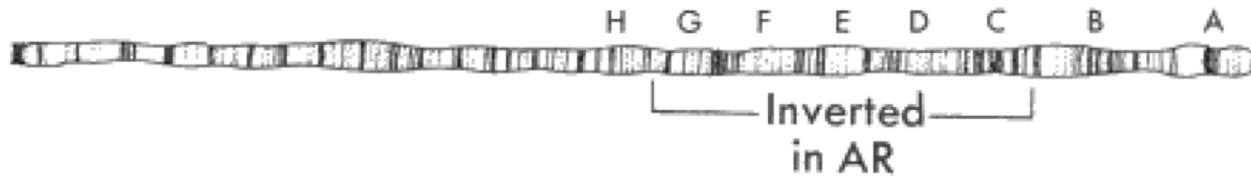
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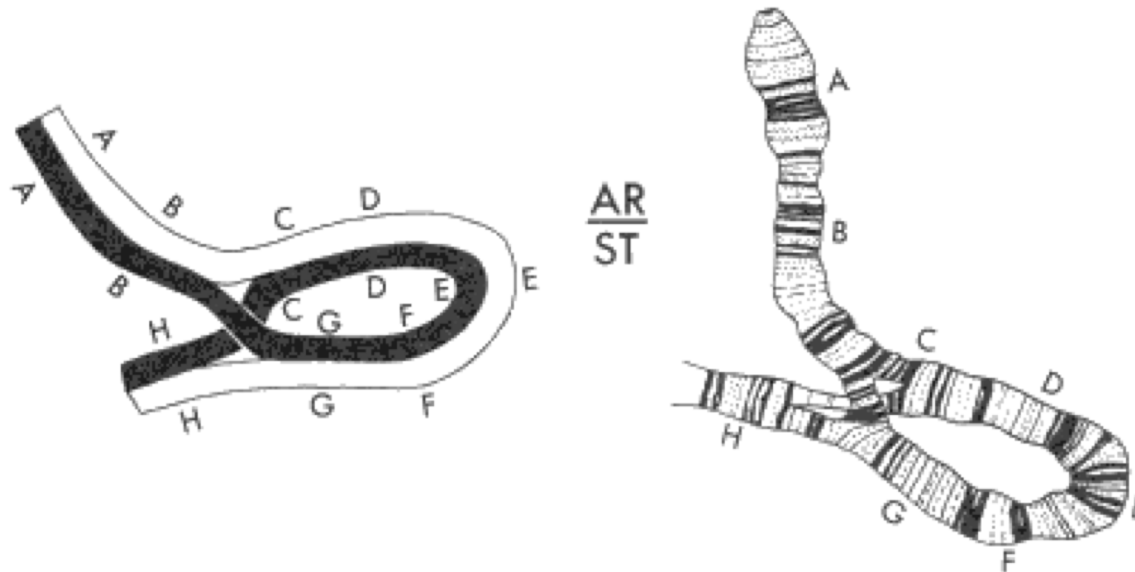
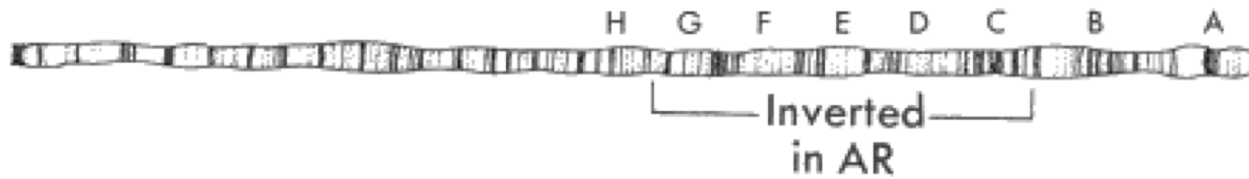
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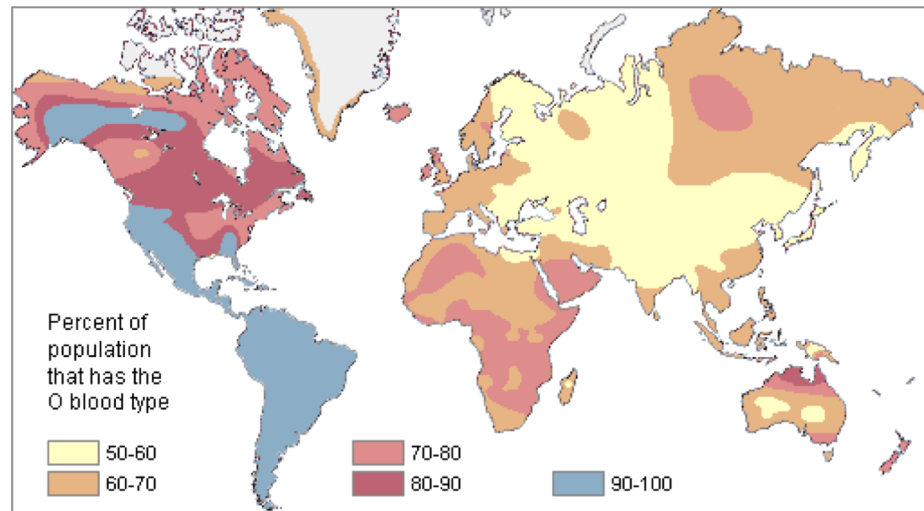
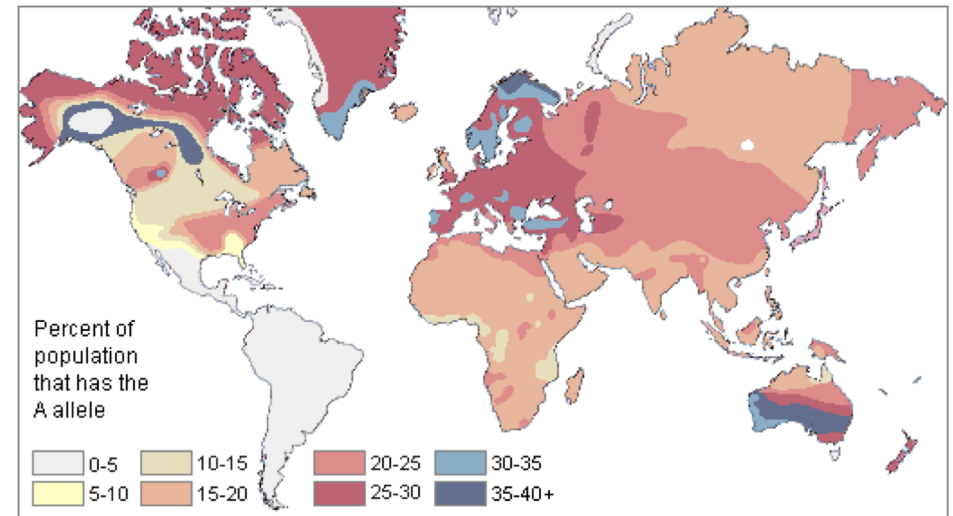
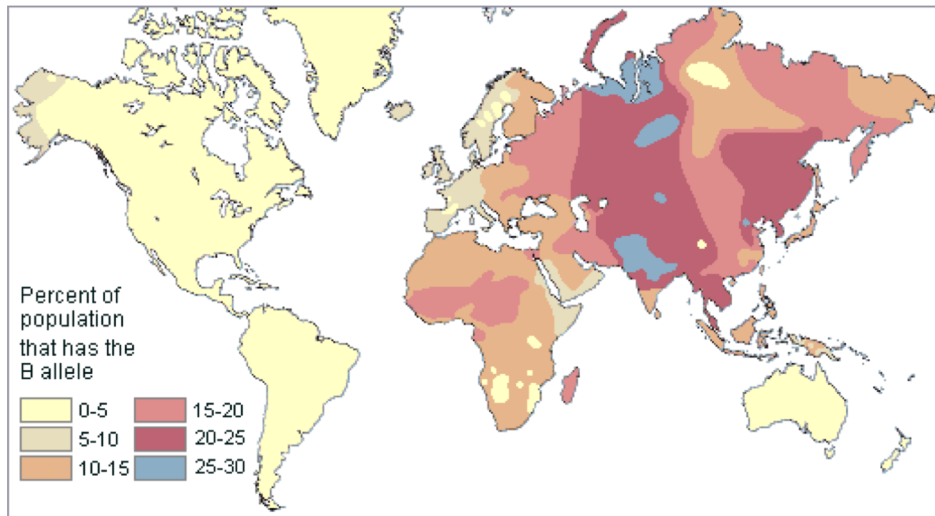


Chromosomal Variation



Protein variation

- ABO blood groups



Protein variation

- Allozymes: variant forms of an enzyme encoded by different alleles at the same locus
- Variation revealed using electrophoresis

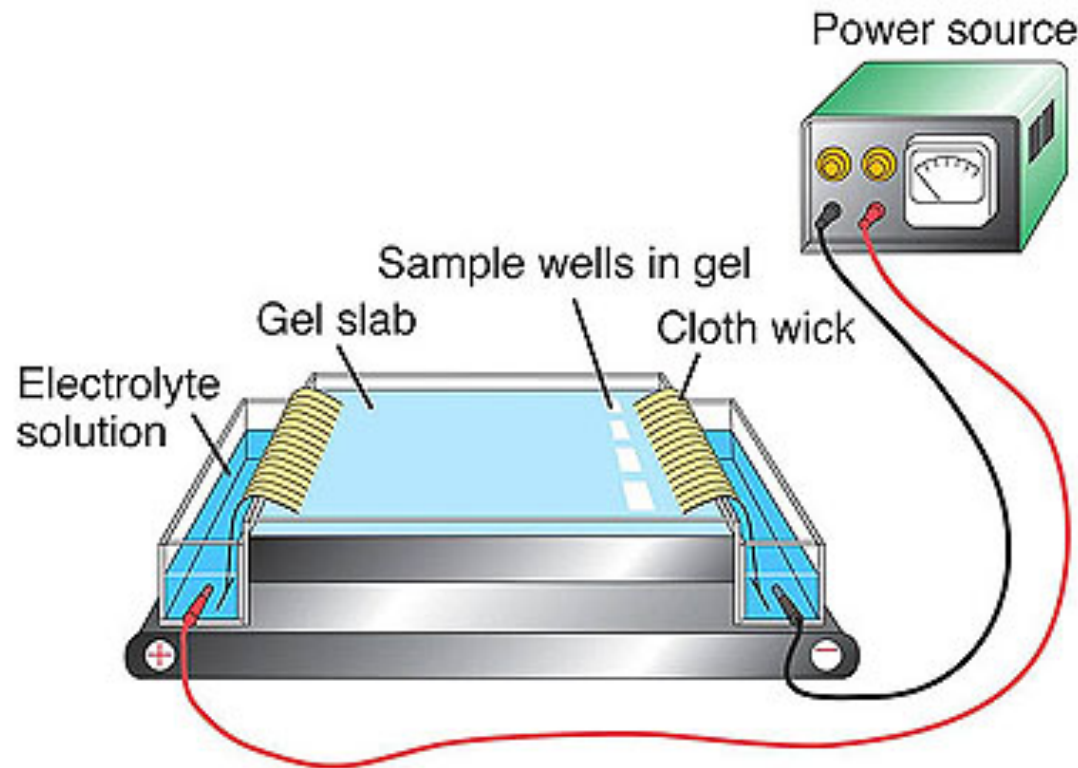
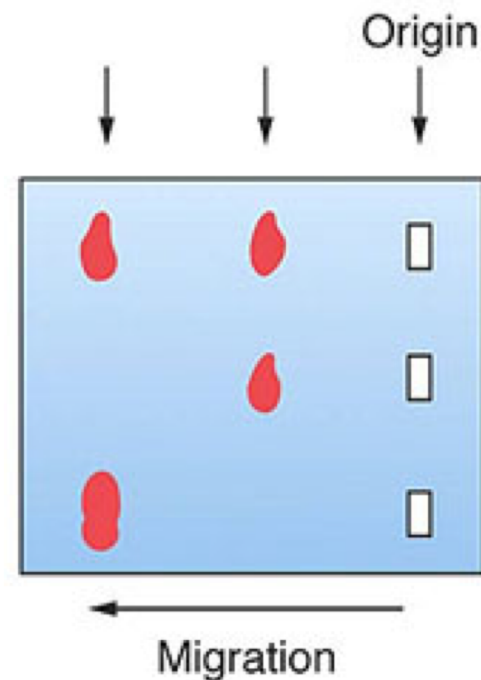


Figure 4: Schematic of devices used in protein electrophoresis

Protein variation

- Allozymes: variant forms of an enzyme encoded by different alleles at the same locus
- Variation revealed using electrophoresis



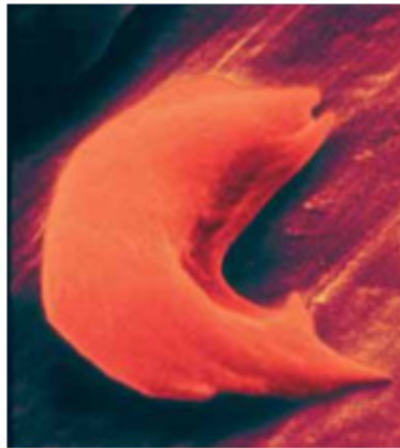
How does it work?

- Nonsynonymous mutations can change enzyme's overall ionic charge
- Leads to differences in electrophoretic mobility

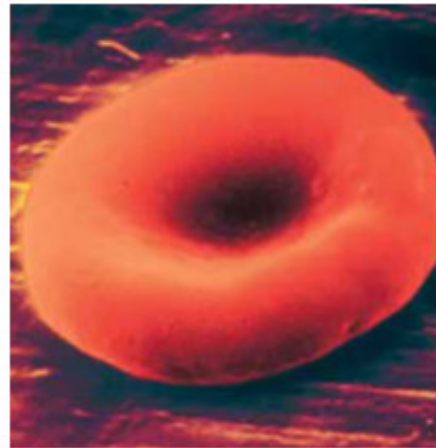
| Amino Acid | 3-Letter | 1-Letter | Side chain polarity | Side chain charge (pH 7.4) |
|---------------|----------|----------|---------------------|--------------------------------|
| Alanine | Ala | A | nonpolar | neutral |
| Arginine | Arg | R | polar | positive |
| Asparagine | Asn | N | polar | neutral |
| Aspartic acid | Asp | D | polar | negative |
| Cysteine | Cys | C | nonpolar | neutral |
| Glutamic acid | Glu | E | polar | negative |
| Glutamine | Gln | Q | polar | neutral |
| Glycine | Gly | G | nonpolar | neutral |
| Histidine | His | H | polar | positive(10%), neutral(90%) |
| Isoleucine | Ile | I | nonpolar | neutral |
| Leucine | Leu | L | nonpolar | neutral |
| Lysine | Lys | K | polar | positive |
| Methionine | Met | M | nonpolar | neutral |
| Phenylalanine | Phe | F | nonpolar | neutral |
| Proline | Pro | P | nonpolar | neutral |
| Serine | Ser | S | polar | neutral |
| Threonine | Thr | T | polar | neutral |
| Tryptophan | Trp | W | nonpolar | neutral |
| Tyrosine | Tyr | Y | polar | neutral |
| Valine | Val | V | nonpolar | neutral |

Protein variation

- Amino acid variation
 - Alternative forms of proteins arising from variation in the amino acid sequence
 - ❖ Sickle-cell disease (HbS): ONE amino acid change in beta-globin chain of hemoglobin



Sickle-cell phenotype



Normal phenotype

DNA variation

- RFLP: Restriction fragment length polymorphism
 - Created by mutation that changes a restriction site

GCCG**C**ATTCTA
CGGC**G**TAAGAT

GCCG**A**ATTCTA
CGGC**T**TAAGAT

DNA variation

- RFLP: Restriction fragment length polymorphism
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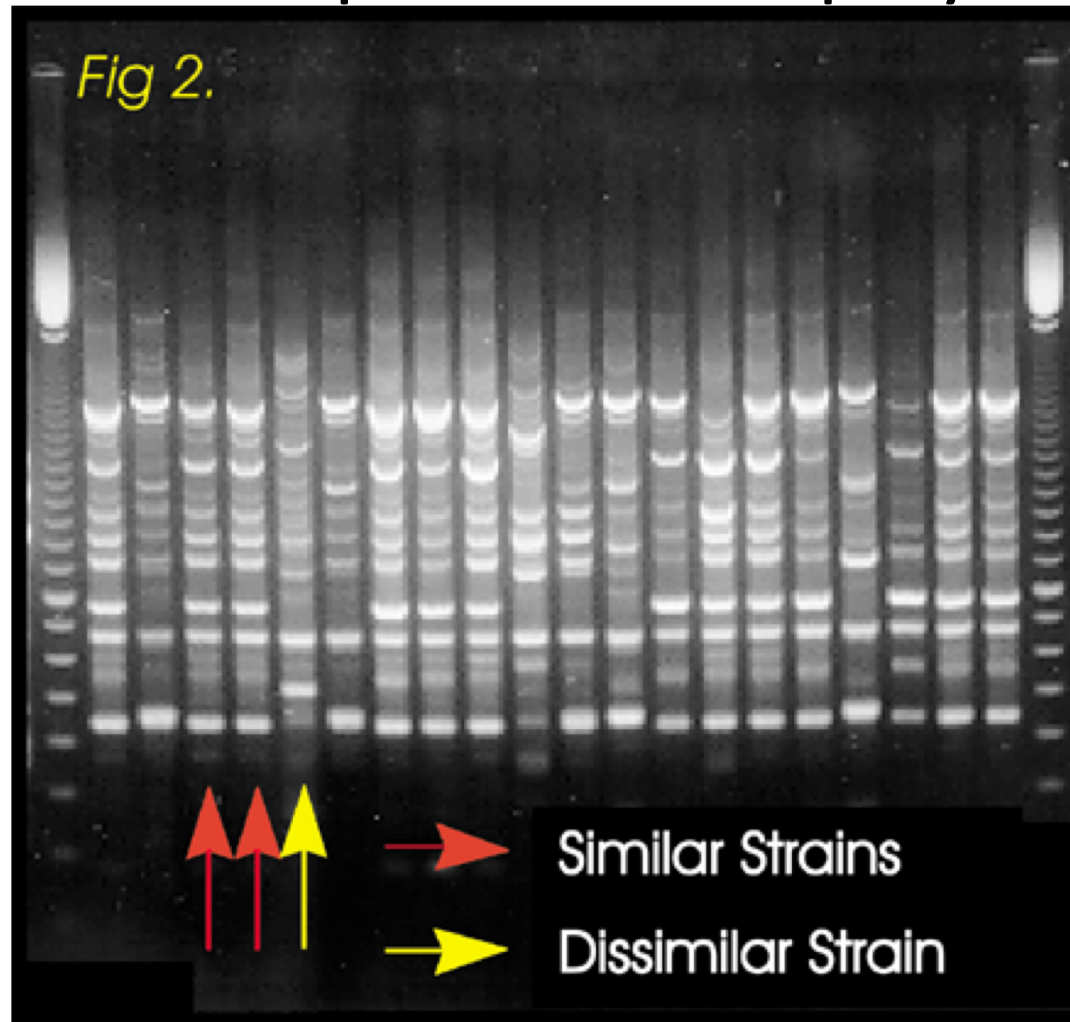


DNA variation

- RFLP
- RAPD: Random amplification of polymorphic DNA
 - Like PCR, but segments are amplified randomly
 - Employs several arbitrary, short primers
 - Need no knowledge of underlying sequence
 - Variation in RAPD profile comes from variation in primer binding sites across individuals

DNA variation

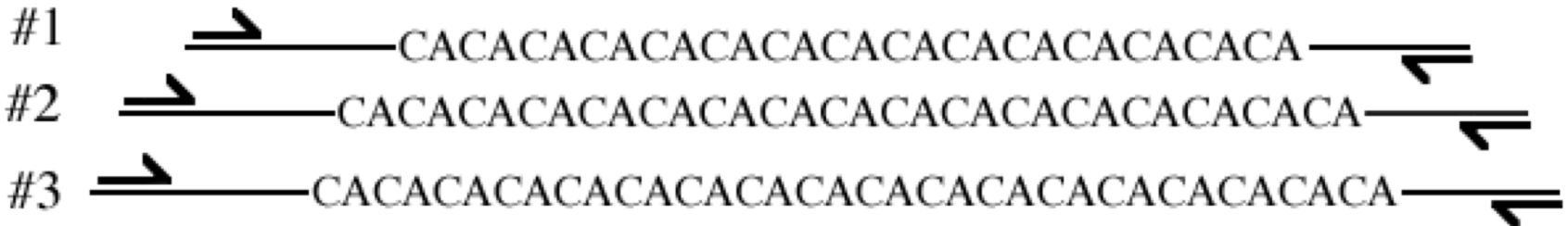
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DNA variation

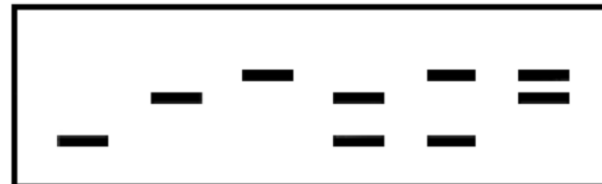
- RFLP
- RAPD
- Microsatellites/minisatellites/VNTRs/SSRs:
Tandemly repeated short sequences

ALLELES



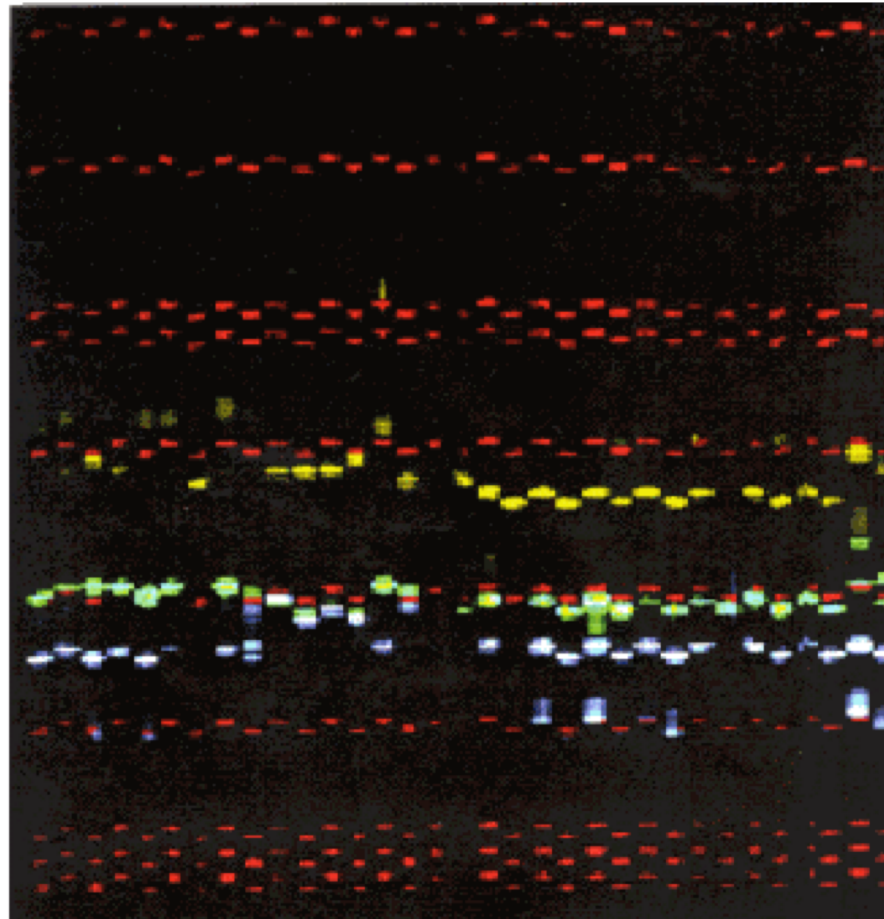
GENOTYPES

1/1 2/2 3/3 1/2 1/3 2/3



DNA variation

- RFLP
- RAPD
- Microsatellites/minisatellites/VNTRs/SSRs:



Leishmania (Viannia)
isolates

From London School of
Hygiene and Tropical
Medicine

DNA variation

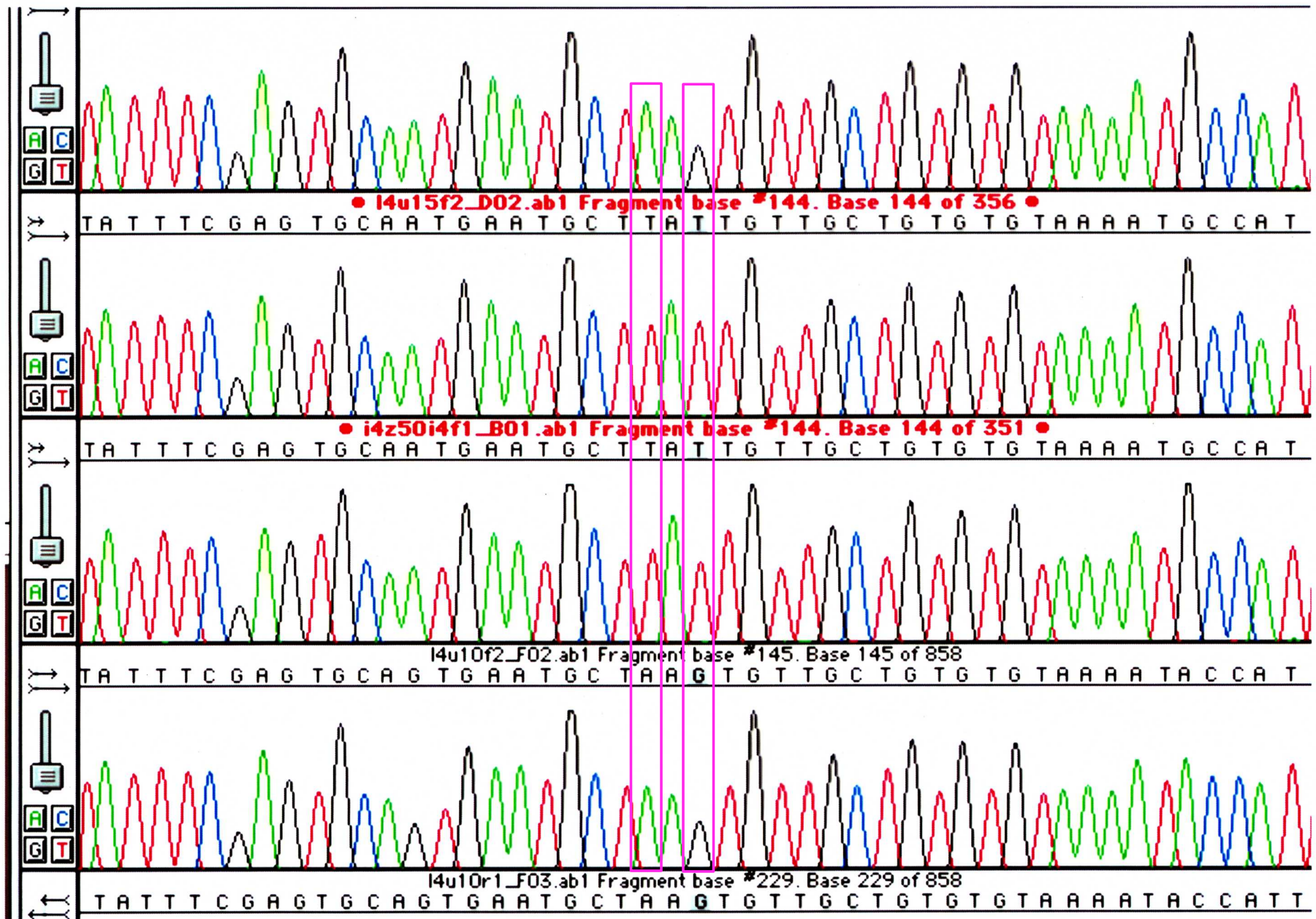
- RFLP
- RAPD
- Microsatellites/minisatellites/VNTRs/SSRs
- Insertion/Deletion: Gain or loss of DNA segment

```
JF330184  GTATGATGCAGGCATGCAGCTACAGTGTATGAACTATGTTGGATGCTTTAACATCATAT—ATACTT—————
JF330186  GTATGATGCAGGCATGCAGCTACAGTGTATGAACTATGTTGGATGCTTTAACATCATAT—ATACTT—————
JF330197  GTATGATGCAGGCATGCAGCTACAGTGTATGAACTATGTTGGATGCTTTAACATCATAT—ATACTT—————
JF330194  GTATGATGCAGGCATGCAGCTACAGTGTATGAACTATGTTGGATGCTTTAACATCATAT—ATACTT—————
JF330196  GTATGATGCAGGCATGCAGCTACAGTGTATGAACTATGTTGGATGCTTTAACATCATAT—ATACTT—————
JF330191  GTATGATGCAGGCATGCAGCTACAGTGTATGAACTATGTTGGATGCTTTAACATCATAT—ATACTT—————
JF330188  GTATGATGCAGGCATGCAGCTACAGTGTATGAACTATGTTGGATGCTTTAACATCATAT—ATACTT—————
JF330185  GTATGATGTAG———CTACAGTGTATGAACTATGTTGAATGCTTTAACITCATCATACTTTA TCAAAAAC TTTAAA———GAAATGATAAT———
JF330190  GTATGATGTAG———CTACAGCGTATGAACTATGTTGAATGCTTTAACITCATCATACTTTA TCAAAAAC TTTAAA———GAAATGATAAT———
JF330192  GTATGATGTAG———CTACAGTGTATGAACTATGTTGAATGCTTTAACITCATCATACTTTA TCAAAAAC TTTAAA———GAAATGATAAT———
JF330193  GTATGATGTAG———CTACAGTGTATGAACTATGTTGAATGCTTTAACITCATCATACTTTA TCAAAAAC TTTAAA———GAAATGATAAT———
JF330198  GTATGATGTAG———CTACAGTGTATGAACTATGTTGAATGCTTTAACITCATCATACTTTA TCAAAAAC TTTAAA———GAAATGATAAT———
JF330189  GTATGATGTAG———CTACAGTGTATGAACTATGTTGGATGCTTTAACITCATCATACTTTA TCAAAAAC TTTAAA———CGAATGATAAT———
JF330196  GTATGATGTAG———CTACAGTGTATGAACTATGTTGAATGCTTTAACITCAACATCATACTTTA TCA TAAAC TTTAAACATTCATACTTACGGAAATGATAAT———
JF330187  GTATGATGCAG———CTACCGTGTATGAACTATGTTGAATGCTTTAACITCAACATCATACTTTA TCAAAAAC TTTTITTTTTC———CGGGATACTTTATCAAAAAC TTT
```


DNA variation

- RFLP
- RAPD
- Microsatellites/minisatellites/VNTRs/SSRs
- Insertion/Deletion
- Single Nucleotide Polymorphism: Differences at a single nucleotide

Sequence reads from 4 individuals



Discrete Genetic Variation

- Chromosomal variation
 - Inversions, chromosomes fusions/fissions
- Protein variation
 - Immunological, allozymes, amino acid variation
- DNA variation
 - RFLP, RAPD, VNTR, Indel, SNP

Where does genetic variation come from?

Mutation is the substrate of evolution

- All (genetic) polymorphisms originate with mutation
- Point mutation (one base for another)

Mutation is the substrate of evolution

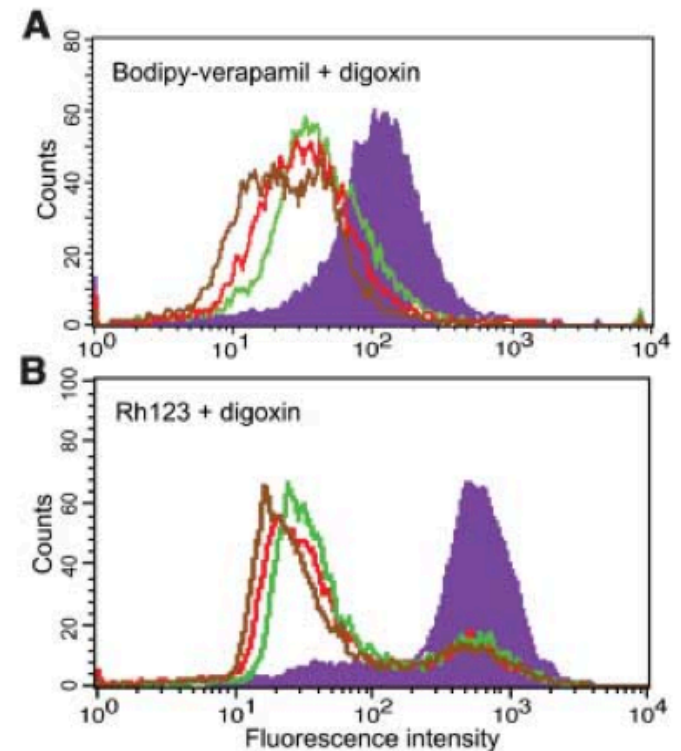
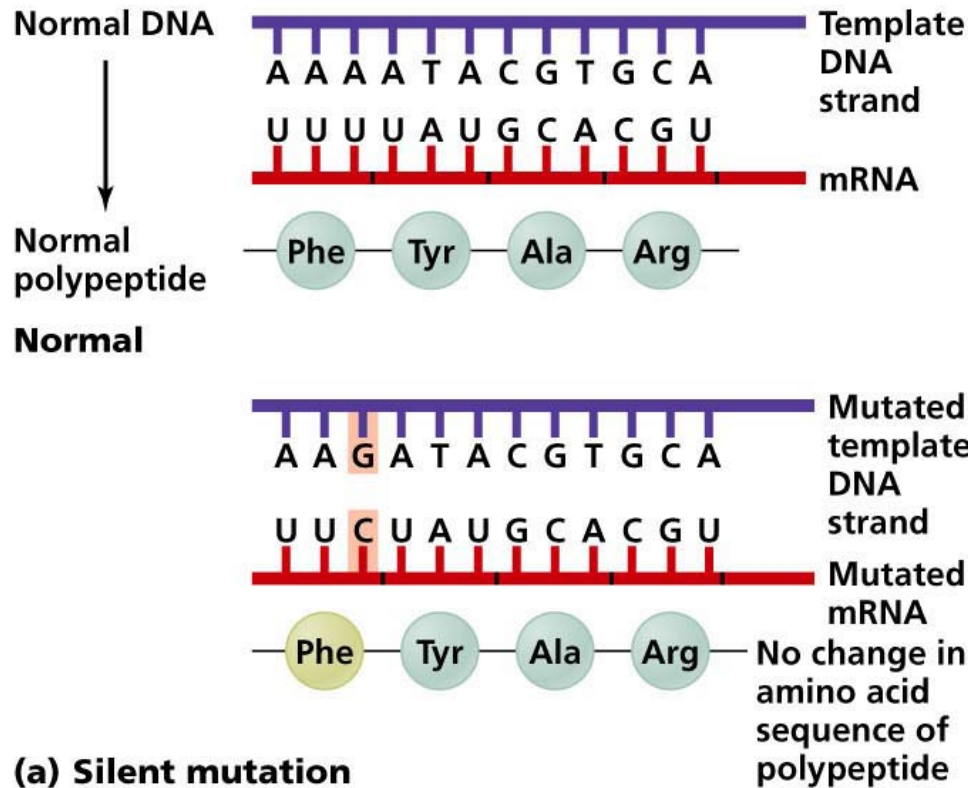
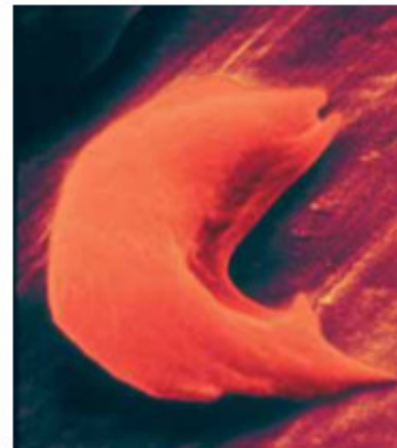
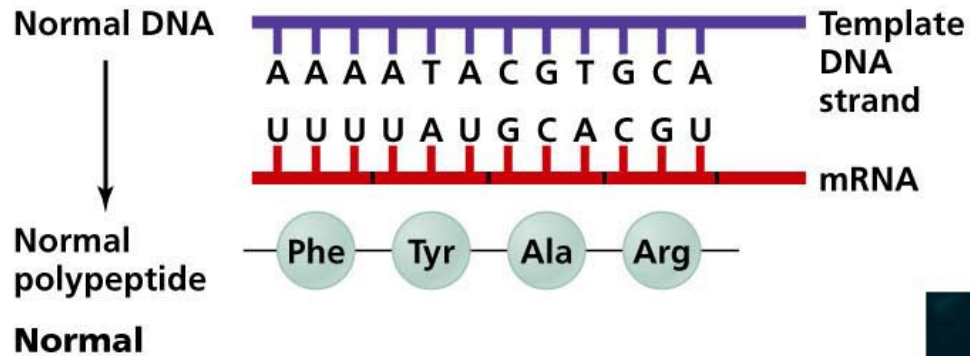
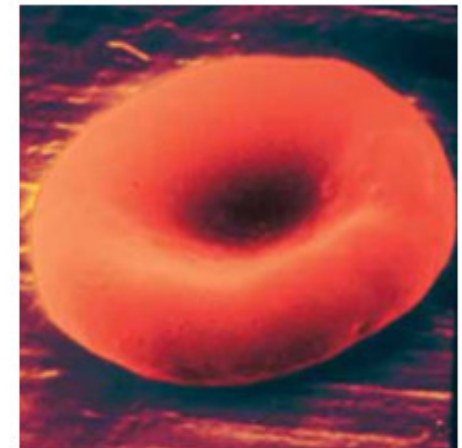


Fig. 4. Drug transport function of wild-type and two MDR1 haplotypes. The drug efflux of vaccinia infected/transfected HeLa cells was determined by FACS analysis (14). Cells were transfected with pTM1 (control; purple), MDR1, (wild-type P-gp; green), C1236T-G2677T-C3435T (red), and C1236T-G2677T-C3435A (brown). (A) 0.5 μ M bodipy-FL-verapamil in the presence of 500 μ M digoxin; (B) 0.5 μ M Rh123 in the presence of 150 μ M digoxin.

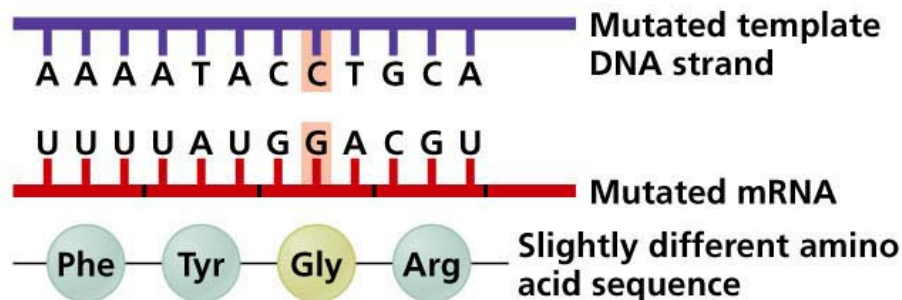
Mutation is the substrate of evolution



Sickle-cell phenotype

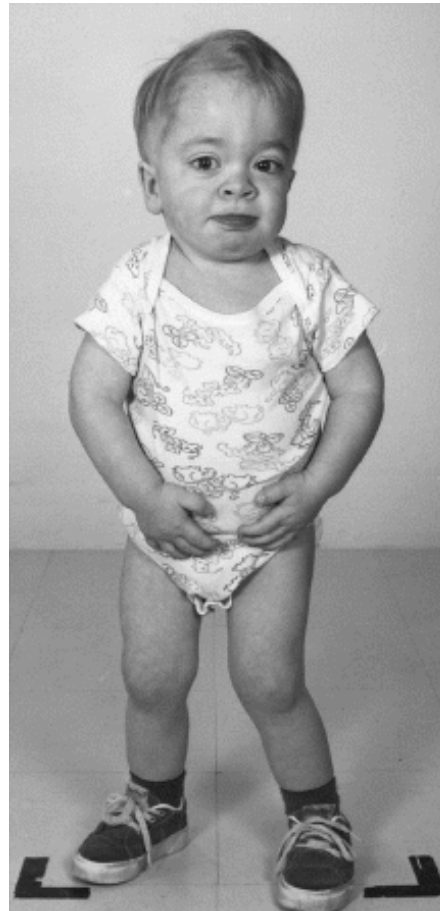
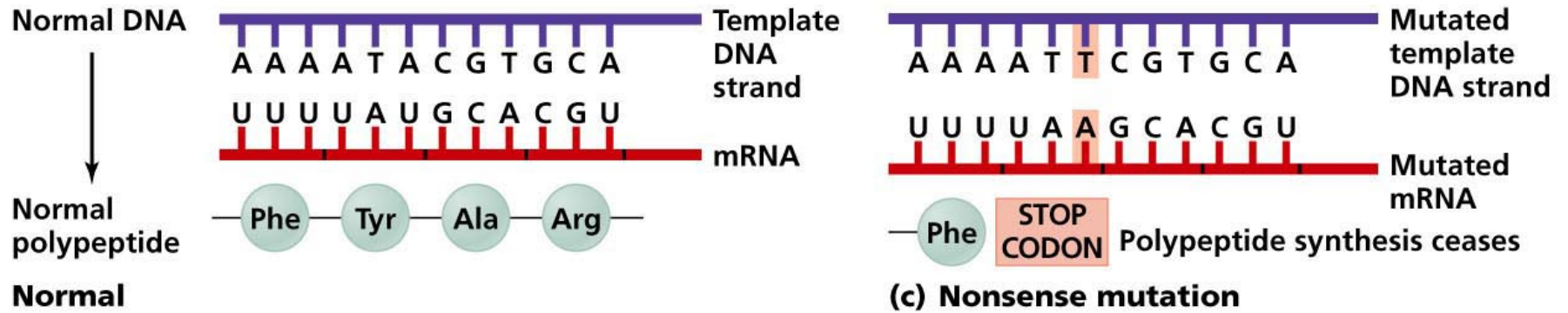


Normal phenotype



(b) Missense mutation

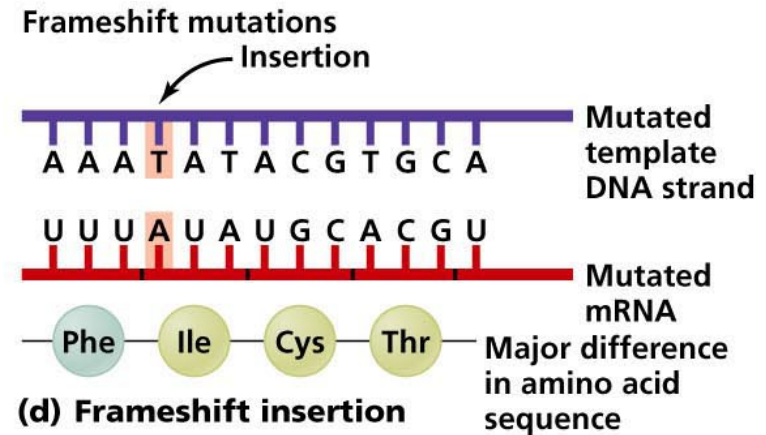
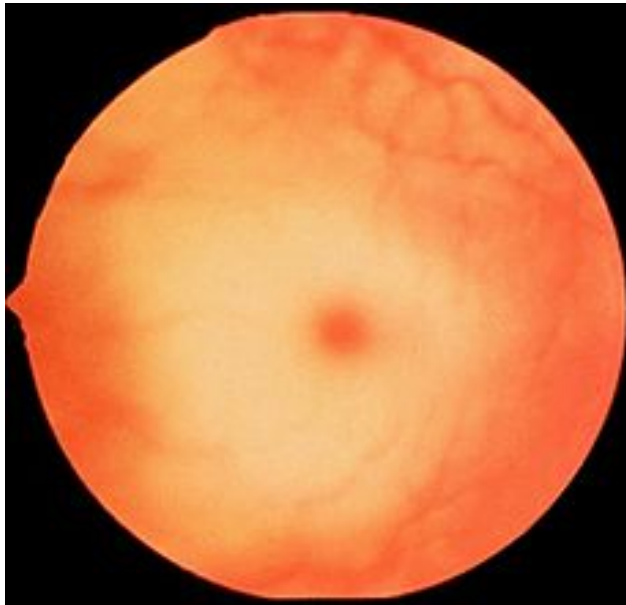
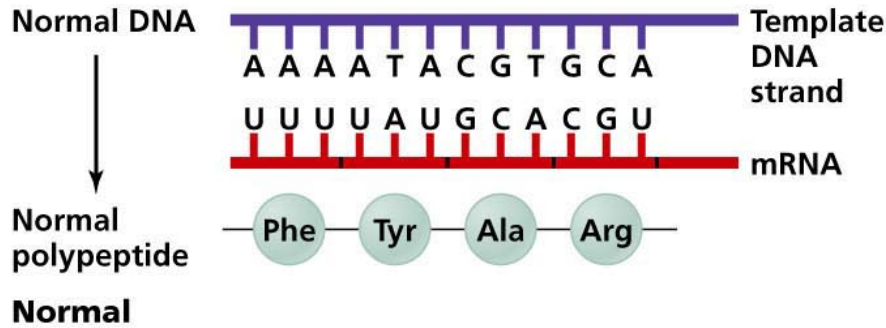
Mutation is the substrate of evolution



Mutation is the substrate of evolution

- All polymorphisms originate with mutation
- Point mutation (one base for another)
- Insertion (addition of DNA)

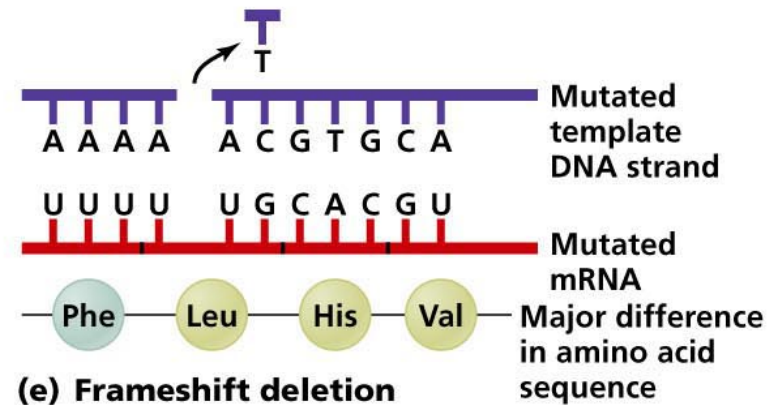
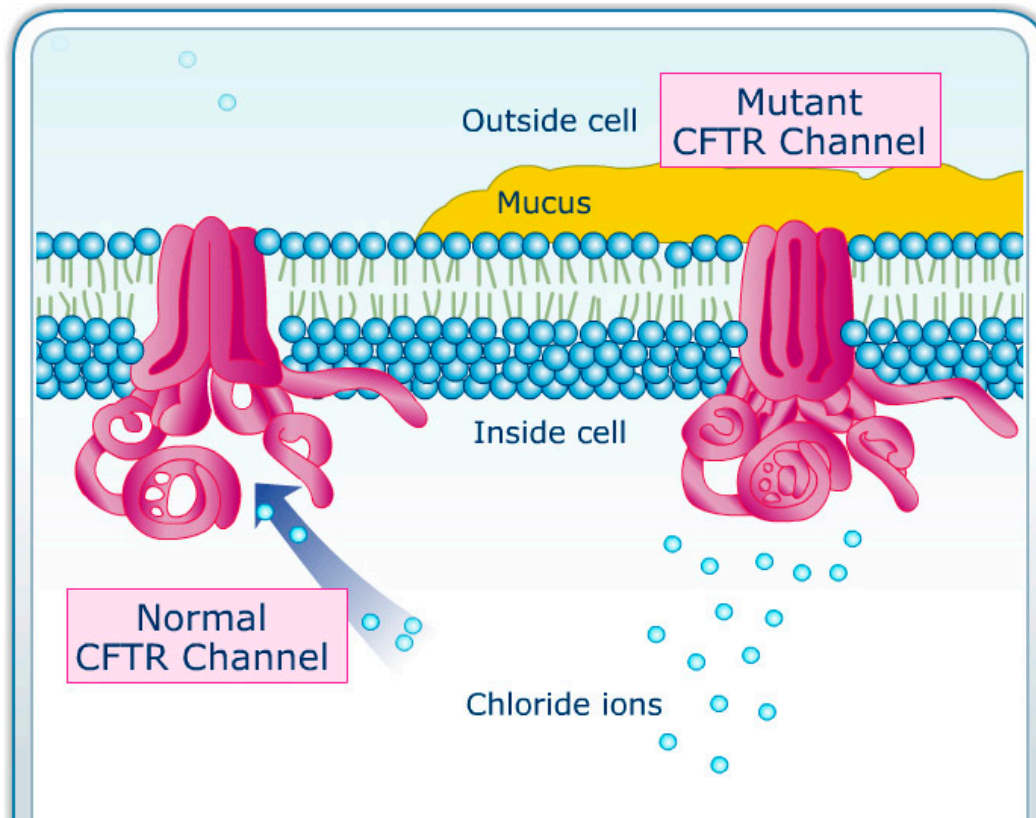
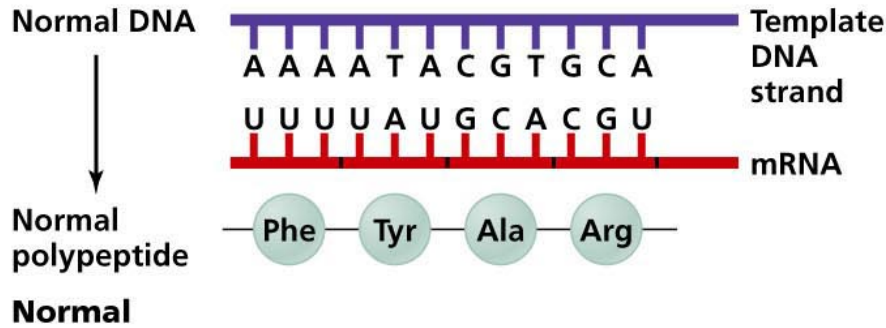
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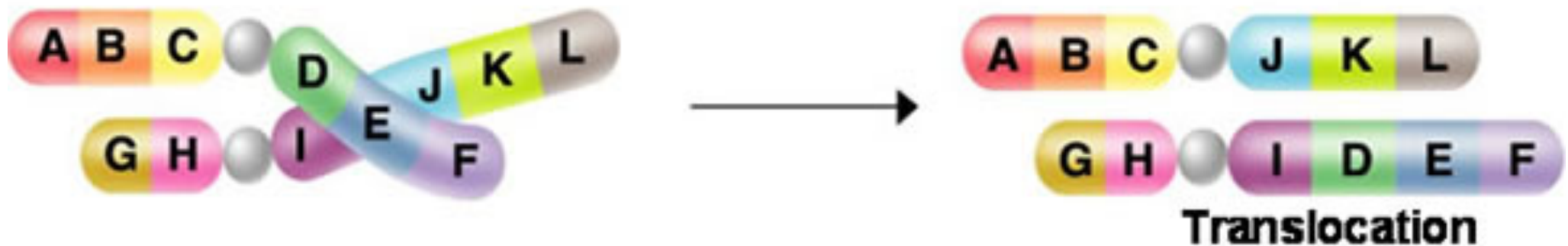
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Mutation is the substrate of evolution

- All polymorphisms originate with mutation
- Point mutation (one base for another)
- Insertion (addition of DNA)
- Deletion (loss of DNA)
- Chromosomal mutations

Mutation is the substrate of evolution



Genetic Variation

- All genetic variation originates with mutation
 - Mutation is the substrate of evolution
- All levels of organization from single base pairs to entire genomes
- Understanding genetic variation has deep implications
- Population genetics aimed at understanding genetic variation within populations

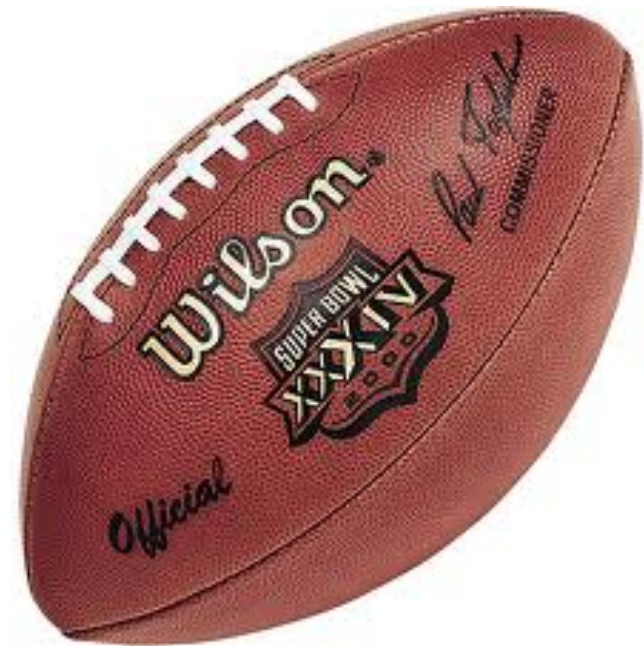
Why do we care about genetic variation?

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 - Including disease risk and responses to drugs and environmental factors



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- Public Health



Why do we care about genetic variation?

- Genetic variation underlies phenotypic differences among individuals
 - Including disease risk and responses to drugs and environmental factors
- Individual identification
- Manage resources
- Public Health
- Improve plant and animal food products
- Understand genetic basis of disease and other complex phenotypes including behaviours
- Insights into evolutionary history, ancestry

Key Terms

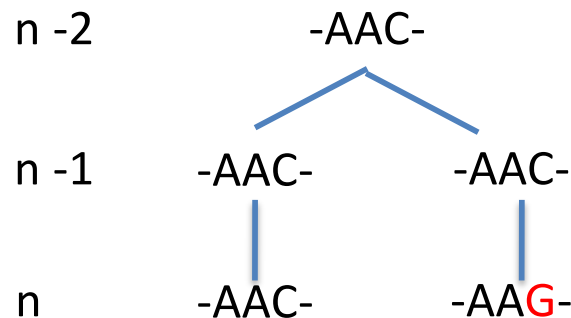
- Population: A group of individuals of a single species that, if sexual, is capable of exchanging genes
- Sample: A finite number of individuals collected from a population
- Polymorphism: Character that is variable within a species
- Allele: Variant at a specific locus in the genome
- Genotype: The allelic makeup of an individual
 - Homozygote (identical alleles at a locus in an individual)
 - Heterozygote (different alleles at a locus in an individual)

Key Terms

- Identical by state
 - Nucleotide level: Alleles have identical nucleotide sequences
 - Amino acid level: Alleles have identical amino acid sequences

Key Terms

- Identical by state
 - Nucleotide level: Alleles have identical nucleotide sequences
 - Amino acid level: Alleles have identical amino acid sequences
- Identical by descent: Alleles share a common ancestor allele (in the short term)
 - Need not be identical by state



Allele Frequency

Individual Allele

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | a | C | A | T | A | G | A | A | C | C | T | G | G | G | C | A | C | T | T | C | A |
| 2 | b | . | . | . | A | . | T | . | . | . | . | G | . | . | . | C | . | . | . | T | . |
| 3 | c | . | . | . | G | . | A | . | . | . | . | G | . | . | . | A | . | . | . | C | . |
| 4 | d | . | . | . | G | . | A | . | . | . | . | T | . | . | . | A | . | . | . | C | . |
| 5 | b | . | . | . | A | . | T | . | . | . | . | G | . | . | . | C | . | . | . | T | . |

- Allele frequency: number of instances of allele/total number of alleles sampled
 - $p_a = 1/5 = 0.2$
 - $p_b = 2/5 = 0.4$
 - $p_c = 1/5 = 0.2$
 - $p_d = 1/5 = 0.2$

Allele Frequency

Individual Allele

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | a | C | A | T | A | G | A | A | C | C | T | G | G | G | C | A | C | T | T | C | A |
| 2 | b | . | . | . | A | . | T | . | . | . | . | G | . | . | . | C | . | . | . | T | . |
| 3 | c | . | . | . | G | . | A | . | . | . | . | G | . | . | . | A | . | . | . | C | . |
| 4 | d | . | . | . | G | . | A | . | . | . | . | T | . | . | . | A | . | . | . | C | . |
| 5 | b | . | . | . | A | . | T | . | . | . | . | G | . | . | . | C | . | . | . | T | . |

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Allele Frequency

Individual Allele

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | a | C | A | T | A | G | A | A | C | C | T | G | G | G | C | A | C | T | T | C | A |
| 2 | b | . | . | . | A | . | T | . | . | . | . | G | . | . | . | C | . | . | . | T | . |
| 3 | c | . | . | . | G | . | A | . | . | . | . | G | . | . | . | A | . | . | . | C | . |
| 4 | d | . | . | . | G | . | A | . | . | . | . | T | . | . | . | A | . | . | . | C | . |
| 5 | b | . | . | . | A | . | T | . | . | . | . | G | . | . | . | C | . | . | . | T | . |

- Allele frequency: number of instances of allele/total number of alleles sampled
 - $p_A = 3/5 = 0.6$
 - $p_G = 2/5 = 0.4$

Allele Frequency

Individual Allele

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | a | C | A | T | A | G | A | A | C | C | T | G | G | G | C | A | C | T | T | C | A |
| 2 | b | . | . | . | A | . | T | . | . | . | . | G | . | . | . | C | . | . | . | T | . |
| 3 | c | . | . | . | G | . | A | . | . | . | . | G | . | . | . | A | . | . | . | C | . |
| 4 | d | . | . | . | G | . | A | . | . | . | . | T | . | . | . | A | . | . | . | C | . |
| 5 | b | . | . | . | A | . | T | . | . | . | . | G | . | . | . | C | . | . | . | T | . |

- Allele frequency: number of instances of allele/total number of alleles
 - Whether estimated per locus or per site, allele frequencies must sum to 1

Genotype Frequency



AA



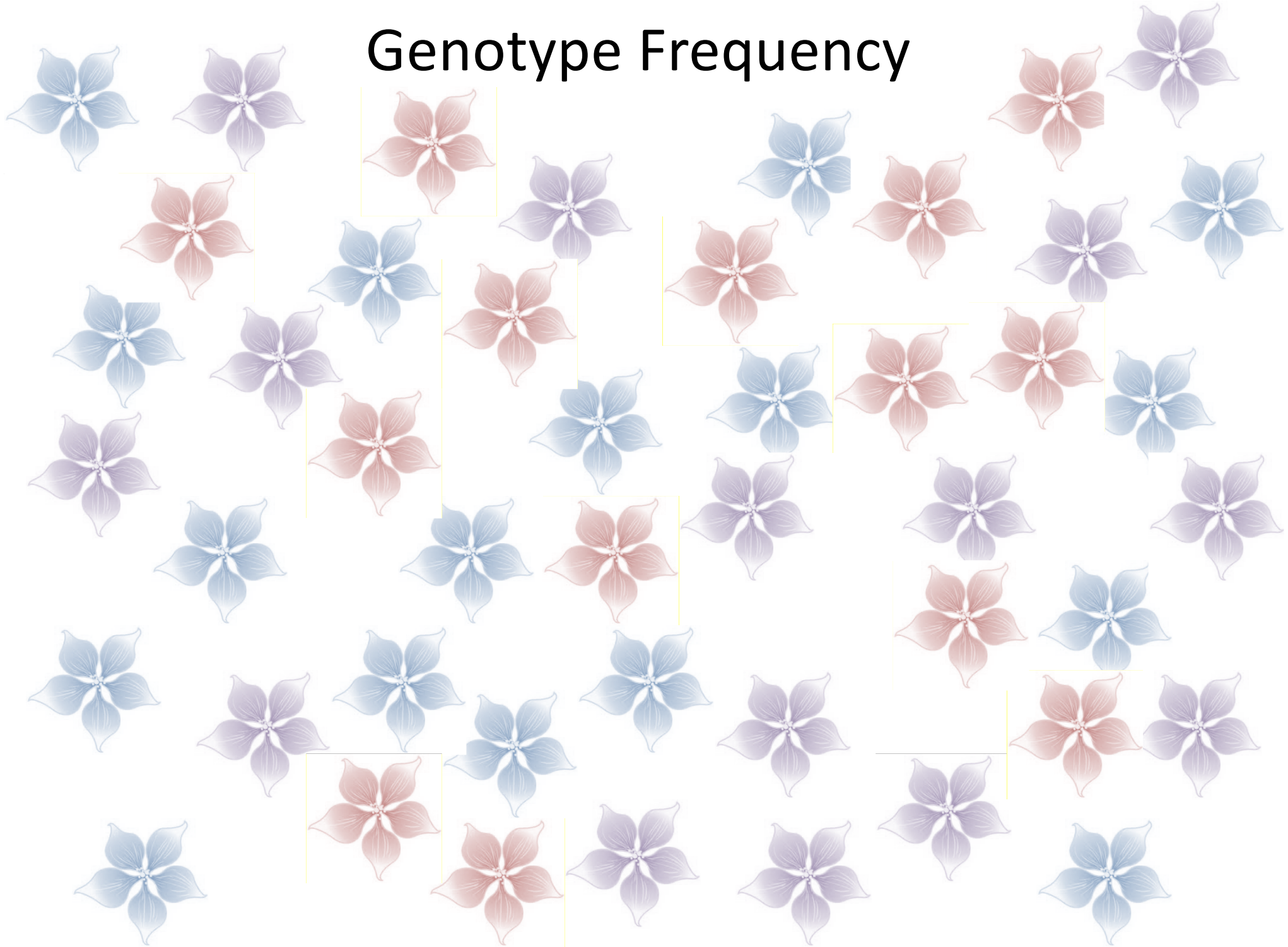
Aa



aa

Genotype

Genotype Frequency



Genotype Frequency



| | | | |
|-----------|------|------|------|
| Genotype | AA | Aa | aa |
| Counts | 17 | 15 | 14 |
| Frequency | 0.37 | 0.33 | 0.30 |

$$p_A = (2 \cdot 17 + 15) / (2 \cdot 46) = 0.53$$

$$p_a = (2 \cdot 14 + 15) / (2 \cdot 46) = 0.47$$