

# Genetic Variation: What it is and how to summarize it

# Genetic Variation

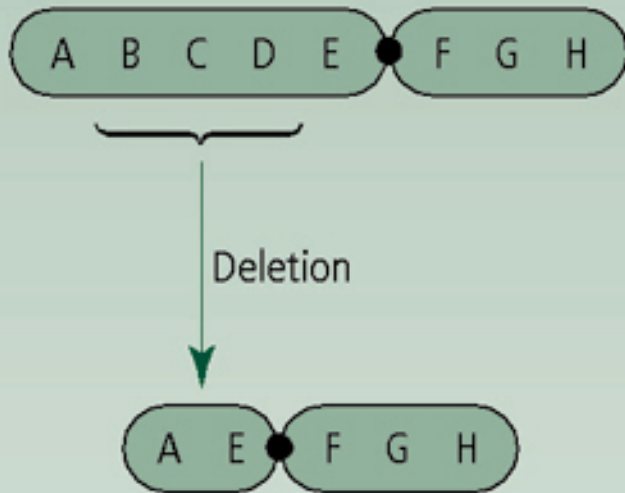
- Chromosomal variation
- Protein variation
- DNA variation

# Chromosomal Variation

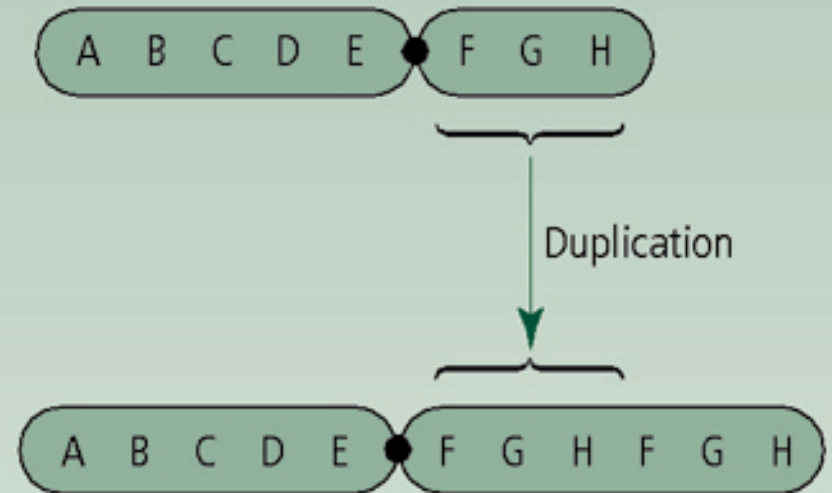
- Variation in chromosome number, gene number, gene order etc.

# Chromosomal rearrangements

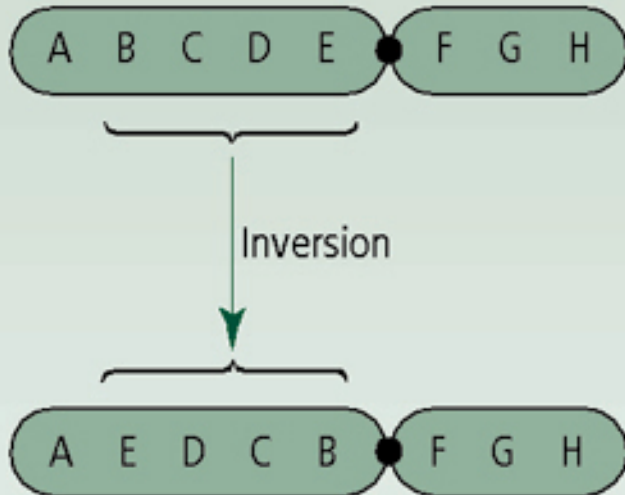
(a)



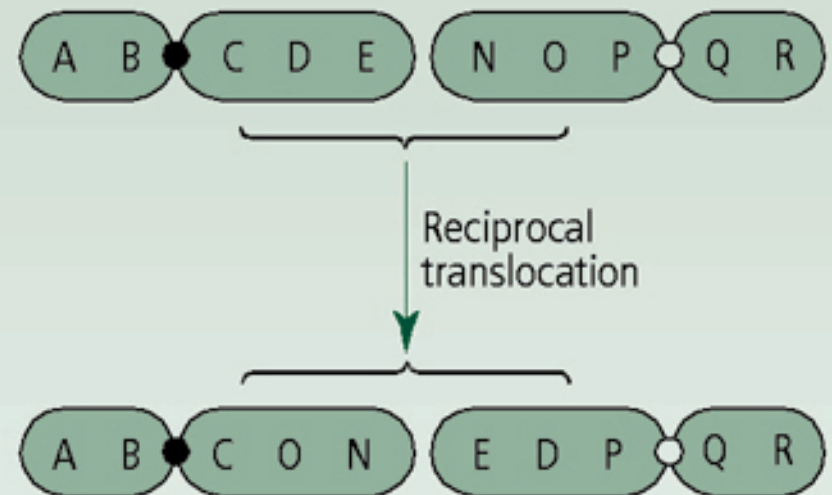
(b)



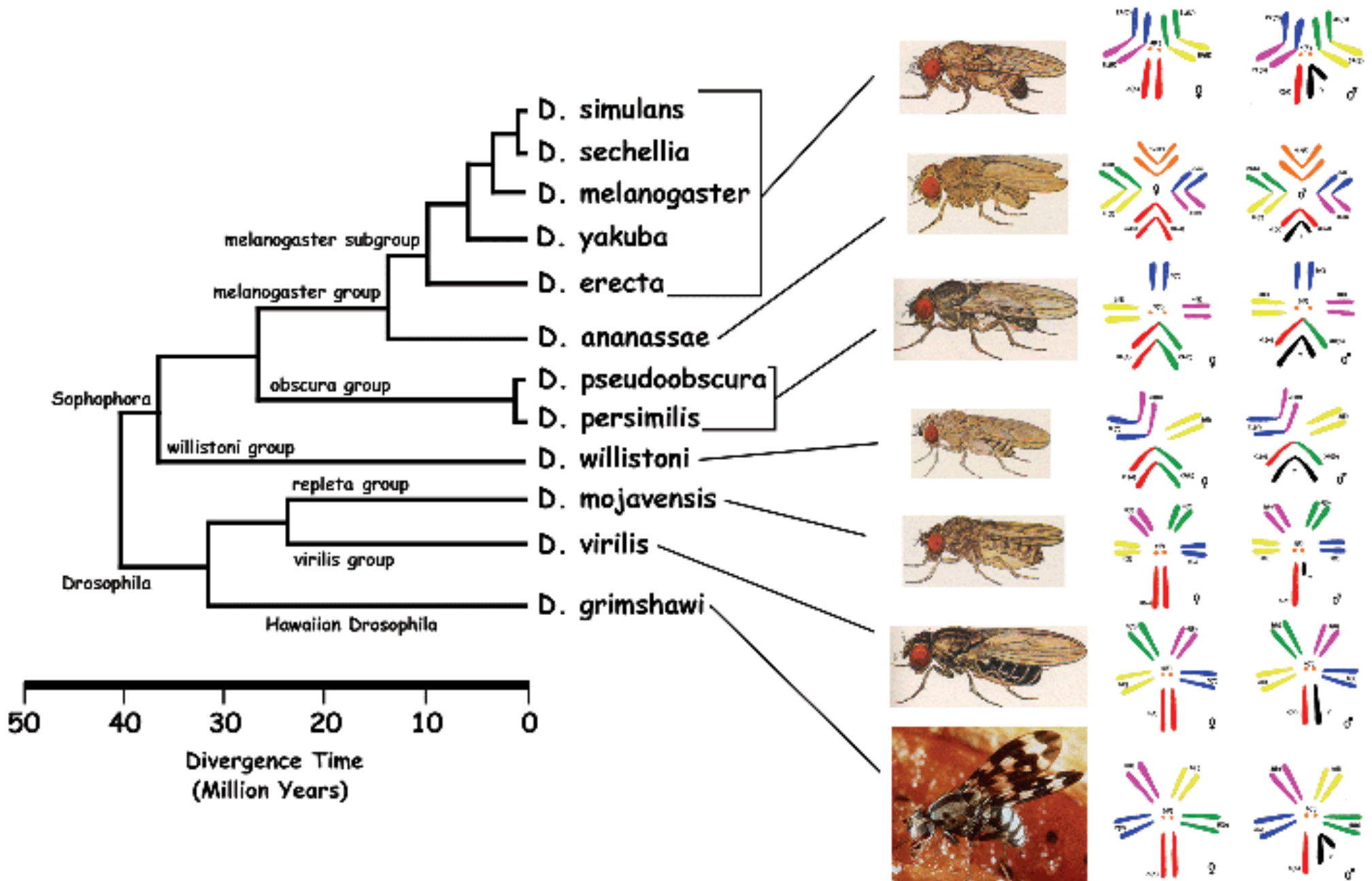
(c)



(d)



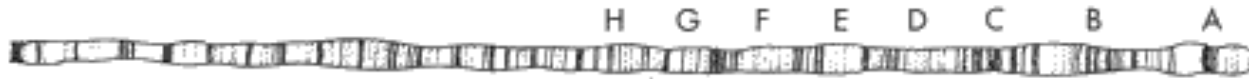
# Chromosomal Variation



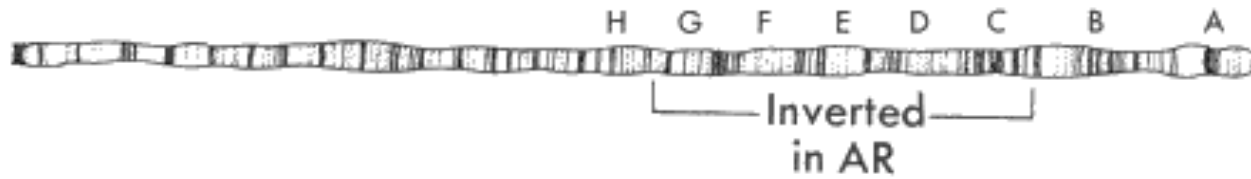
# Chromosomal Variation



# Chromosomal Variation

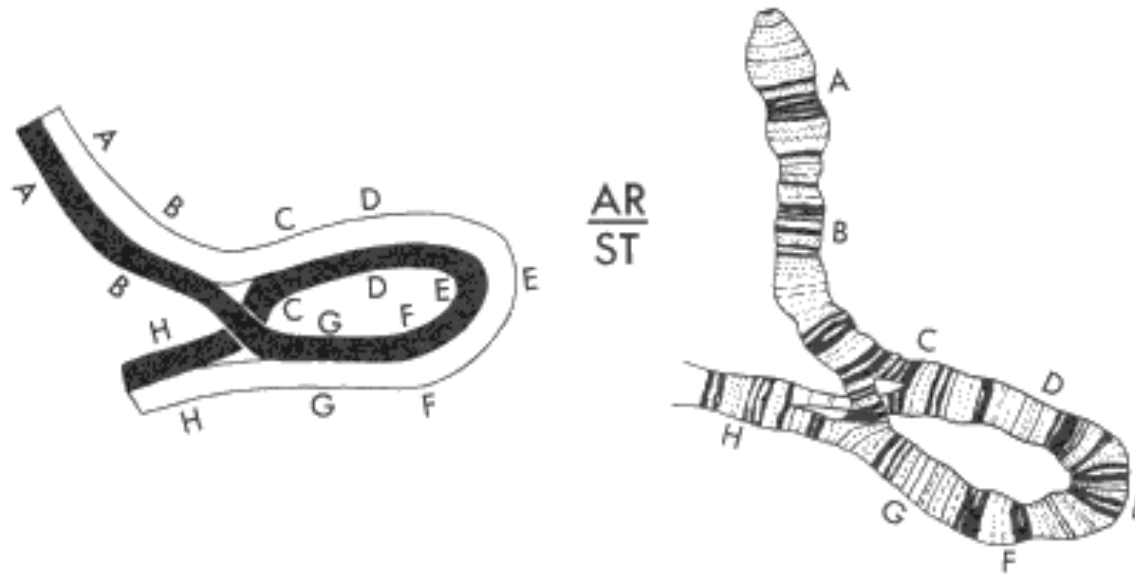
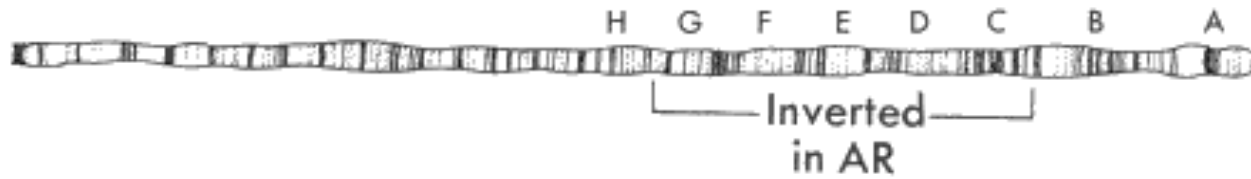


# Chromosomal Variation





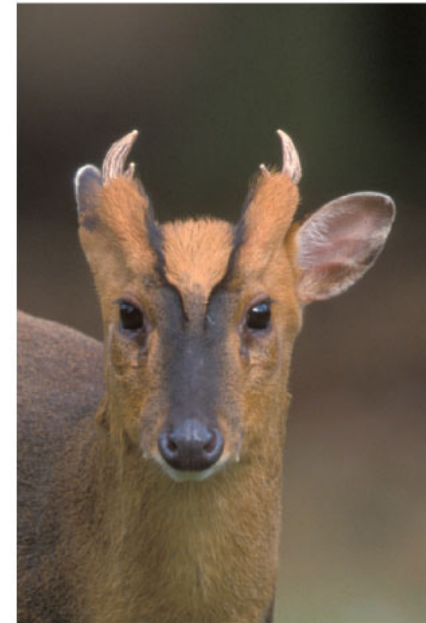
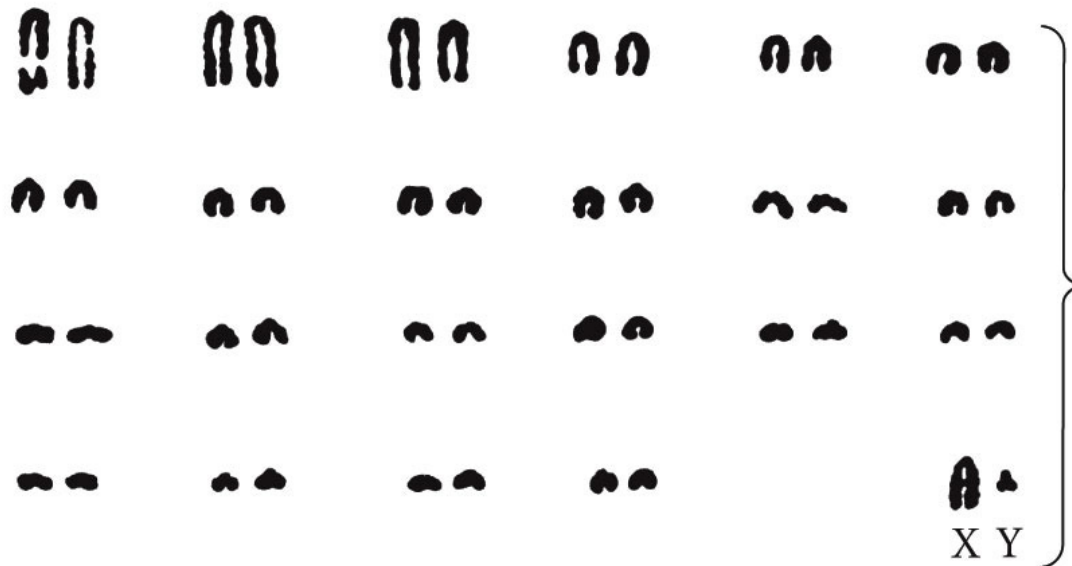
# Chromosomal Variation



From Dobzhansky and Sturtevant

# Chromosomal number changes

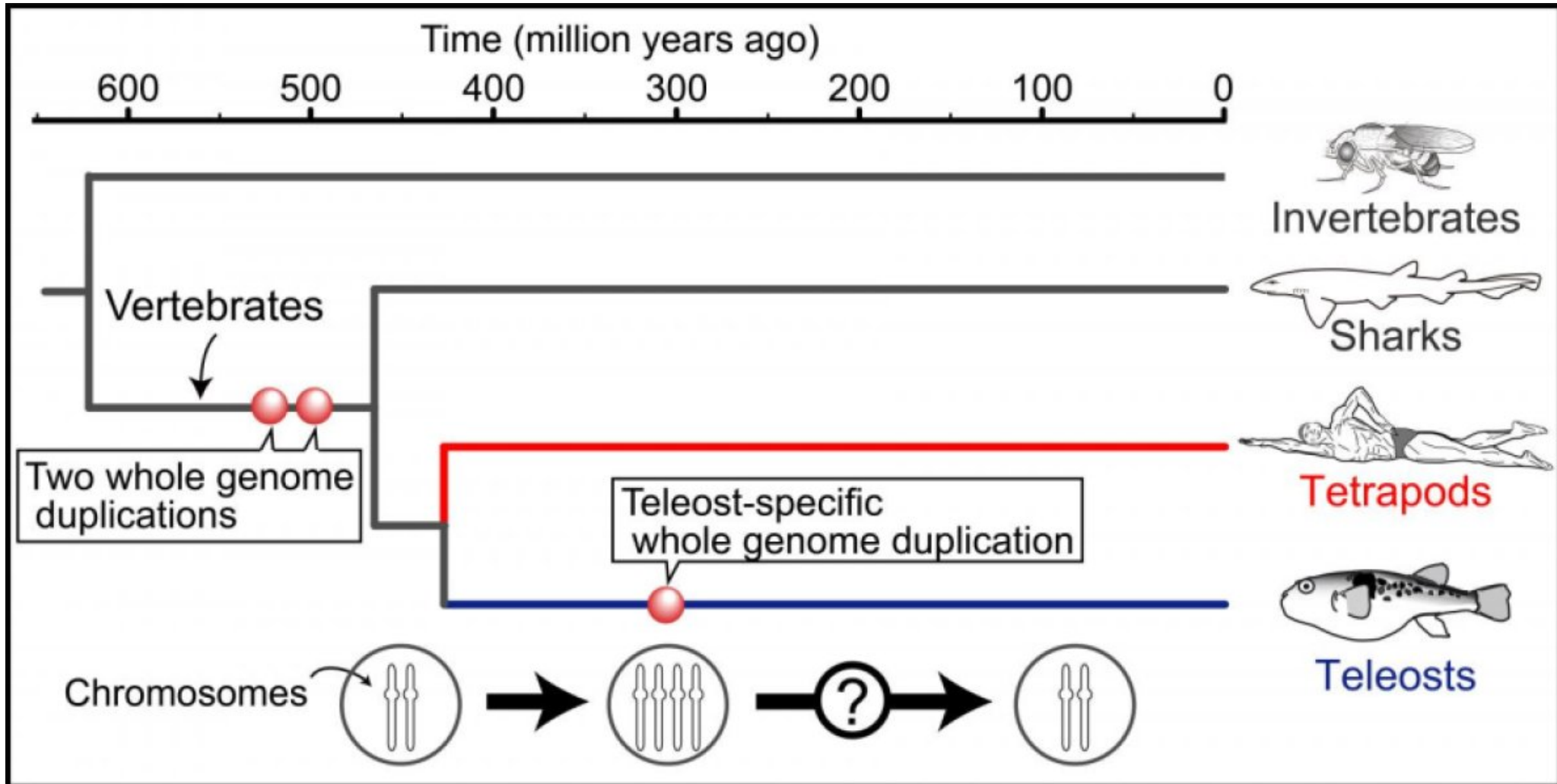
*Muntiacus reevesii* ( $2N = 46$ )



*Muntiacus muntiacus* ( $2N = 8$ )

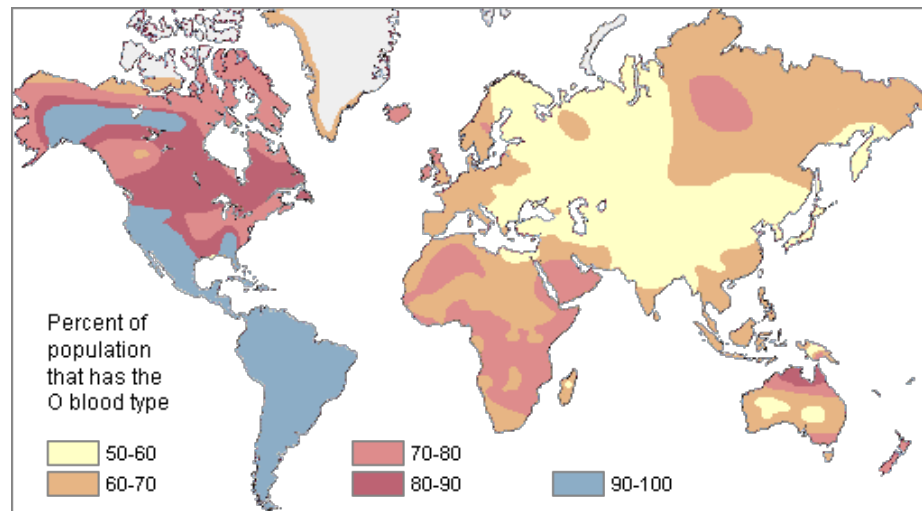
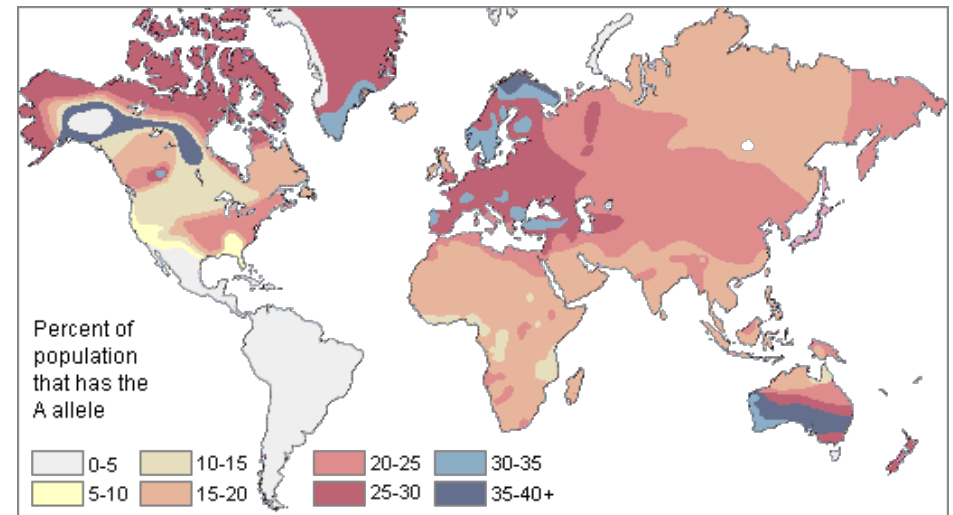
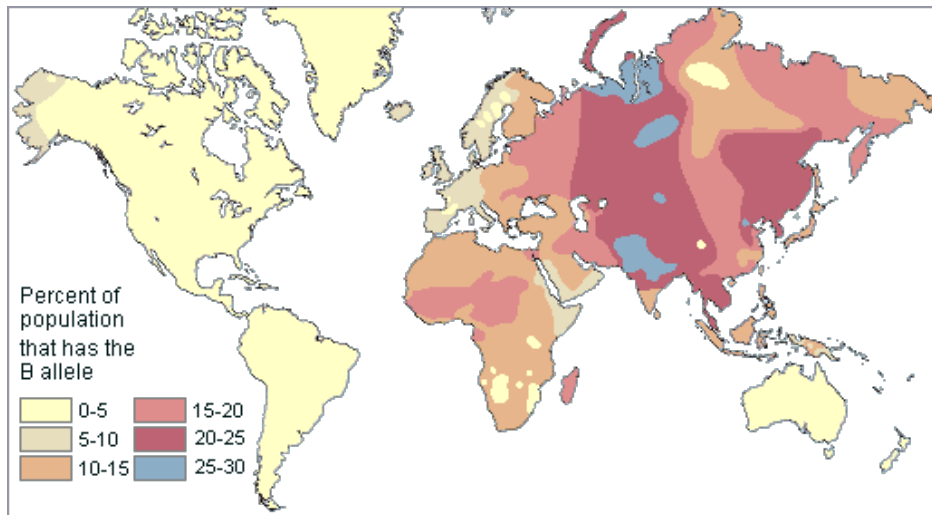


# Genome Duplication



# 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

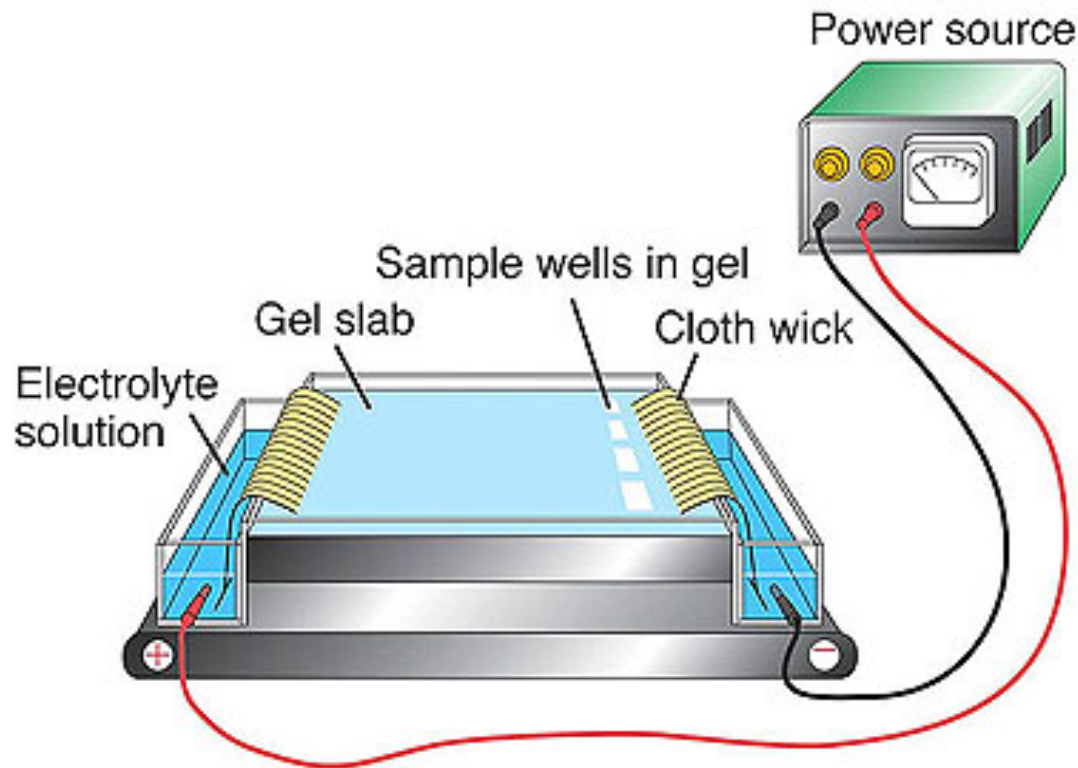
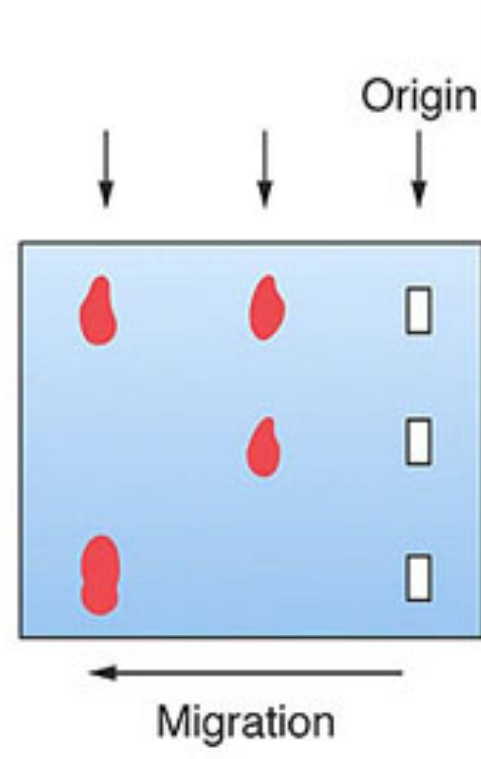


Figure 4: Schematic of devices used in protein electrophoresis

# Protein variation

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- Variation revealed using electrophoresis

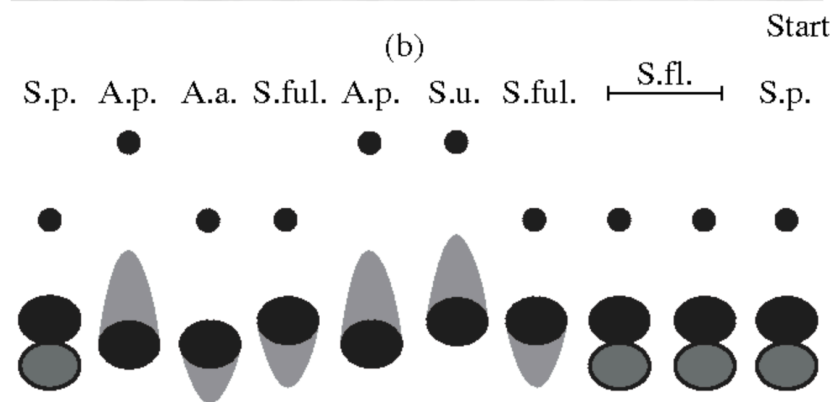
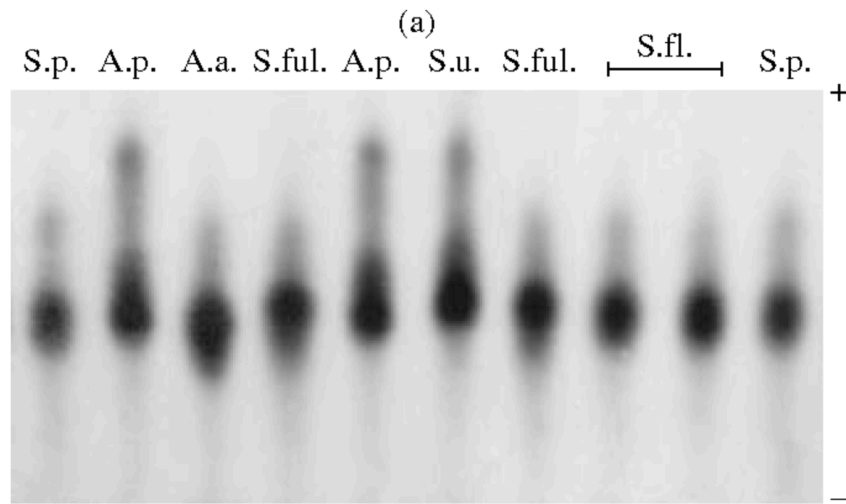


# How does it work?

- 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

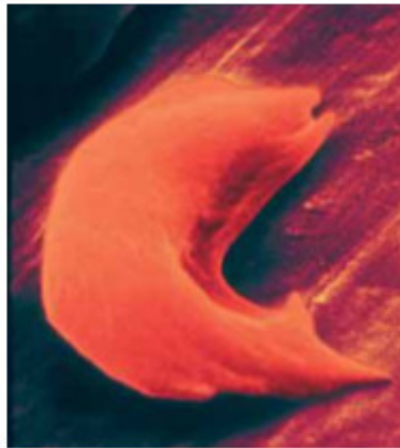


- HB-1
- HB-2
- HB-3
- HB-4

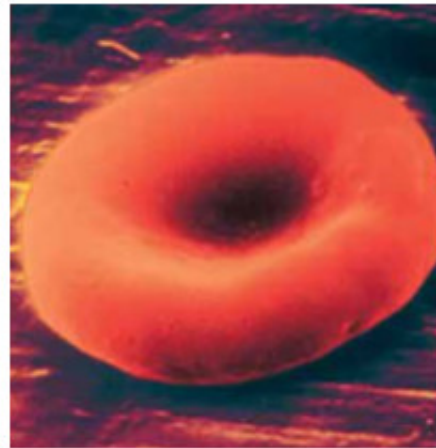


# Protein variation

- 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

– Created by mutations that alter the restriction site



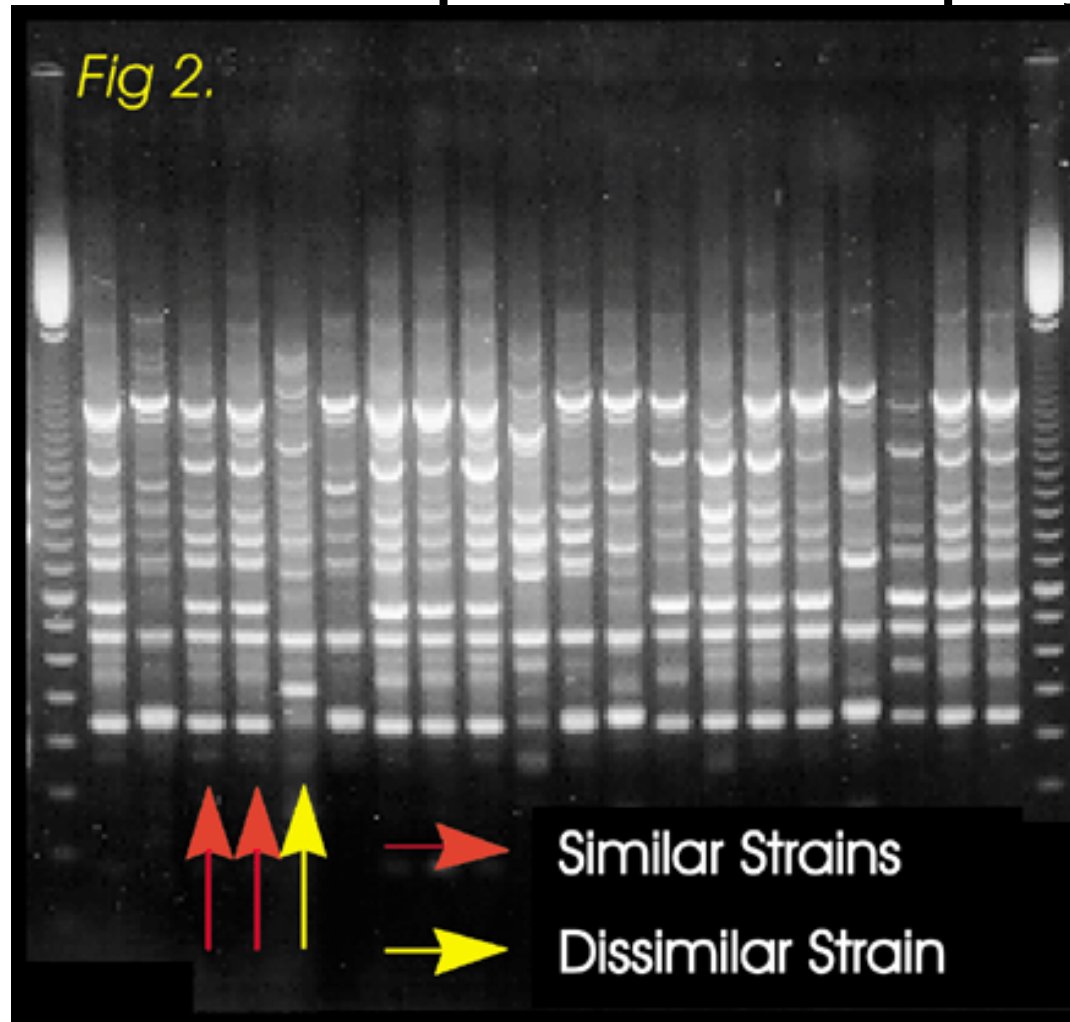
# DNA variation

- 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

- RFLP
- RAPD: Random amplification of polymorphic DNA

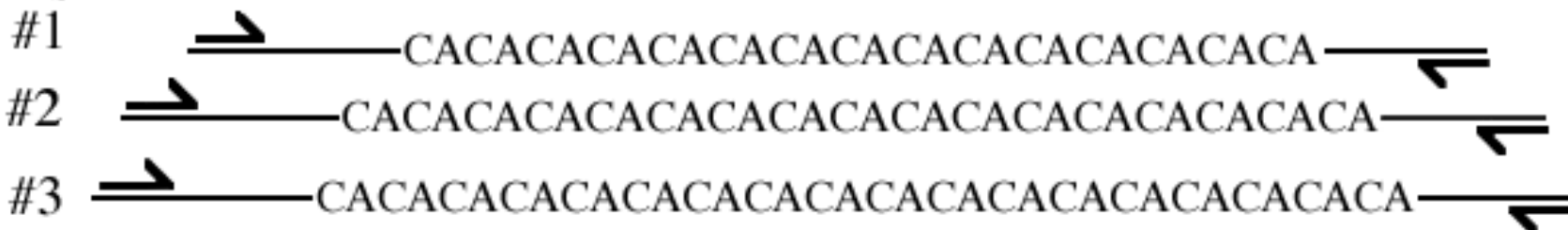
Strains of  
Lactobacillus  
from 18  
types of  
Cheddar  
Cheese



# DNA variation

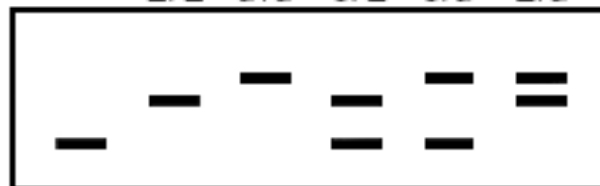
- RFLP
- RAPD
- Microsatellites/minisatellites/VNTRs/SSRs:  
Tandemly repeated short sequences

ALLELES



GENOTYPES

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



# Errors in mispairing during replication and DNA repair

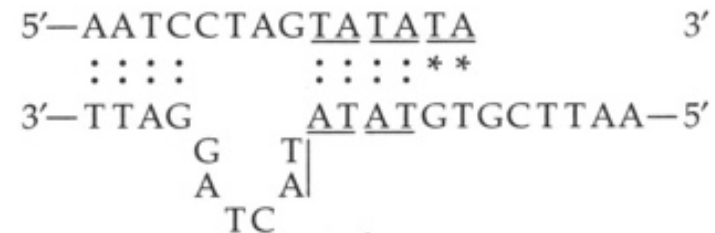
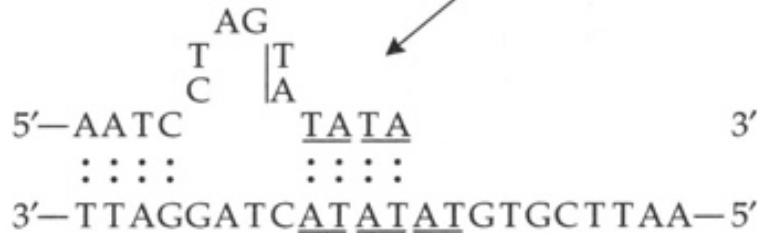
(a)

Normal pairing  
during DNA replication



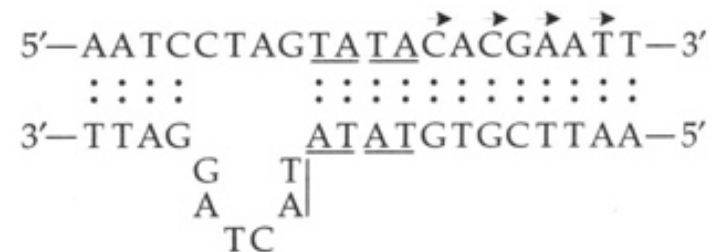
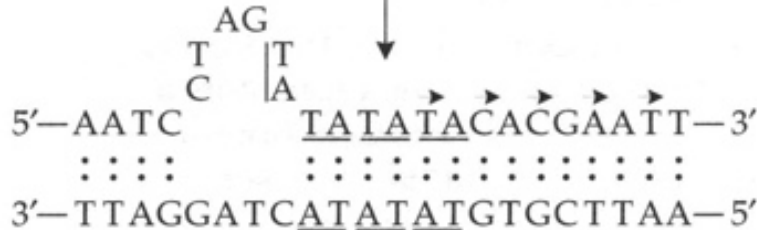
Slipped-strand mispairing

Slipped-strand mispairing



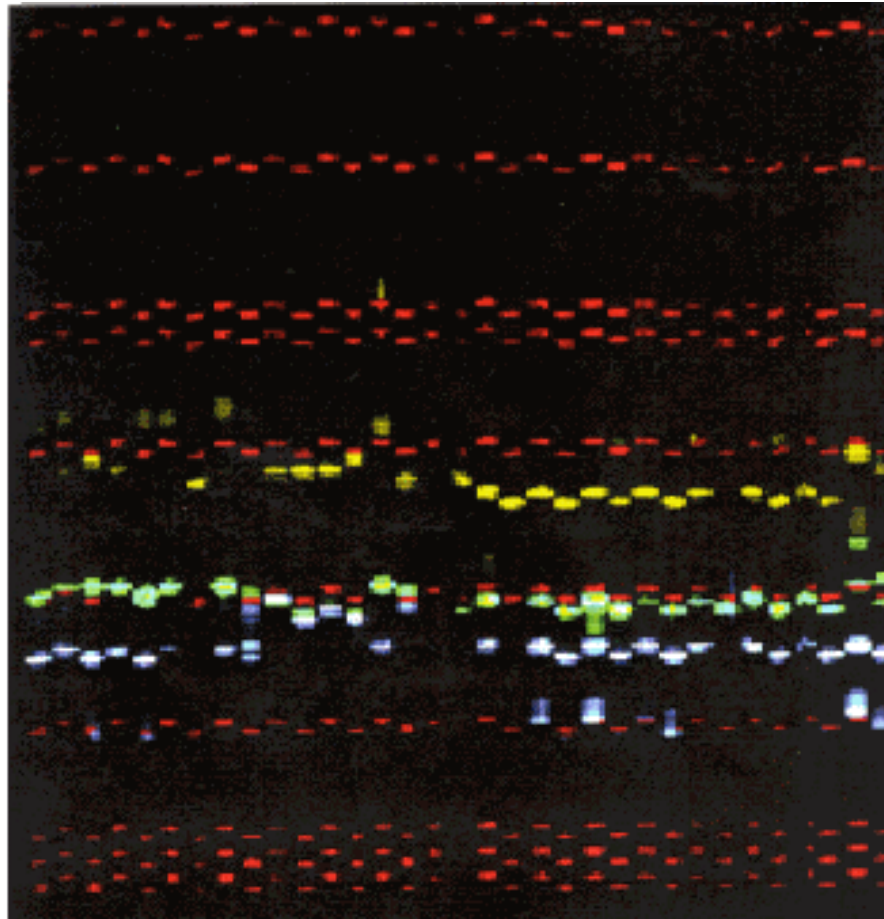
Replication continues  
inserting TA repeat unit

Replication continues after  
excision of unpaired TA repeat unit



# DNA variation

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



Leishmania  
(Viannia) isolates

From London School of  
Hygiene and Tropical  
Medicine

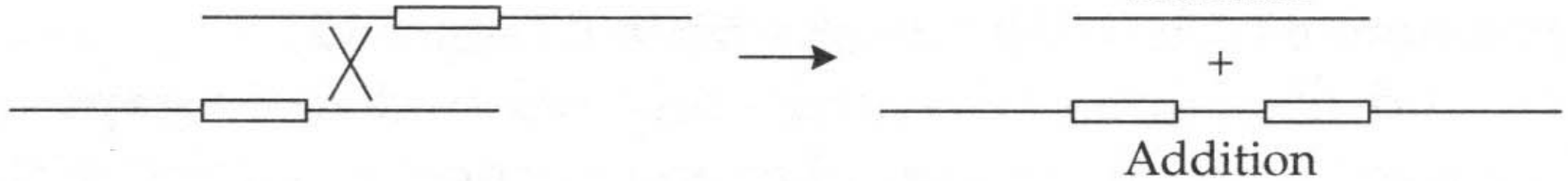


# DNA variation

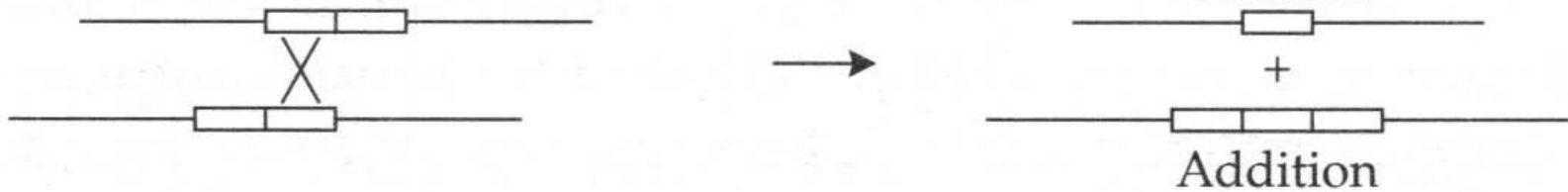
- RFLP
- RAPD
- Microsatellites/minisatellites/VNTRs/SSRs
- Insertion/Deletion: Gain or loss of DNA segment

# Small Scale Insertion & Deletions (InDels)

(a)



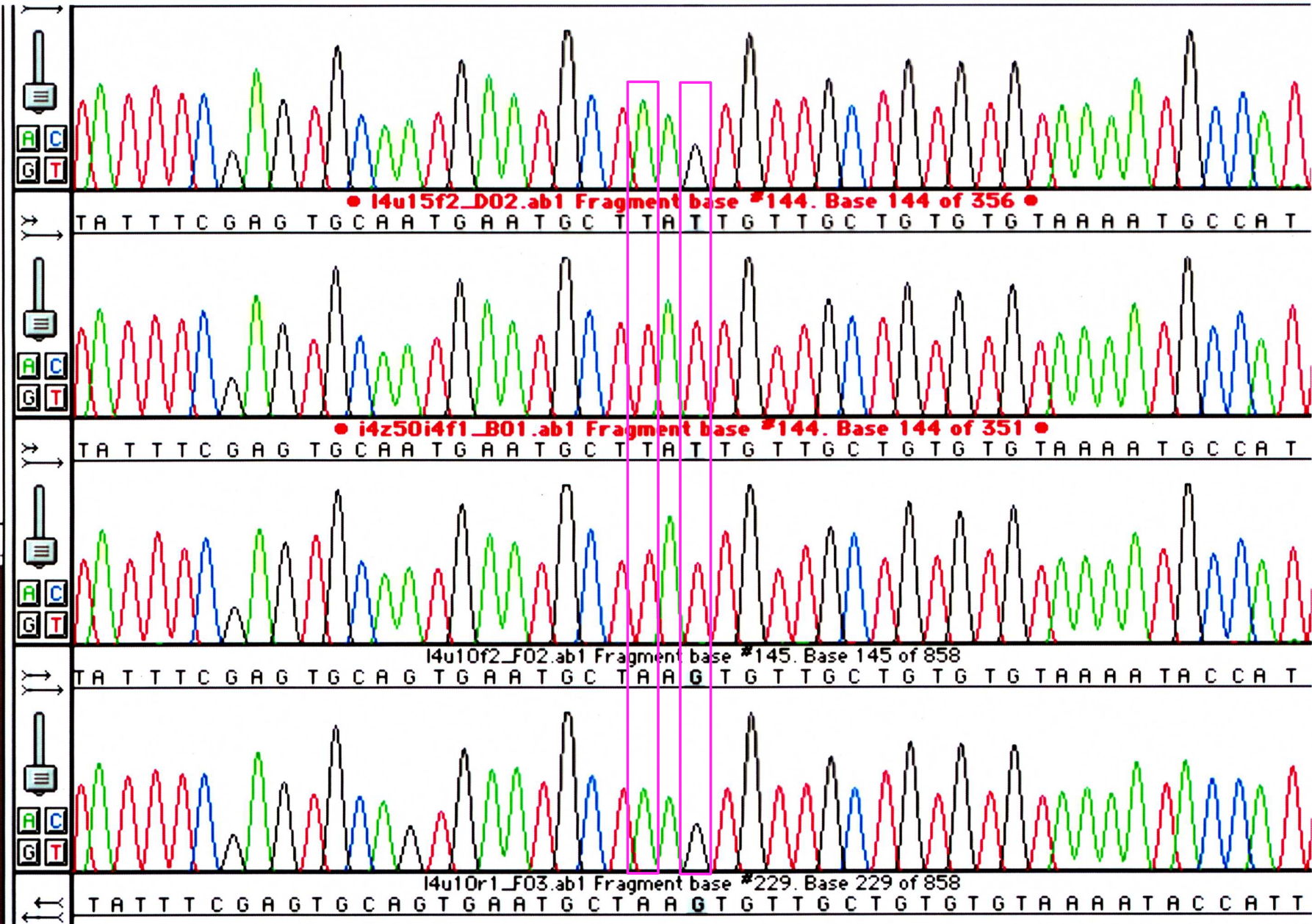
(b)



# 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)

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- Insertion (addition of DNA)
- Deletion (loss of DNA)



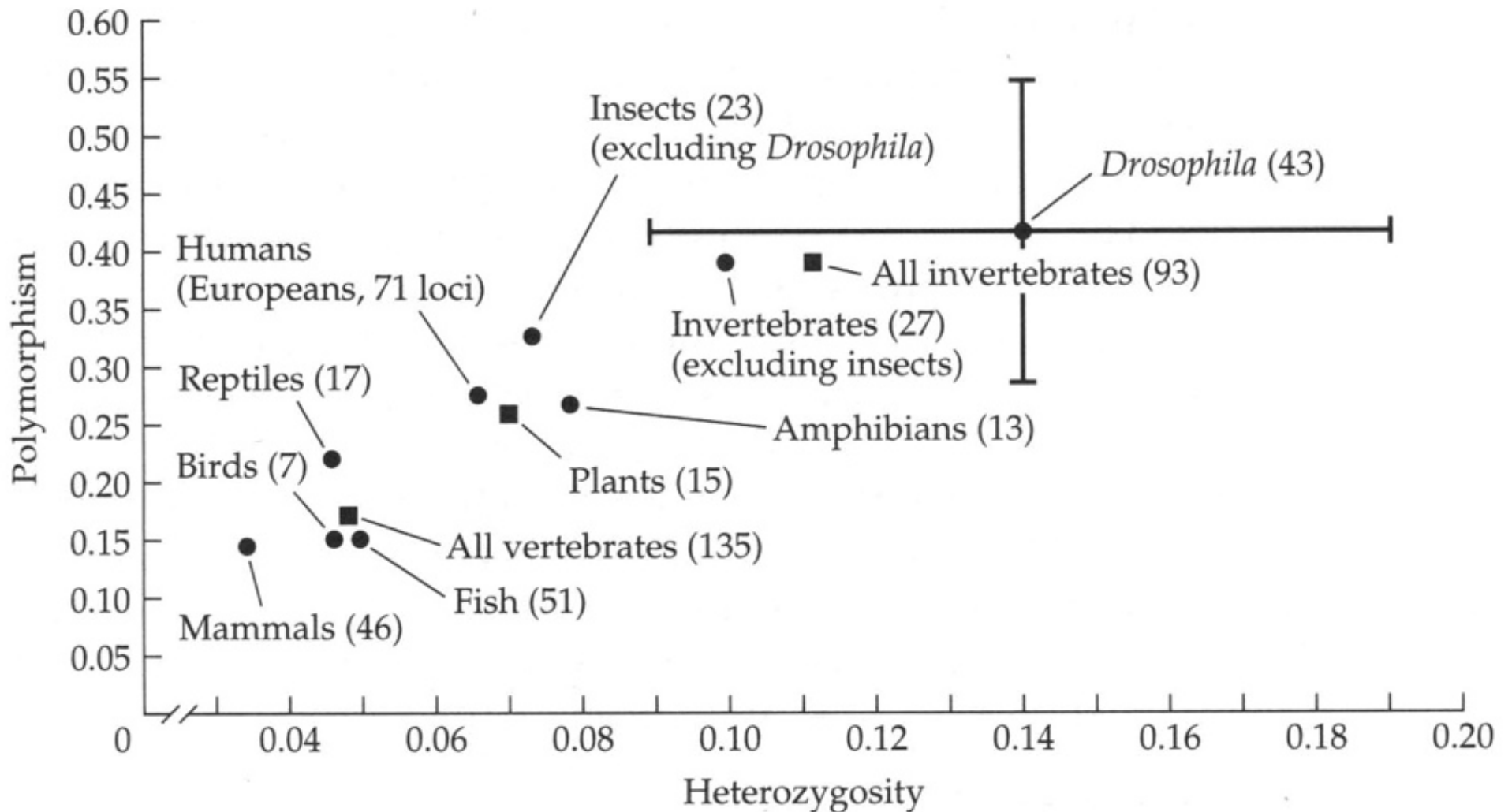
# Mutation is the substrate of evolution

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

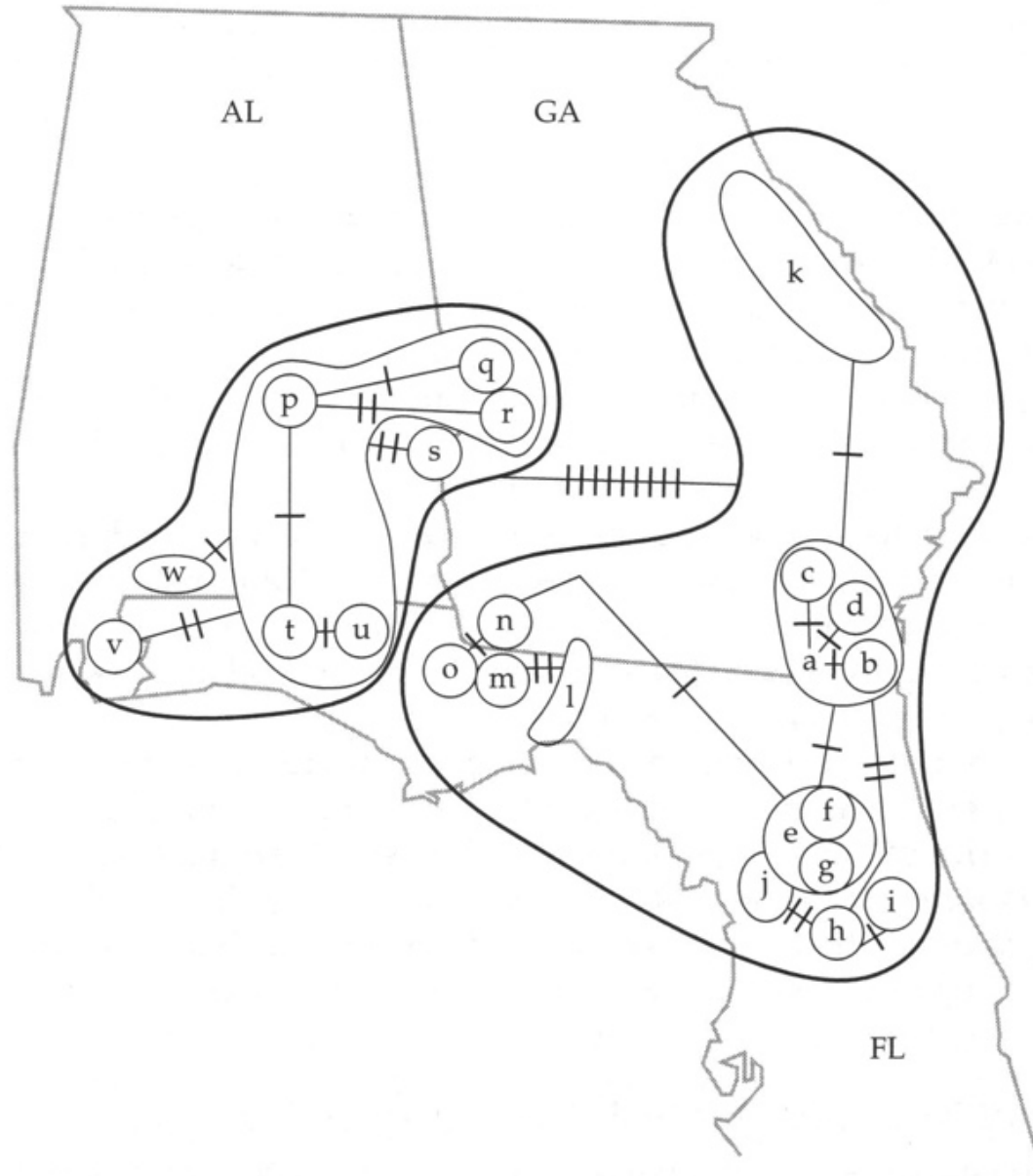
# Genetic Variation

- 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

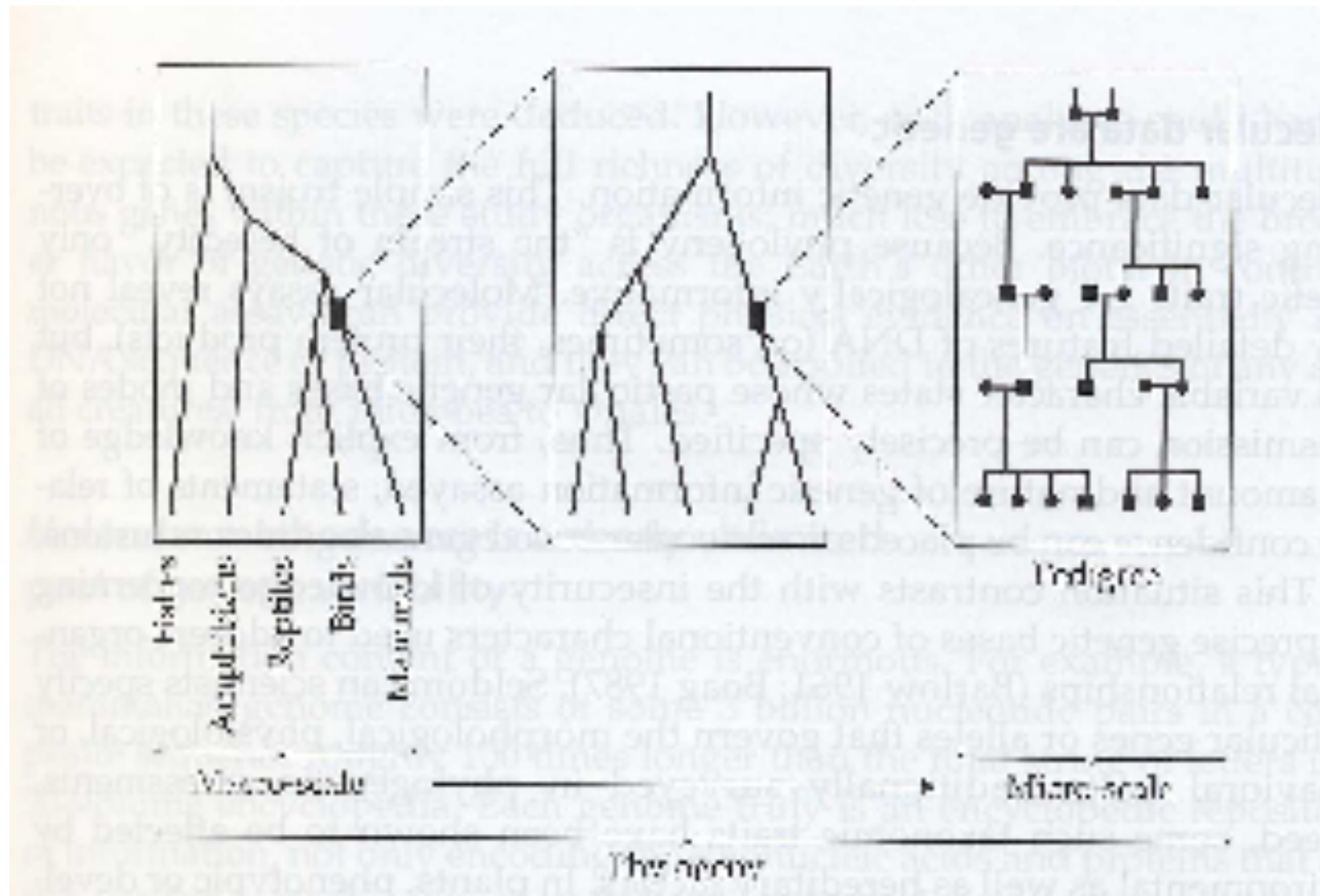
# Genetic variation varies greatly among organisms

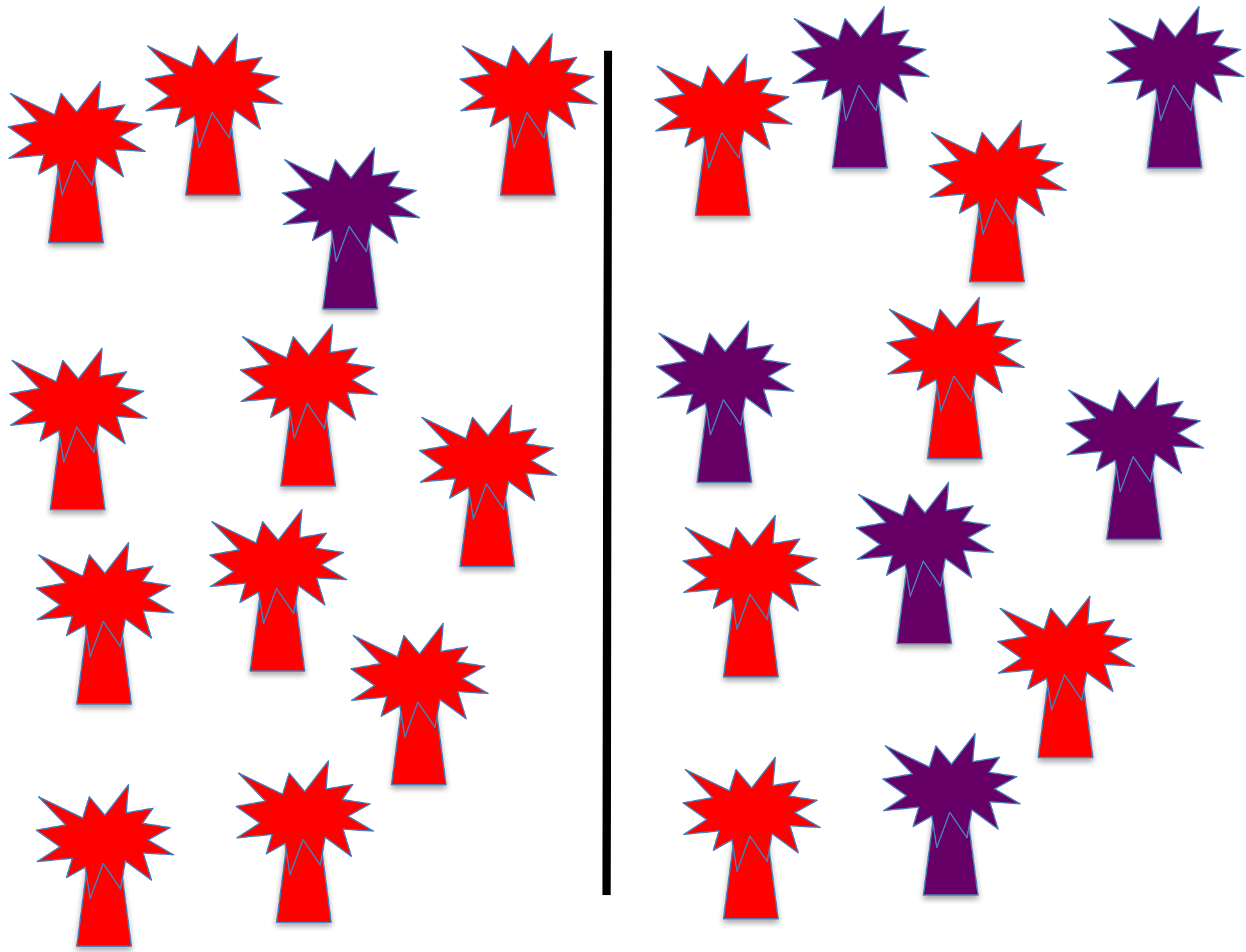


# Genetic variation is distributed geographically



# Genetic variation is nested phylogenetically





# Summarizing molecular data

```
#1 CTGCCACCTTTTGTGGGTCTTAGTCCGCAGTGCACTTGTGCCGCCGAGGGGAATGTGGTGCCTTCCATTGTCCGGATG
#2 .....C.....T.....C.....
#3 .....
#4 .A.....C.....T.....C.....
#5 .....G.....A.....
#6 .....
#7 .....C.....C.....
#8 .....T.....A.....
#9 .....A.....
#10 .....A.....
#11 .....C.....C.....C.....
#12 .....C.....C.....C.....
```

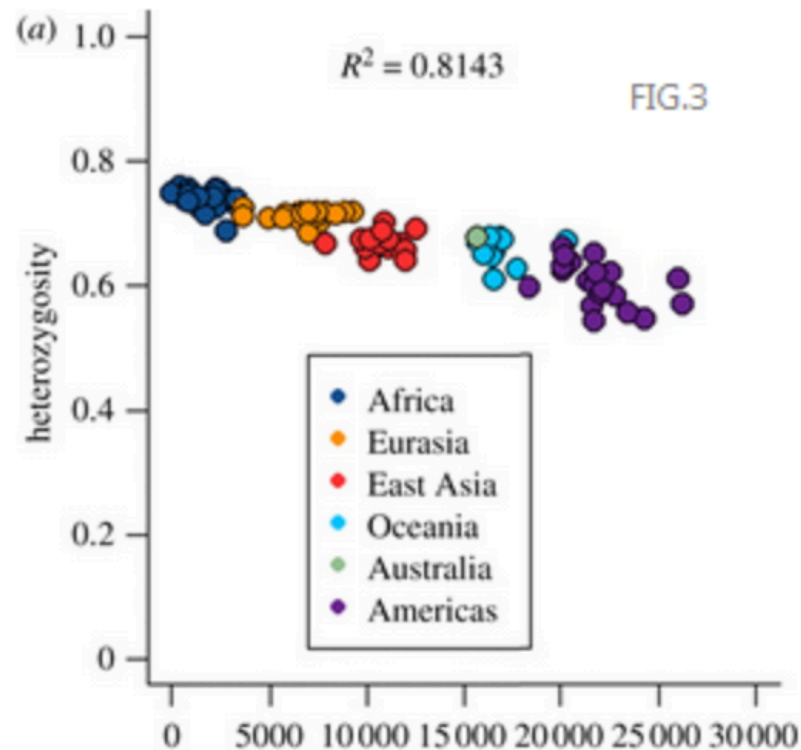
# Key terms

- Gene
- Locus
- Allele
- Genotype
- Haplotype
- Homozygote
- Heterozygote
- Polymorphism



# Heterozygosity

- Expected probability that an individual will be heterozygous at a locus
- Expected proportion of heterozygotes in a population at a locus



Microsatellite heterozygosity vs. geographical distance

# Allelic diversity

- Number of alleles per locus

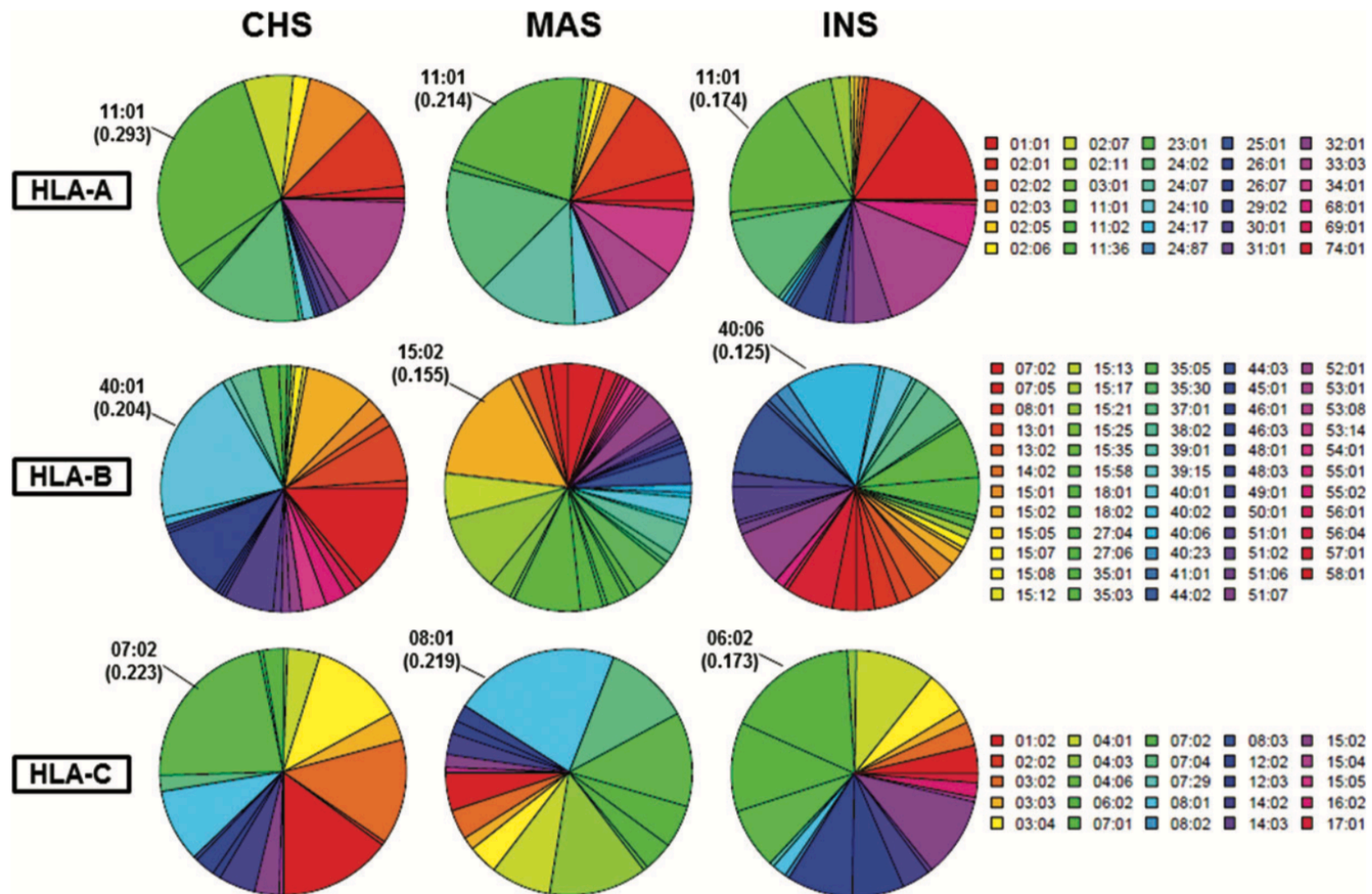
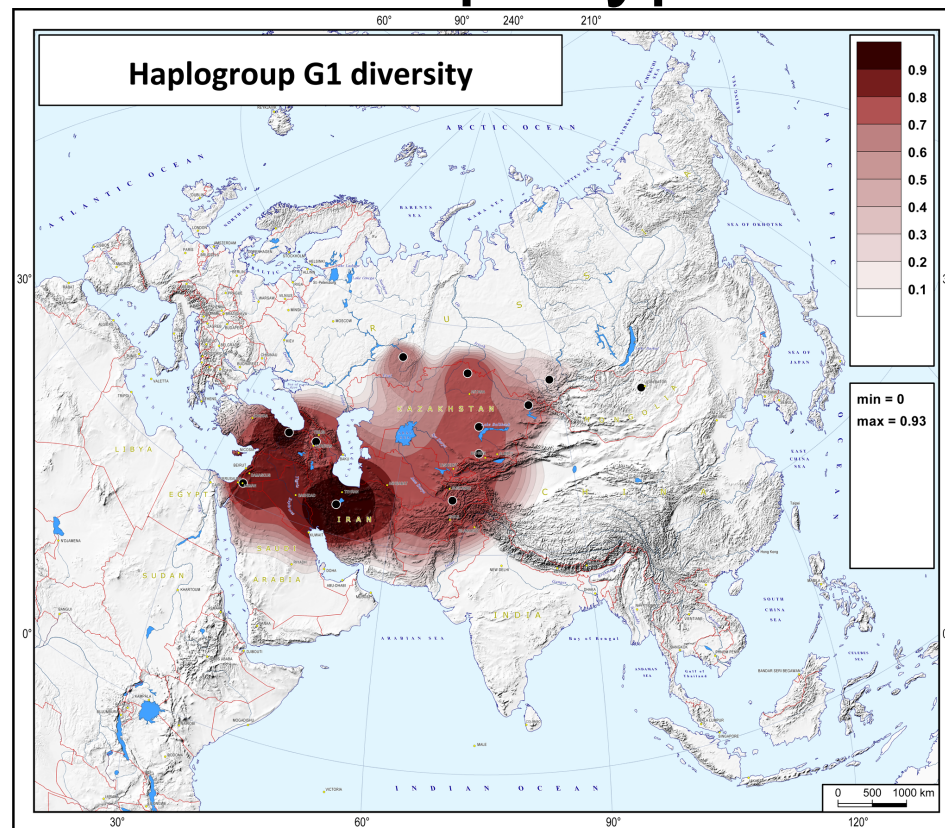


Figure 1. Allelic diversity and distribution in HLA Class I genes. Pie charts illustrating the allelic diversity of the three genes in HLA Class I in the three populations.

# Haplotype indices

- Haplotype number
- Unique ('private') haplotypes
- Haplotype diversity: probability that two randomly chosen haplotypes are different



# Nucleotide-level Indices

- $\Theta_w$

- Watterson's estimator

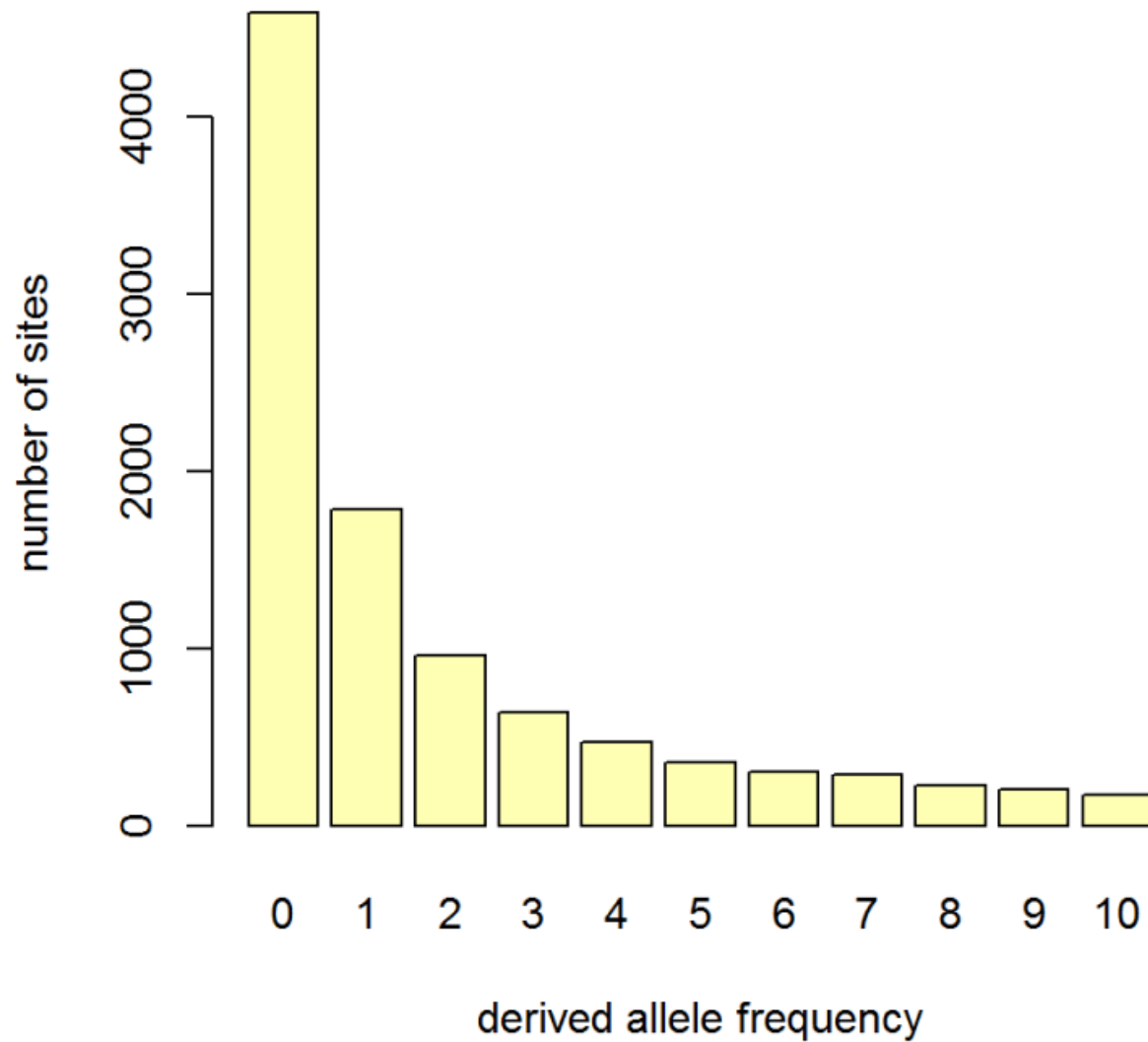
- $$= \frac{S}{\sum_{i=1}^{n-1} \frac{1}{i}}$$

- $\pi$

- Average pairwise difference between alleles

# Site Frequency Spectrum

5 diploid individuals  
10,000



# Genetic Variation: Software

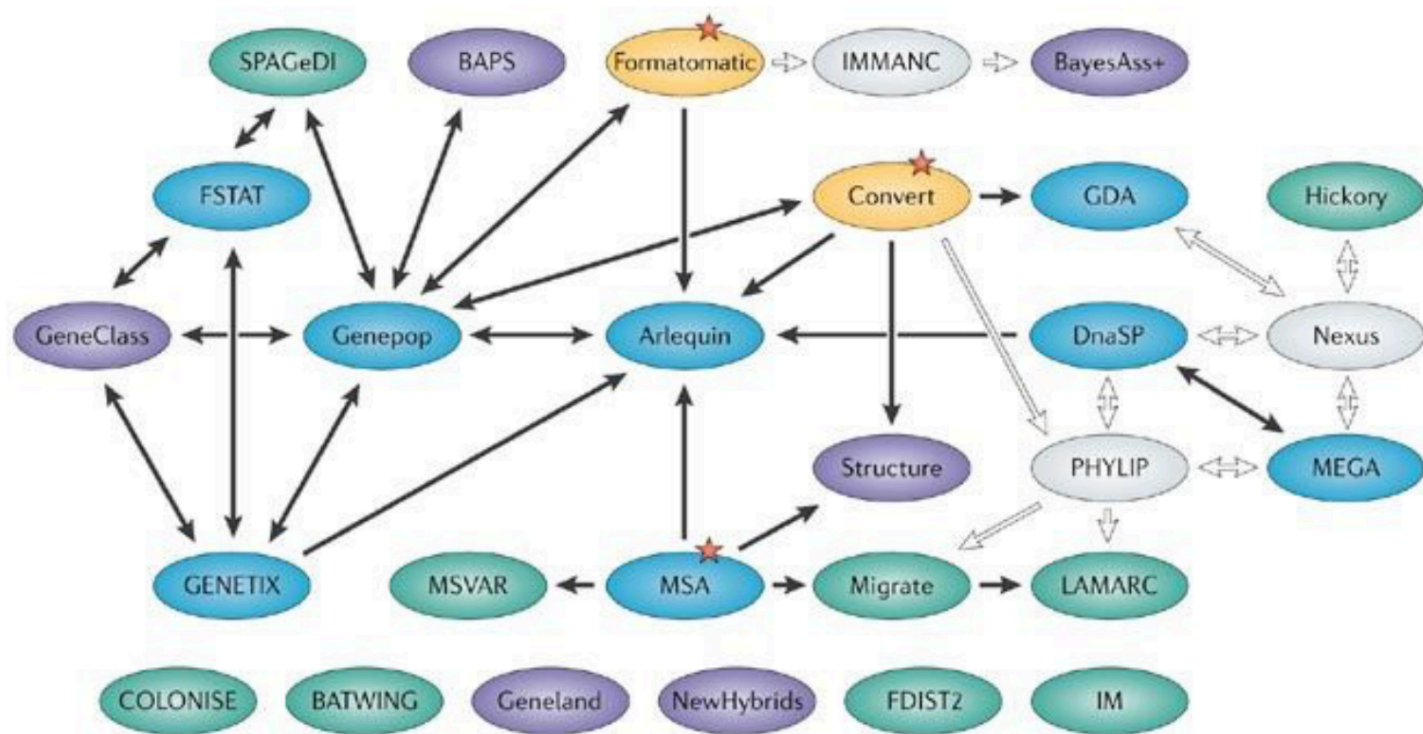
- DnaSP (DNA sequence polymorphism)
- DNA sequence
- Basic population genetic analyses
- Estimate genetic diversity
- Within/Between populations
- LD, recombination, gene flow, gene conversion
- Neutrality tests

# Genetic Variation: Software

- Arlequin
- MEGA
- PHYLIP
- ...
- Excoffier and Heckel 2006: Computer programs for population genetic data analysis: a survival guide

# Genetic Variation: Software

From: Computer programs for population genetics data analysis: a survival guide





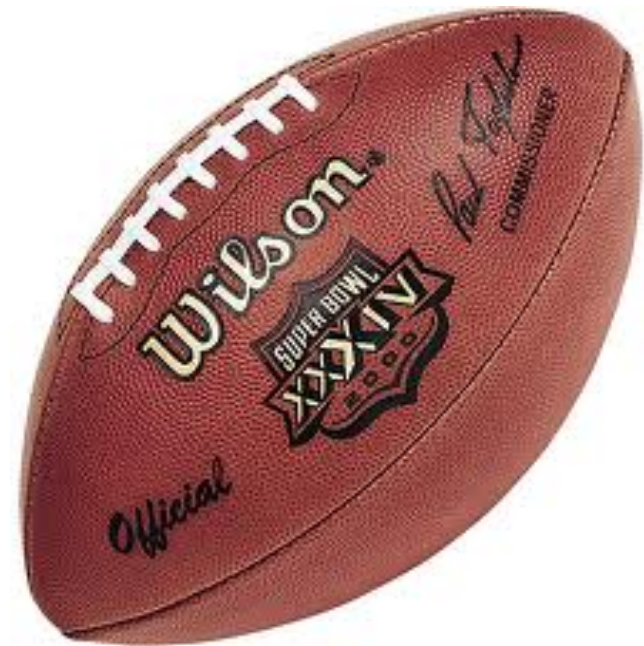
# Why do we care about genetic variation?

- Genetic variation underlies phenotypic differences among individuals
  - Including disease risk and responses to drugs and environmental factors



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- Individual identification
- Manage resources
- Public Health

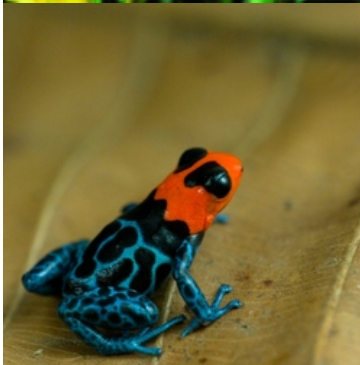


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- Genetic variation underlies phenotypic differences among individuals
  - Including disease risk and responses to drugs and environmental factors
- Individual identification
- Manage resources
- Public Health
- Improve plant and animal food products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

# Conservation genetics

- Use of genetic theories and techniques to study the loss and restoration of genetic diversity
- Derived from ecological, evolutionary, and quantitative genetics
- Focuses on small populations



# Why is conservation important?

- Sixth mass extinction
- Aesthetic value
- Bioresources
- Ecosystem services
- Ethical, moral considerations



# How can genetics help?

- Minimize inbreeding and loss of genetic variation
- Identify populations of concern
- Resolve population structure
- Resolve taxonomic uncertainty
- Define management units
- Detect hybridization
- Detect and define invasive species
- Estimate population size and sex ratio
- Establish parentage
- Understand population connectivity
- Aid in management
- Enhance reproductive capacity of organisms
- How do genetic factors affect extinction risk?
- How can we best genetically rescue populations?
- What can we use genetics to identify hotspots?
- Applied genetic detective work
- ...

# Future of conservation genetics

- Open questions:
  - Genetic variation and fitness
  - Mechanism connecting genetic variation and fitness
  - Genotype by environment interaction
  - Intermediate phenotypes
- New technologies
  - DNA sequencing