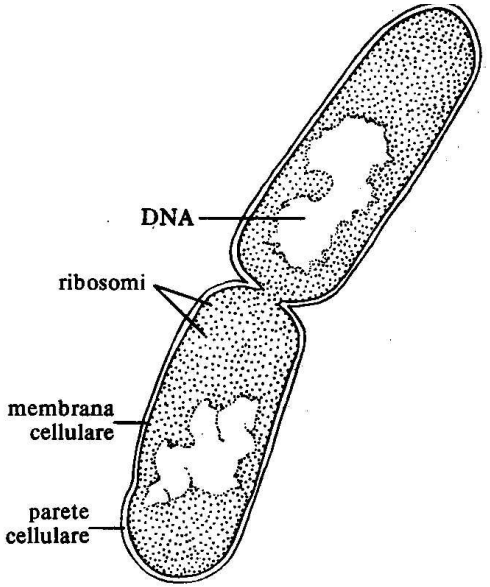
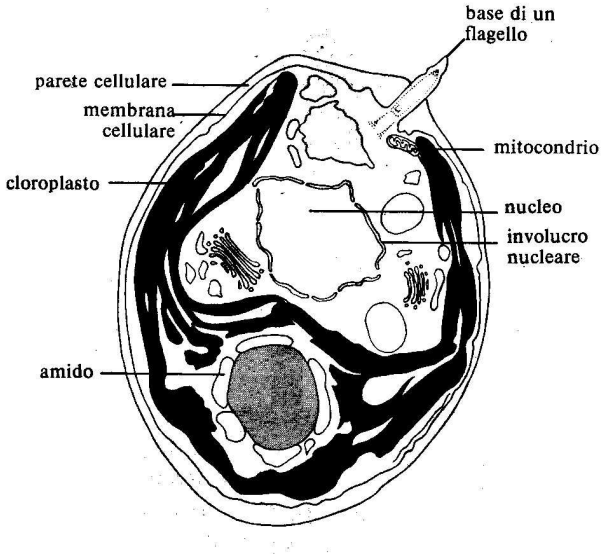
The cell

PROKARYOTES
(1-5 µm)



Bacterium
(*Escherichia coli*)

EUKARYOTES
(10-50 µm)



Green alga
(*Chlamydomonas sp.*)

lacks a membrane-bound nucleus (nucleoid)

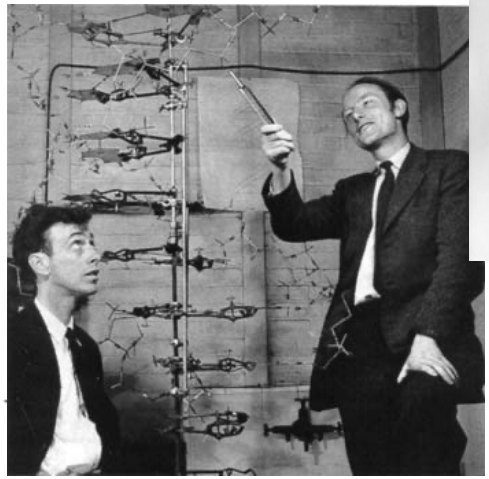
Nucleoid and nucleus contain DNA

The brick of life

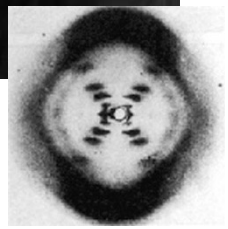
DNA structure

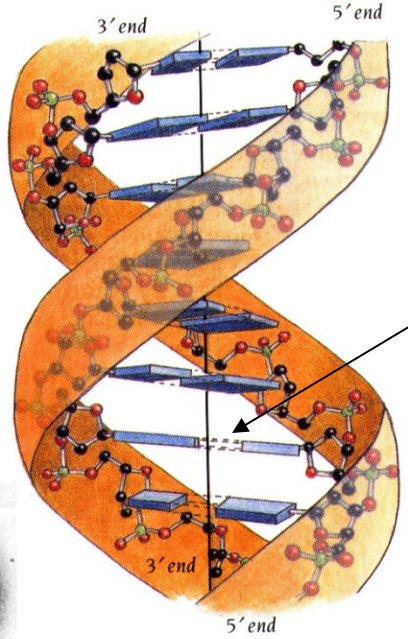
This figure is purely diagrammatic. The two ribbons symbolize the two phosphate—sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical line marks the fibre axis

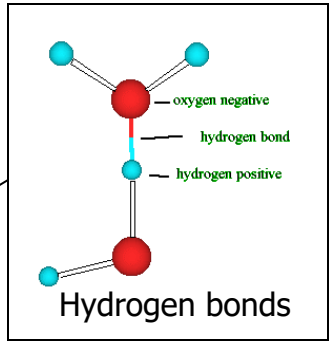
Watson and Crick

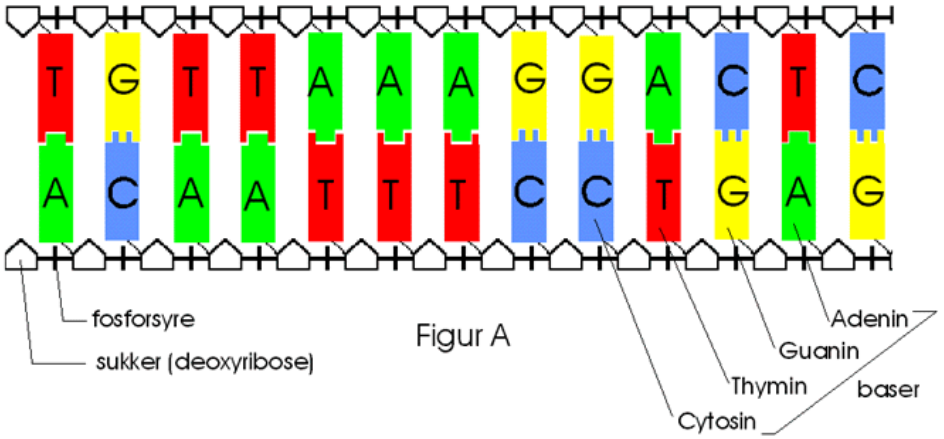


Rosalind Franklin







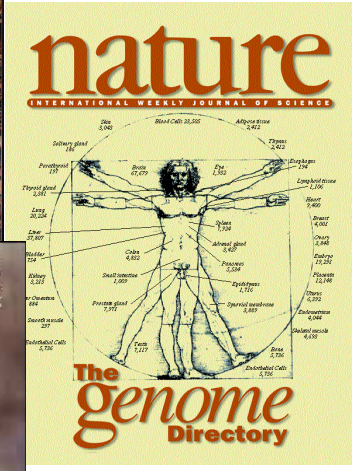


Nucleotide = nitrogenous base+
+ sugar/phosphate group

Codon = base triplet that codes for an amino acid

Amino acid = one of the 20 bricks of proteins

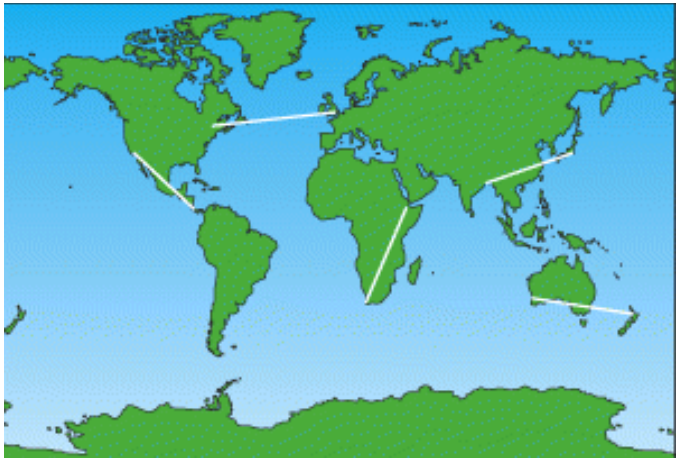
15/16 February 2001



One thing that the gene catalog cannot tell us, and will not be able to tell us even when it is complete, is what makes a human being […] On the basis of gene number we are only three times more complex than a fruit fly and only twice as complex as the microscopic worm *Caenorhabditis elegans*. More detailed studies of how the human genome functions may reveal key features that underlie some of the special attributes of human beings, but genomics will never explain why a human was able to compose Mozart's 40th symphony, or indeed why it was composed by Mozart and not by an ordinary human.

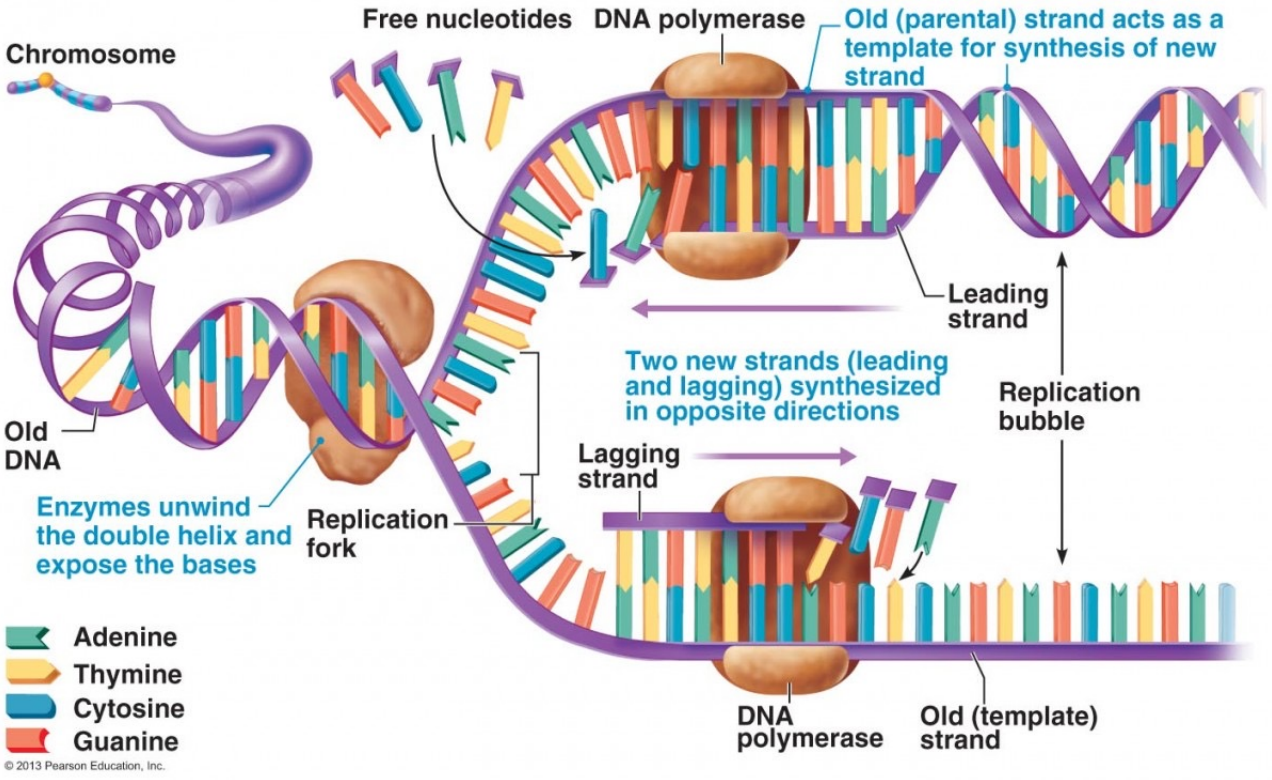
[Google for *Genome 2*]

What do we mean by *the* human genome?

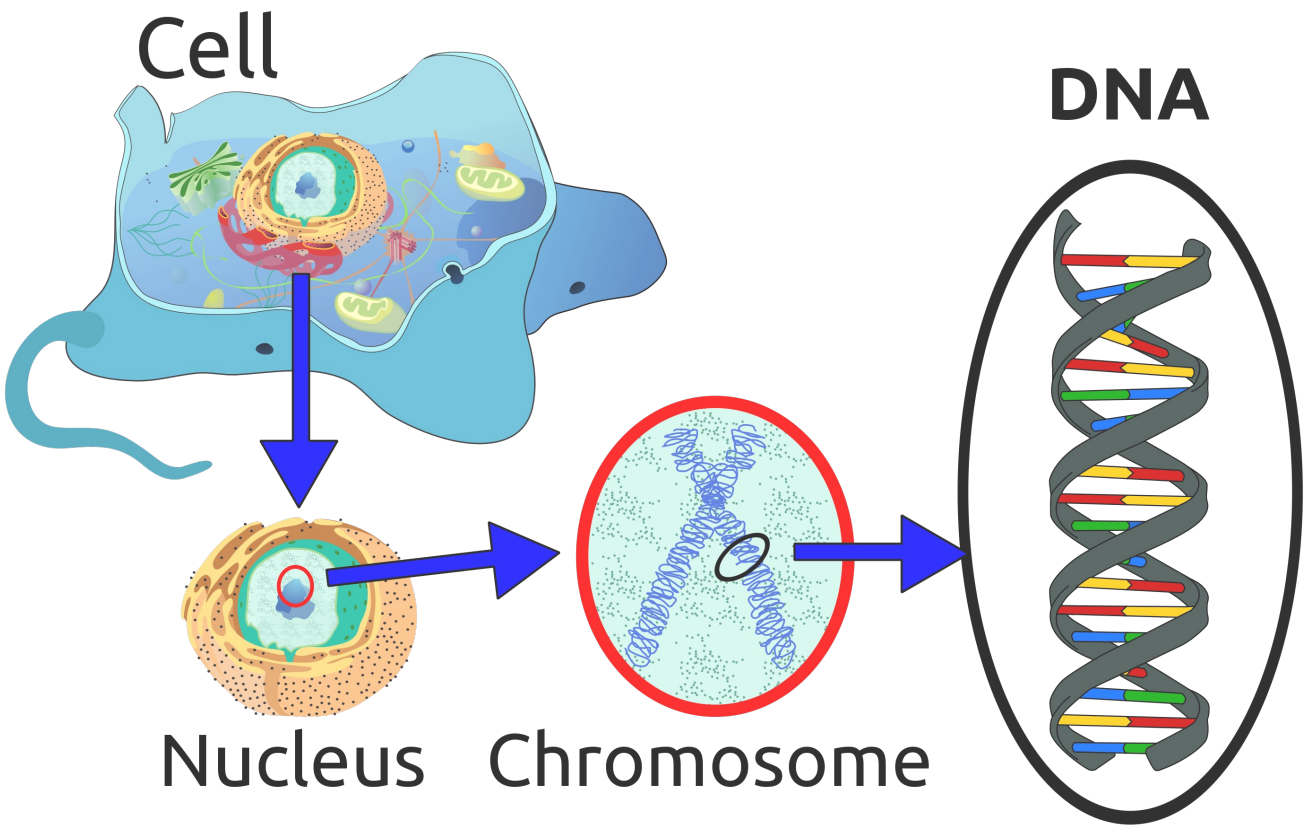


Approximate length of human genome in 12 point font

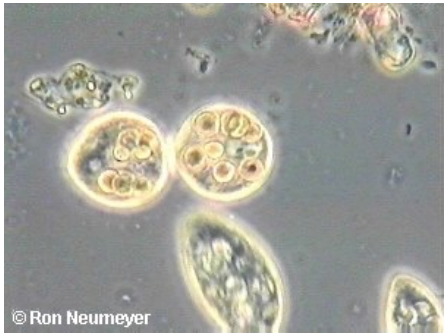
DNA replication



DNA and chromosomes



Reproduction in asexual organisms



a) *Protozoon*

b) *Hydra viridis*

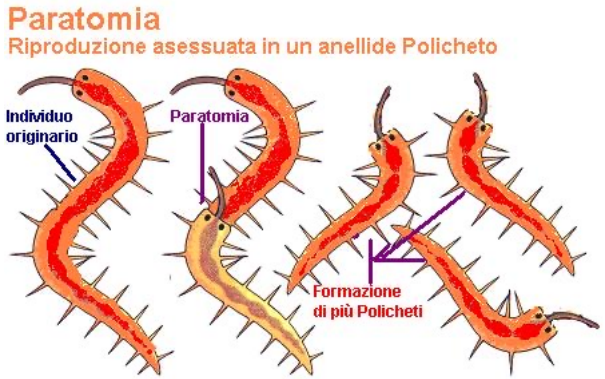
a) Fission

b) Budding

c) Vegetative reproduction

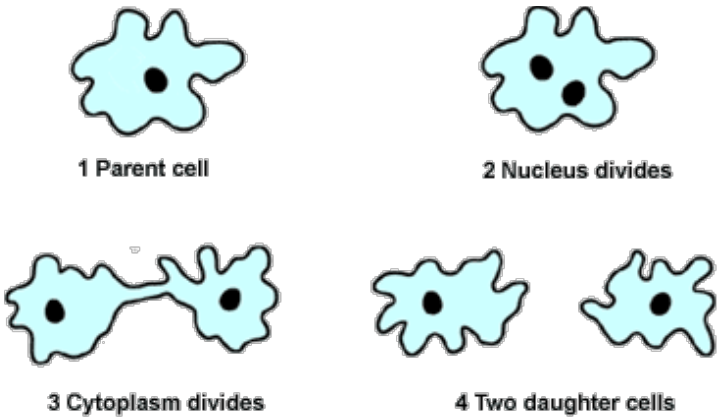
d) Fragmentation

c) *Iris versicolor*

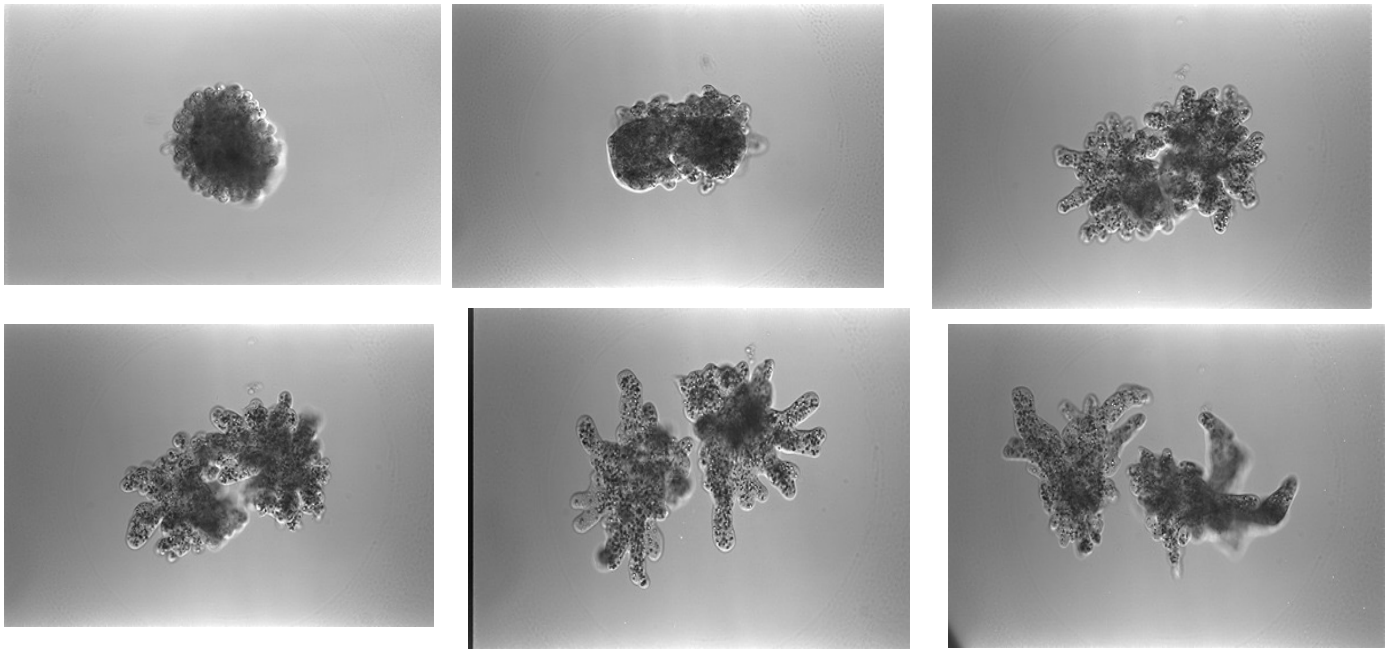


d) *Microstomum lineare*

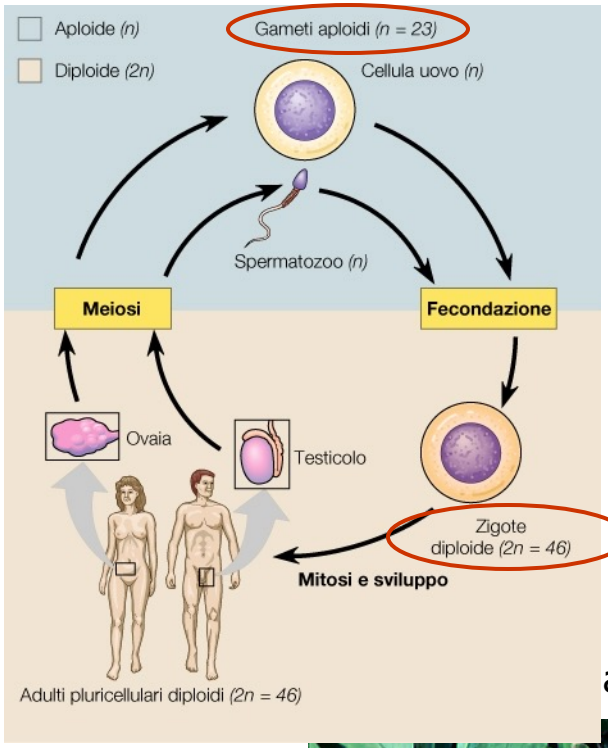
Amoeba proteus



Haploid cell, 500-1000 small chromosomes



Reproduction of sexual organisms



a) *Homo sapiens*

Haploid gametes
Diploid zygotes

a) Dioecious reproduction (separate sexes)

b) Monoecious reproduction (non separate sexes) or hermaphrodite

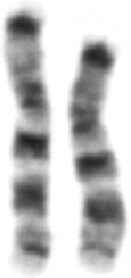
c) Parthenogenesis

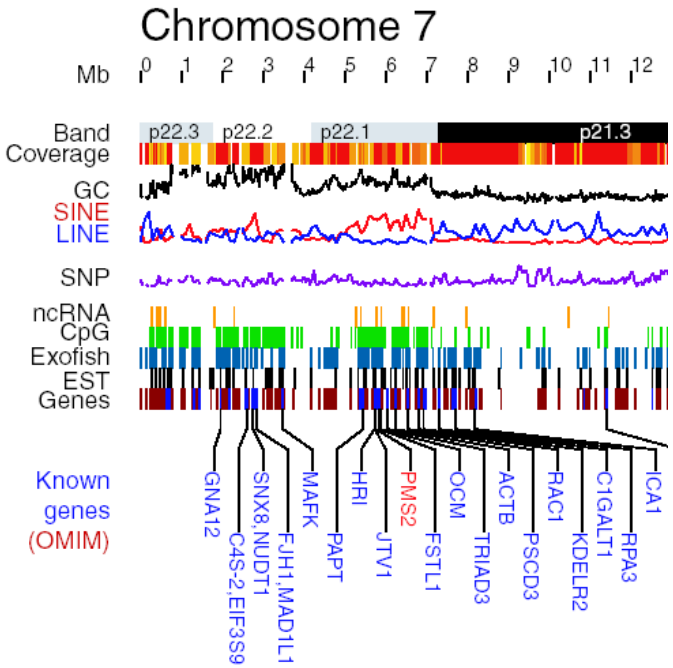
b) *Betula nigra*

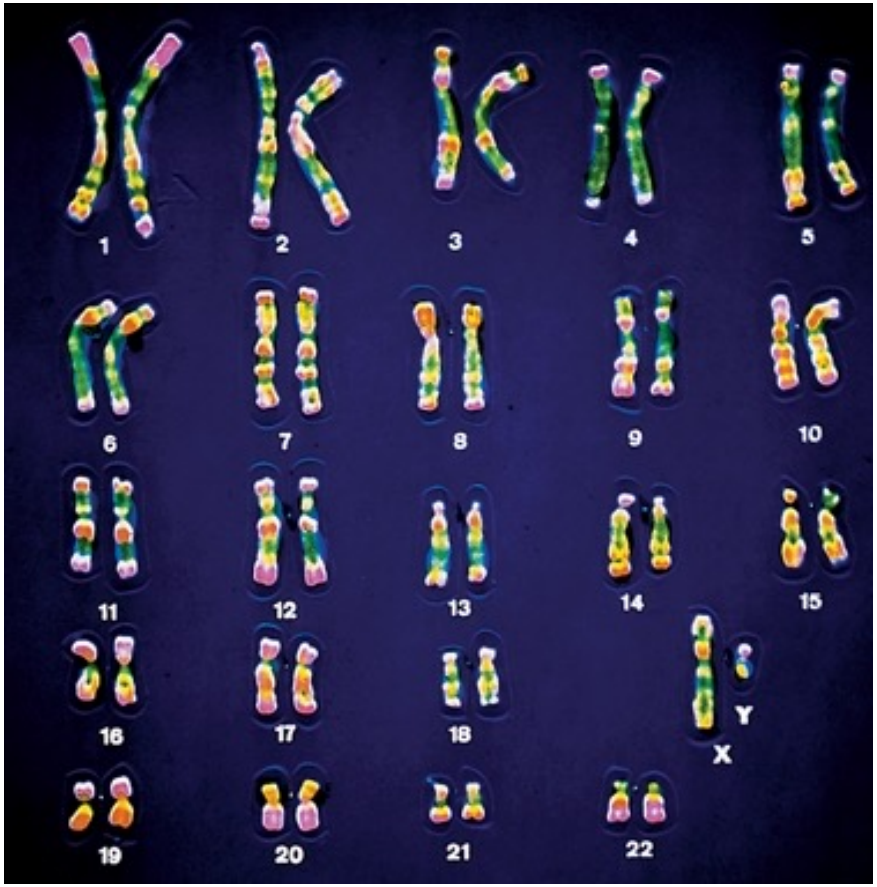
a) *Ilex decidua*

c) *Brachionus rotundiformis* with egg

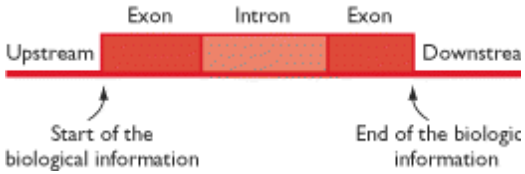
Lepidodactylus lugubris

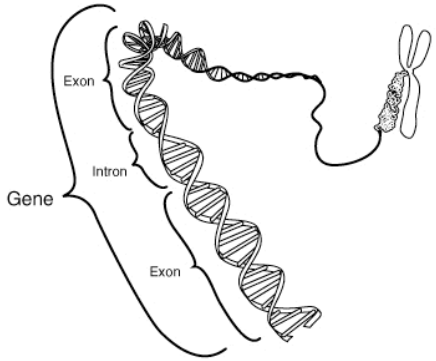






Gene (Locus)
= expression unit

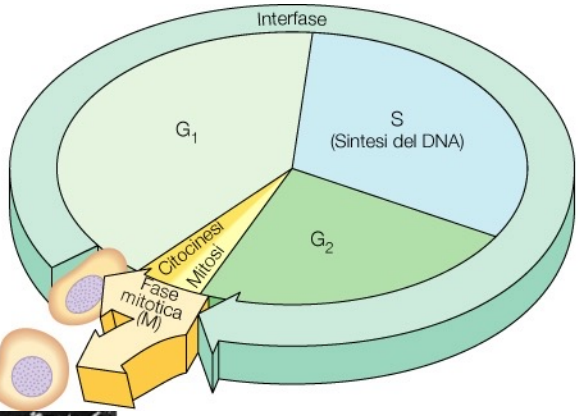




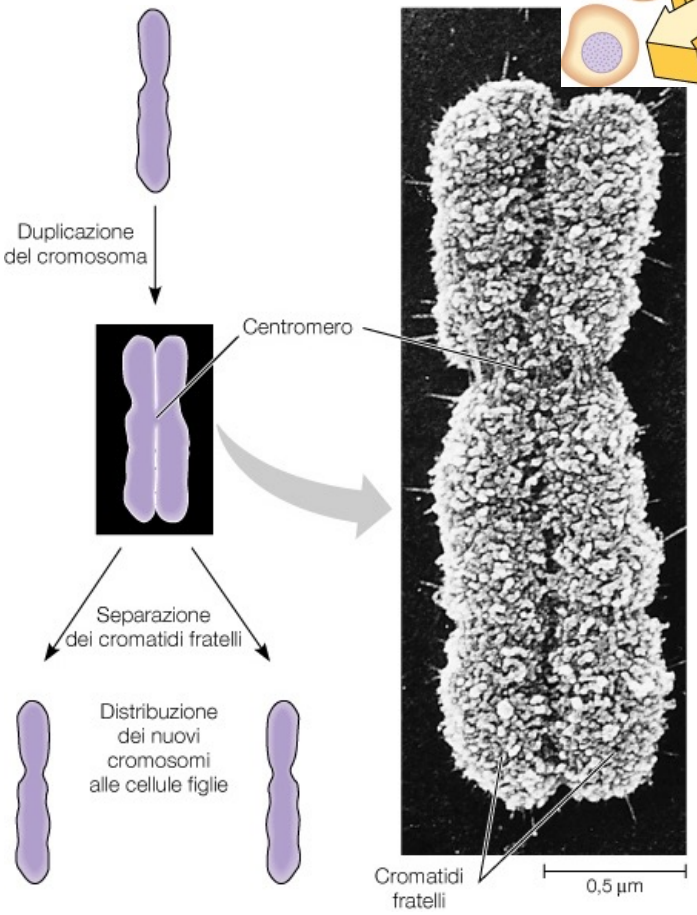
In the same locus one can have variants of a gene: the alleles

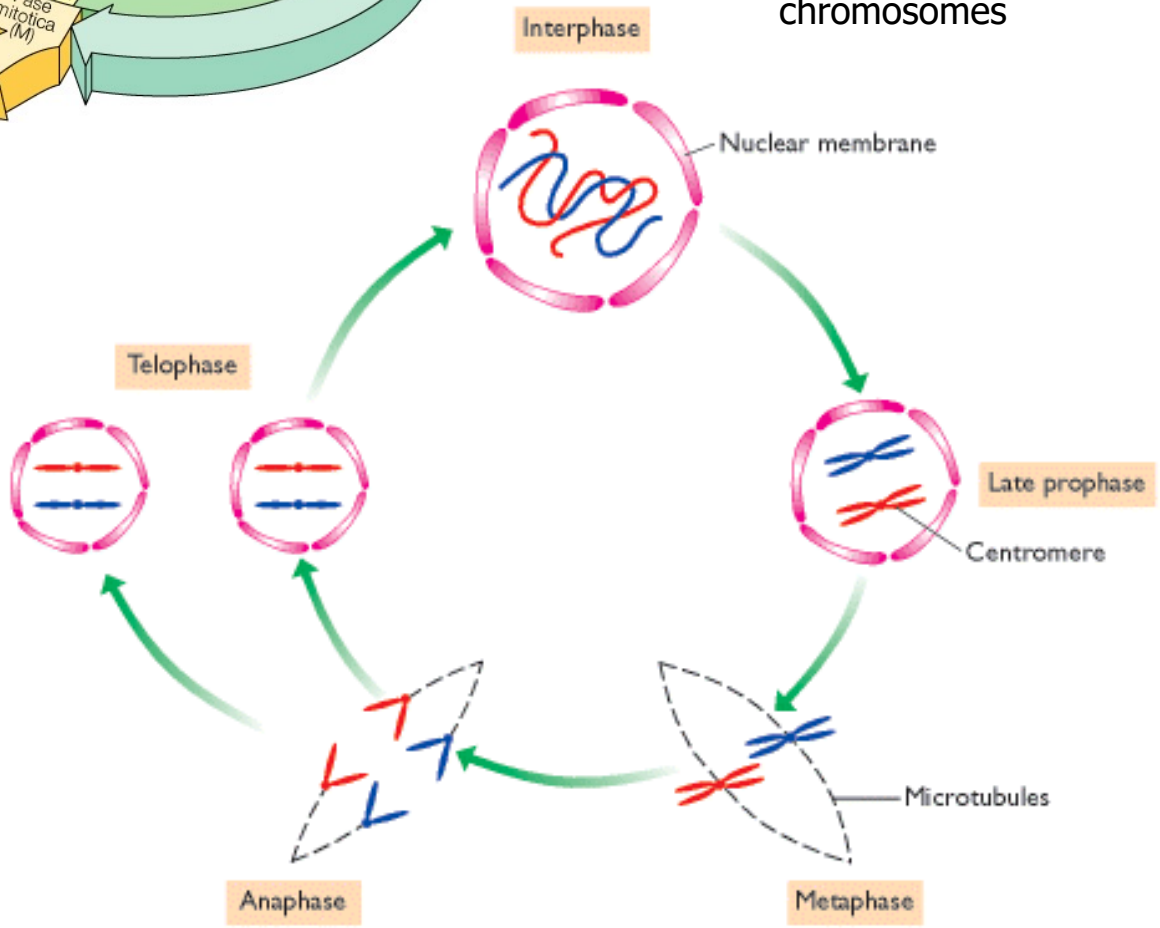
http://www.cellsalive.com/mitosis.htm

Cell cycle and mitosis

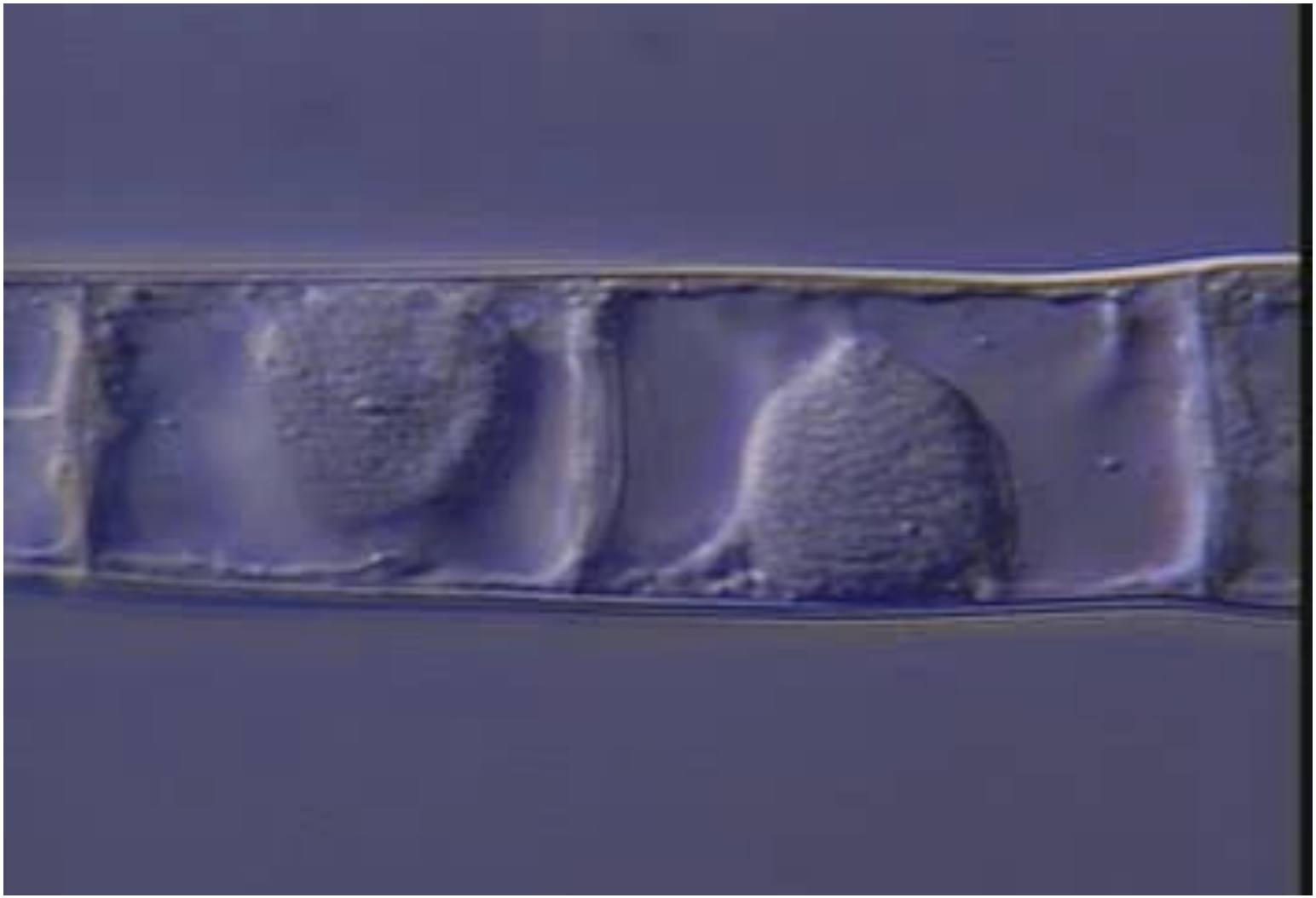


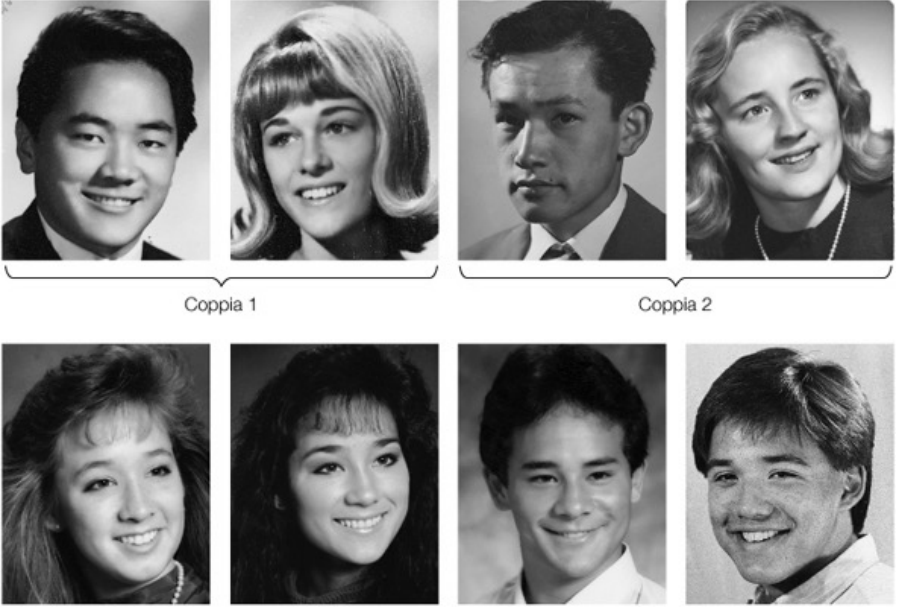
Pay attention: red and blue are two nonpaired chromosomes



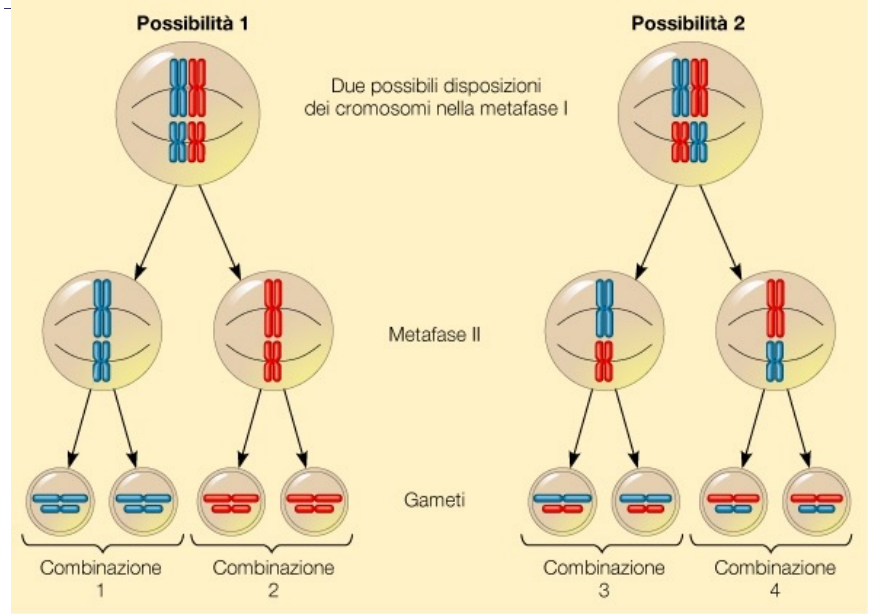


Mitosis in a plant cell (*Tradescantia*)





Sexual reproduction produces genetic variability



Number of possible combinations from *n* chromosomes is 2^n

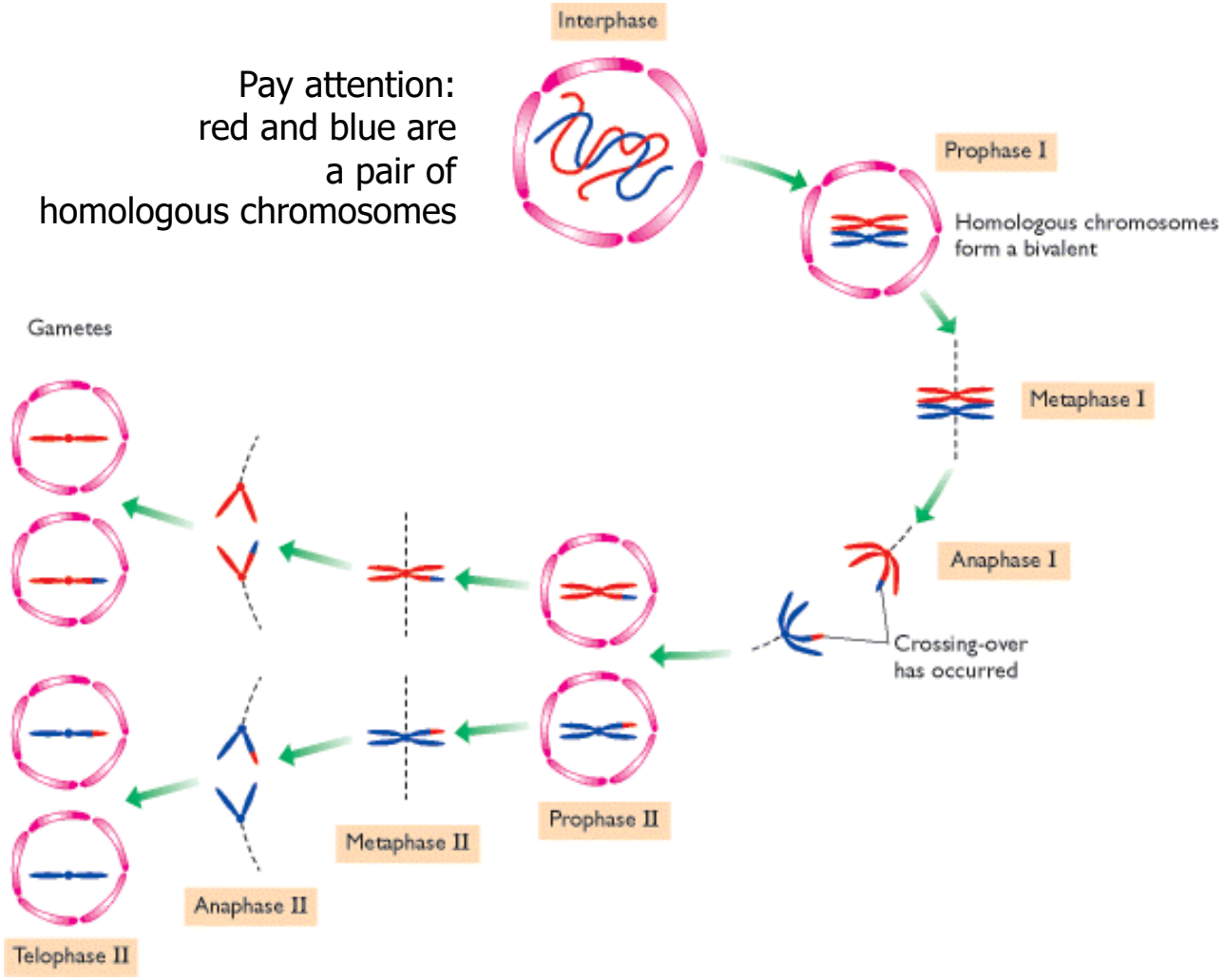
$$2^{23} \times 2^{23} = 7 \times 10^{13}$$

Main reasons:

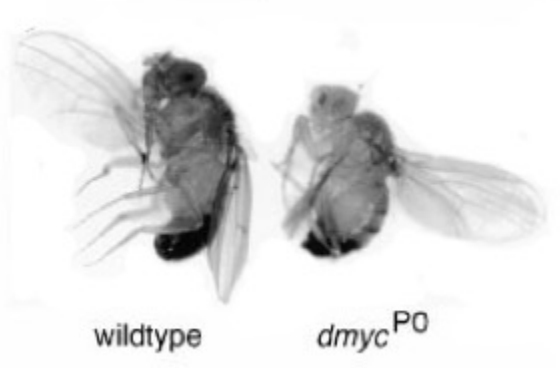
- Independent assortment of chromosomes
- Crossing over

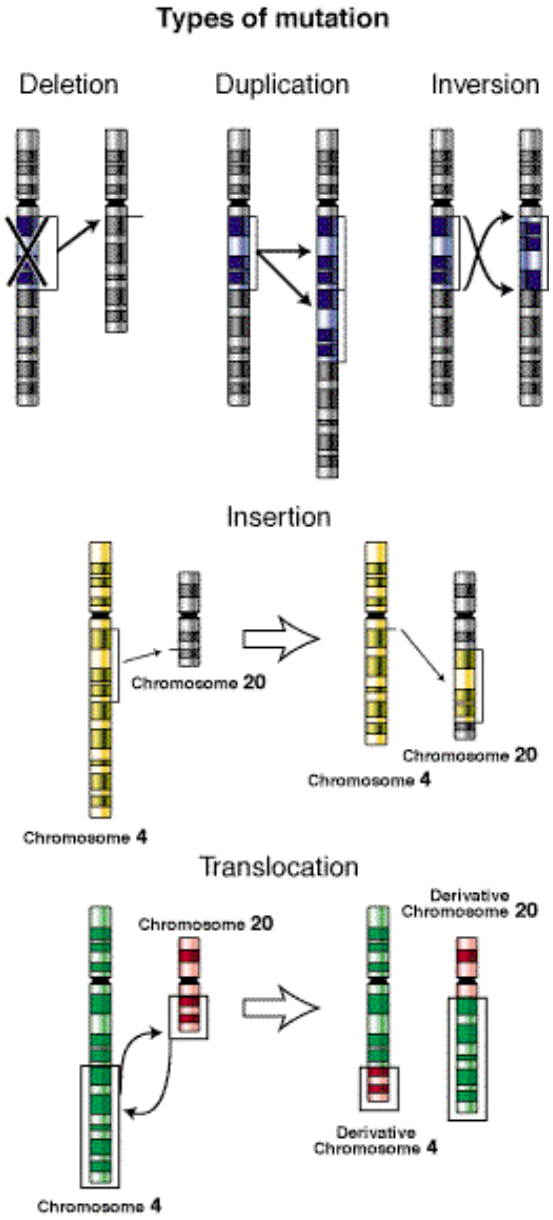
Meiosis

Pay attention:
red and blue are
a pair of
homologous chromosomes



Mutations



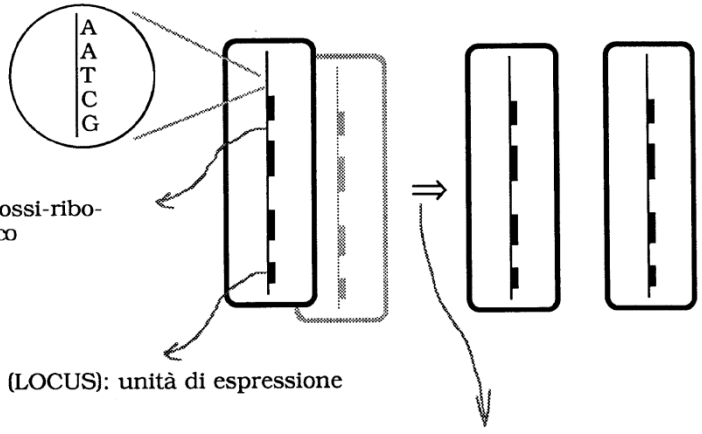


Mutation in a male *Drosophila*

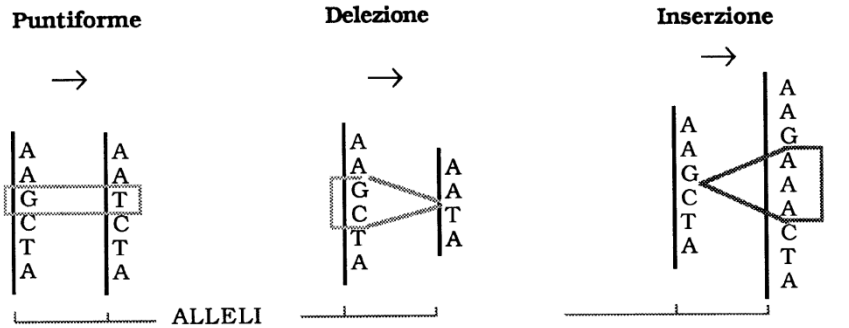
Mutations are rare ~ 10^{-6} per base per generation

Elementi di Genetica

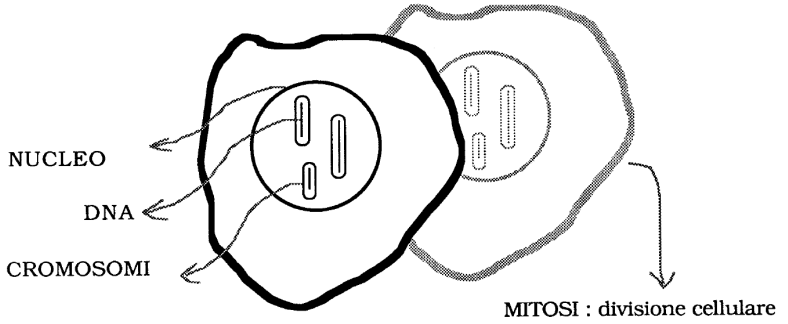
Organismi Unicellulari Semplici (batteri)



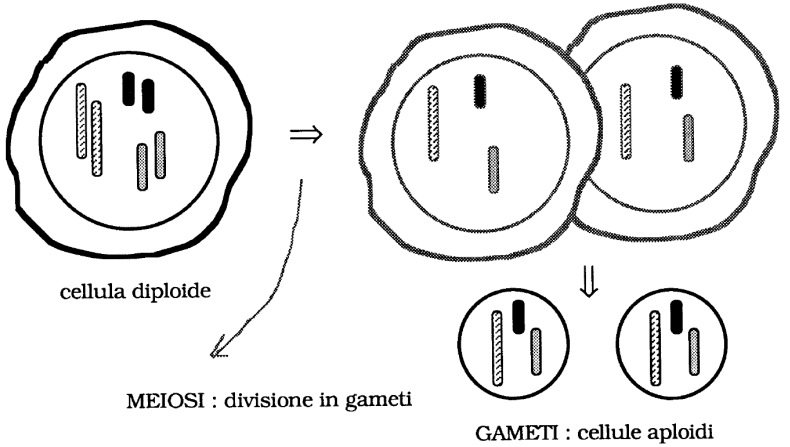
Le Mutazioni

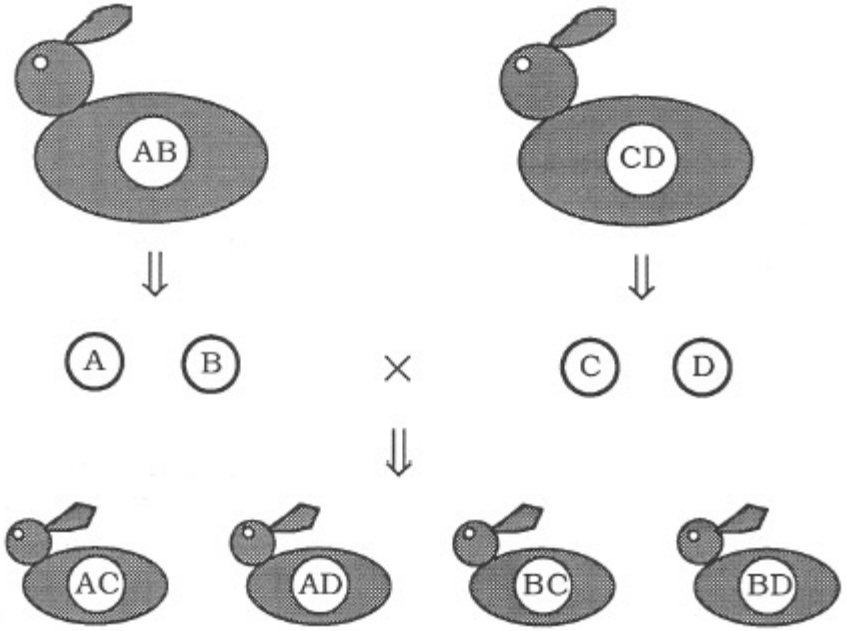


Organismi Unicellulari Complessi (protozoi)



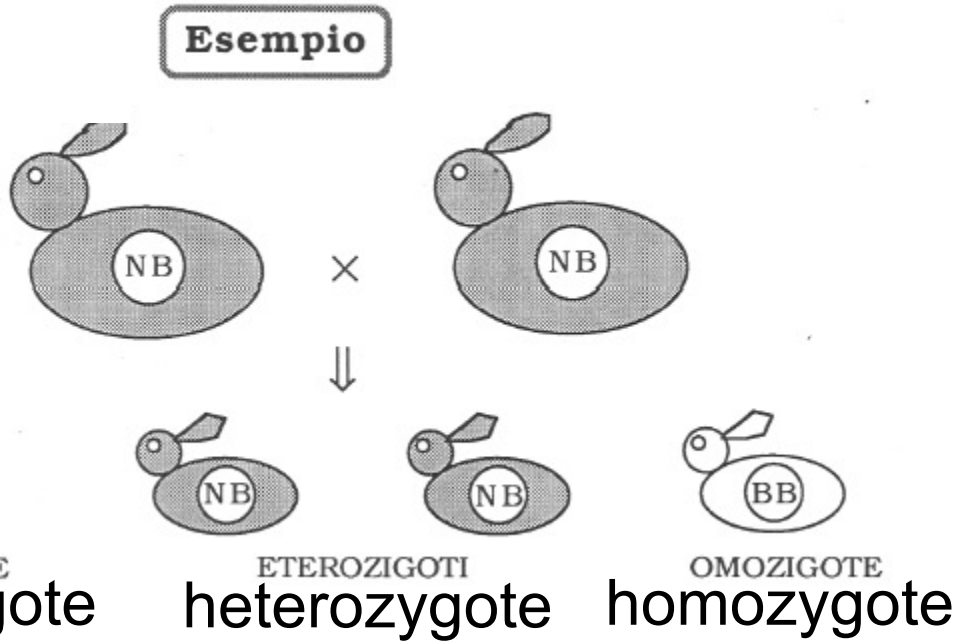
Organismi Complessi Sessuati





One-locus formal genetics
(A,B,C,D: alleles of the same gene)

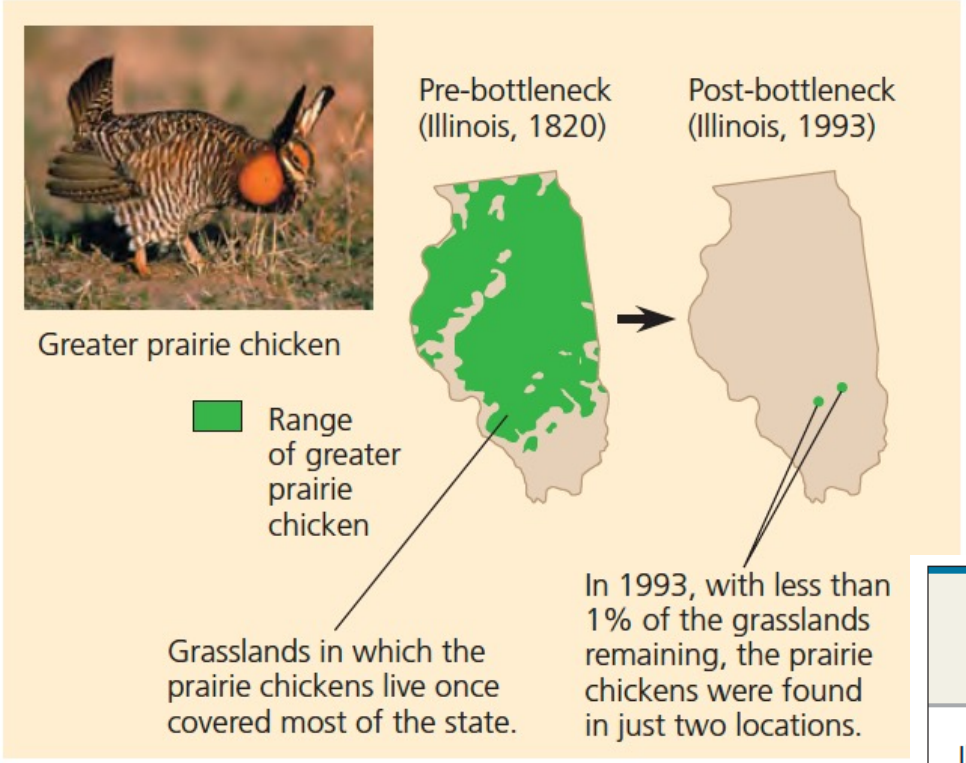
Genotype and phenotype



homozygote heterozygote homozygote

N.B. Sometimes alleles can be dominant or recessive

Genetic deterioration



The example of prairie chicken (*Tympanuchus cupido*)
Low genetic diversity implies low birth rate

Location	Population size	Number of alleles per locus	Percentage of eggs hatched
Illinois			
1930–1960s	1,000–25,000	5.2	93
1993	<50	3.7	<50

Hardy-Weinberg law (large populations)

- One locus with two alleles A and a
- Possible genotypes AA, aa (homozygotes) and Aa (heterozygotes)
- Genotypic frequencies $D=N_{AA}/N$; $H=N_{Aa}/N$ and $R=N_{aa}/N$
  where $N= N_{AA} + N_{Aa} + N_{aa}$
- Allelic (or genic) frequencies

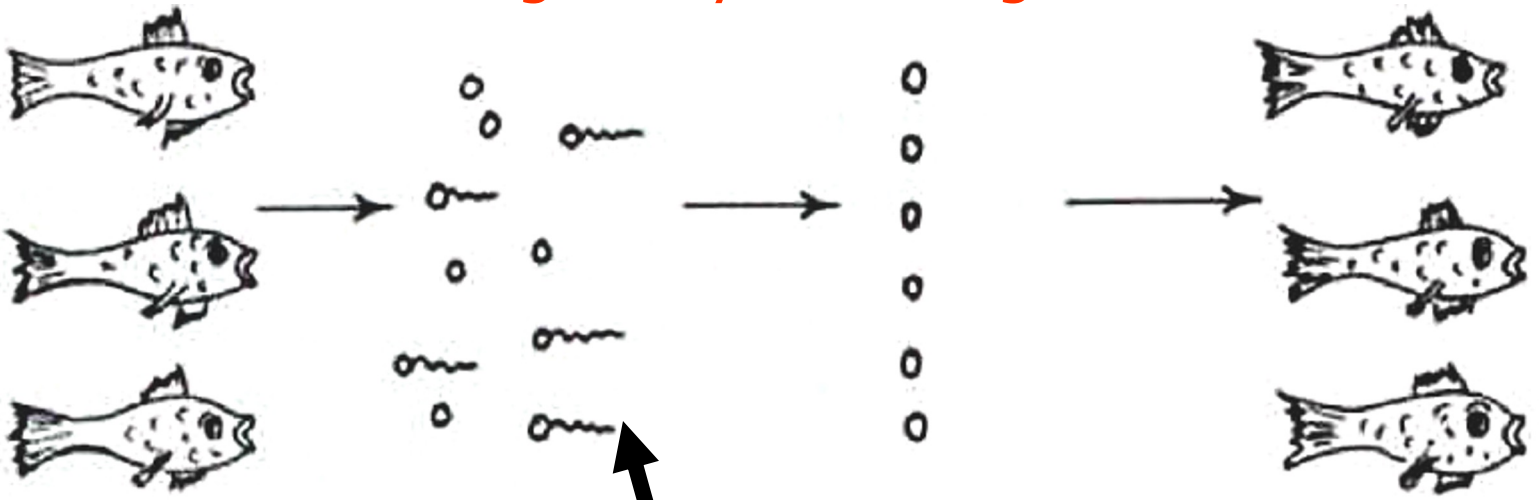
$$p = \frac{2N_{AA} + N_{Aa}}{2N} = D + \frac{1}{2}H \qquad q = \frac{2N_{aa} + N_{Aa}}{2N} = R + \frac{1}{2}H$$

Hardy-Weinberg law

Initial genotypic frequencies: D_0 , H_0 , R_0 whatsoever
Allelic frequencies: $p_0 = D_0 + H_0/2$ $\quad q_0 = R_0 + H_0/2$
In one generation, genotypic frequencies in the population stabilize to the following values

$$D = p_0^2 \qquad H = 2p_0q_0 \qquad R = q_0^2$$

Deriving Hardy-Weinberg law



At time t the population consists of adults who are about to breed

At this point the population breeds by random union of gametes

At this point the population consists of zygotes

At this point the population again consists of adults who are about to breed. This time is called $t + 1$

D_t , H_t , R_t

$$p_t = D_t + H_t/2$$
$$q_t = R_t + H_t/2$$

f = fertility

Gametes A $= f(D_t + H_t/2)N_t$

Gametes a $= f(R_t + H_t/2)N_t$

$$p_t = D_t + H_t/2$$
$$q_t = R_t + H_t/2$$

$$D_{t+1} = p_t^2$$
$$H_{t+1} = 2p_tq_t$$
$$R_{t+1} = q_t^2$$

$p_{t+1} = p_t$ for all t

Assumptions underlying H-W law

1. Discrete generations;
2. Random encounters(*random union* of gametes);

   Can be replaced by random mating
3. No selective pressure (same genotypic fertility and survival);
4. No immigration/emigration;
5. No mutation;
6. Genotypic frequencies equally distributed in the two sexes; not strictly necessary
7. Population size very large (infinite in the limit!)

Exercises

Exercise 1: In an insect pest population with sexual reproduction the percentage of recessive homozygotes (genotype aa) is 36%. Calculate:

i. The frequency of recessive and dominant alleles in the population

ii. The frequency of dominant homozygotes and of heterozygotes

iii. The frequency of the two possible phenotypes under the assumption that A is completely dominant with respect to a.

Exercise 2: Assume that 96% of the Algerian human population has dark eyes (dominant allele A). What would the heterozygote frequency be in the population?

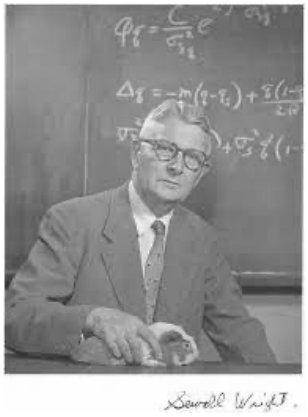
Loss of genetic variability

- Random genetic drift
- Inbreeding and outbreeding depression
- Bottleneck and founder effects

Program Populus 5.3: freely downloadable at

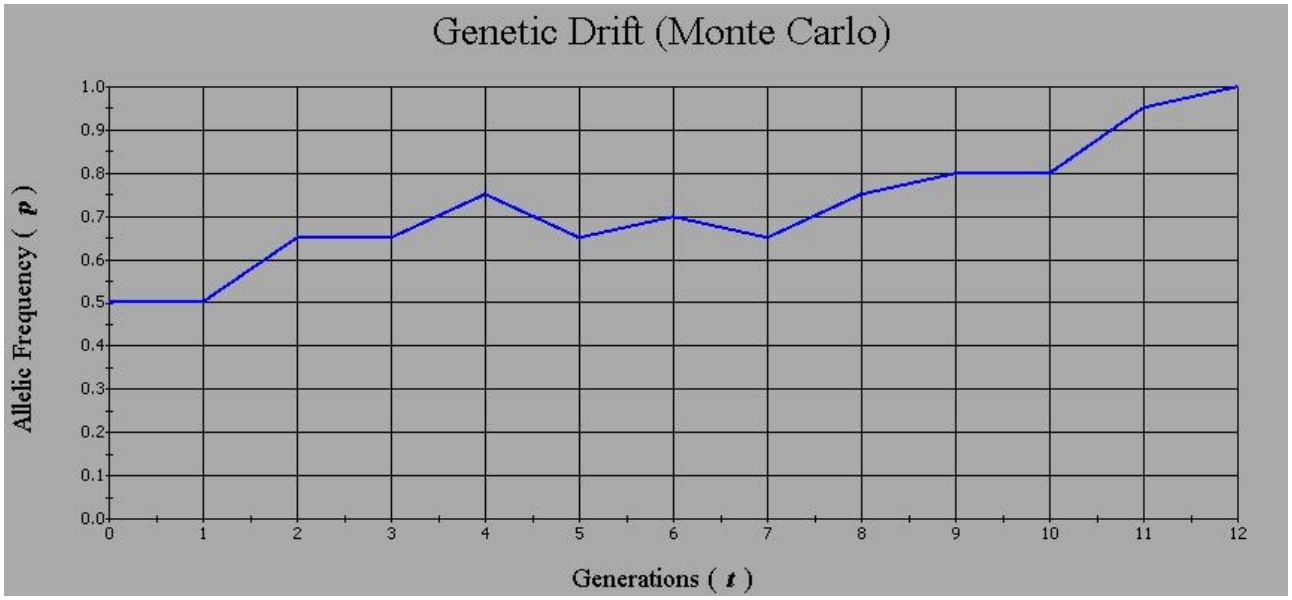
http://www.cbs.umn.edu/populus/installer

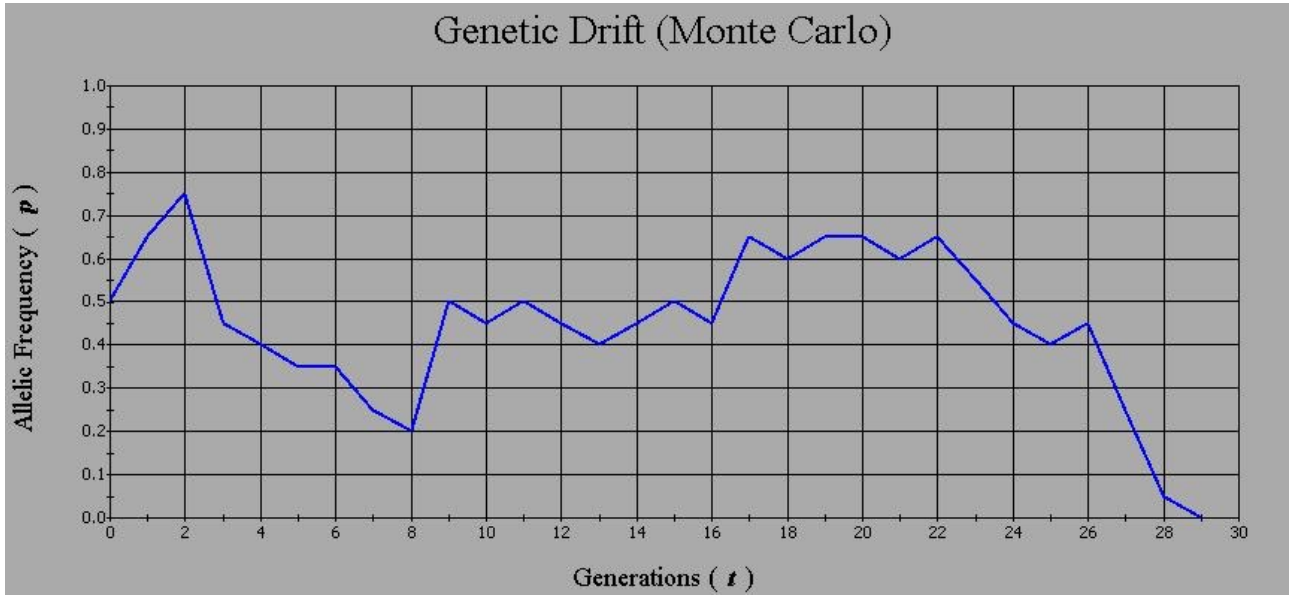
Genetic drift (Wright 1931)



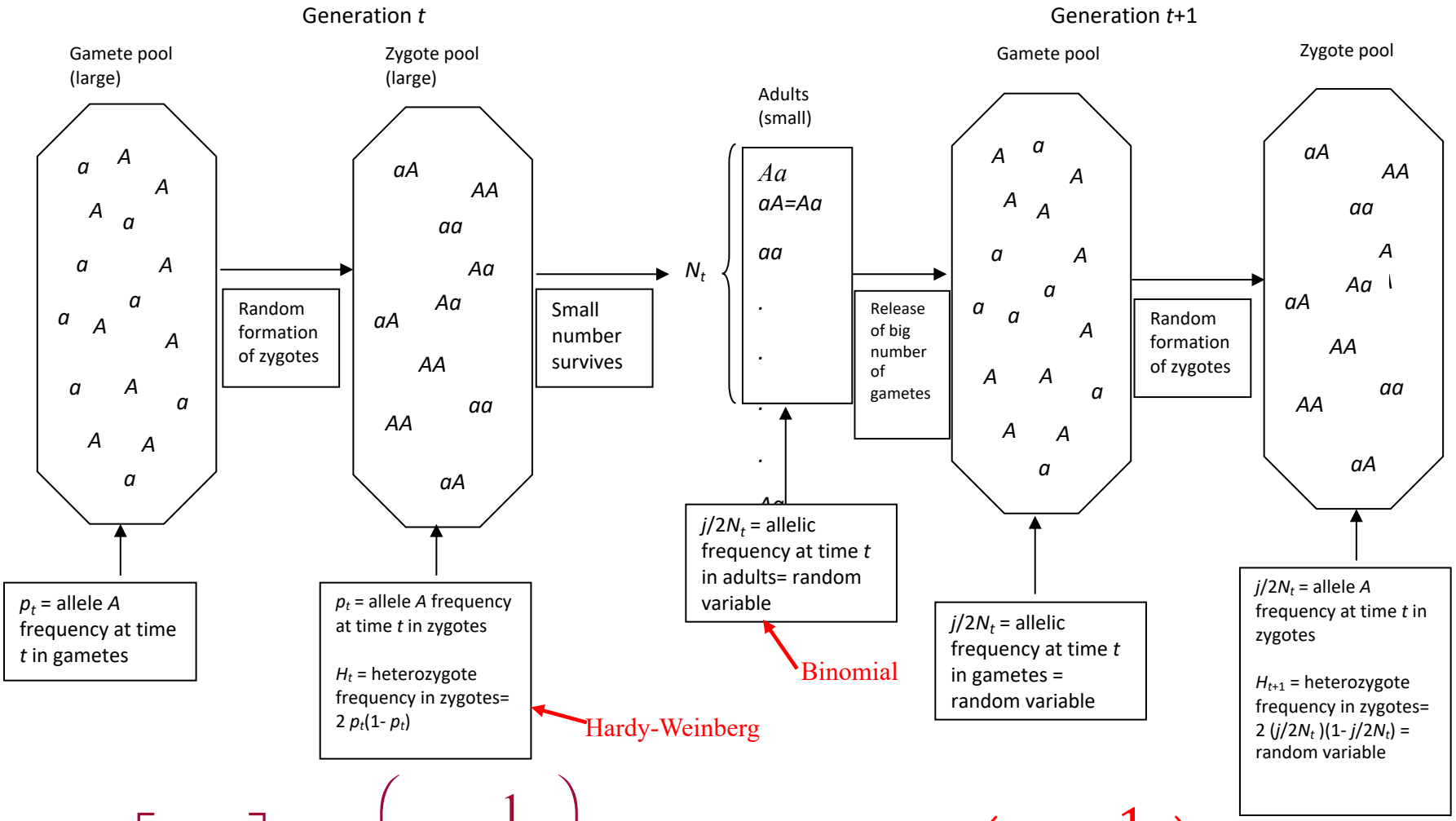
Sewall Wright

p_0=0.5
Hardy-Weinberg
$H_0=2p_0(1-p_0)=0.5$





Genetic drift (Wright 1931)



$$E\left[H_{t+1}\right] = H_t\left(1-\frac{1}{2N_t}\right)$$

$$\bar{H}_{t+1} = \bar{H}_t\left(1-\frac{1}{2N_t}\right)$$

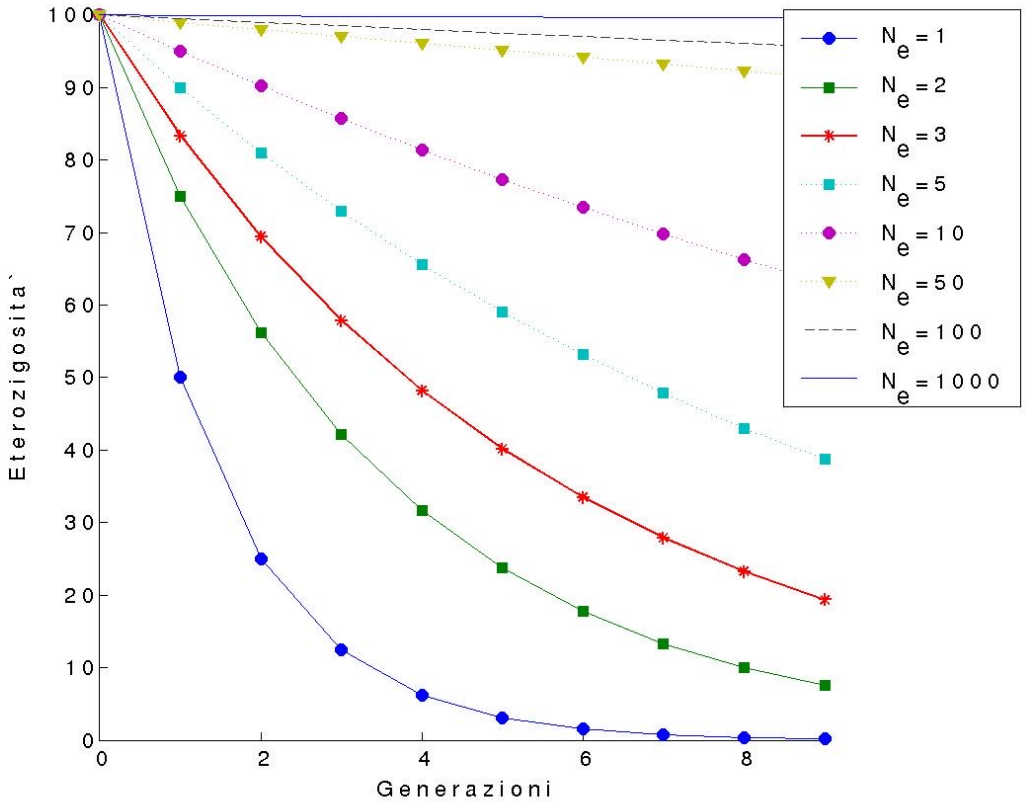
Genetic drift (Wright 1931)

N_e = effective population size= No. of individuals actually reproducing

t = number of generations

$$\bar{H}_t = \bar{H}_0 \left(1 - \frac{1}{2N_e}\right)^t$$

with N_e constant



Mutations and gene flow (immigration) can nullify the effect of the drift

Mutations for $N_e > 100$, Immigration > 5 per generation

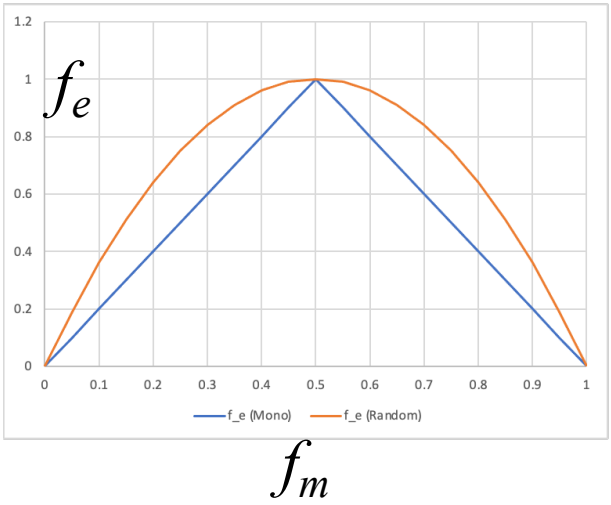
Effective population size

- Unequal sex ratio

N_m = # of males N_f = # of females $N = N_m + N_f$ = total potentially reproducing

$$N_e = 2\min(N_m, N_f)$$ ← Monogamous species

$$N_e = \frac{4N_m N_f}{N_m + N_f}$$ ← Random mating



N_e is max if sex ratio is 1:1, i.e. $N_m = N_f$

$f_e = N_e/N$ $f_m = N_m/N$ $f_f = N_f/N = 1 - f_m$

- Fluctuations in time

$$\overline{H}_t = \overline{H}_0\left(1-\frac{1}{2N_{e,0}}\right)\left(1-\frac{1}{2N_{e,1}}\right)\ldots\left(1-\frac{1}{2N_{e,t-1}}\right)$$

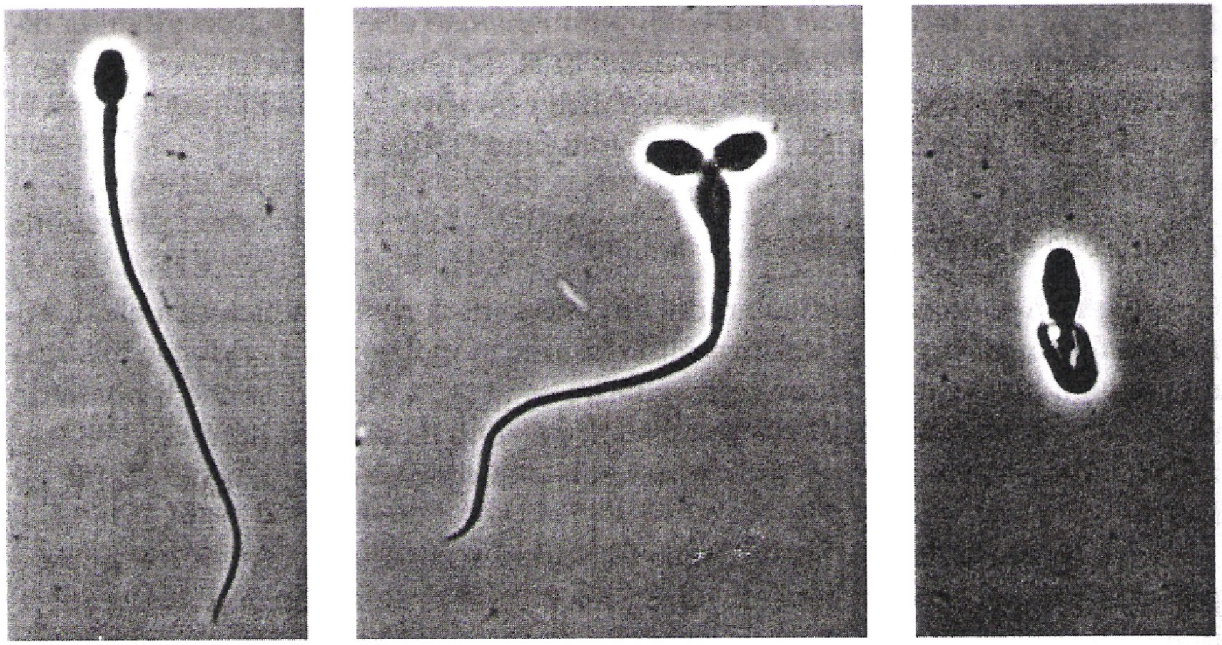
Founder effect and bottlenecks

Ngorongoro crater lions

Beginning of 1960's: about 70 individuals

1962: killed by stinging flies and reduced to 9 females + 1 male + 7 new males

Founder effect



(A) (B) (C)

Figura 3.4 Anomalie negli spermatozoi dei leoni del cratere di Ngorongoro (Tanzania), conseguenza della bassa variabilità genetica intrapopolazione imputabile all'effetto fondatore, all'isolamento e all'alto tasso di inbreeding. (A) Spermatozoo normale. (B) Spermatozoo bicefalo. (C) Spermatozoo afunzionale con flagello avvolto a spirale. (Fotografie di D.E.Wildt e J.Howard, National Zoological Park, Smithsonian Institute.)

Inbreeding and outbreeding depression

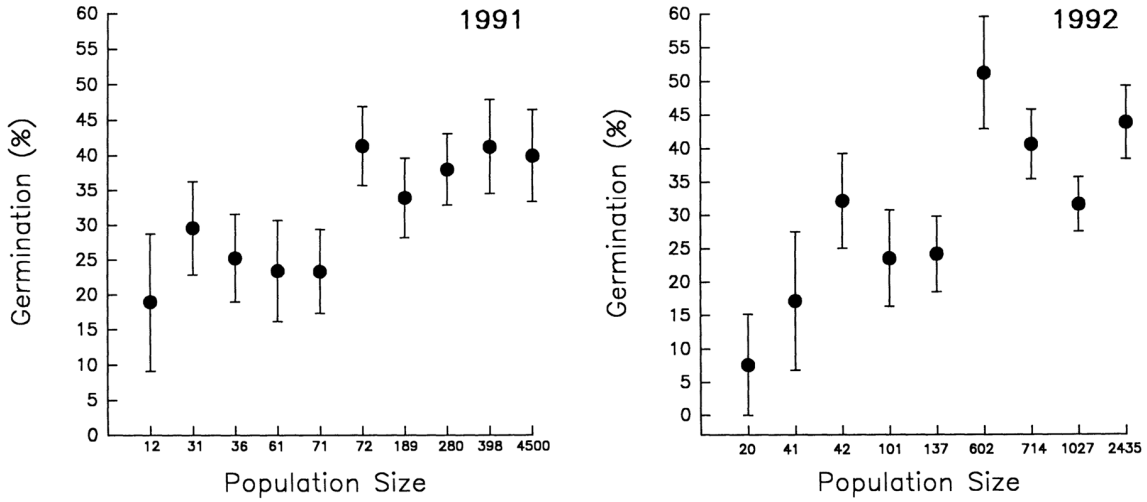
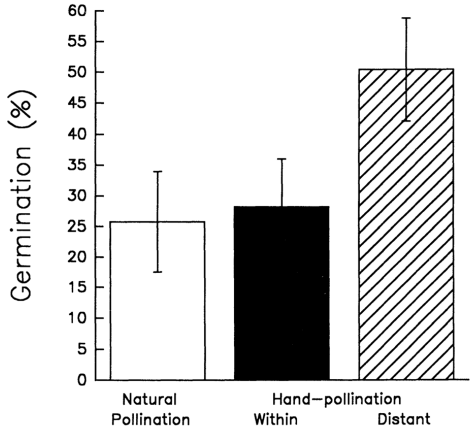


Figure 2. Individual population data on percentage of seed germination success for 1991 and 1992. Means ± S.E. are shown (F = 1.48, df = 9,96, p = 0.168, 1991, although not statistically significant, the trend is in the same direction as seed size data; F = 3.56, df = 8,69, p = 0.0016, 1992).

Ipomopsis aggregata



small populations

Heschel M.S, Paige K.N. 1995 *Conservation Biology*, 9:126:133

The deer at Mesola

60 residual deer

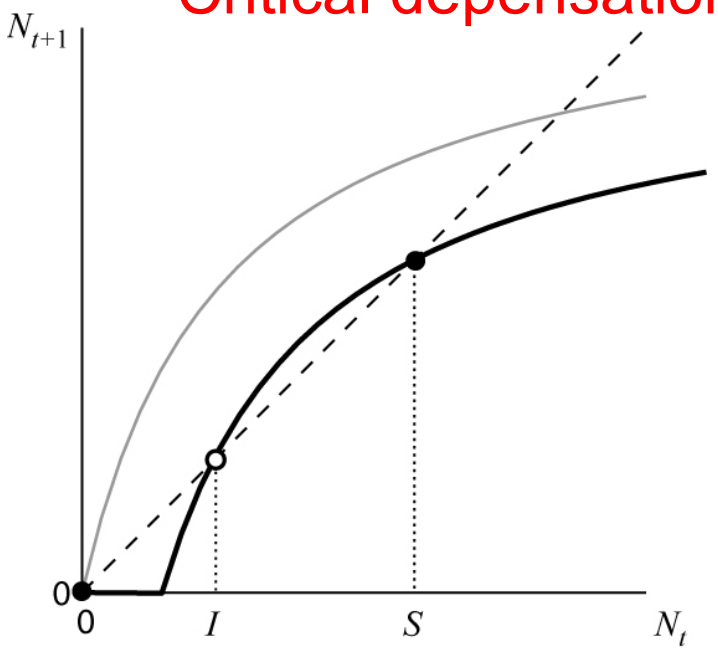
N_e = 10-20

Cervus elaphus

Effects of genetic drift on population dynamics

$$N_{t+1} = \left(1 - \frac{1}{2\gamma N_t}\right) \Lambda(N_t) N_t$$

Critical depensation!



N_t = total population size

$\Lambda(N_t)$ = finite rate of increase with no genetic deterioration

N_{et} = effective population size $= \gamma N_t$

$0 < \gamma \leq 1$ fraction of reproducing individuals

$1 - \frac{1}{2\gamma N_t}$ Wright's factor (=0 if $\gamma N_t \leq 0.5$)