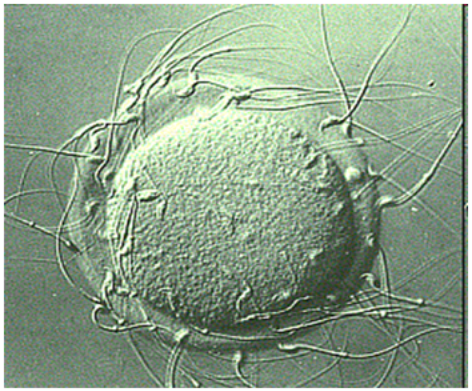
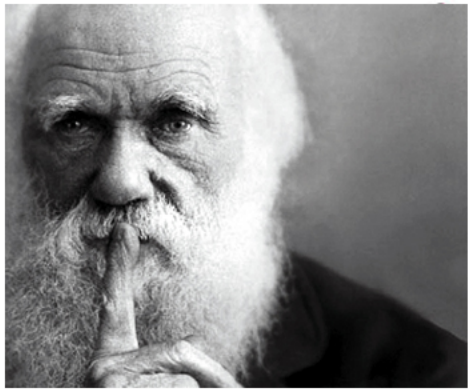


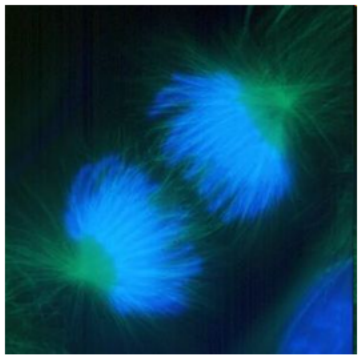
പ്രപഞ്ചവും ജീവനും

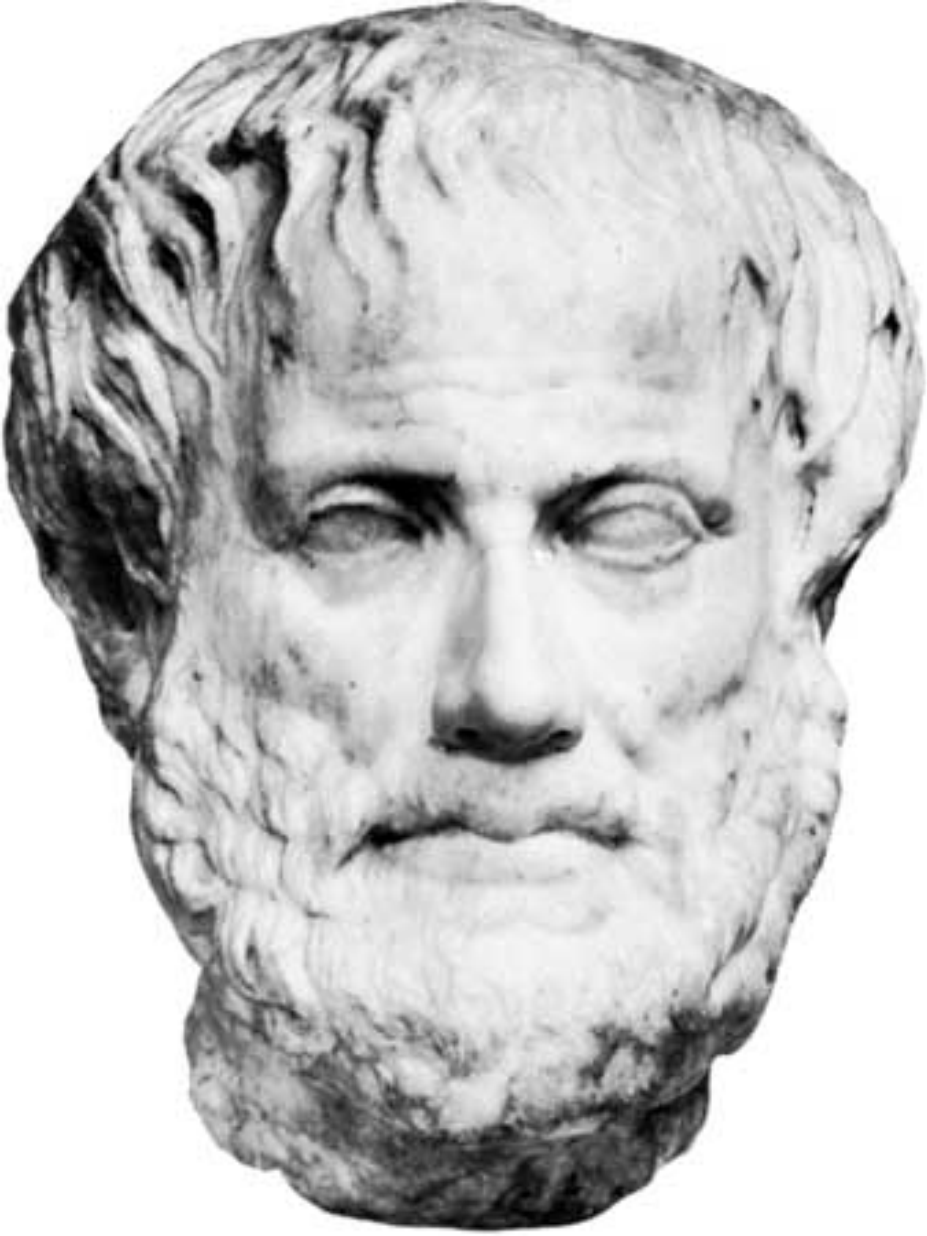
സയൻസ്ക്ലാസുകൾ



ഡാർവിൻ മുതൽ ജിനോം വരെ

കേരള ശാസ്ത്രസാഹിത്യ പരിഷത്ത്





CAROLI LINNÆI

EQUITIS DE STELLA POLARI,

ARCHIATRI REGII, MED. & BOTAN. PROFESS. UPSAL.;
ACAD. UPSAL. HOLMENS. PETROPOL. BEROL. IMPER.
LOND. MONSPEL. TOLOS. FLORENT. SOC.

SYSTEMA NATURÆ

PER

REGNA TRIA NATURÆ,

SECUNDUM

CLASSES, ORDINES,
GENERA, SPECIES,

CUM

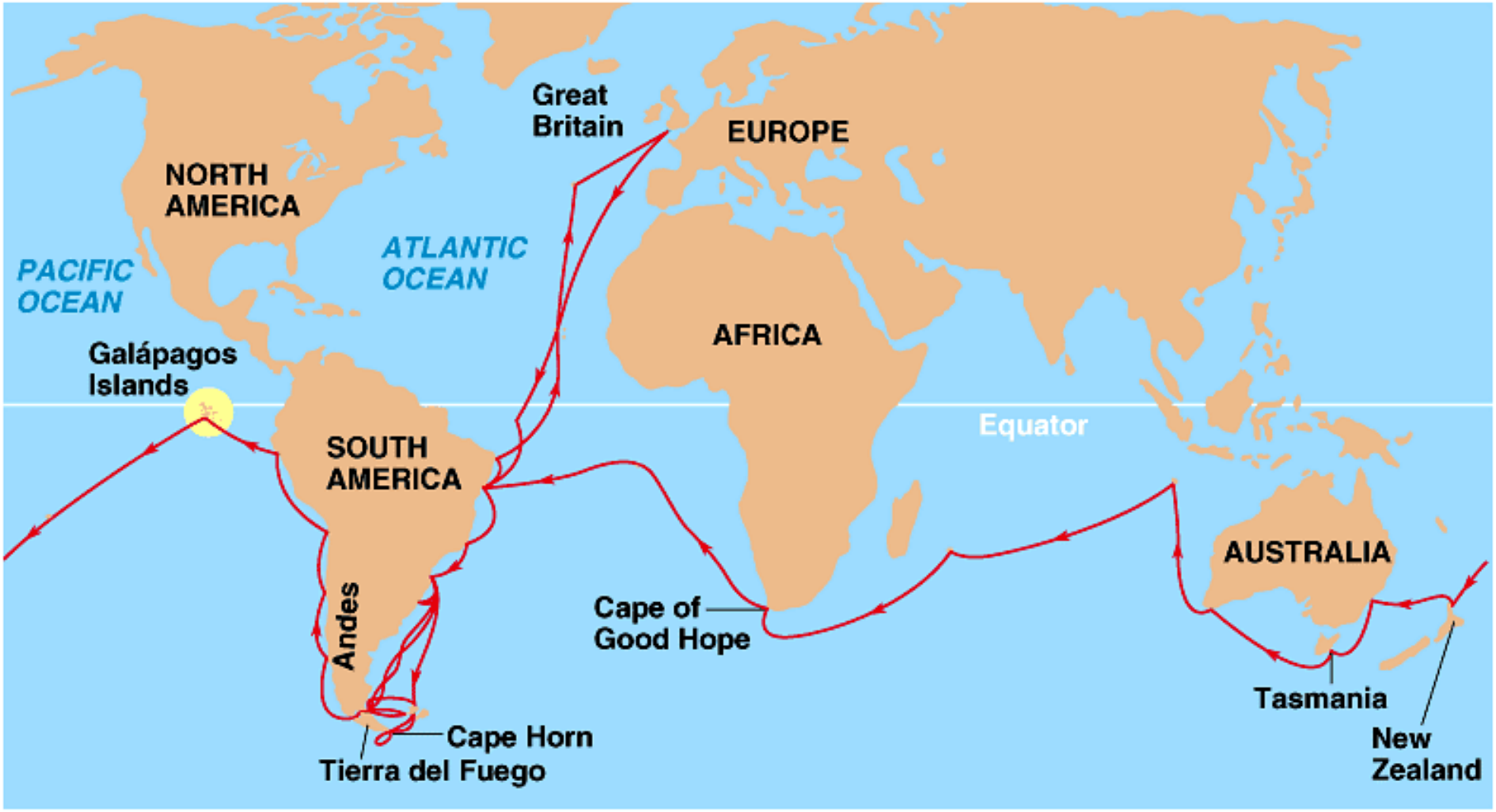
CHARACTERIBUS, DIFFERENTIIS,
SYNONYMIS, LOCIS.

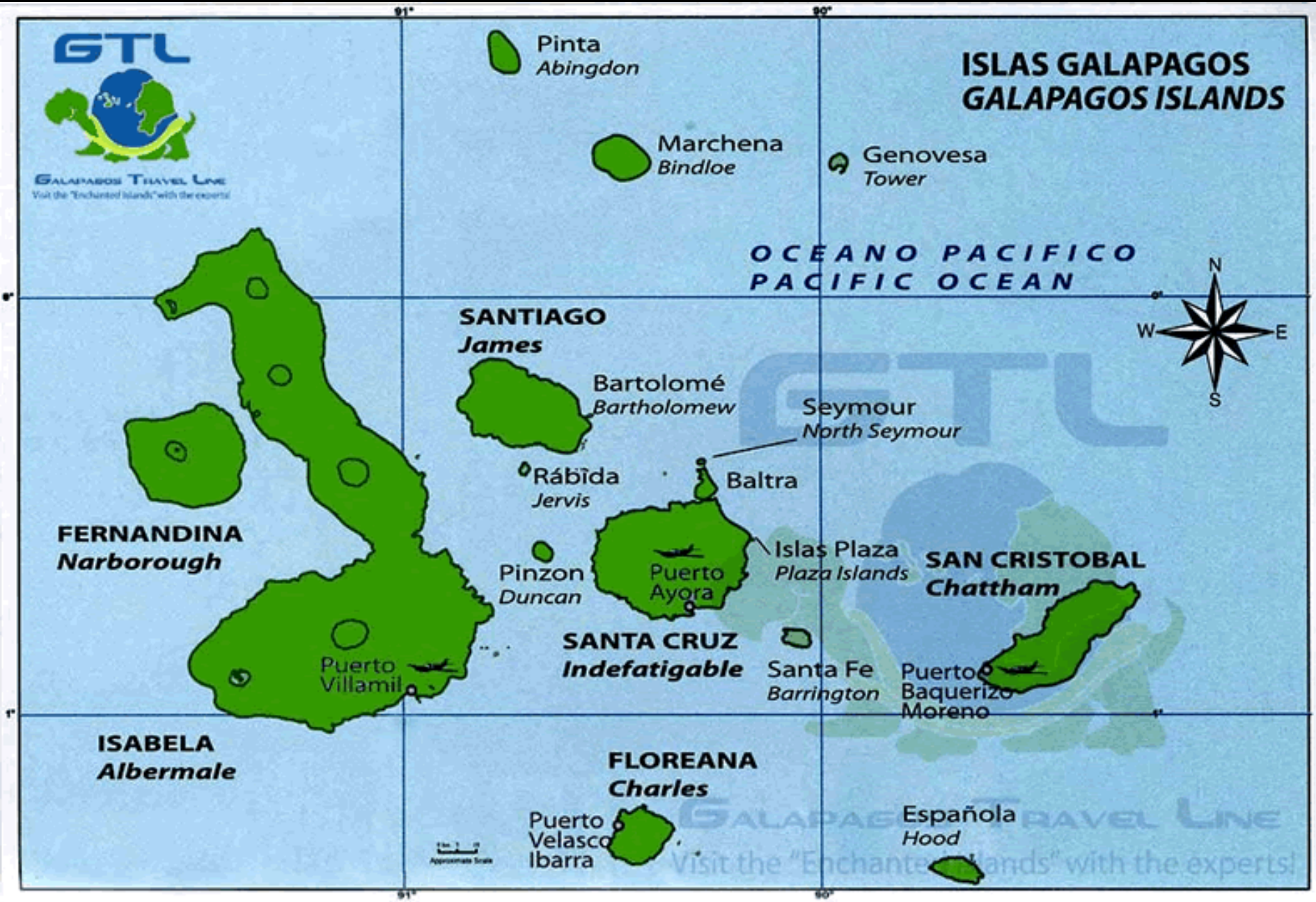
TOMUS I.

EDITIO DECIMA, REFORMATA.

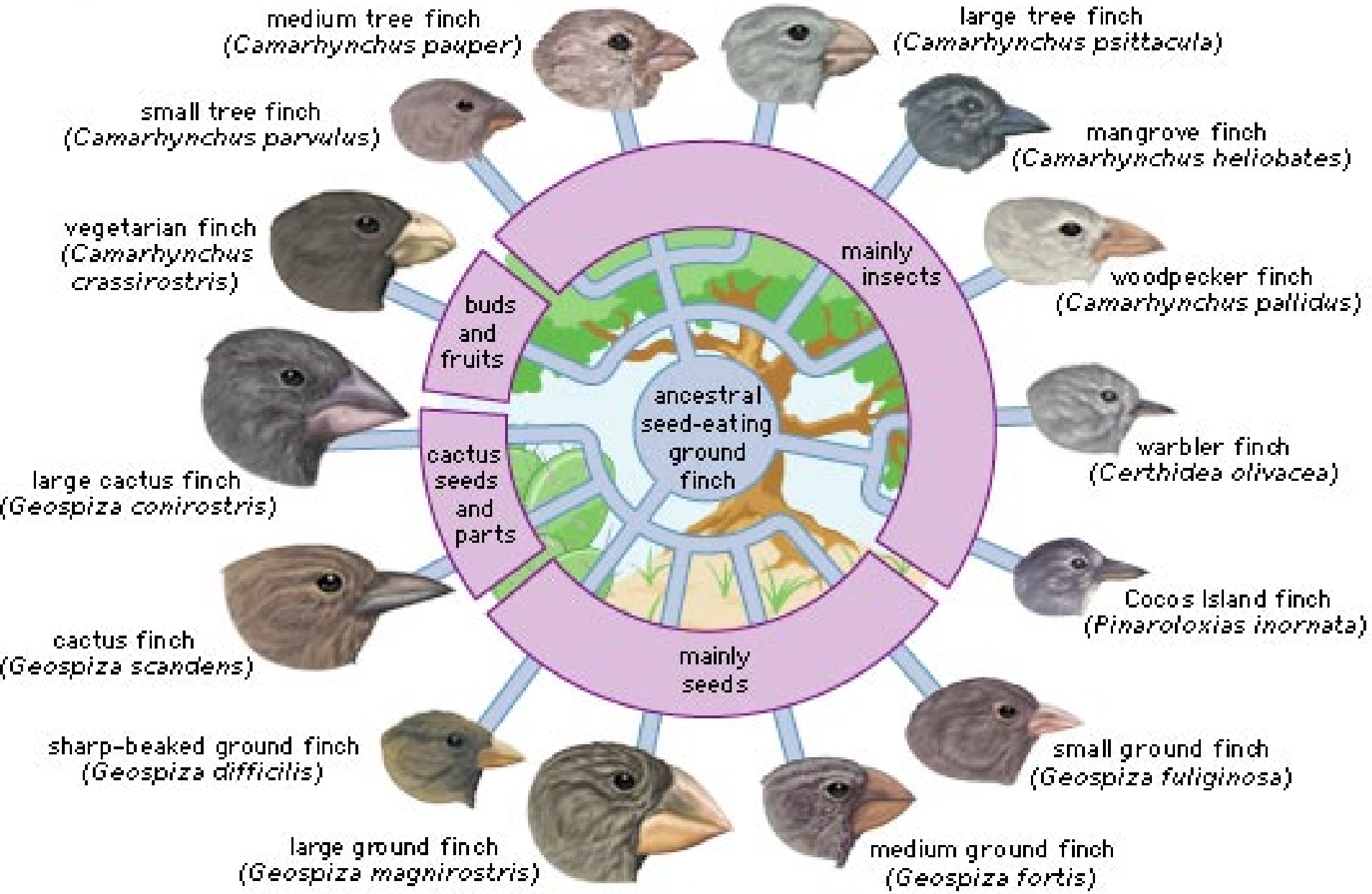
Cum Privilegio S:æ R:æ M:tis Sveciæ.

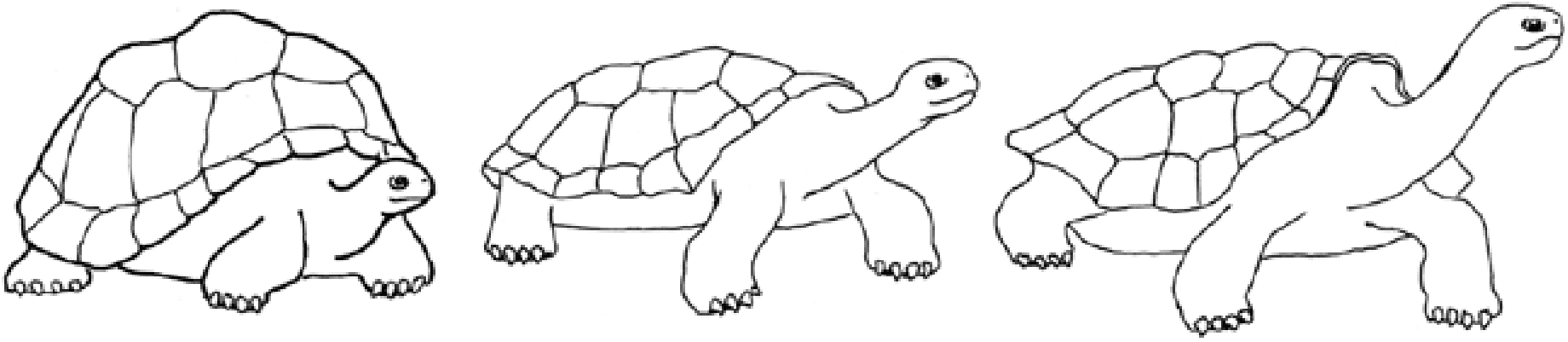
HOLMIÆ,
IMPENSIS DIRECT. LAURENTII SALVII,
1758.




GTL
Galapagos Travel Line
Visit the "Enchanted Islands" with the experts!
ISLAS GALAPAGOS
GALAPAGOS ISLANDS
Pinta
Abingdon
Marchena
Bindloe
Genovesa
Tower
OCEANO PACIFICO
PACIFIC OCEAN
N
W
E
S
SANTIAGO
James
Bartolomé
Bartholomew
Seymour
North Seymour
Rábida
Jervis
Baltra
FERNANDINA
Narborough
Islas Plaza
Plaza Islands
SAN CRISTOBAL
Chattham
Pinzon
Duncan
Puerto
Ayora
SANTA CRUZ
Indefatigable
Santa Fe
Barrington
Puerto
Baquerizo
Moreno
Puerto
Villamil
ISABELA
Albermale
FLOREANA
Charles
Puerto
Velasco
Ibarra
Española
Hood
Approximate Scale
Galapagos Travel Line
Visit the "Enchanted Islands" with the experts!

Adaptive radiation in Galapagos finches





പ്രകൃതി നിർധാരണം


Woods

ON

THE ORIGIN OF SPECIES

BY MEANS OF NATURAL SELECTION,

OR THE

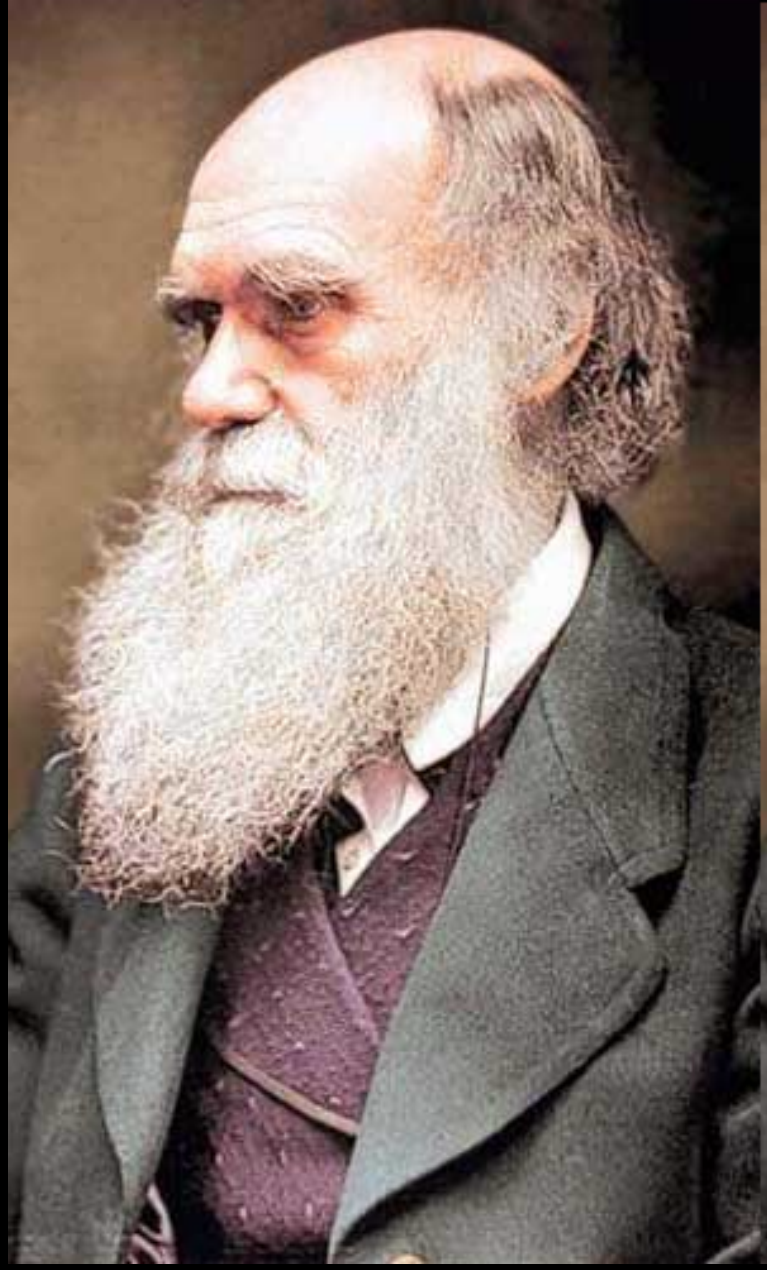
PRESERVATION OF FAVOURED RACES IN THE STRUGGLE FOR LIFE.

By CHARLES DARWIN, M.A.,

FELLOW OF THE ROYAL, GEOLOGICAL, LINNÆAN, ETC., SOCIETIES;
AUTHOR OF 'JOURNAL OF RESEARCHES DURING H. M. S. BEAGLE'S VOYAGE ROUND THE WORLD.'

LONDON:
JOHN MURRAY, ALBEMARLE STREET.
1859.

പാരമ്പര്യം



The Variation of

Animals and Plants

Under Domestication

Second Edition, Revised

Charles Darwin

New York: D. Appleton & Co.

1883

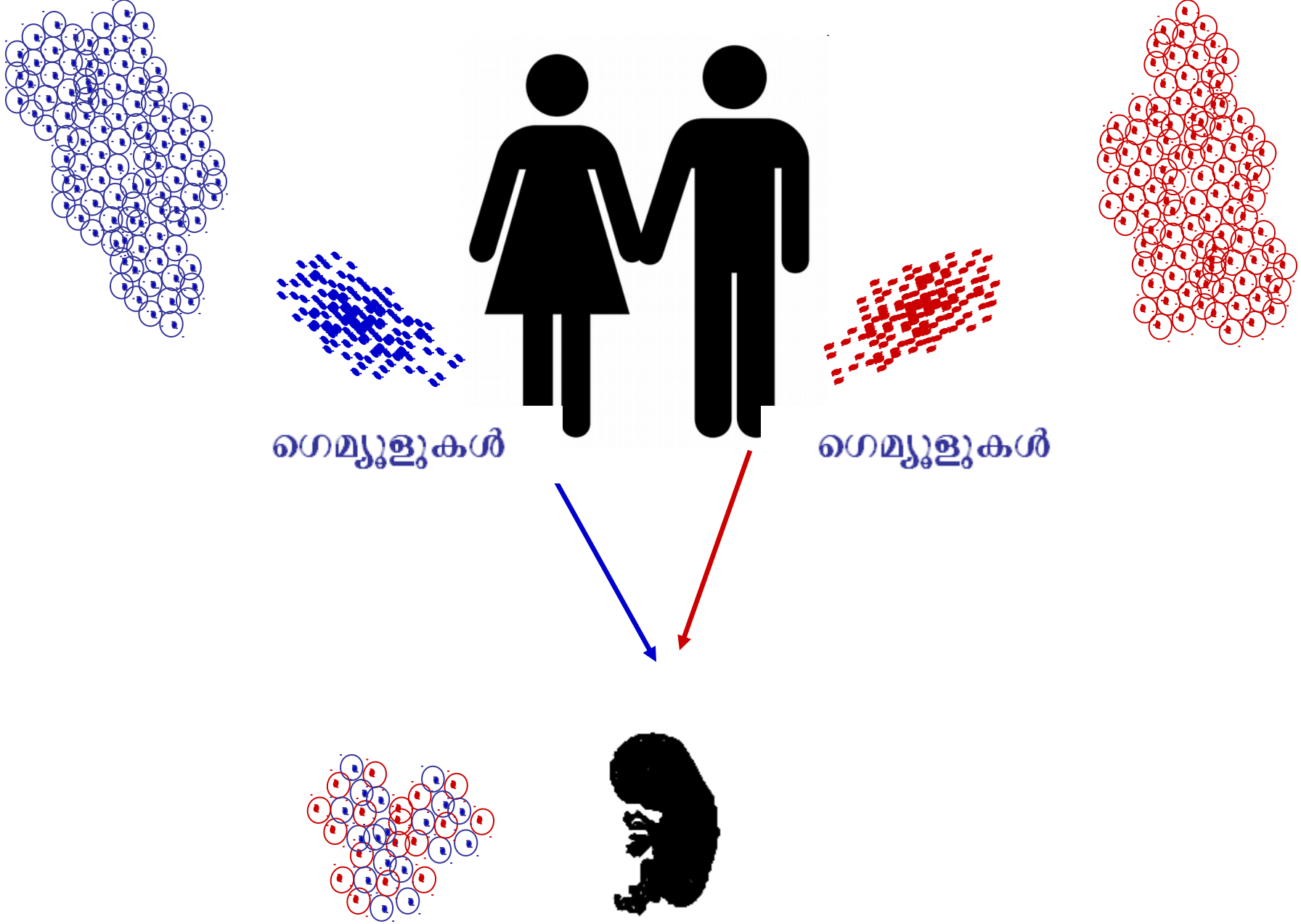
CHAPTER XXVII.

PROVISIONAL HYPOTHESIS OF PANGENESIS.

PRELIMINARY REMARKS—FIRST PART:—THE FACTS TO BE CONNECTED UNDER A SINGLE POINT OF VIEW, NAMELY, THE VARIOUS KINDS OF REPRODUCTION—RE-GROWTH OF AMPUTATED PARTS—GRAFT-HYBRIDS—THE DIRECT ACTION OF THE MALE ELEMENT ON THE FEMALE—DEVELOPMENT—THE FUNCTIONAL INDEPENDENCE OF THE UNITS OF THE BODY—VARIABILITY—INHERITANCE—REVERSION.

SECOND PART:—STATEMENT OF THE HYPOTHESIS—HOW FAR THE NECESSARY ASSUMPTIONS ARE IMPROBABLE—EXPLANATION BY AID OF THE HYPOTHESIS OF THE SEVERAL CLASSES OF FACTS SPECIFIED IN THE FIRST PART—CONCLUSION.

IN the previous chapters large classes of facts, such as those bearing on bud-variation, the various forms of inheritance, the causes and laws of variation, have been discussed; and it is obvious that these subjects, as well as the several modes of reproduction, stand in some sort of relation to one another. I


ഗെമ്യൂളുകൾ
ഗെമ്യൂളുകൾ

Seed shape

Spherical

Dented

Seed color

Yellow

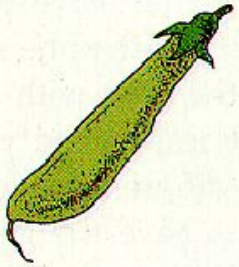
Green

Flower color

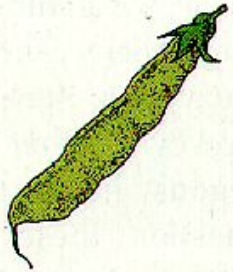
Purple

White

Pod shape

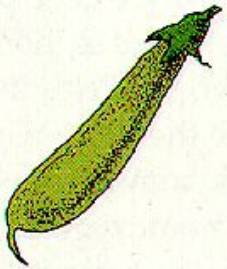


Inflated

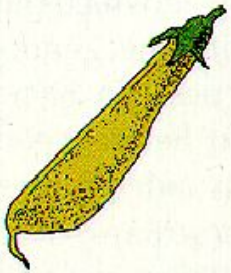


Constricted

Pod color



Green



Yellow

Flower position

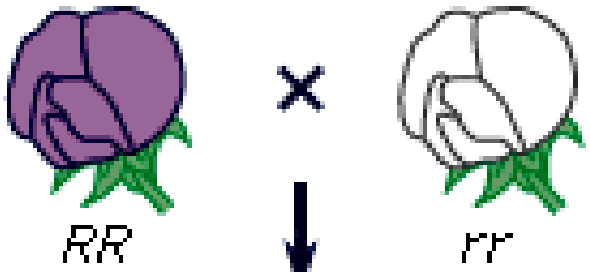
Axial

Terminal

Stem height

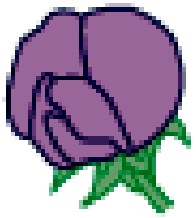
Tall

Dwarf

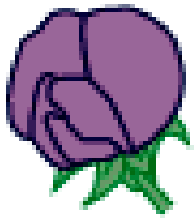
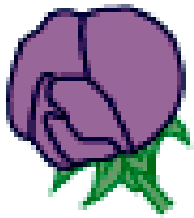
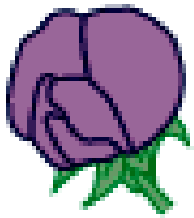


parental generation (P)

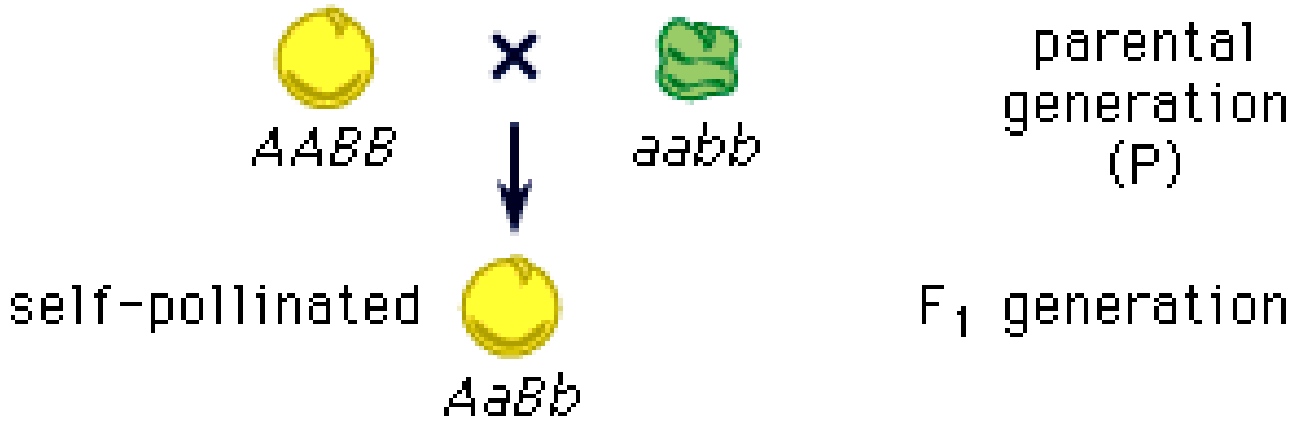
self-pollinated



F_1 generation

♀ \ ♂		pollen	
		R	r
ovules	R	 RR	 Rr
	r	 Rr	 rr

F_2 generation



♀ \ ♂		pollen			
		AB	*Ab*	*aB*	*ab*
ovules	*AB*	*AABB*	*AABb*	*AaBB*	*AaBb*
	Ab	*AABb*	*AAbb*	*AaBb*	*Aabb*
	aB	*AaBB*	*AaBb*	*aaBB*	*aaBb*
	ab	*AaBb*	*Aabb*	*aaBb*	*aabb*

F_2 generation

9:3:3:1

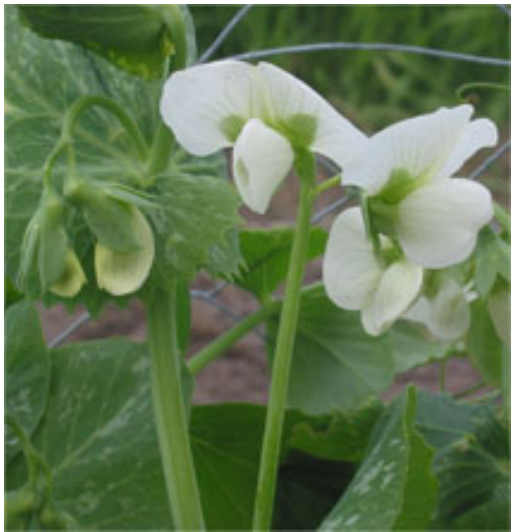
Hugo de Vries

Erich Tschermak

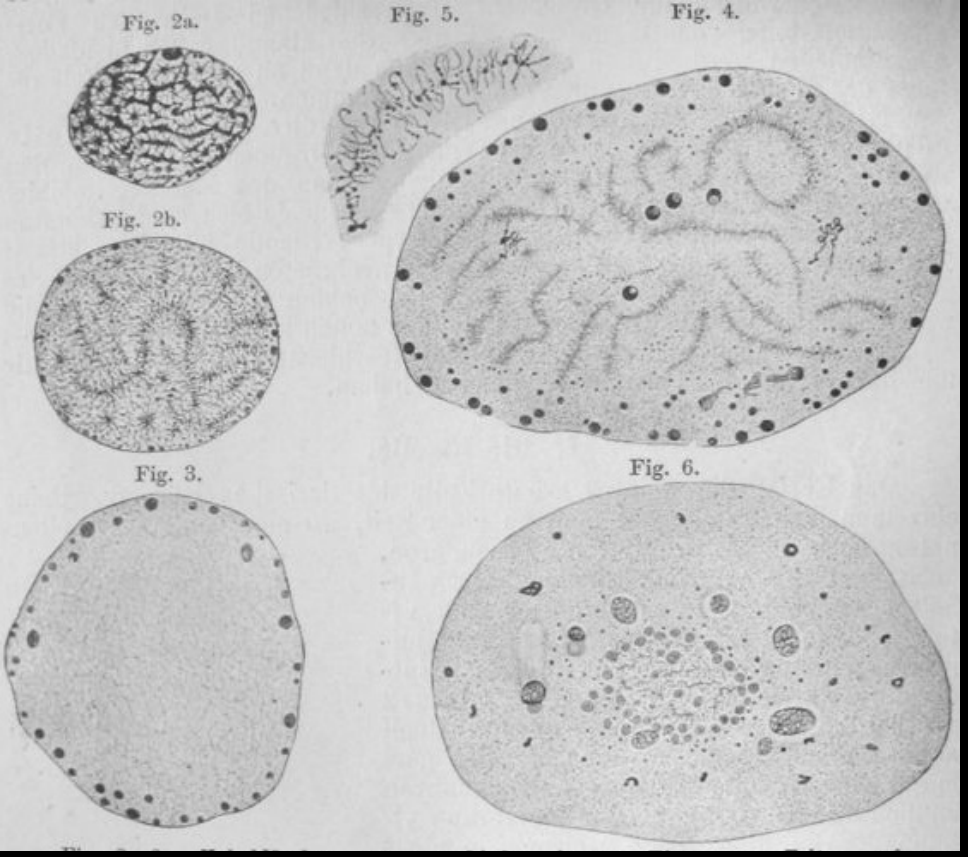
Carl Correns

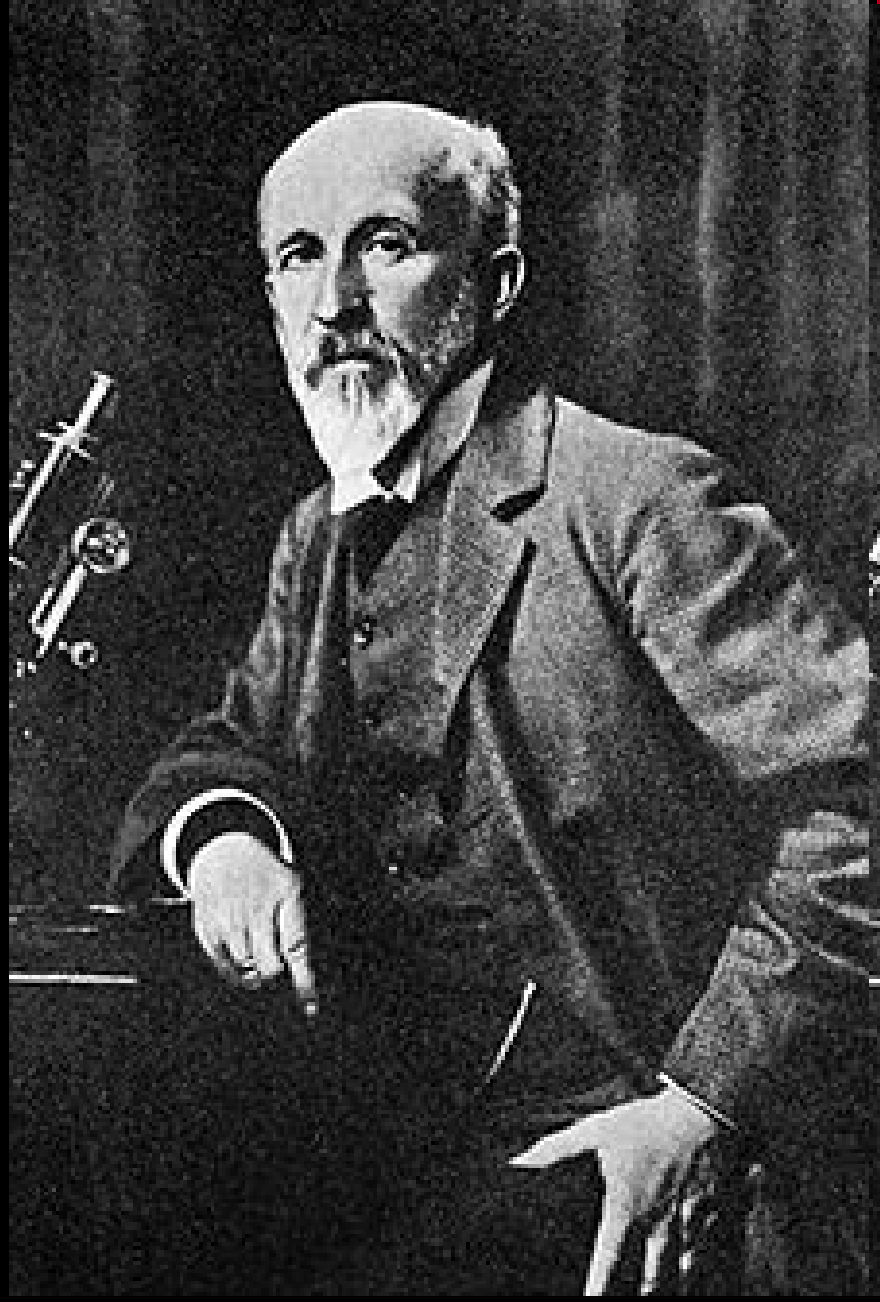
Evening primrose

Pea

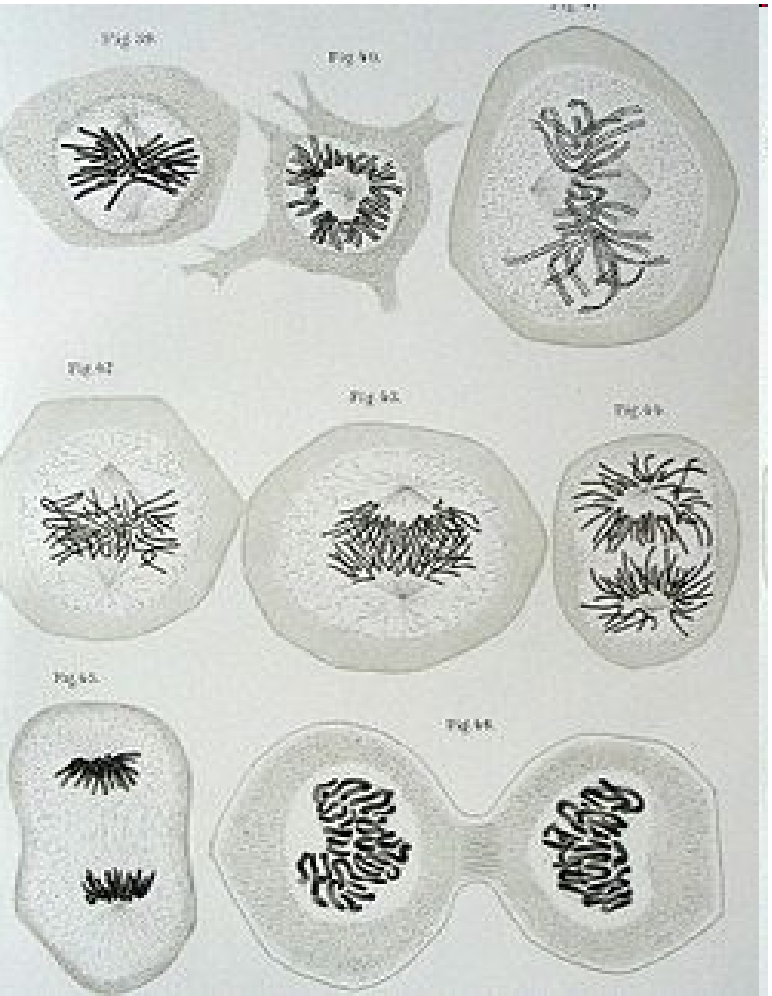


Hawkweed



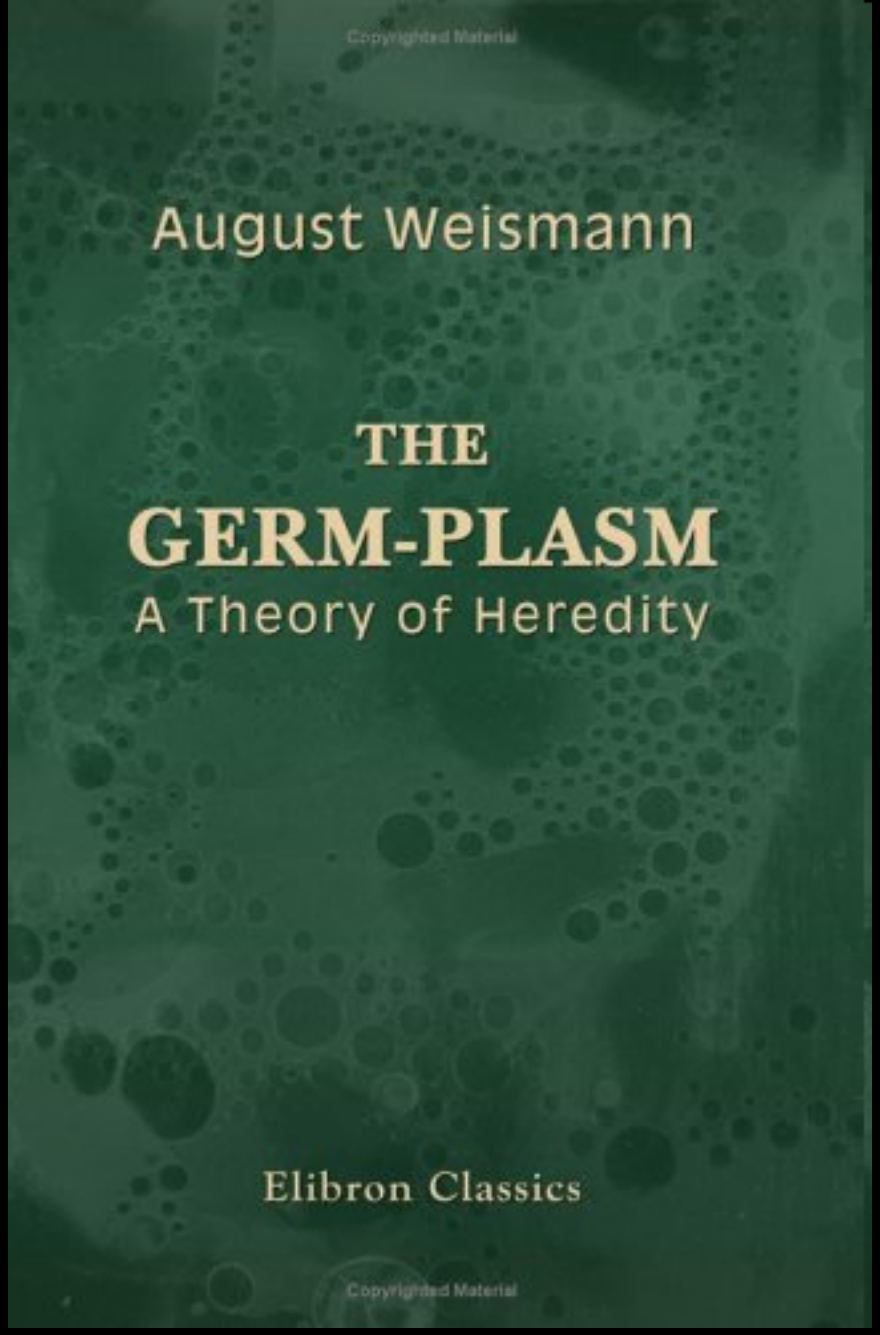


Oscar Hertwig 1876

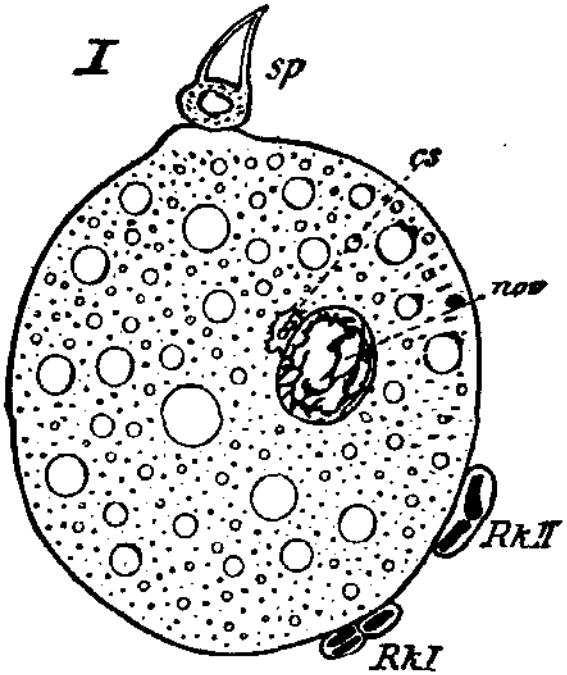


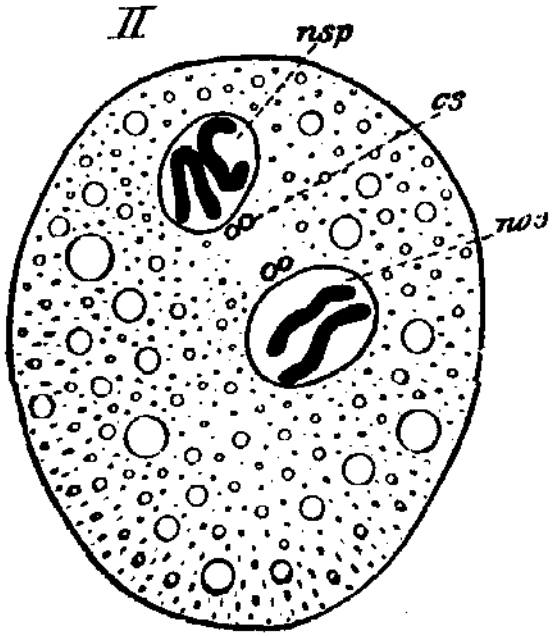
Walther Flemming

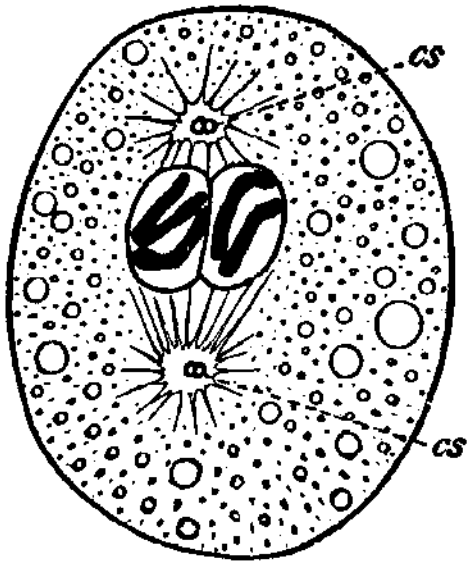
1878

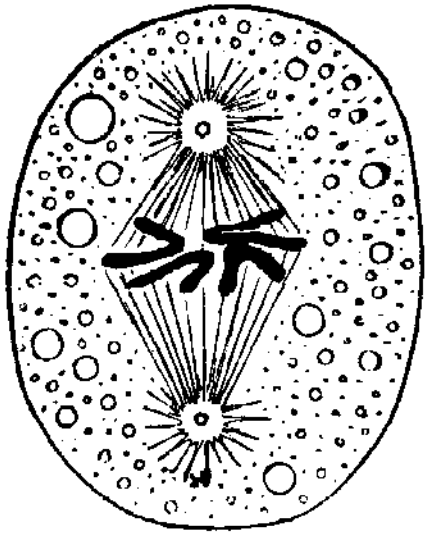


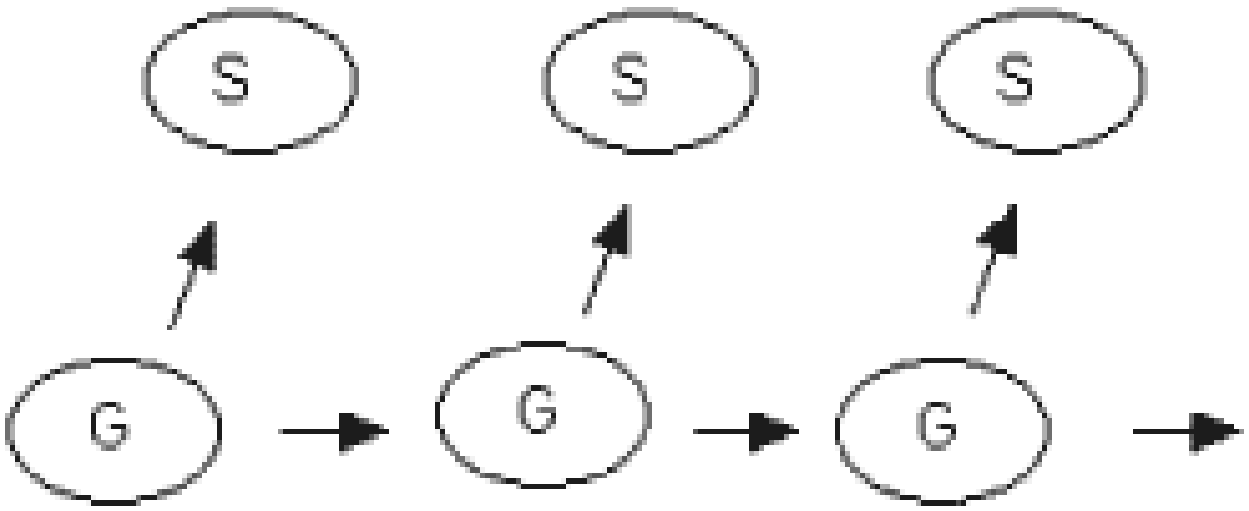
August Weismann **1893**


I
sp
cs
RkII
RkI


II
nsp
cs


III
cs
cs


IV



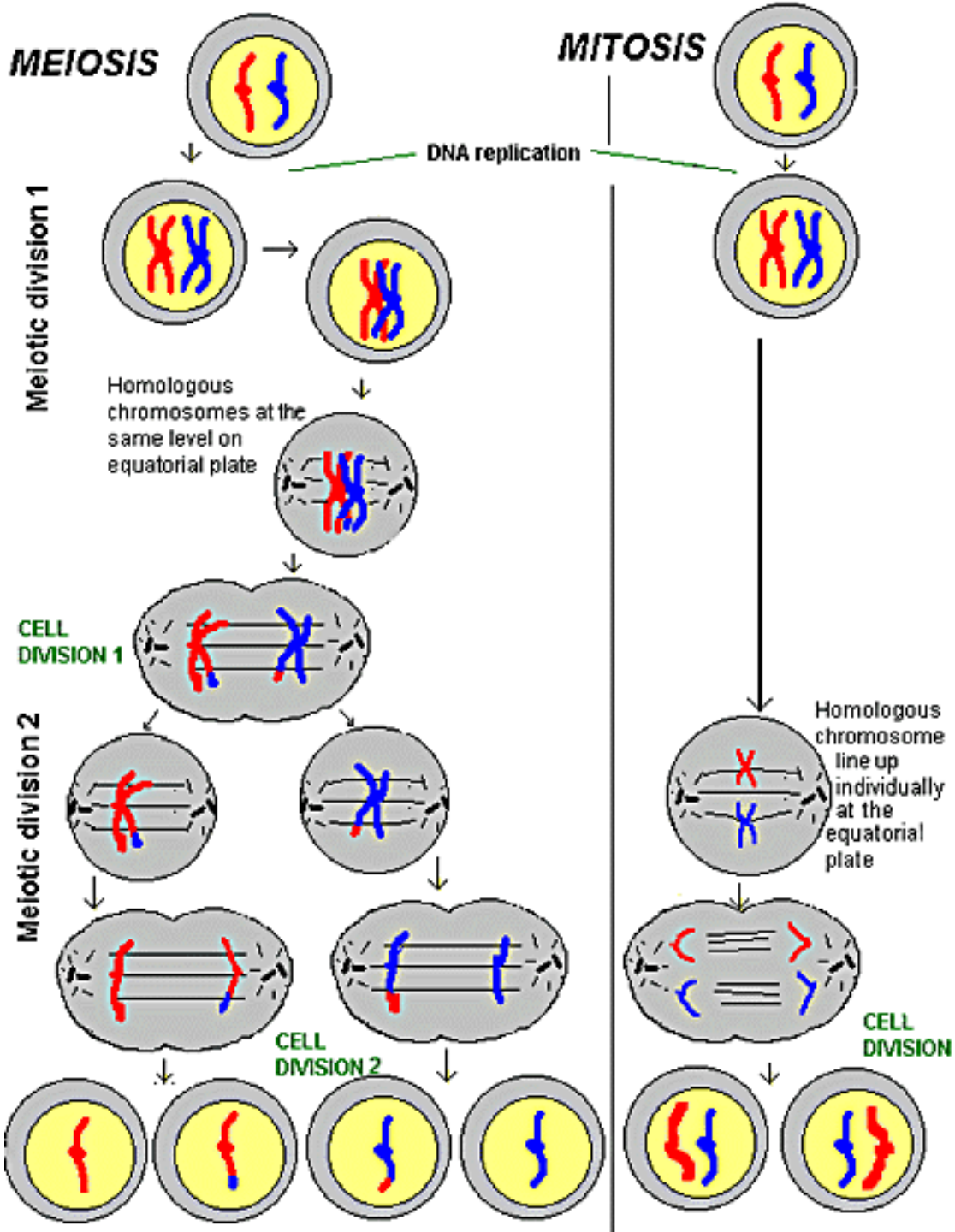
Weismann barrier

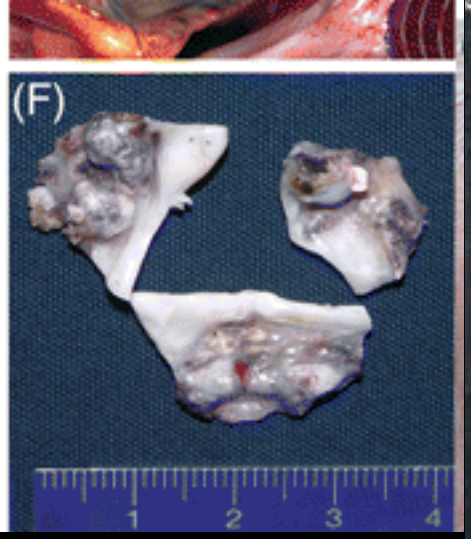
William Sutton

Theodor Boveri

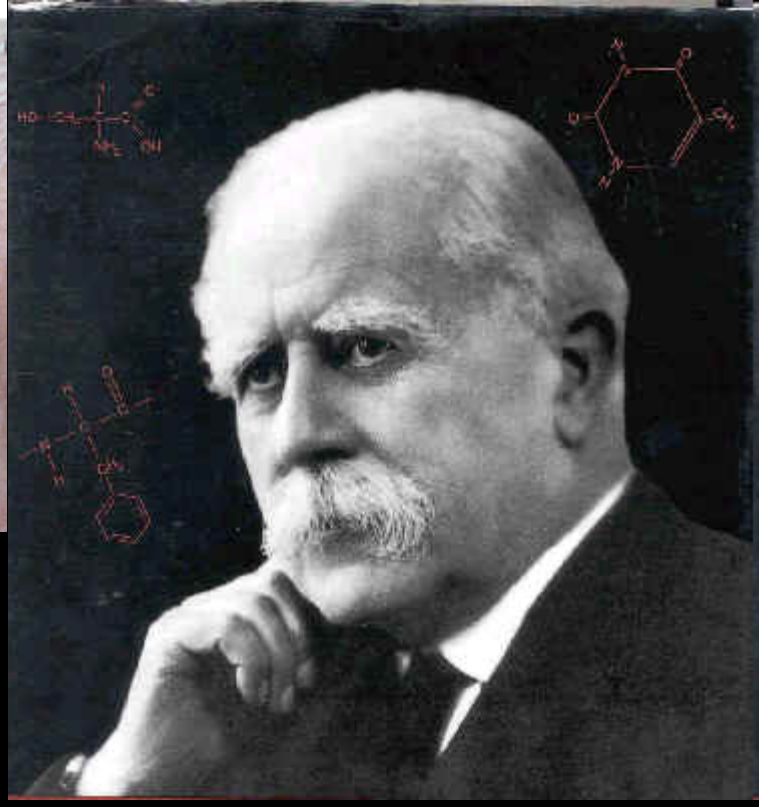
പാരമ്പര്യത്തിൻെറ ക്രോമോസോം സിദ്ധാന്തം

1902


MEIOSIS
MITOSIS
DNA replication
Meiotic division 1
Homologous chromosomes at the same level on equatorial plate
CELL DIVISION 1
Meiotic division 2
CELL DIVISION 2
Homologous chromosome line up individually at the equatorial plate
CELL DIVISION



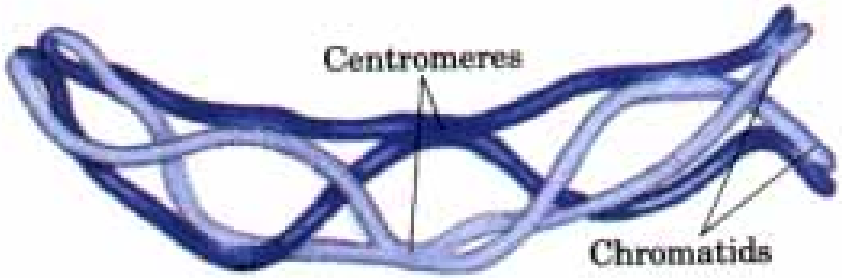
Total number of family (brothers and sisters)	Number of Alkaptonuric members	Number of normal members
14	4	10
4	3	1
7	3	4
2	1	1
2	2	0
1	1	0
10	1	9
5	2	3
3	2	1
48	19	29

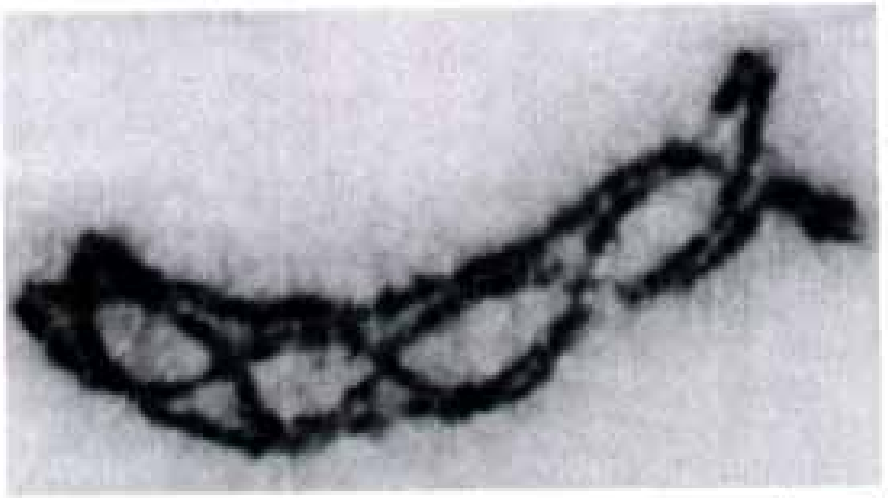


Archibald Garrod

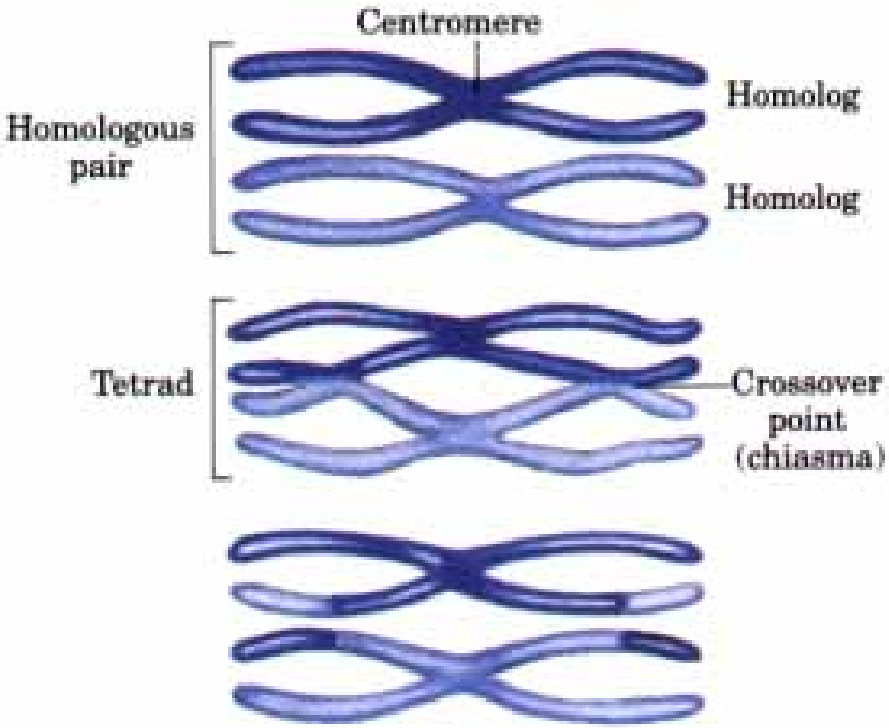
Thomas Hunt Morgan

1866 - 1945





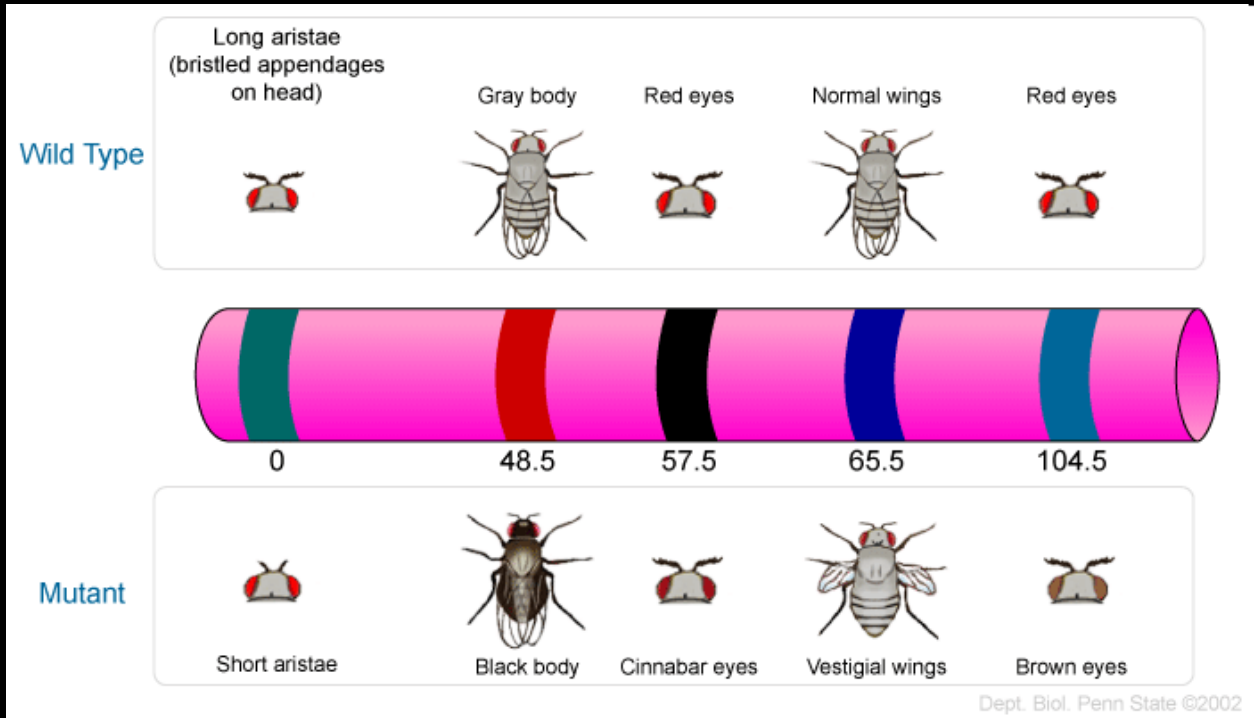
(a)



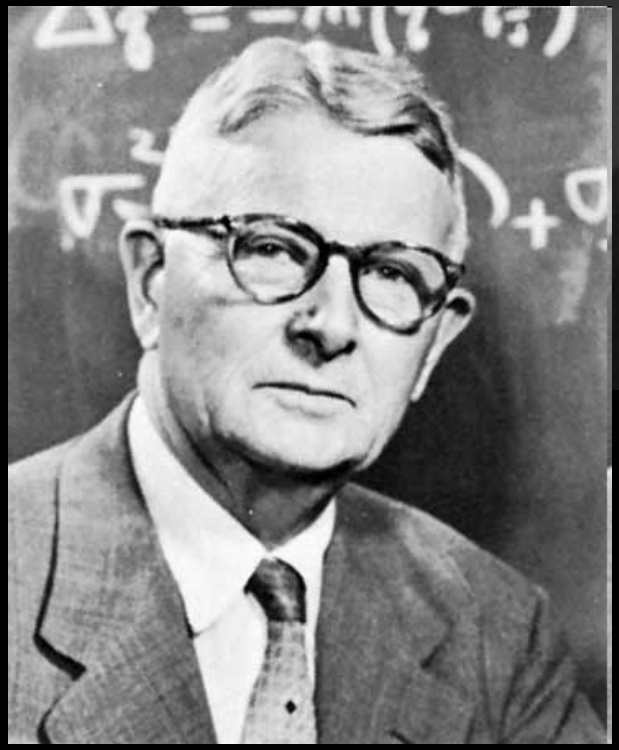
(b)

Figure 24–26 Crossing over. **(a)** The homologous chromosomes of a grasshopper are shown during prophase I of meiosis. Multiple points of joining (chiasmata) are evident between the two homolo-

Alfred Sturtevant



RA Fisher



Sewall Wright

JBS Haldane

T Dobzhansky

Ernst Mayr

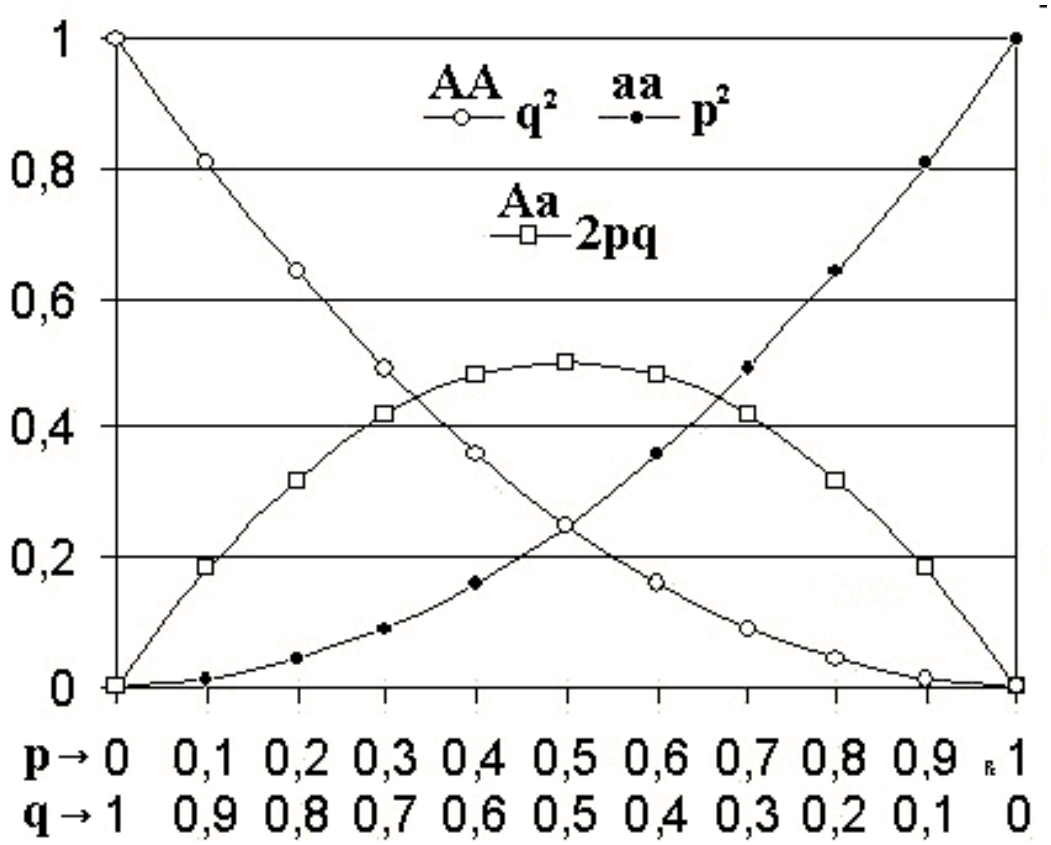
സാംഖിക ശാസ്ത്രം + ജനിതകം

ആധുനിക സംശ്ലേഷണം

(Modern Evolutionary synthesis)

ഹാർഡി വീൻബെർഗ് നിയമം

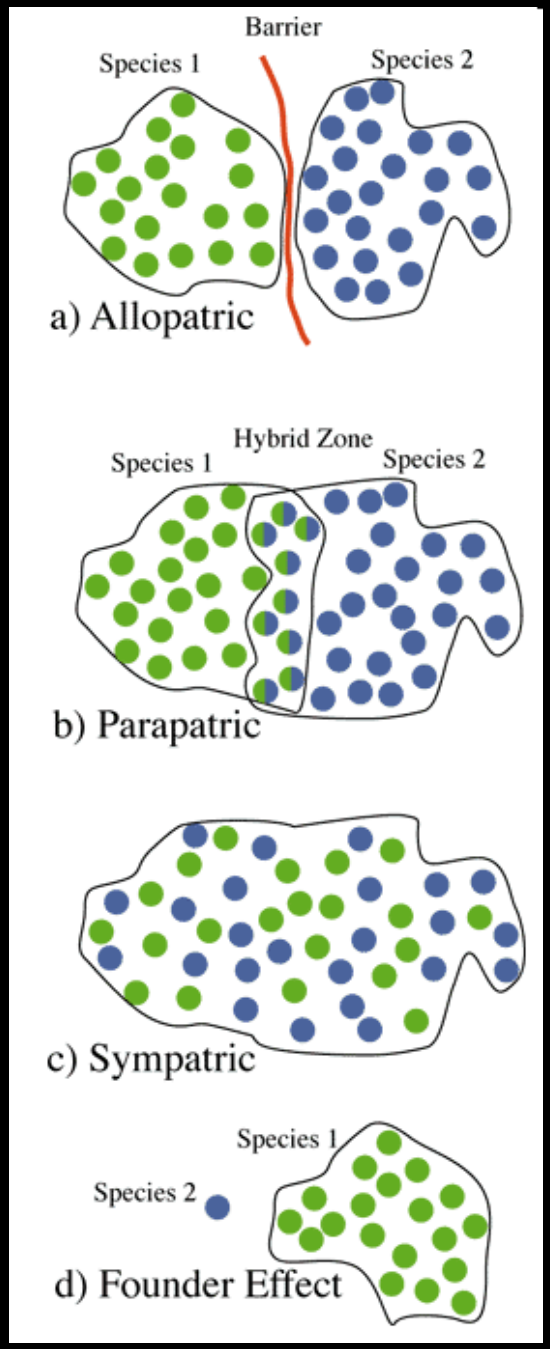
(ജനിതക സന്തുലിതാവസ്ഥ)



$$p^2 + q^2 + 2pq = 1$$

സന്തുലിതാവസ്ഥയിലുള്ള മാറ്റങ്ങൾ

- മ്യൂട്ടേഷൻ
- പുനസംയോജനം
- ജനിതക ഡ്രിഫ്റ്റ്
- പ്രകൃതിനിർധാരണം


Barrier
Species 1
Species 2
a) Allopatric
Hybrid Zone
Species 1
Species 2
b) Parapatric
c) Sympatric
Species 1
Species 2
d) Founder Effect

George Beadle

Edward Tatum

*GENETIC CONTROL OF BIOCHEMICAL REACTIONS IN NEUROSPORA**

By G. W. Beadle and E. L. Tatum

Biological Department, Stanford University

Communicated October 8, 1941

From the standpoint of physiological genetics the development and functioning of an organism consist essentially of an integrated system of chemical reactions controlled in some manner by genes. It is entirely tenable to suppose that these genes which are themselves a part of the system, control or regulate specific reactions in the system either by acting directly as enzymes or by determining the specificities of enzymes.[1] Since the components of such a system are likely to be interrelated in complex ways, and since the synthesis of the parts of individual genes are presumably dependent on the functioning of other genes, it would appear that there must exist orders of directness of gene control ranging from simple one-to-one relations to relations of great complexity. In investigating the rôles of genes, the physiological geneticist usually attempts to determine the physiological and biochemical bases of already known hereditary traits. This approach, as made in the study of anthocyanin pigments in plants,[2] the fermentation of sugars by yeasts[3] and a number of other instances,[4] has established that many biochemical reactions are

*GENETIC CONTROL OF BIOCHEMICAL REACTIONS IN NEUROSPORA**

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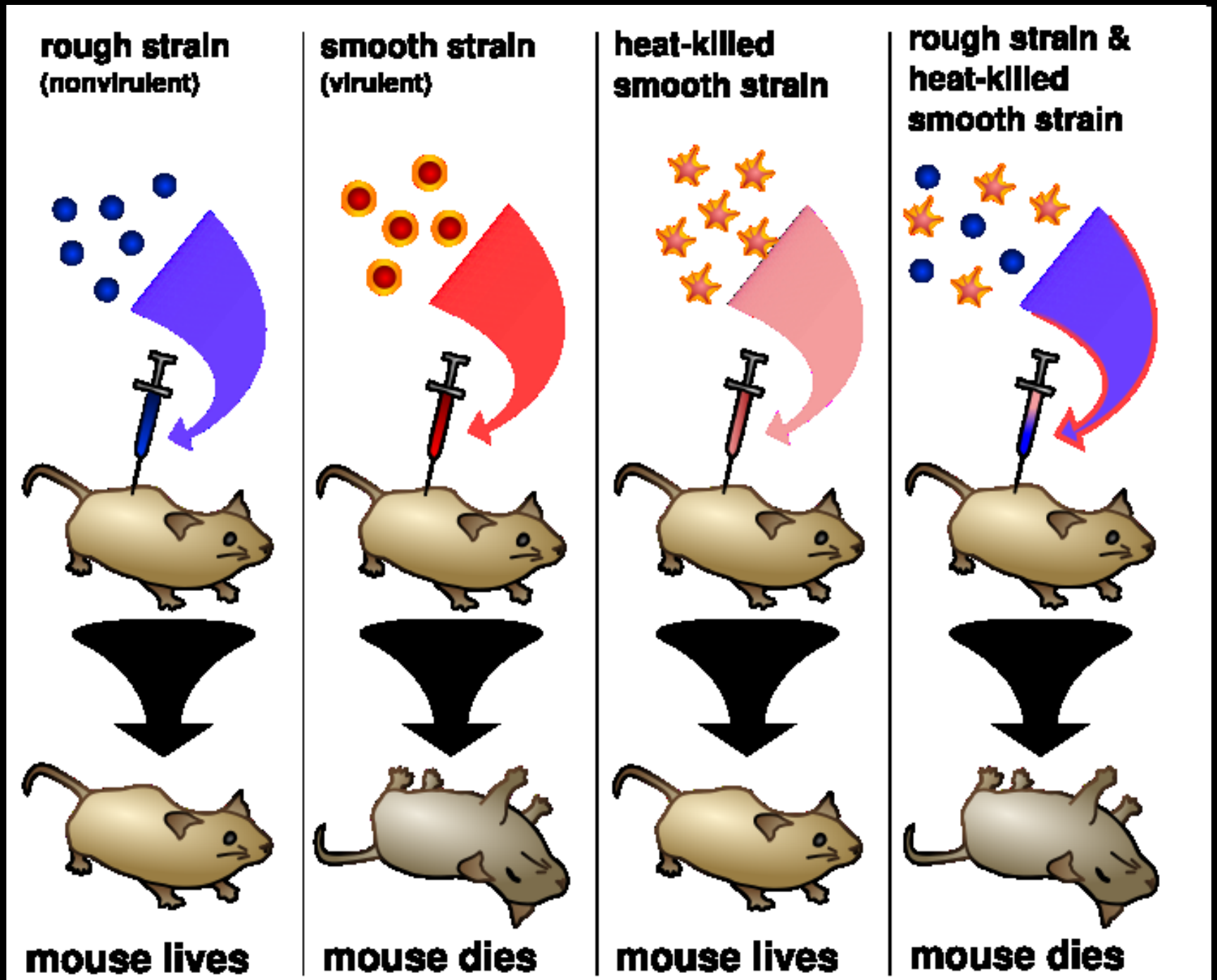
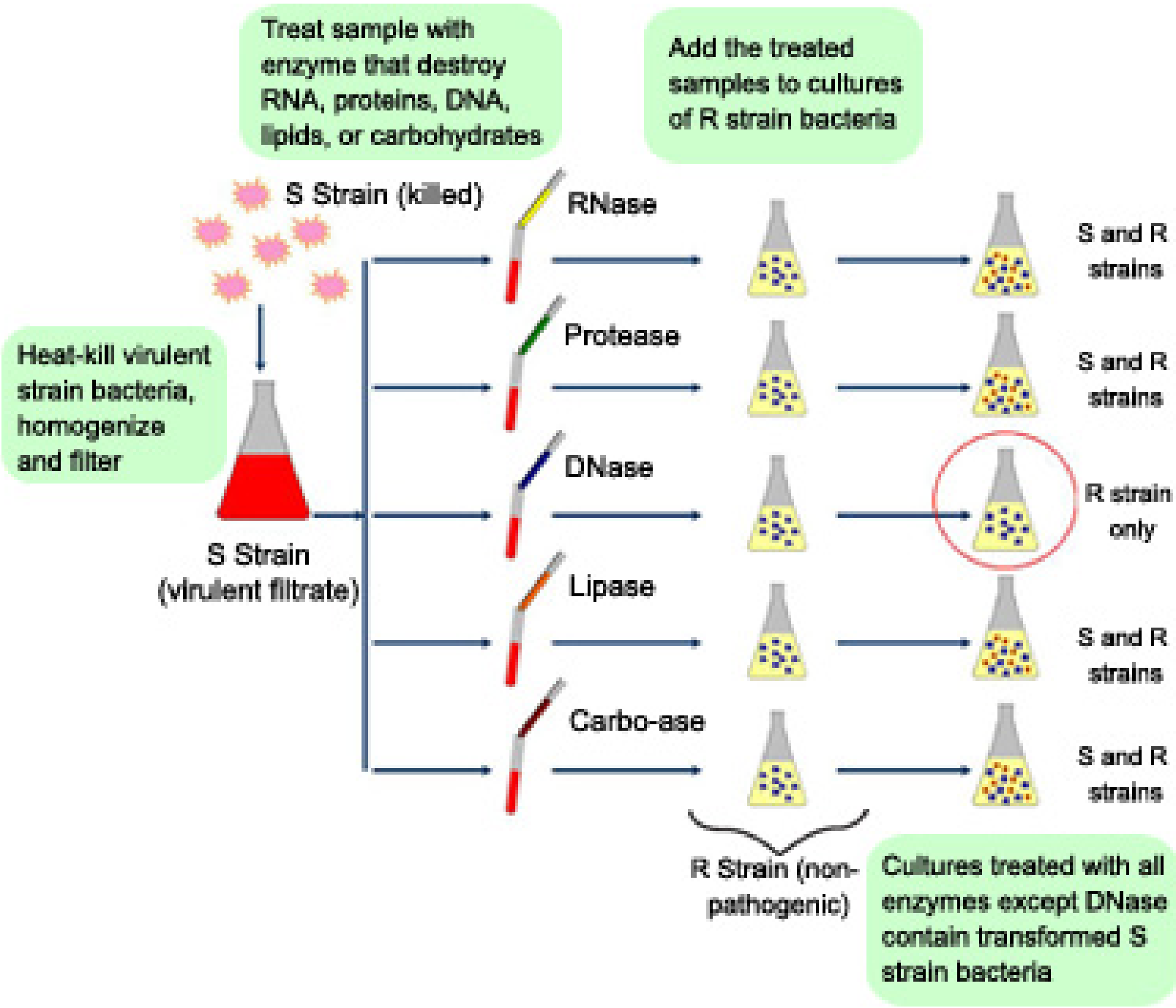
ഒരു ജീൻ ഒരു പ്രോട്ടീൻ

Colin Macleod

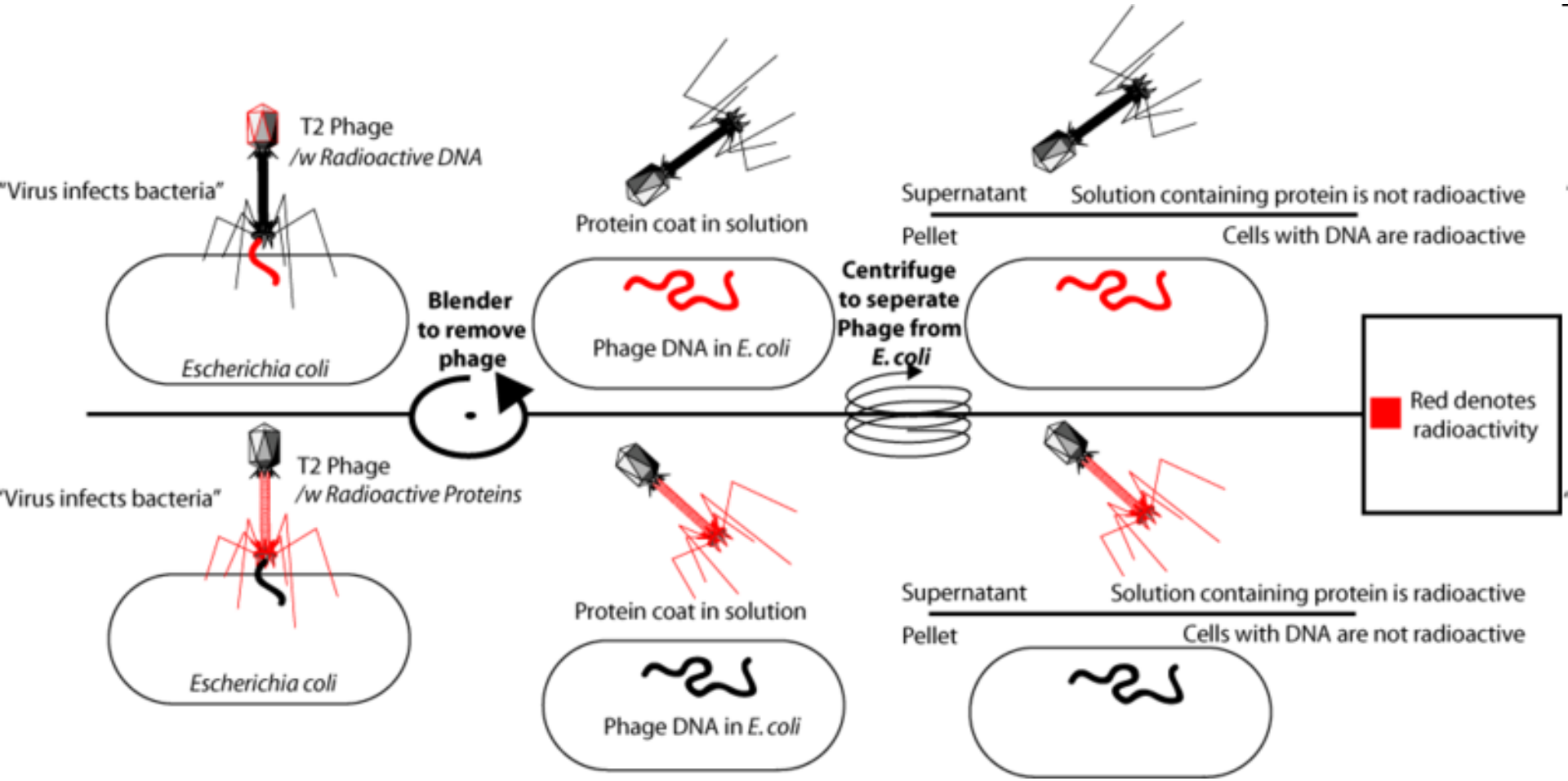
Maclyn McCarty

Oswald T Avery


rough strain
(nonvirulent)
smooth strain
(virulent)
heat-killed
smooth strain
rough strain &
heat-killed
smooth strain
mouse lives
mouse dies
mouse lives
mouse dies

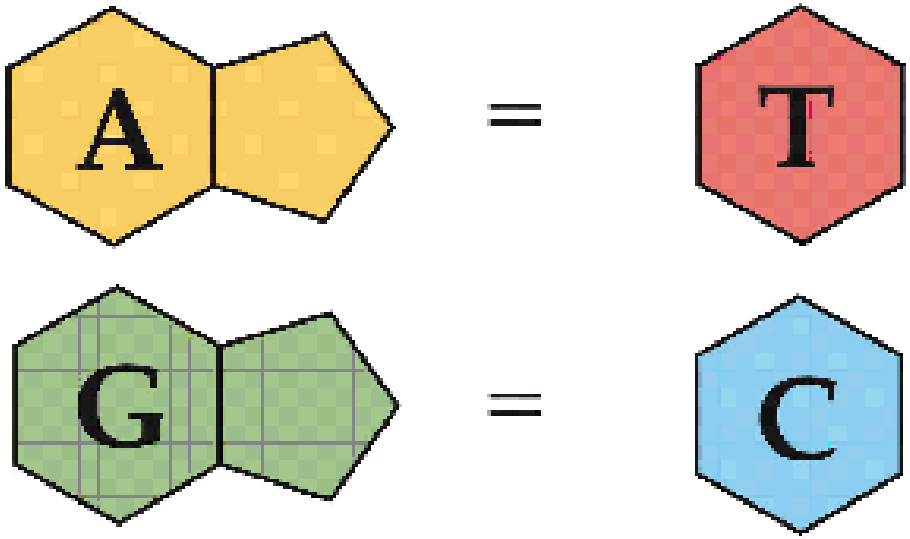

Treat sample with enzyme that destroy RNA, proteins, DNA, lipids, or carbohydrates
Add the treated samples to cultures of R strain bacteria
S Strain (killed)
Heat-kill virulent strain bacteria, homogenize and filter
S Strain (virulent filtrate)
RNase
Protease
DNase
Lipase
Carbo-ase
S and R strains
S and R strains
R strain only
S and R strains
S and R strains
R Strain (non-pathogenic)
Cultures treated with all enzymes except DNase contain transformed S strain bacteria

ഹെർഷി–ചേസ് പരീക്ഷണം (1952)

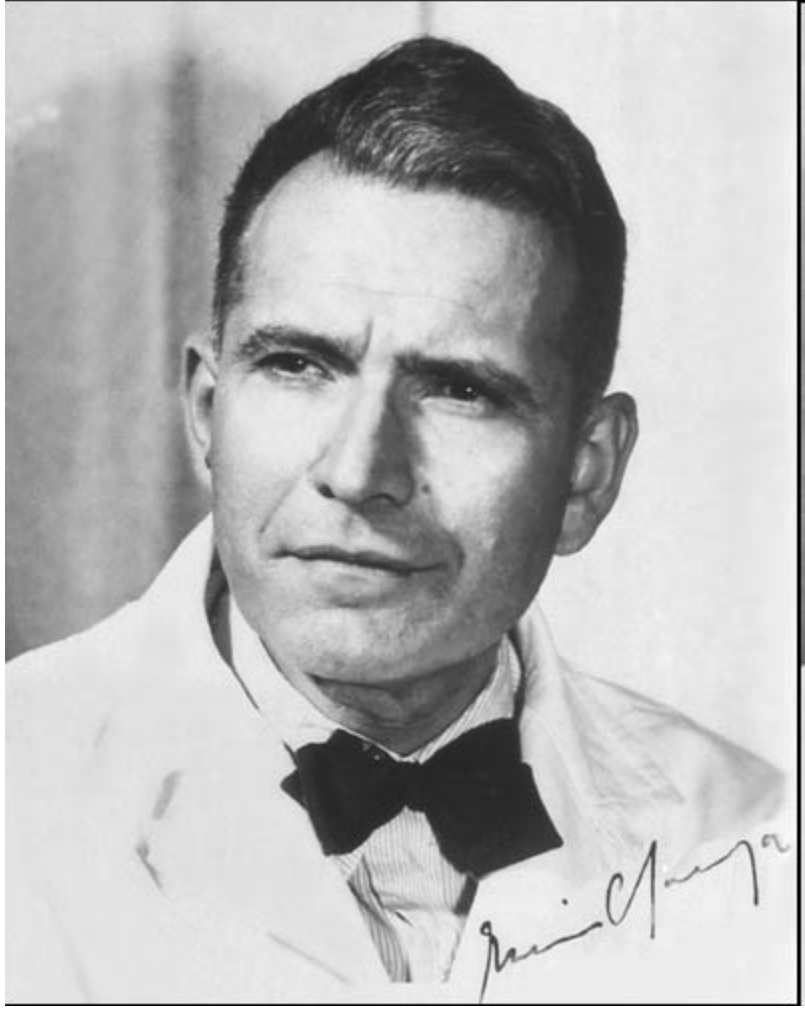


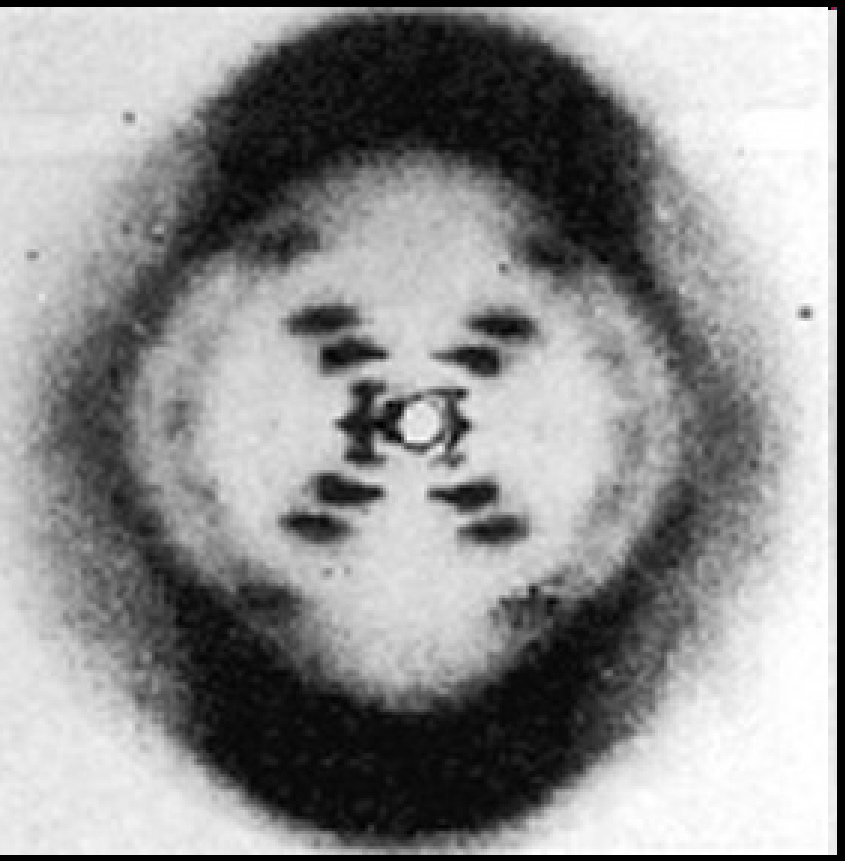
Erwin Chargaff

(1950)



Purines = Pyrimidines



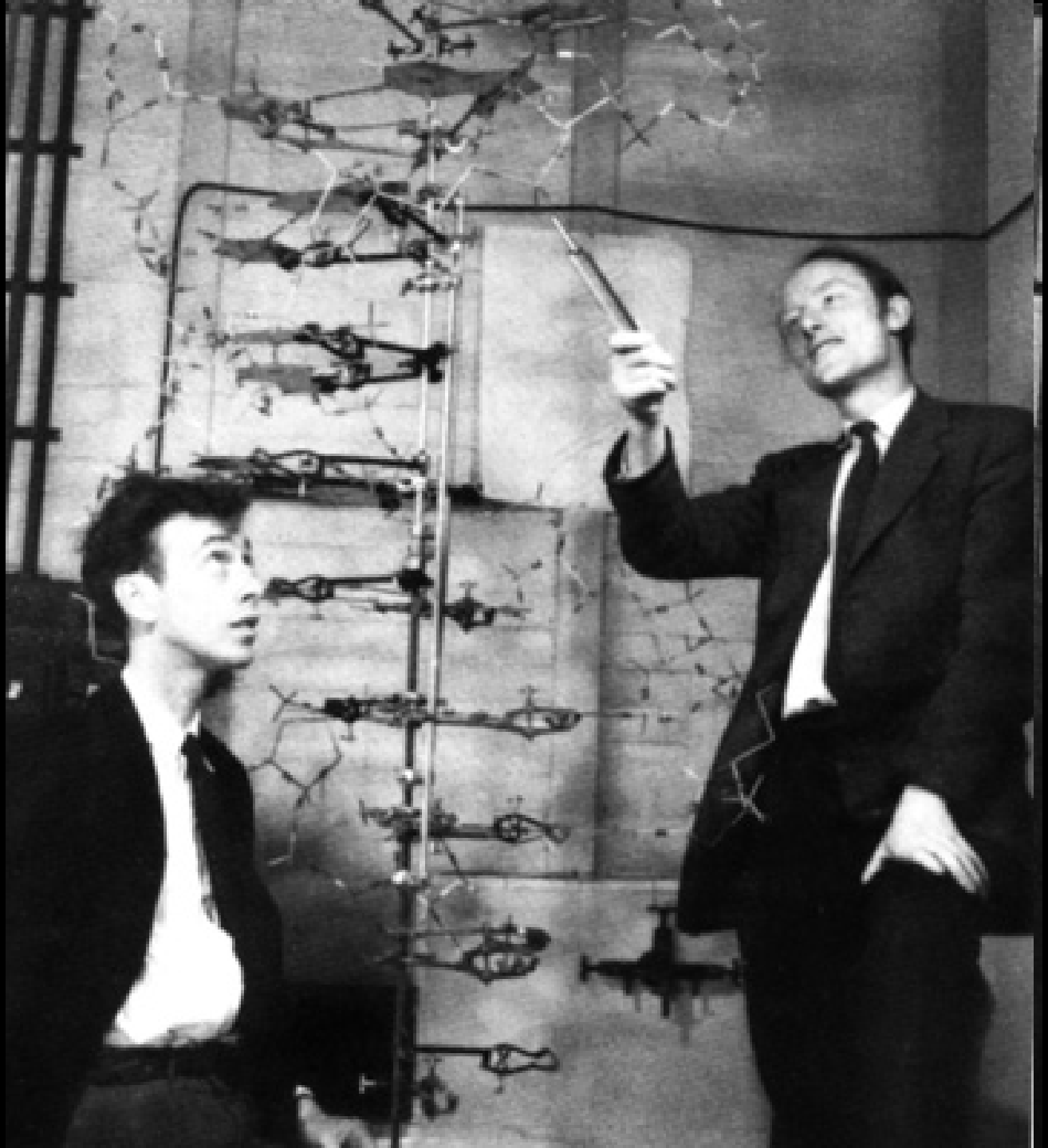


Photograph 51

Rosalind Franklin

Francis Crick James Watson

1953



equipment, and to Dr. G. E. R. Deacon and the captain and officers of R.R.S. *Discovery II* for their part in making the observations.

[1] Young, F. B., Gerrard, H., and Jevons, W., *Phil. Mag.*, **40**, 140 (1920).
[2] Longuet-Higgins, M. S., *Mon. Not. Roy. Astro. Soc., Geophys. Supp.*, **5**, 285 (1949).
[3] Van Arx, W. S., Woods Hole Papers in Phys. Oceanog., Meteor., **11** (3) (1950).
[4] Ekman, V. W., *Arkiv. Mat. Astron. Fysik. (Stockholm)*, **2** (11) (1905).

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Corey[1]. They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons: (1) We believe that the material which gives the X-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.

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

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate diester groups joining β-D-deoxyribofuranose residues with 3′,5′ linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furberg's[2] model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration', the sugar being roughly perpendicular to the attached base. There is a residue on each chain every 3·4 A. in the z-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 A. The distance of a phosphorus atom from the fibre axis is 10 A. As the phosphates are on the outside, cations have easy access to them.

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

The novel feature of the structure is the manner in which the two chains are held together by the purine and pyrimidine bases. The planes of the bases are perpendicular to the fibre axis. They are joined together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so that the two lie side by side with identical z-co-ordinates. One of the pair must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows: purine position 1 to pyrimidine position 1; purine position 6 to pyrimidine position 6.

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) it is found that only specific pairs of bases can bond together. These pairs are: adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, on either chain, then on these assumptions the other member must be thymine; similarly for guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted in any way. However, if only specific pairs of bases can be formed, it follows that if the sequence of bases on one chain is given, then the sequence on the other chain is automatically determined.

It has been found experimentally[4,5] that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribose nucleic acid.

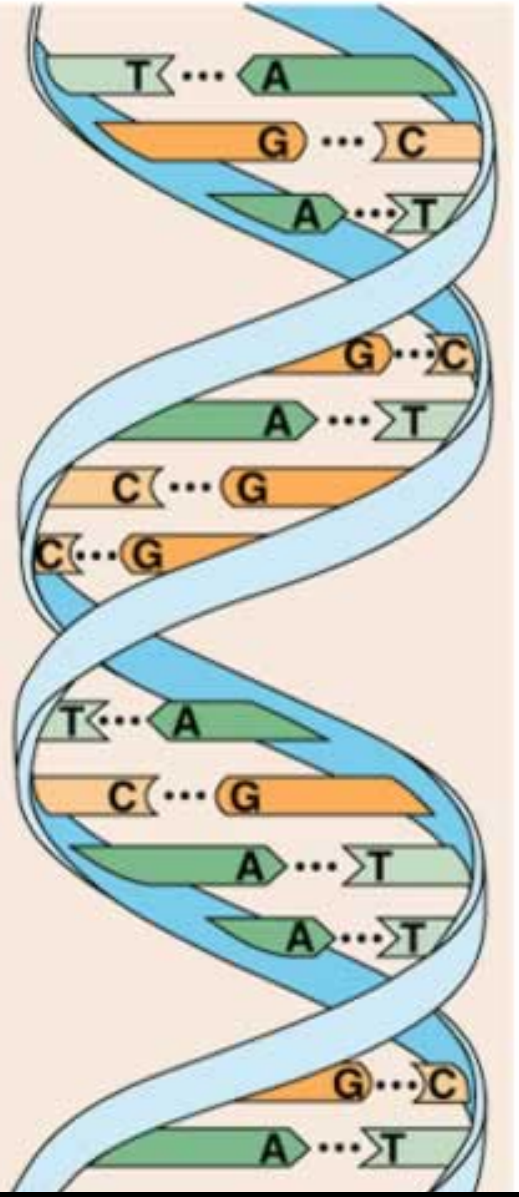
It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atom would make too close a van der Waals contact.

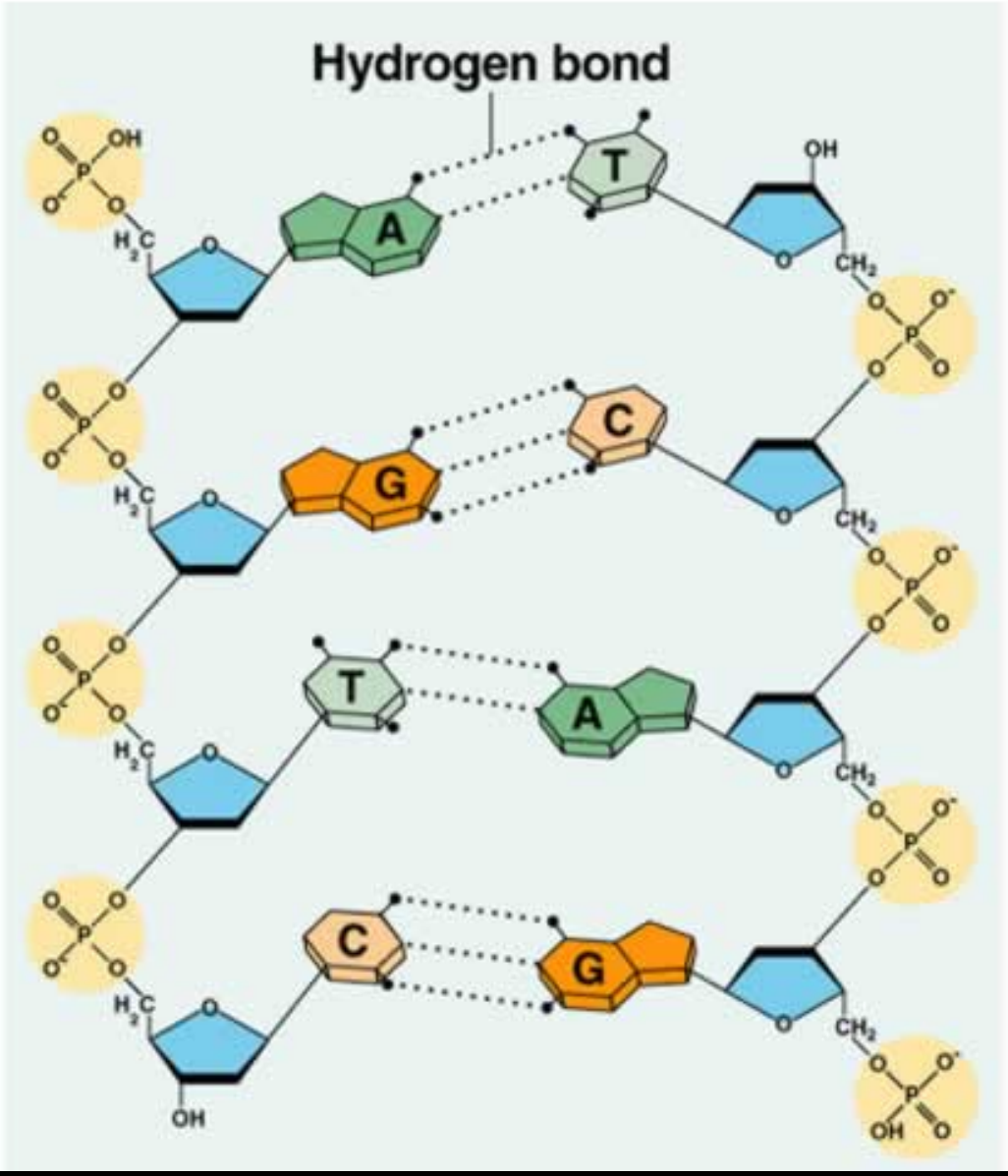
The previously published X-ray data[3,6] on deoxyribose nucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in the following communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on published experimental data and stereochemical arguments.

It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material.

Full details of the structure, including the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on interatomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F. Wilkins, Dr. R. E. Franklin and their co-workers at


T ··· A
G ··· C
A ··· T
G ··· C
A ··· T
C ··· G
C ··· G
T ··· A
C ··· G
A ··· T
A ··· T
G ··· C
A ··· T


Hydrogen bond
T
A
C
G
T
A
C
G

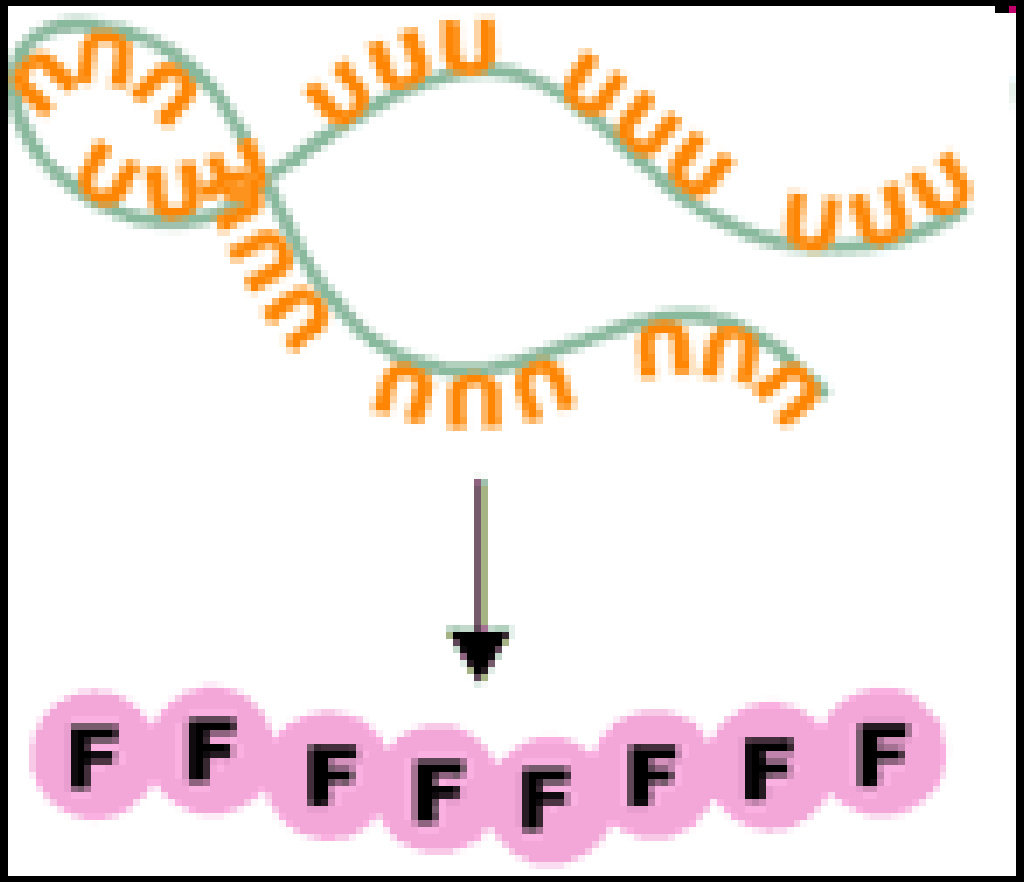
മൂന്നക്ഷരങ്ങൾ?

George Gamow

RNA tie club

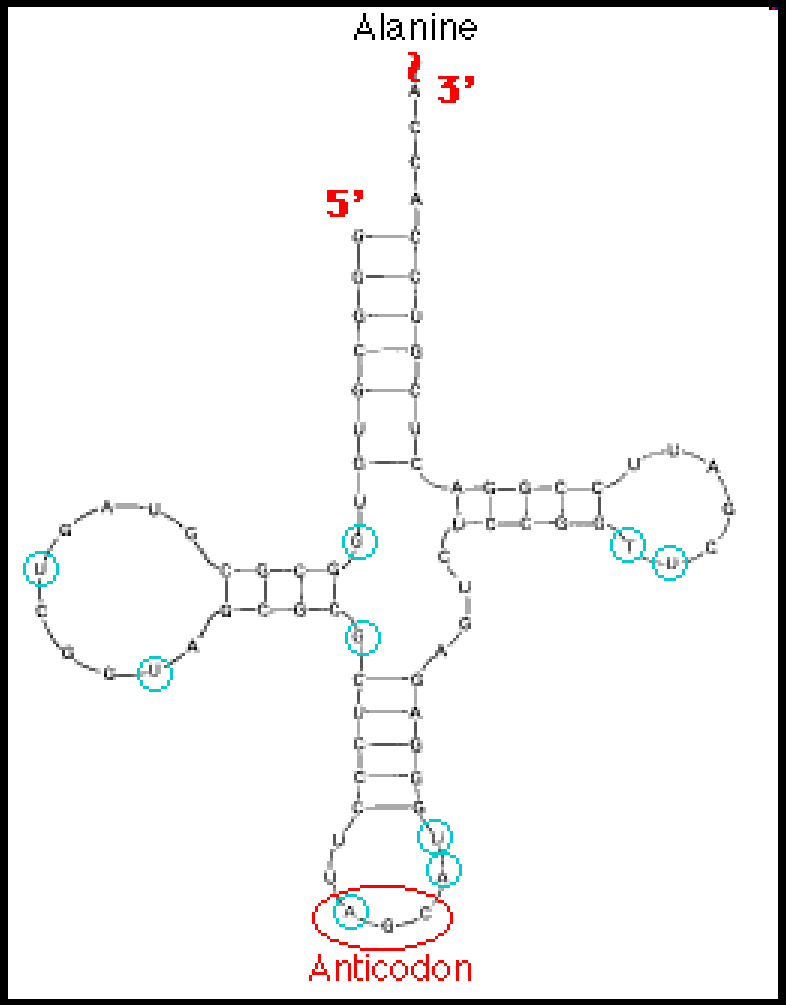
? Adaptor molecule

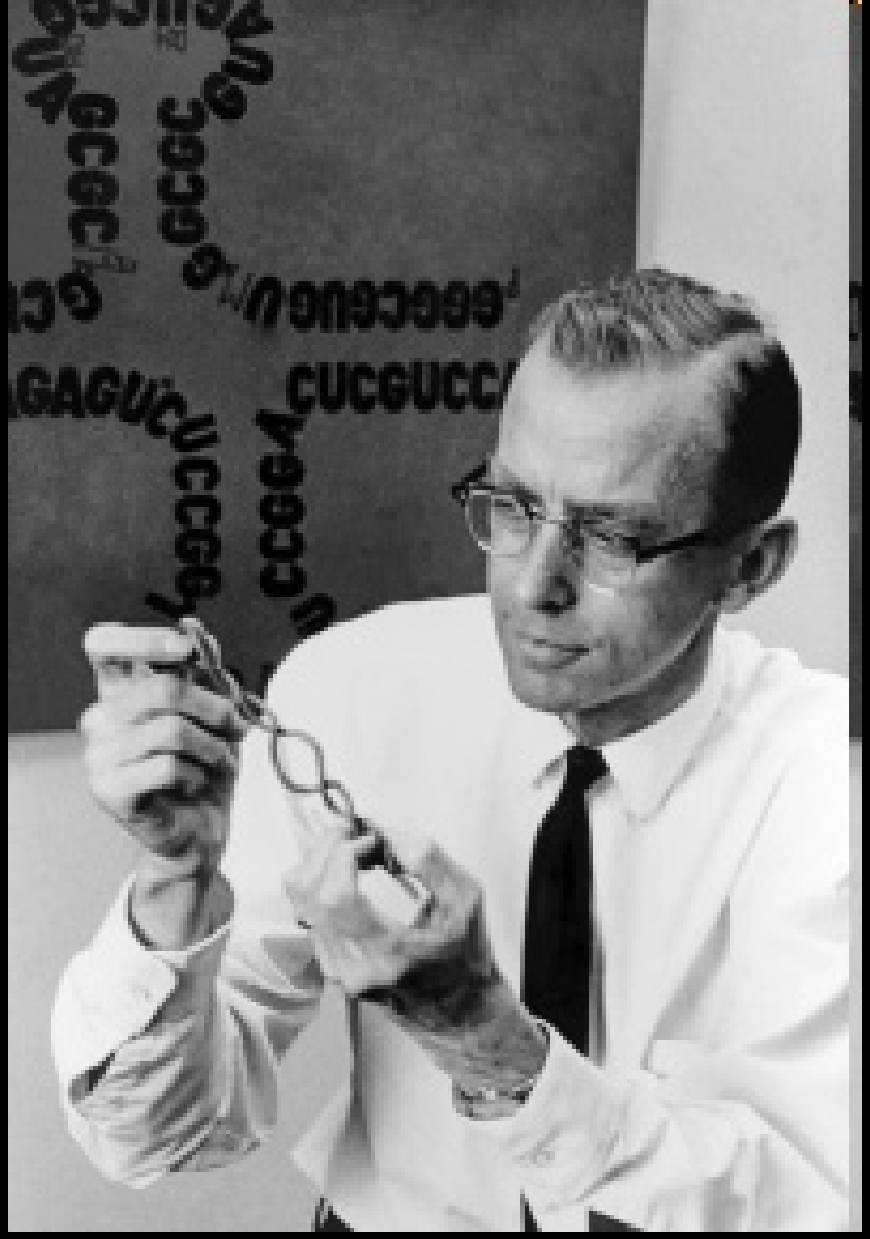
Francis Crick



Marshall Nirenberg & Heinrich Matthaei

Hargobind Khorana



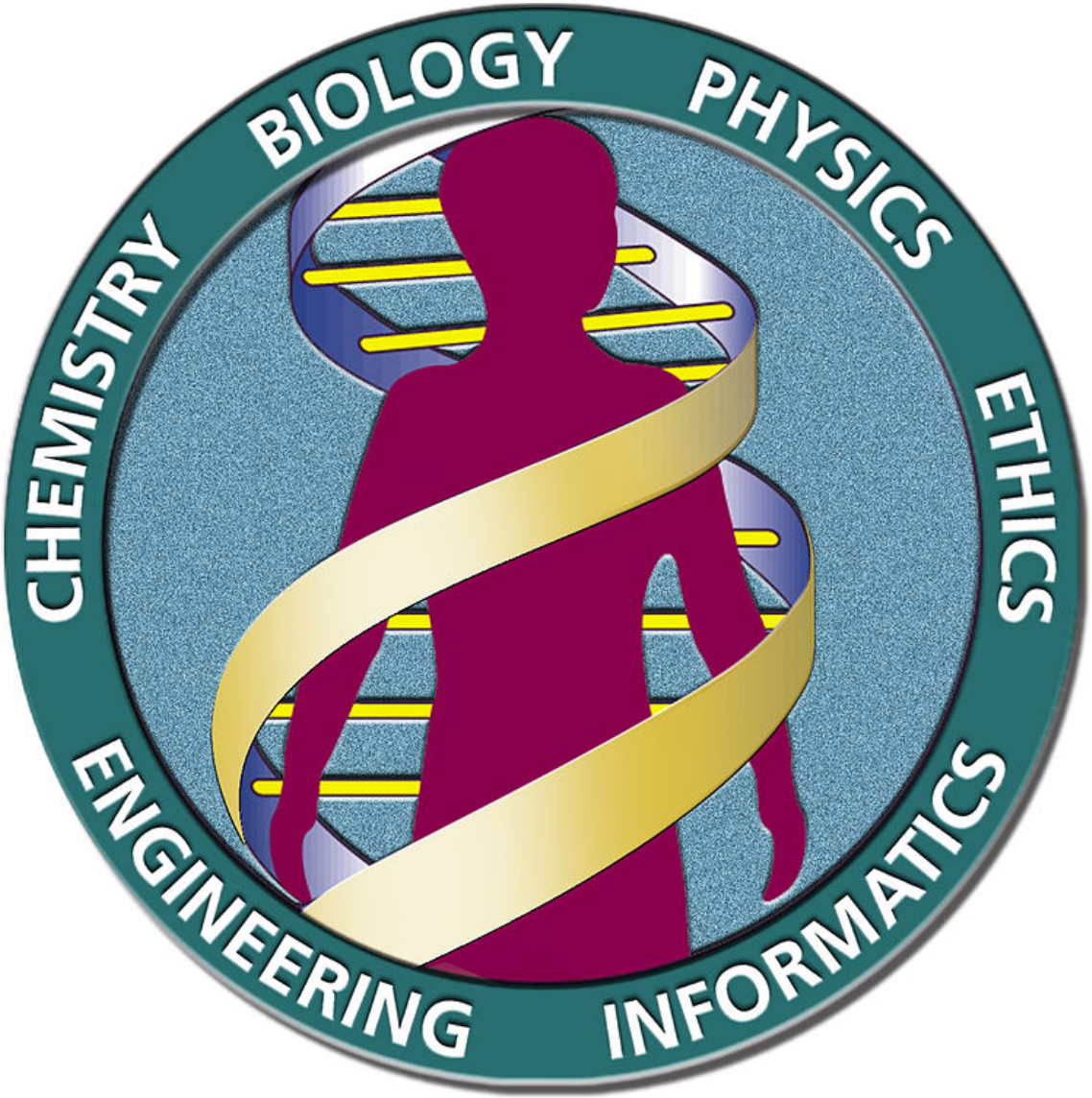


Robert Holley

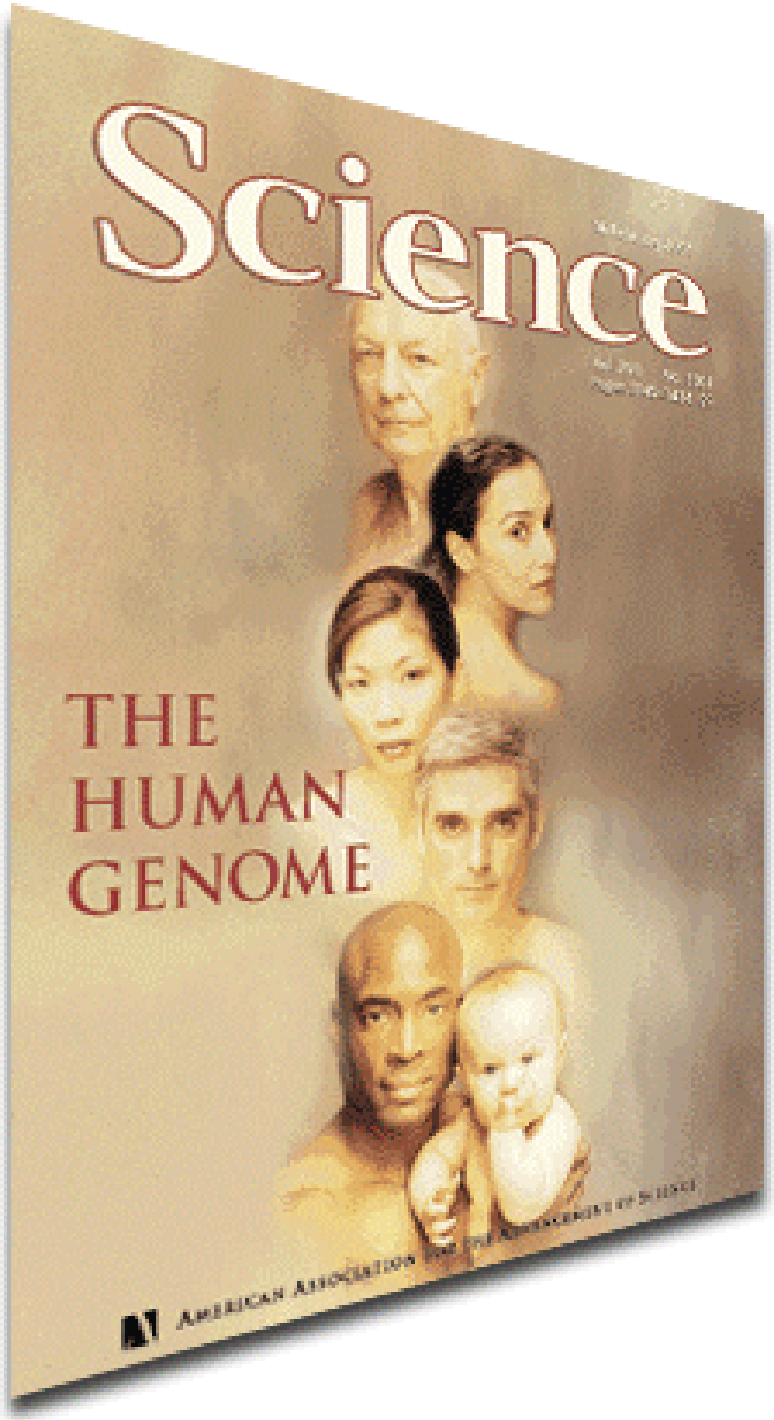
Nobel prize 1968

Herbert Boyer

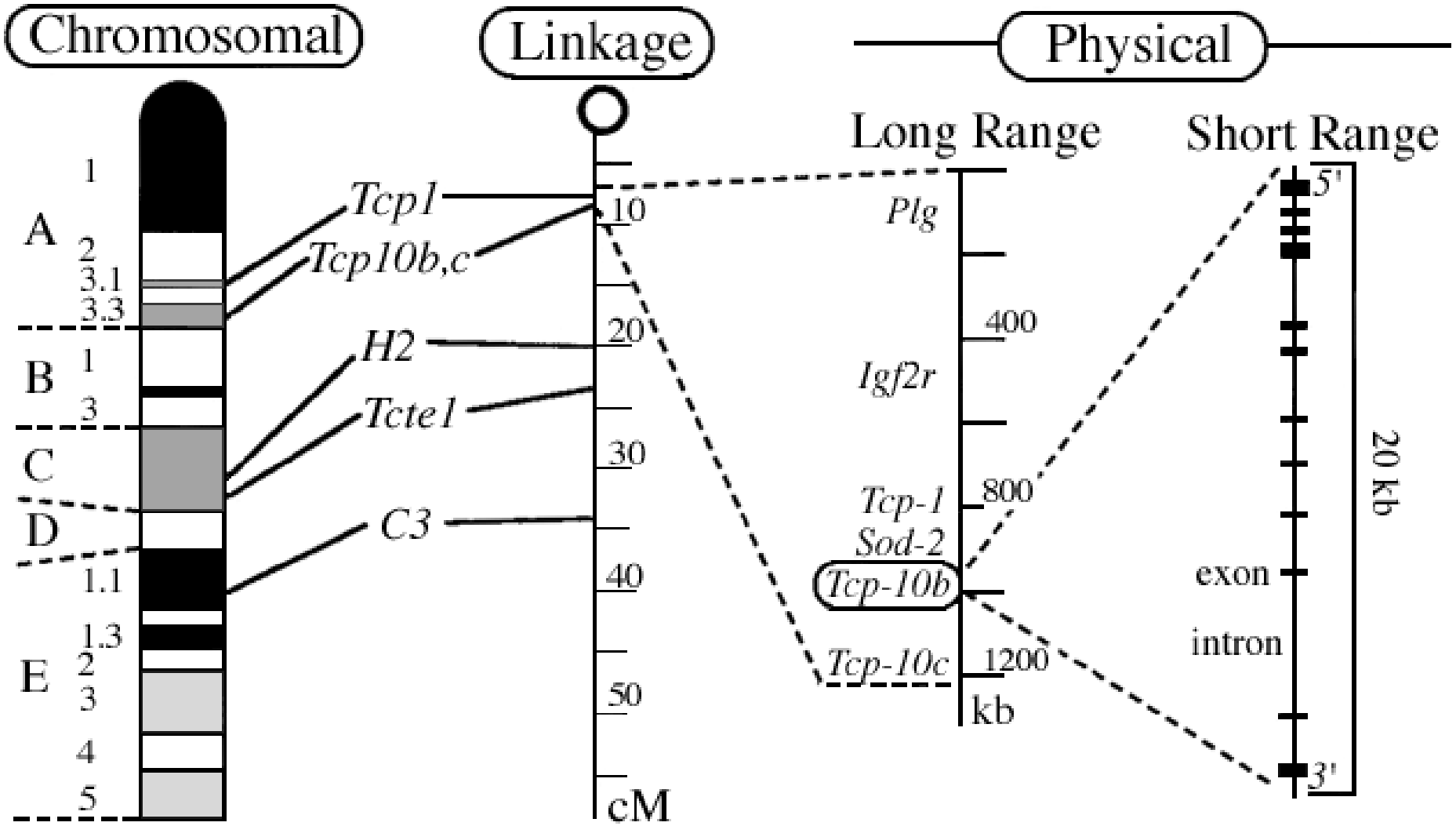
Stanley Cohen



The Human Genome Project


Science
THE
HUMAN
GENOME


nature
the
human
genome


Chromosomal
Linkage
Physical
Long Range
Short Range
A
B
C
D
E
1
2
3.1
3.3
1
3
1.1
1.3
2
3
4
5
Tcp1
Tcp10b,c
H2
Tcte1
C3
10
20
30
40
50
cM
Plg
Igf2r
Tcp-1
Sod-2
Tcp-10b
Tcp-10c
400
800
1200
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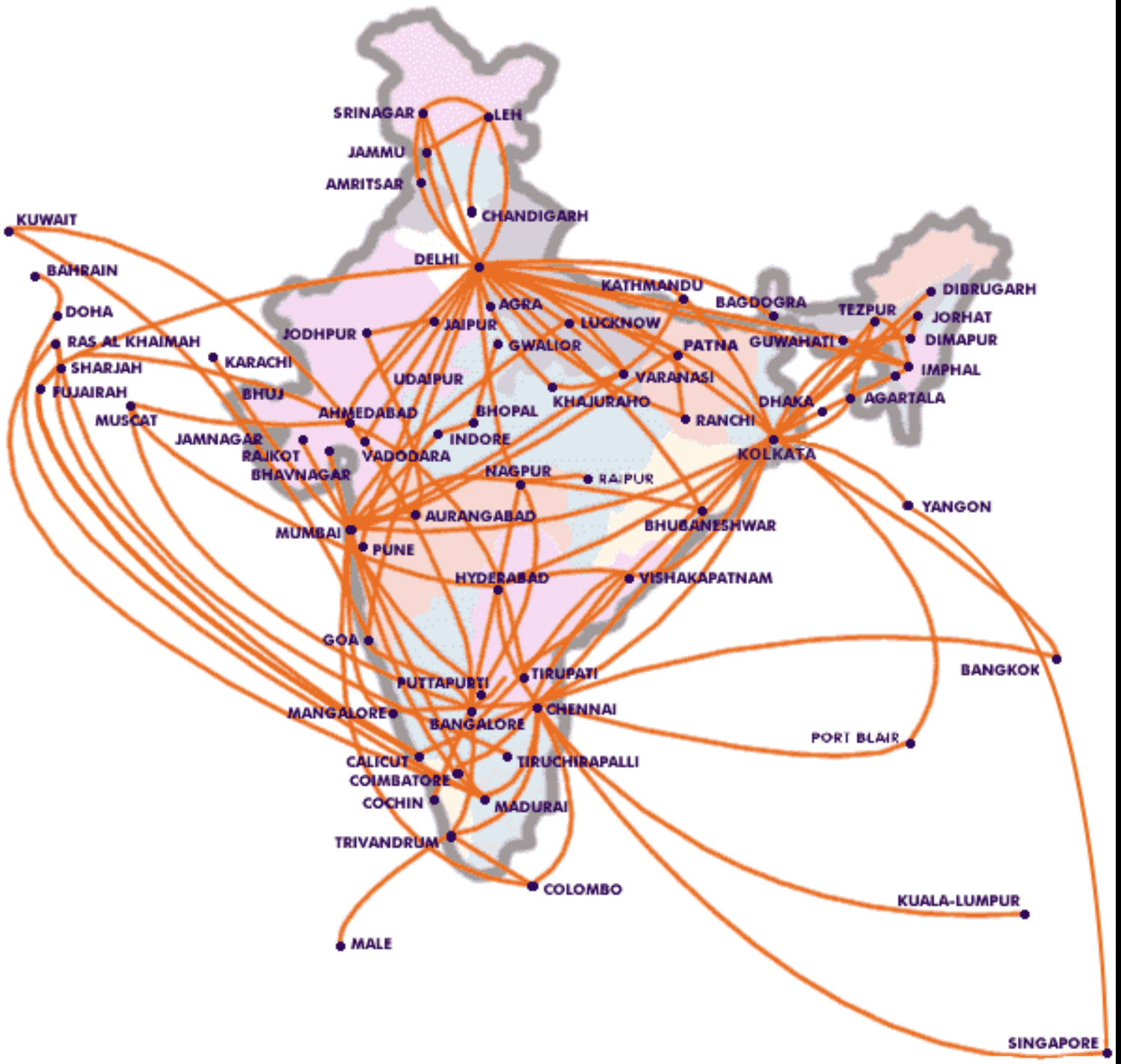
exon
intron
20 kb


SRINAGAR
LEH
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BAHRAIN
DELHI
KATHMANDU
BAGDOGRA
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DIBRUGARH
JORHAT
DIMAPUR
IMPHAL
AGARTALA
DHAKA
GUWAHATI
DOHA
AGRA
JAIPUR
LUCKNOW
JODHPUR
GWALIOR
PATNA
RAS AL KHAIMAH
KARACHI
SHARJAH
UDAIPUR
VARANASI
FUJAIRAH
BHUJ
KHAJURAHO
MUSCAT
AHMEDABAD
BHOPAL
RANCHI
JAMNAGAR
INDORE
RAJKOT
VADODARA
KOLKATA
BHAVNAGAR
NAGPUR
RAIPUR
YANGON
AURANGABAD
BHUBANESHWAR
MUMBAI
PUNE
HYDERABAD
VISHAKAPATNAM
GOA
BANGKOK
TIRUPATI
PUTTAPURTI
MANGALORE
CHENNAI
BANGALORE
PORT BLAIR
CALICUT
TIRUCHIRAPALLI
COIMBATORE
COCHIN
MADURAI
TRIVANDRUM
COLOMBO
KUALA-LUMPUR
MALE
SINGAPORE

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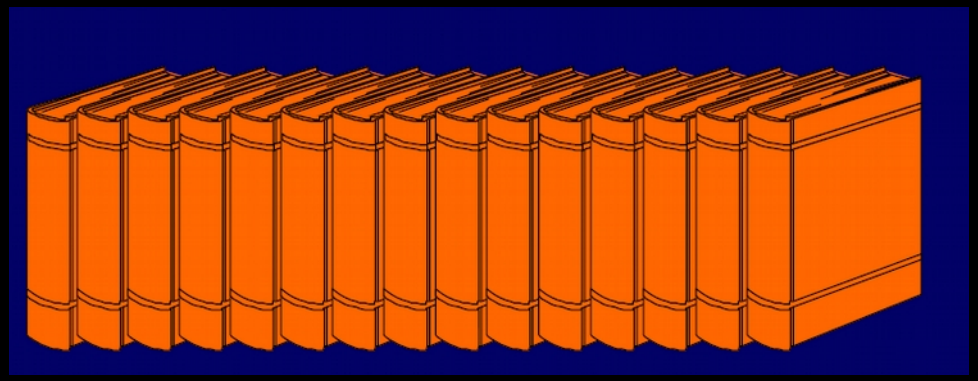
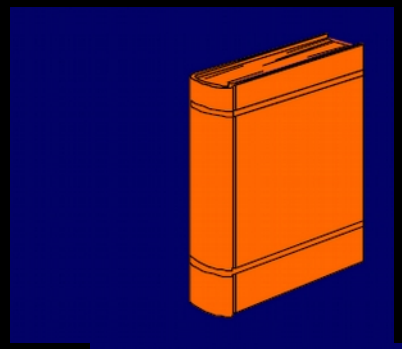
40 boxes x 5000 pages per box x 5000 bases per page
= 3,000,000,000 bases!

Finding a mutation in the genome



Genome



Chromosome

Gene

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accggtaccatgtatagg
tacccgggtaccctaccc
cggcacc T Agcatca
tataggacacatactgat
catgcattacggatcgta
cgtaggtcagtttaccggt
accatgtataggtacccg
ggtaccctacccgggga

Normal

atcgtacgtaggtcagttt
accggtaccatgtatagg
tacccgggtaccctaccc
cggcacc A agcatca
tataggacacatactgat
catgcattacggatcgta
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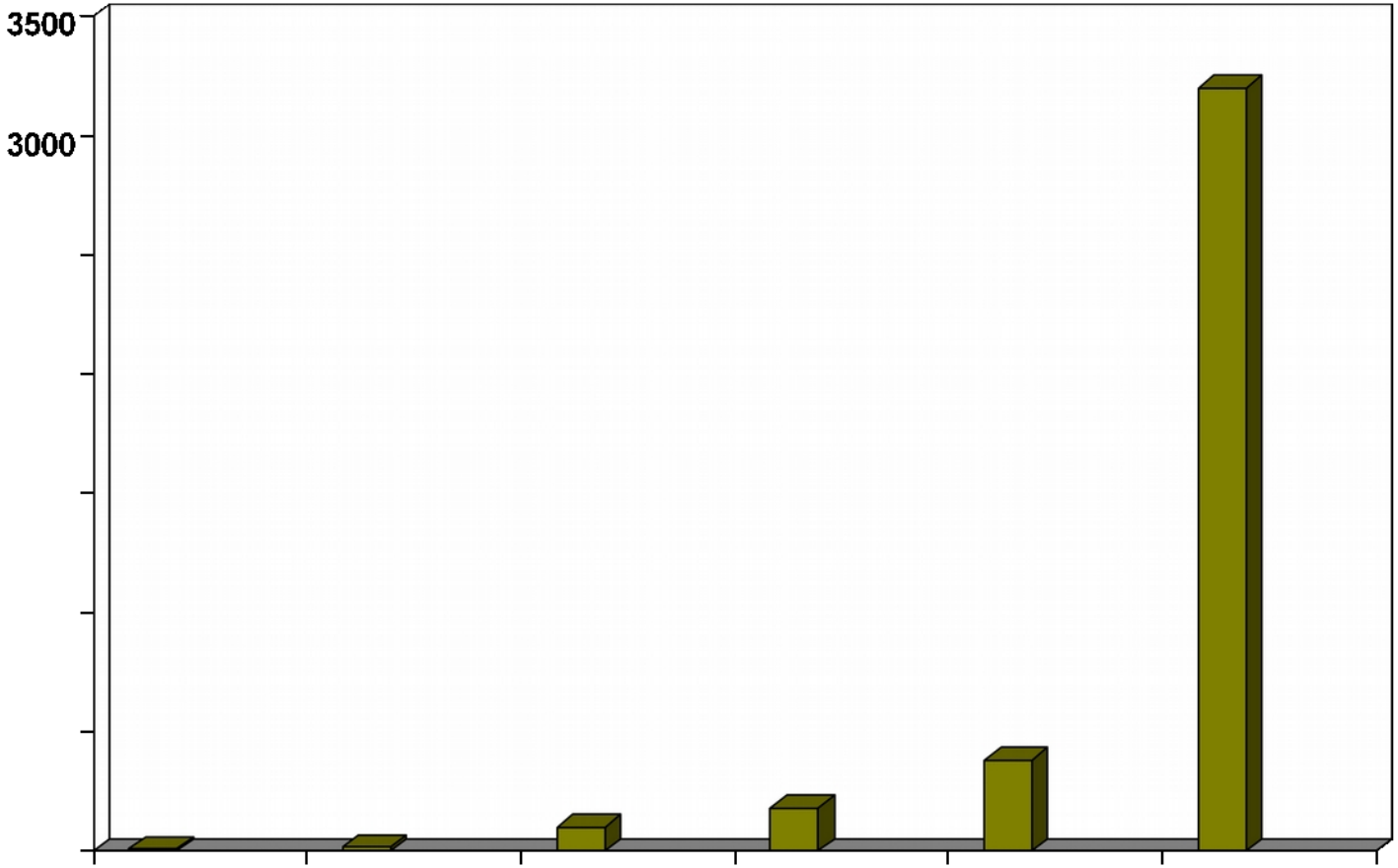
accatgtataggtacccg
ggtaccctacccaggga

Patient

Size of the genome




700000
600000