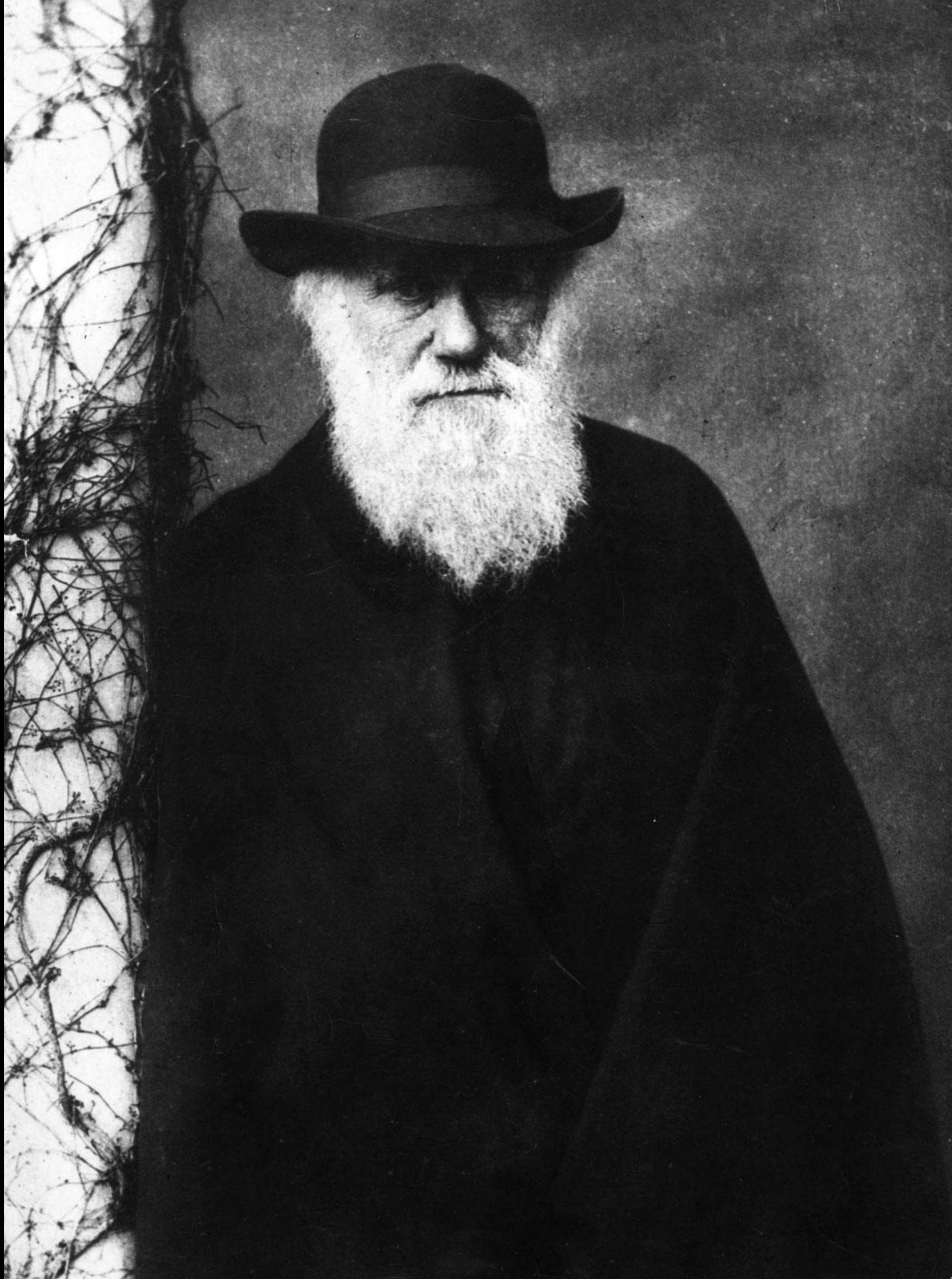


"It has often and confidently been asserted, that man's origin can never be known: but ignorance more frequently begets confidence than does knowledge: it is those who know little, and not those who know much, who so positively assert that this or that problem will never be solved by science."

Charles Darwin

Djetinjstvo

,,Razmišljajući o velikoj sličnosti građe toplokrvnih životinja, i istodobno o velikim promjenama koje su pretrpjele i prije i nakon rođenja; i razmatranjem u koliko kratkom vremenu su nastale mnoge od gore opisanih promjena životinja; bi li bilo previše smjelo zamisliti da u velikom vremenskom razdoblju, otkako je Zemlja počela postojati, možda milijunima godina ... da su sve toplokrvne životinje nastale iz jedne žive niti, kojoj je VELIKI PRVI UZROK dodijelio animalnost ... i time posjedovati sposobnost da se nastavlja poboljšavati vlastitom inherentnom aktivnošću i da ta poboljšanja generira prema svojim potomcima, svijetu bez kraja?"

Erasmus Darwin - Zoonomia; or the Laws of Organic Life (1794-96)

Školovanje

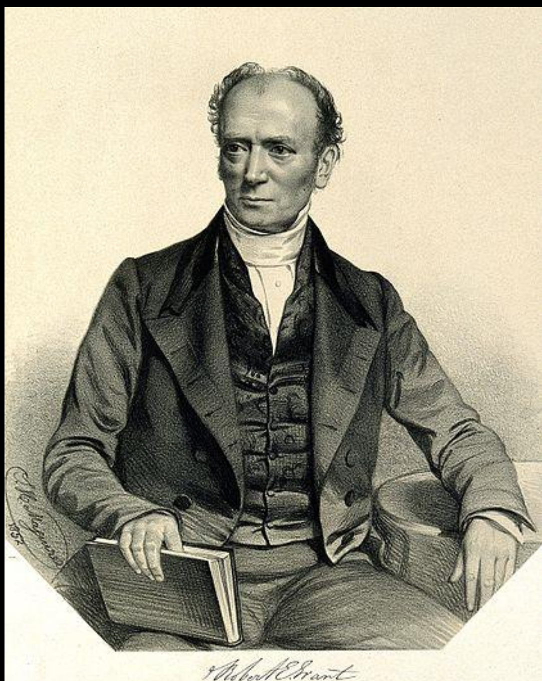
Anglican Shrewsbury School (1818 – 1825)

University of Edinburgh Medical School (1825 – 1828)

Christ's College University of Cambridge (1828 – 1831)

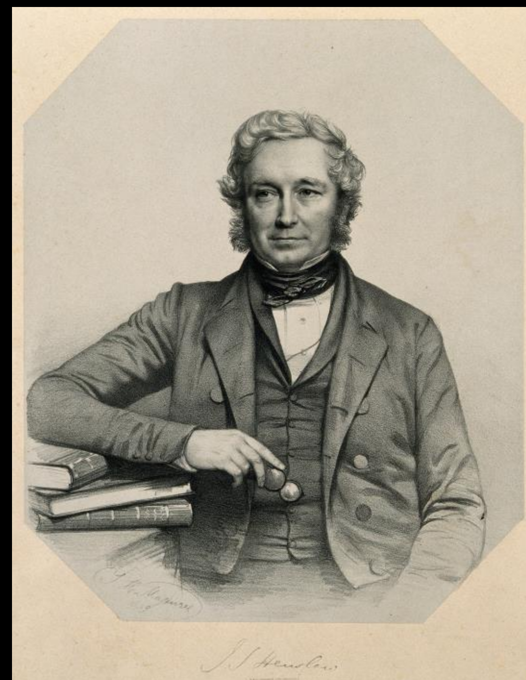
Mentori

Robert Edmond Grant



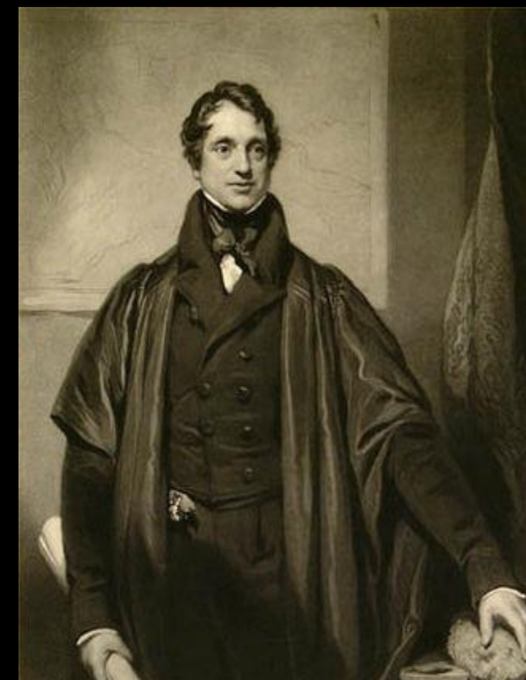
Marine invertebrates
&
Lamarck

Revd. John Stevens Henslow



„The man who walks
with Henslow"
Botany & Beagle

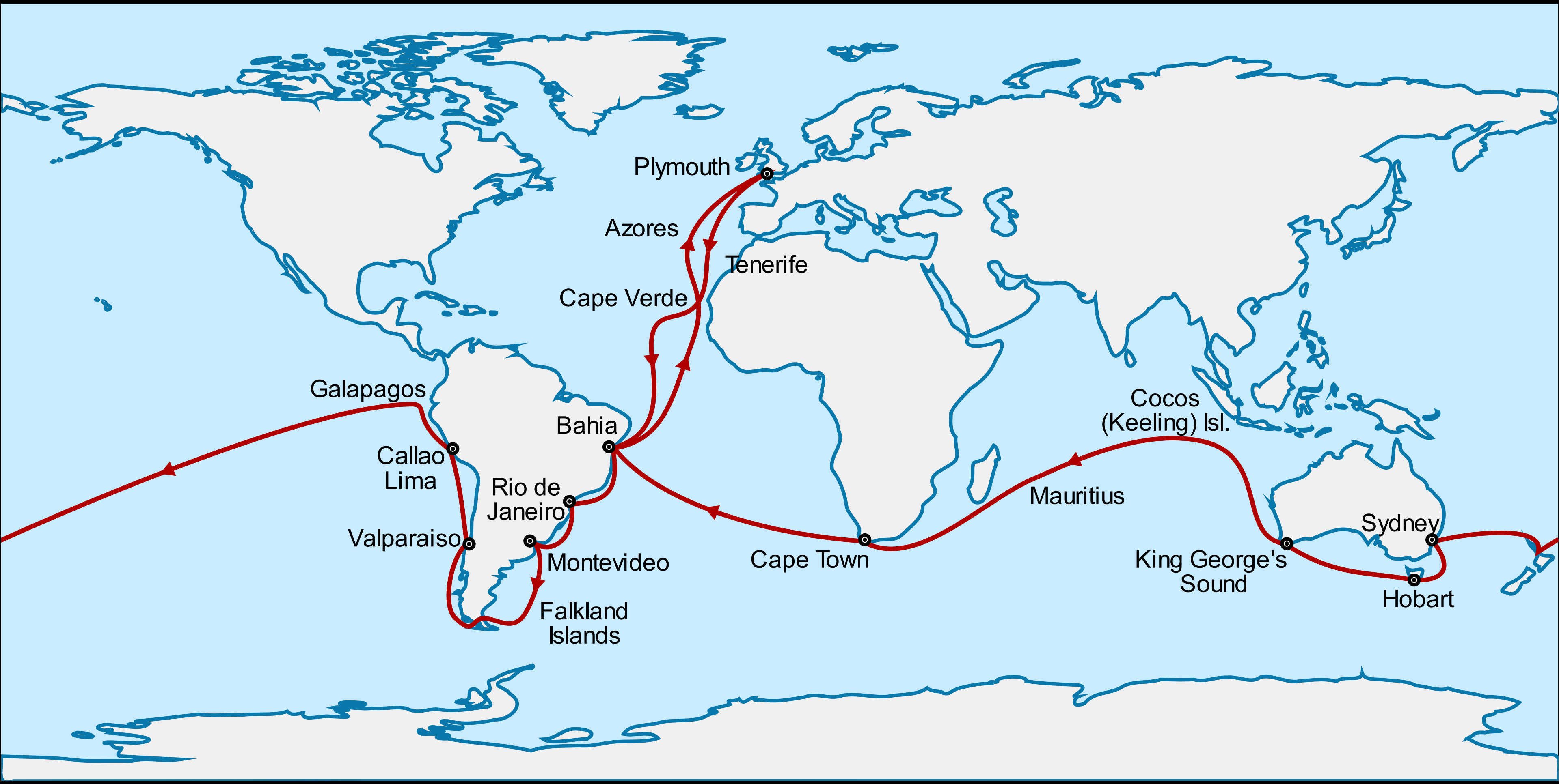
Revd. Adam Sedgwick



Geology

Putovanje

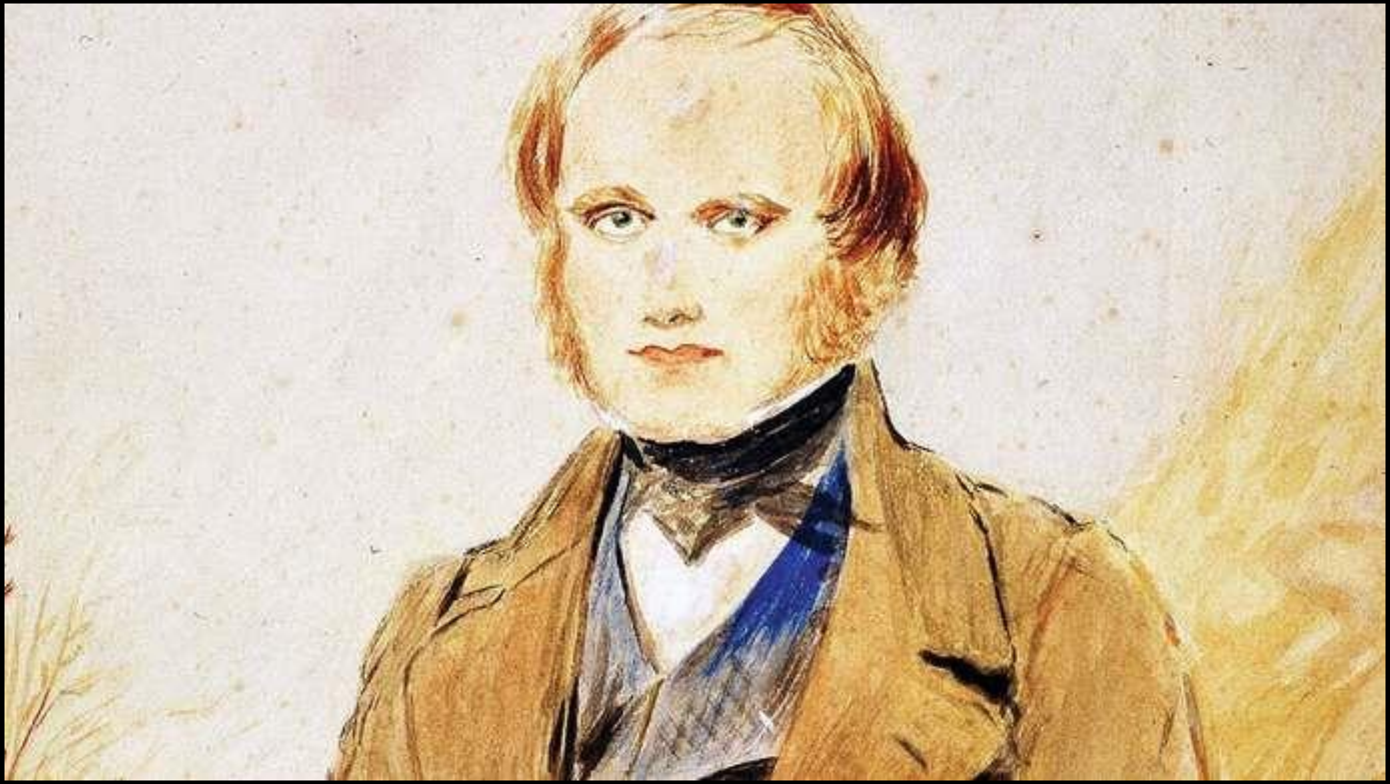
HMS Beagle



1831–1836

Povratak

1837 – 1839 & 1839-1859



Believing in evolution was like confessing a murder.

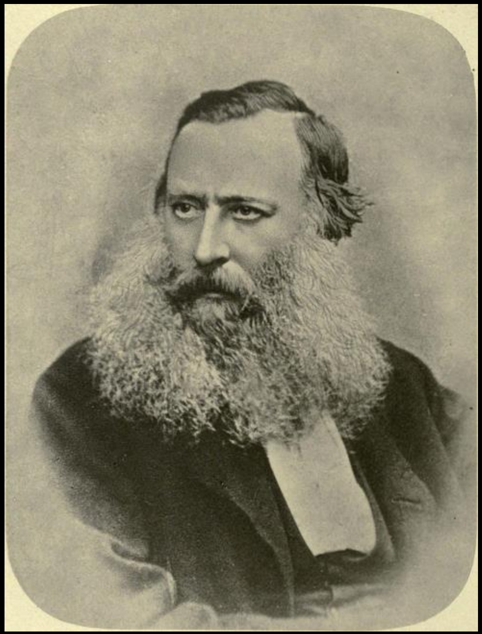
P.S. prije

James Hutton (1794) - *An Investigation of the Principles of Knowledge: And of the Progress of Reason, From Sense to Science and Philosophy*

...if an organised body is not in the situation and circumstances best adapted to its sustenance and propagation, then, in conceiving an indefinite variety among the individuals of that species, we must be assured, that, on the one hand, those which depart most from the best adapted constitution, will be the most liable to perish, while, on the other hand, those organised bodies, which most approach to the best constitution for the present circumstances, will be best adapted to continue, in preserving themselves and multiplying the individuals of their race.

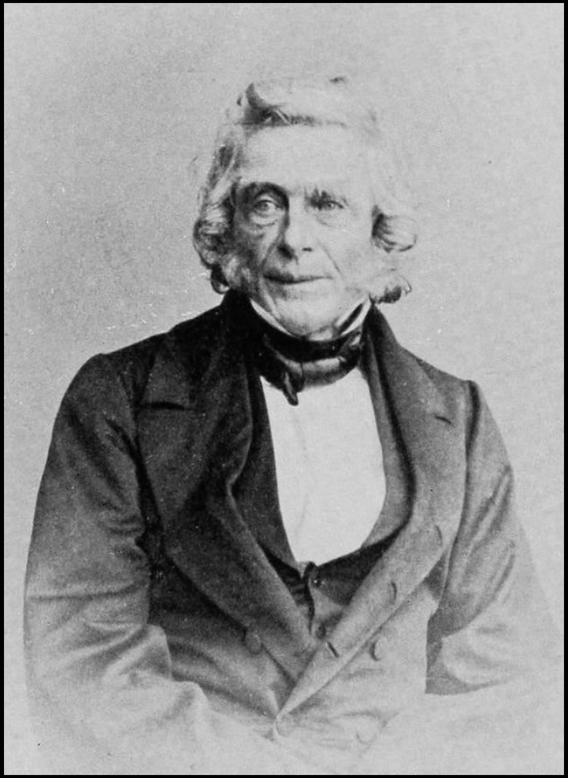
William Charles Wells (1813) - *Two Essays... with some observations on the causes of the differences of colour and form between the white and negro races of men. By the Late W.C. Wells…with a Memoir of his life, written by himself.*

"[What was done for animals artificially] seems to be done with equal efficiency, though more slowly, by nature, in the formation of varieties of mankind, fitted for the country which they inhabit. Of the accidental varieties of man, which would occur among the first scattered inhabitants, some one would be better fitted than the others to bear the diseases of the country. This race would multiply while the others would decrease, and as the darkest would be the best fitted for the [African] climate, at length [they would] become the most prevalent, if not the only race."



Edward Blyth (1835 – 1837) - *The Magazine of Natural History*

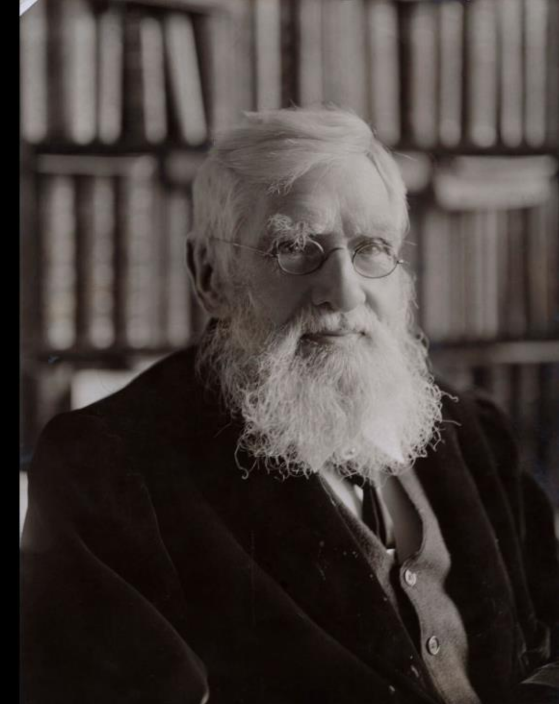
Three articles on variation, discussing the effects of artificial selection and describing the process in nature as restoring organisms in the wild to their archetype (rather than forming new species). However, he never actually used the term "natural selection„.



Patrick Matthew (1831) – *On Naval Timber and Arboriculture with critical notes on authors who have recently treated the subject of planting*

The self-regulating adaptive disposition of organised life, may, in part, be traced to the extreme fecundity of Nature, who, as before stated, has, in all the varieties of her offspring, a prolific power much beyond (in many cases a thousandfold) what is necessary to fill up the vacancies caused by senile decay. As the field of existence is limited and pre-occupied, it is only the hardier, more robust, better suited to circumstance individuals, who are able to struggle forward to maturity, these inhabiting only the situations to which they have superior adaptation and greater power of occupancy than any other kind; the weaker, less circumstance-suited, being prematurely destroyed.

Alfred Russel Wallace (8.1.1823. – 7.11.1913.)



8/9

13

4

8

125.660

5000

10.10.1855 - "On the Law which has Regulated the Introduction of New Species"

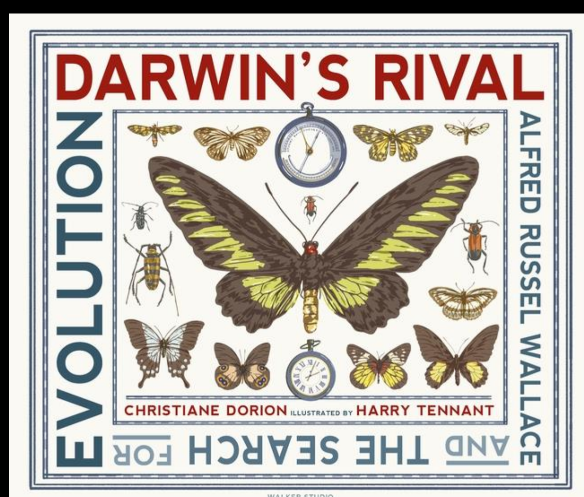
18.6.1858 - ”On the Tendency of Varieties to Depart Indefinitely From the Original Type„

22

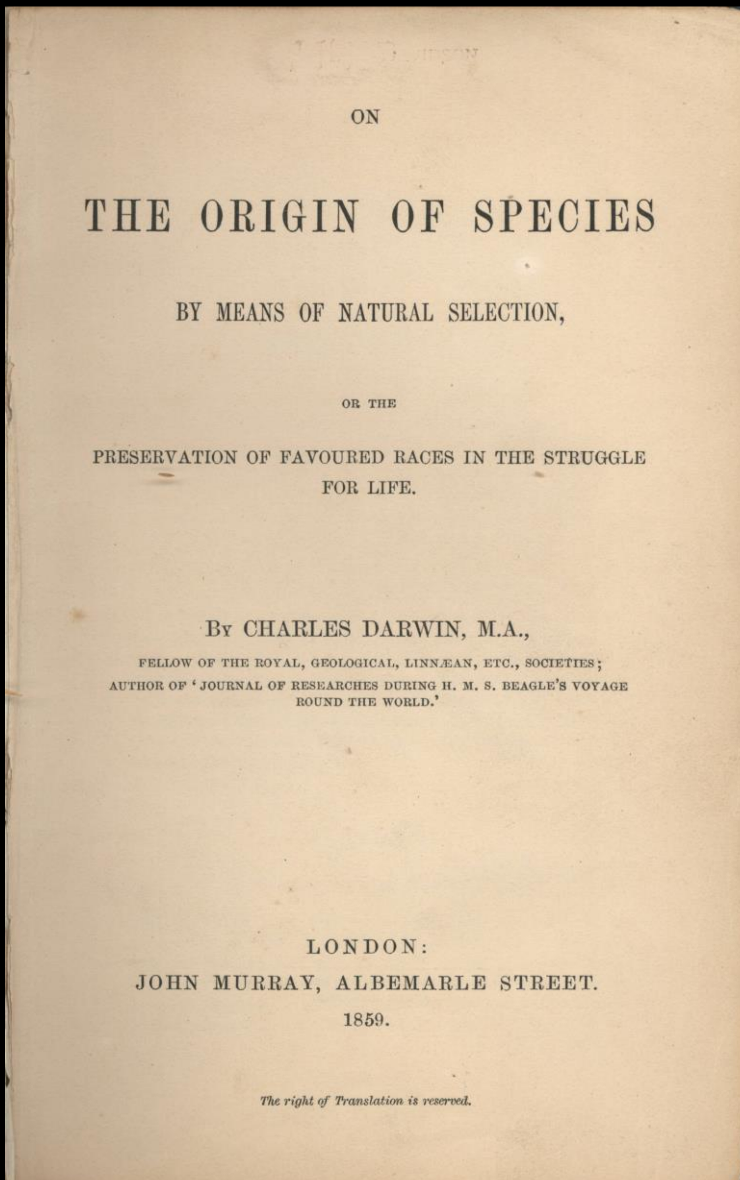
1000 (508)

191

750



O porijeklu



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.,

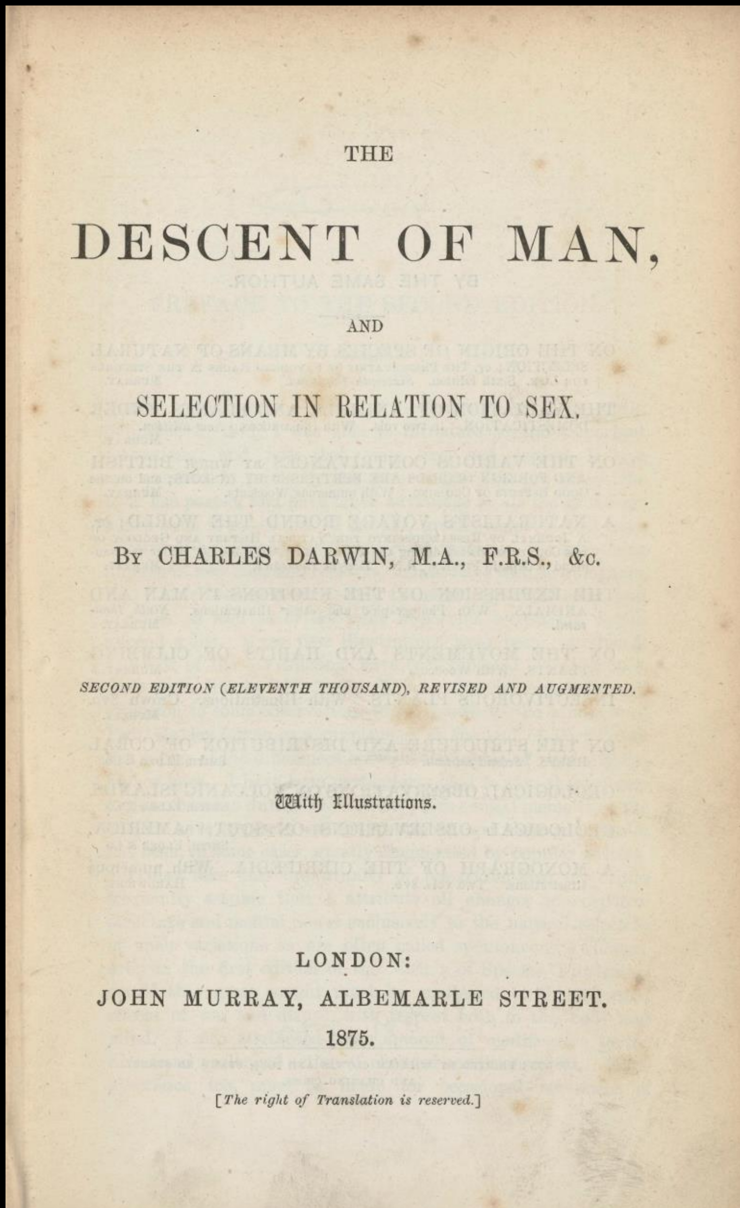
FELLOW OF THE ROYAL, GEOLOGICAL, LINNÆAN, ETC., SOCIETIES;
AUTHOR OF 'JOURNAL OF RESEARCHES DURING H. M. S. BEAGLE'S VOYAGE ROUND THE WORLD.'

LONDON:
JOHN MURRAY, ALBEMARLE STREET.
1859.

The right of Translation is reserved.

- Svaka je vrsta dovoljno plodna da će populacija rasti ako bi preživjelo svo potomstvo.
- Unatoč povremenim fluktuacijama, populacije ostaju približno iste veličine.
- Resursi poput hrane ograničeni su i u vremenu su relativno stabilni.
- Slijedi borba za opstanak.
- Pojedinci se u populaciji međusobno značajno razlikuju.
- Većina ove varijacije nasljedna je.
- Pojedinci slabije prilagođeni okolišu imaju manju vjerojatnost da će preživjeti i rjeđe se razmnožavati; jedinke prilagođenije okolišu imaju veću vjerojatnost da će preživjeti i vjerojatnije će se razmnožavati i ostavljati će tako svoje nasljedne osobine budućim naraštajima, što provodi proces prirodne selekcije.
- Ovaj proces rezultira promjenom populacija kako bi se prilagodile svom okolišu, te se u konačnici te varijacije akumuliraju kako bi stvorile nove vrste.

Porijeklo


THE

DESCENT OF MAN,

AND

SELECTION IN RELATION TO SEX.

BY CHARLES DARWIN, M.A., F.R.S., &c.

SECOND EDITION (ELEVENTH THOUSAND), REVISED AND AUGMENTED.

With Illustrations.

LONDON:
JOHN MURRAY, ALBEMARLE STREET.
1875.

[*The right of Translation is reserved.*]

1. Razmotriti jesu li ljudi porijeklom od već postojećeg oblika
2. Razmotriti prirodu ljudskog razvoja
3. Razmotriti razlike između "ljudskih rasa".

Ljudi potječu iz Afrike

Nema temeljne razlike između čovjeka i viših sisavaca

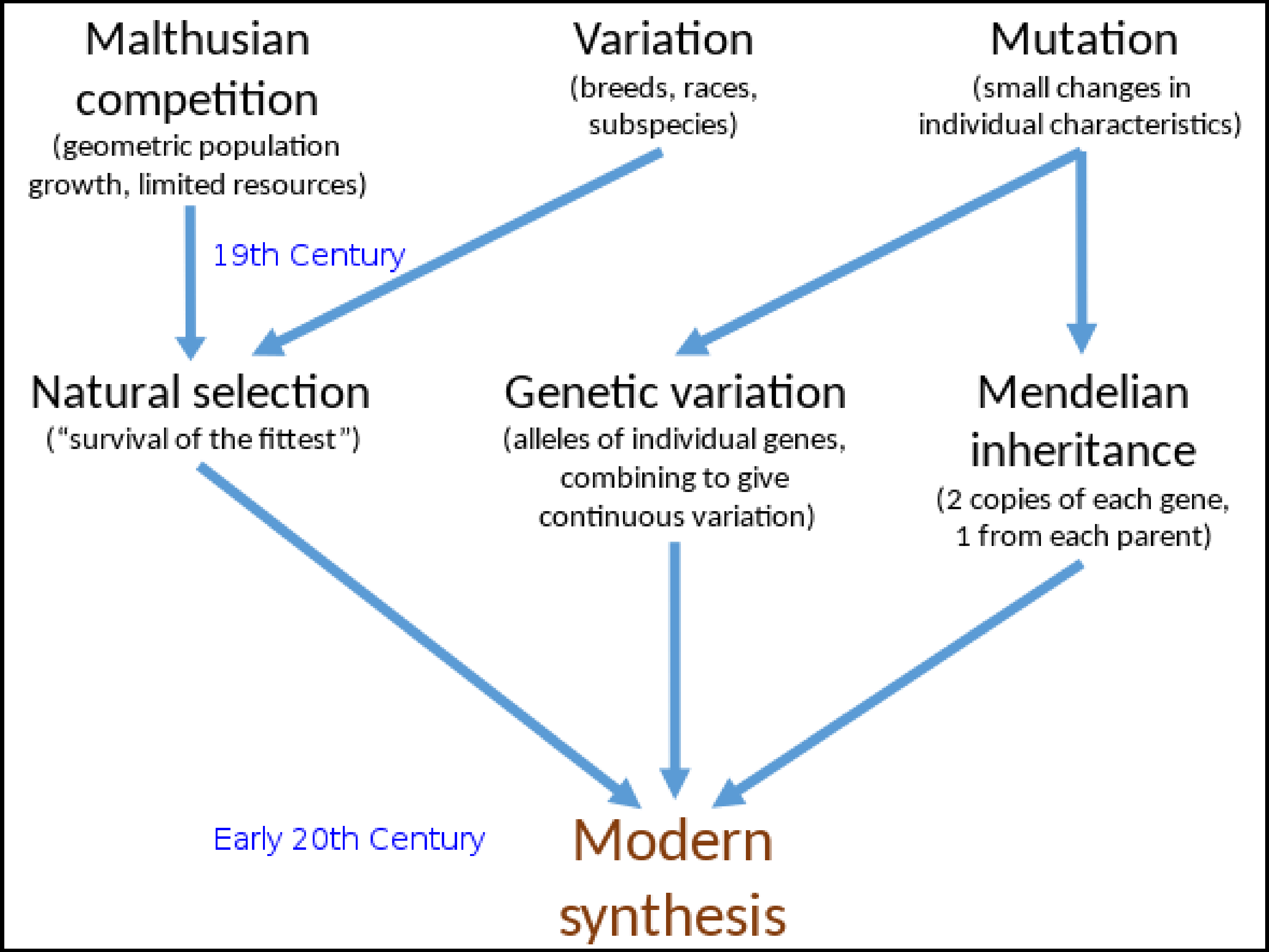
Moral je proizvod čimbenika povezanih s borbom za opstanak i reprodukciju, a nije božanski određen.

Monogenizam

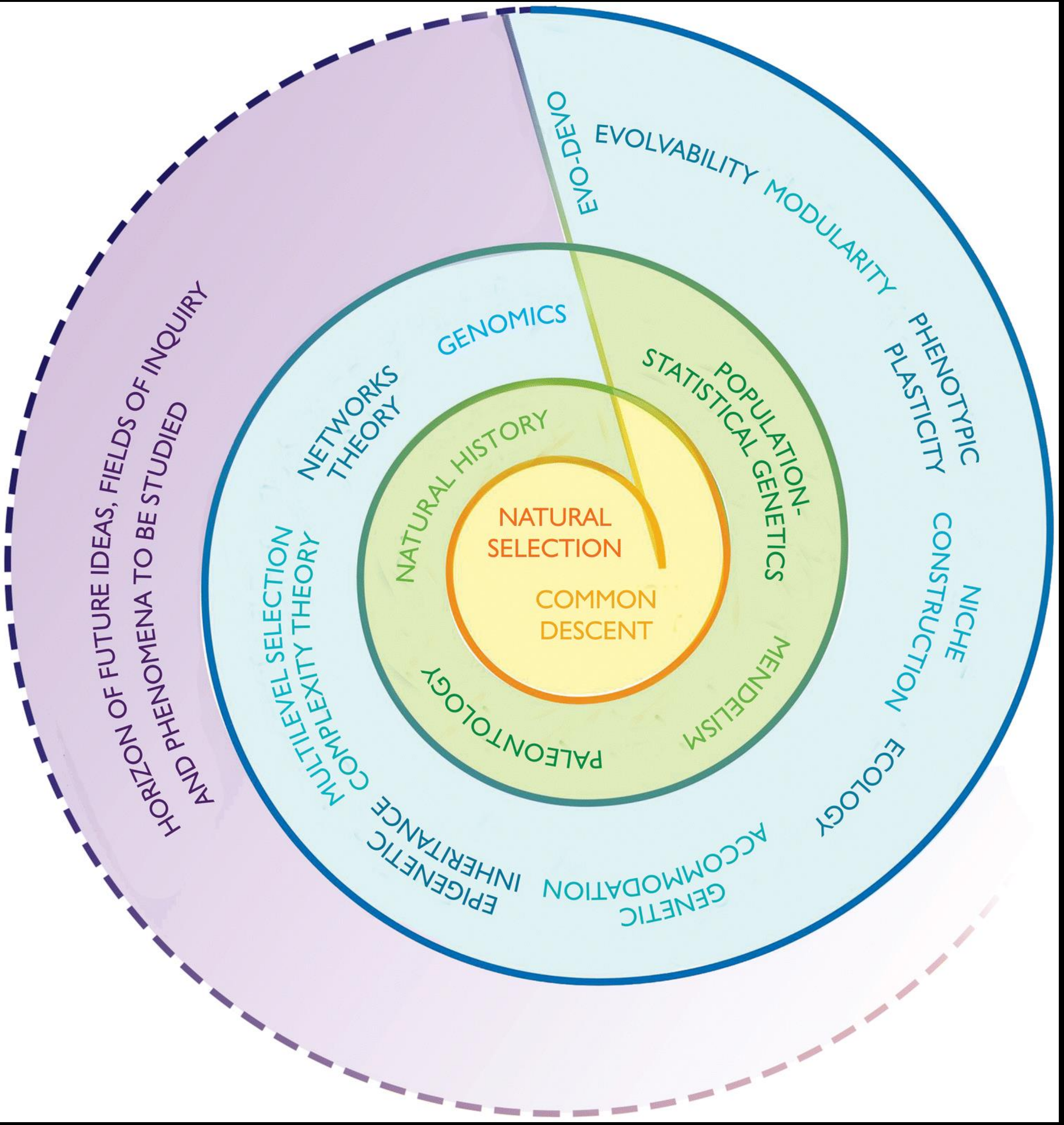
Seksualni odabir objasnio je kako je borba za partnere dovela do prilagodbi bez koristi za preživljavanje.

Neo-Darvinizam

Moderna sinteza 1918 - 1942

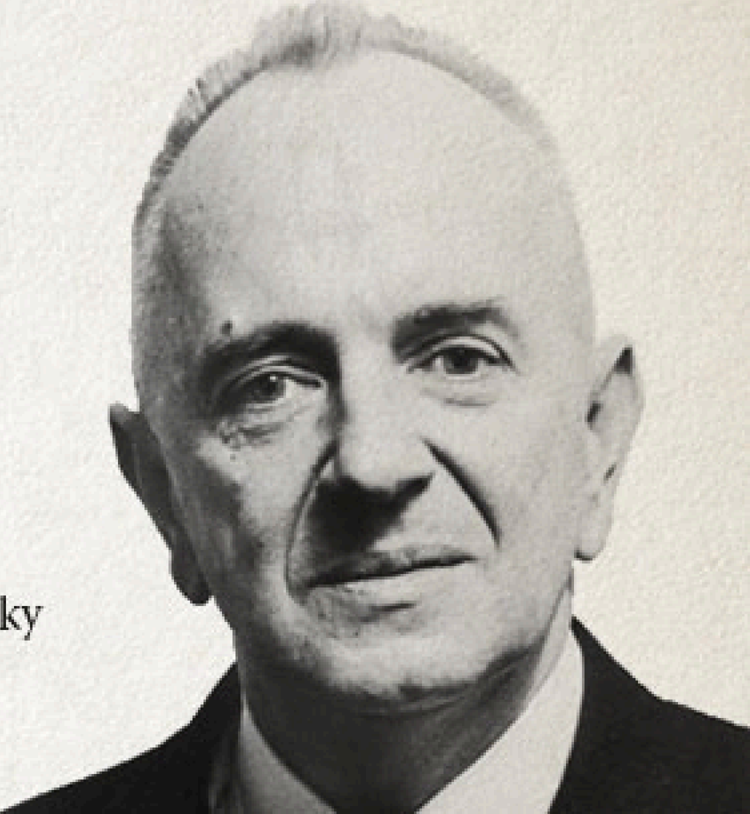


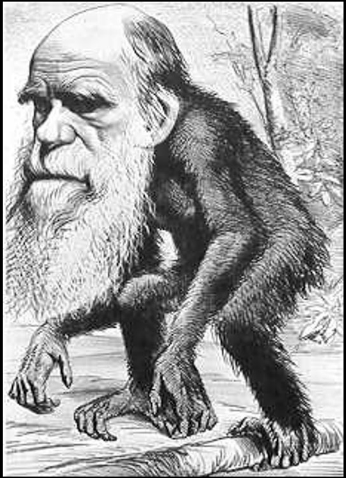
Proširena evolucijska sinteza 1950 - 2007

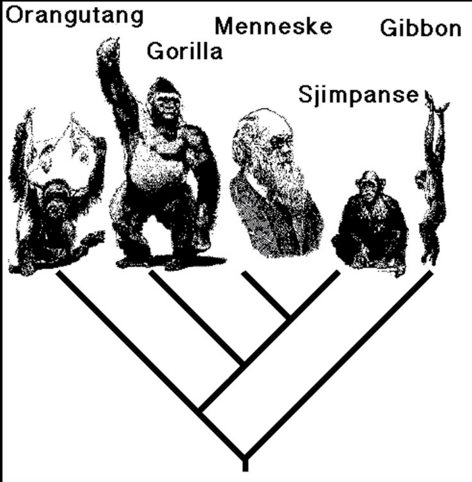


“Ništa u biologiji nema smisla,
osim u svjetlu evolucije.“

—Theodosius Dobzhansky

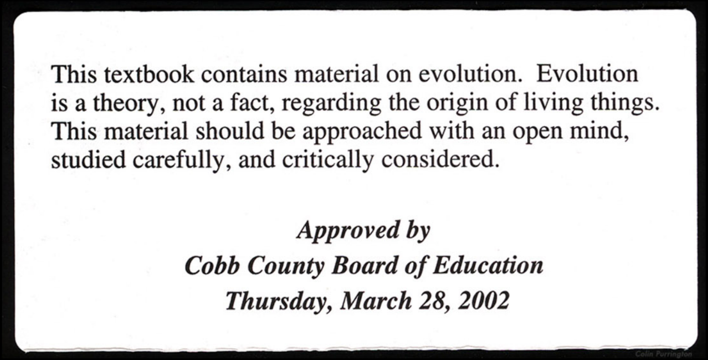





Orangutang
Gorilla
Menneske
Sjimpanse
Gibbon

Butler Act & Scopes Trial – Tennessee (1925)

Edwards vs Aguillard – Louisiana (1987)



This textbook contains material on evolution. Evolution is a theory, not a fact, regarding the origin of living things. This material should be approached with an open mind, studied carefully, and critically considered.

Approved by
Cobb County Board of Education
Thursday, March 28, 2002

Kitzmiller vs Dover Area School District – Pensylvannia (2005)

Senate Bill 893 a.k.a Monkey Bill – Tennessee (2012)

Znanstvena teorija:

a) je objašnjenje nekog fenomena ili grupe fenomena u prirodi putem niza testova koji su **reproducibilni**
b) ostaje otvorena novim testiranjima revizijama i posljedičnim **prihvaćanjima ili odbacivanjima**.
c) ne može ju postaviti jedan znanstvenik već ponovljeni testovi niza znanstvenika; jedan znanstvenik postavlja **hipotezu koja postaje teorija**
d) ima znatan broj **empirijskih dokaza**
e) nikako se ne smije poistovjećivati s **laičkim teorijama**

Evolucija nije "samo teorija" već znanstvena teorija bazirana na 150 godina konstantnog preispitivanja i istraživanja tisuća znanstvenika u cijelom svijetu.

Paleontologija, biogeografija, anatomija, embriologija, fiziologija, biokemija i molekularna biologija

Znanstvena teorija vs znanstveni zakon

Zajedničko:

Izvedeni iz pažljivo formuliranih hipoteza nastalih na osnovi dugotrajnog istraživanja i uočavanja prirodnih fenomena

Prihvaćeni od znanstvene zajednice i služe predviđanjima određenih događaja

Znanstvena teorija s vremenom postaje zakon?

Razlike:

Teorija mnogo kompleksnija od zakona.

Višekomponentna.

Podložna promjenama.

Obrazlaže čitav niz povezanih fenomena.

Kaosa – Relativnosti – Kontinentalnog drifta

Znanstveni zakon:

striktno empirijski i objašnjiv jednom ili nizom akcija

ponekad i jednom jedinom jednadžbom

(Zakoni termodinamike, Newtonov zakon gravitacije, Hookov zakon elastičnosti, Ohmov zakon)

mogu biti i komponente teorije

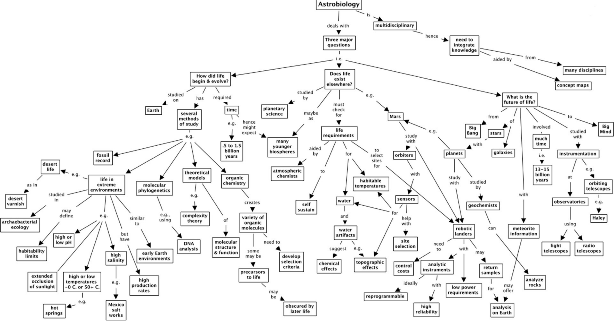
(Newtonov zakon gravitacije sadržan je u Einsteinovoj teoriji relativnosti)

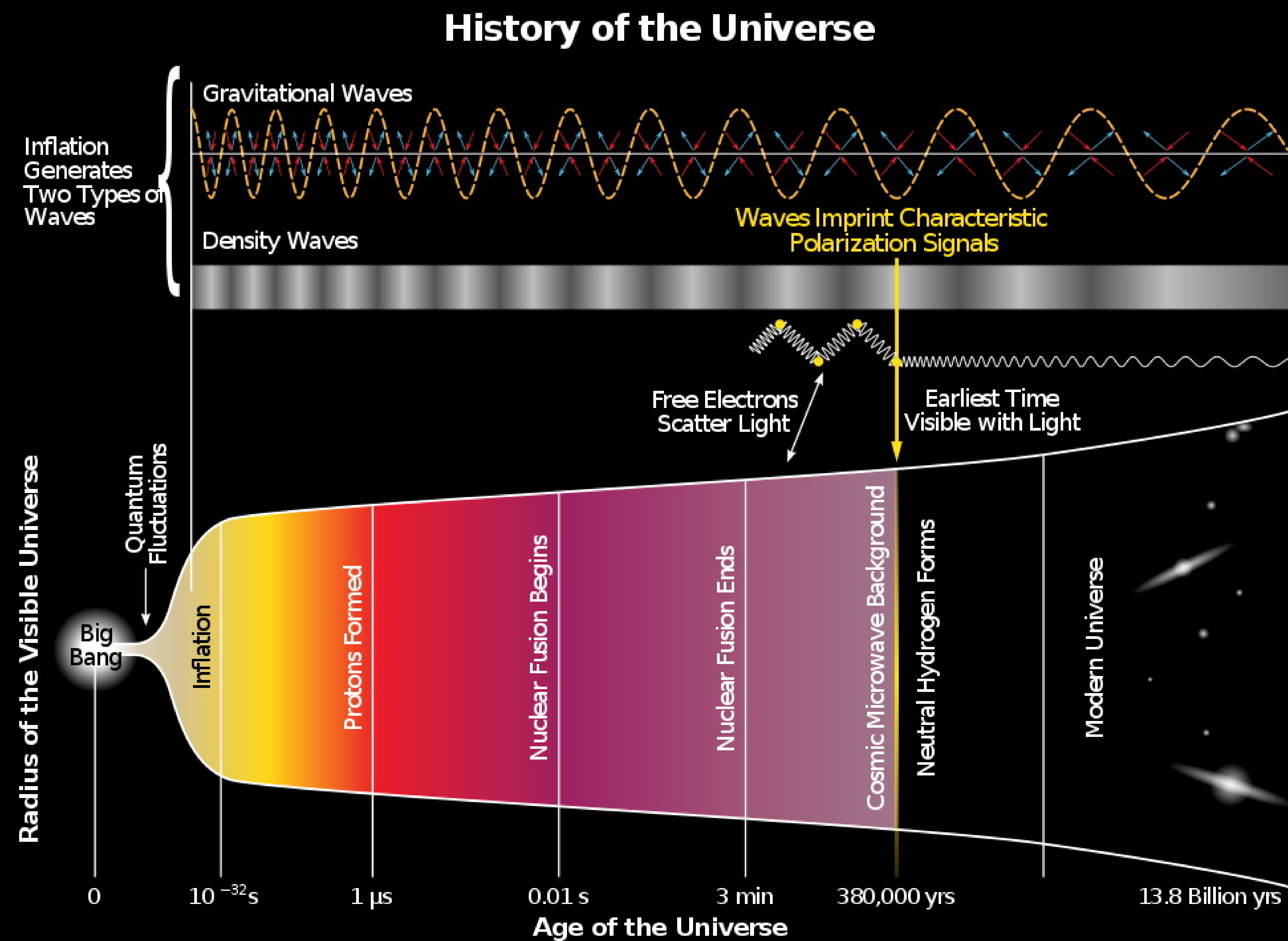
ID:

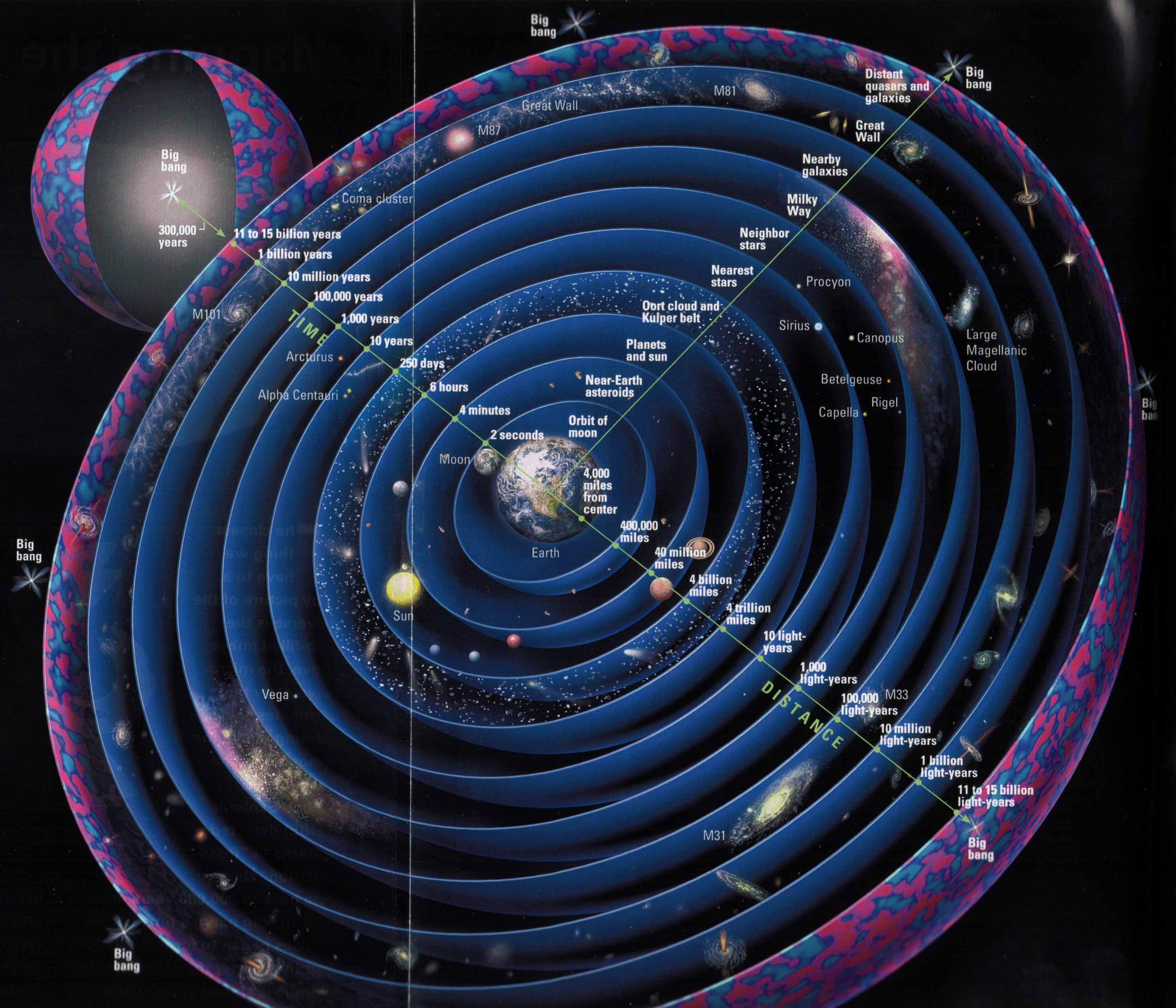
bazirana na uvjerenju ne na empirijskim dokazima

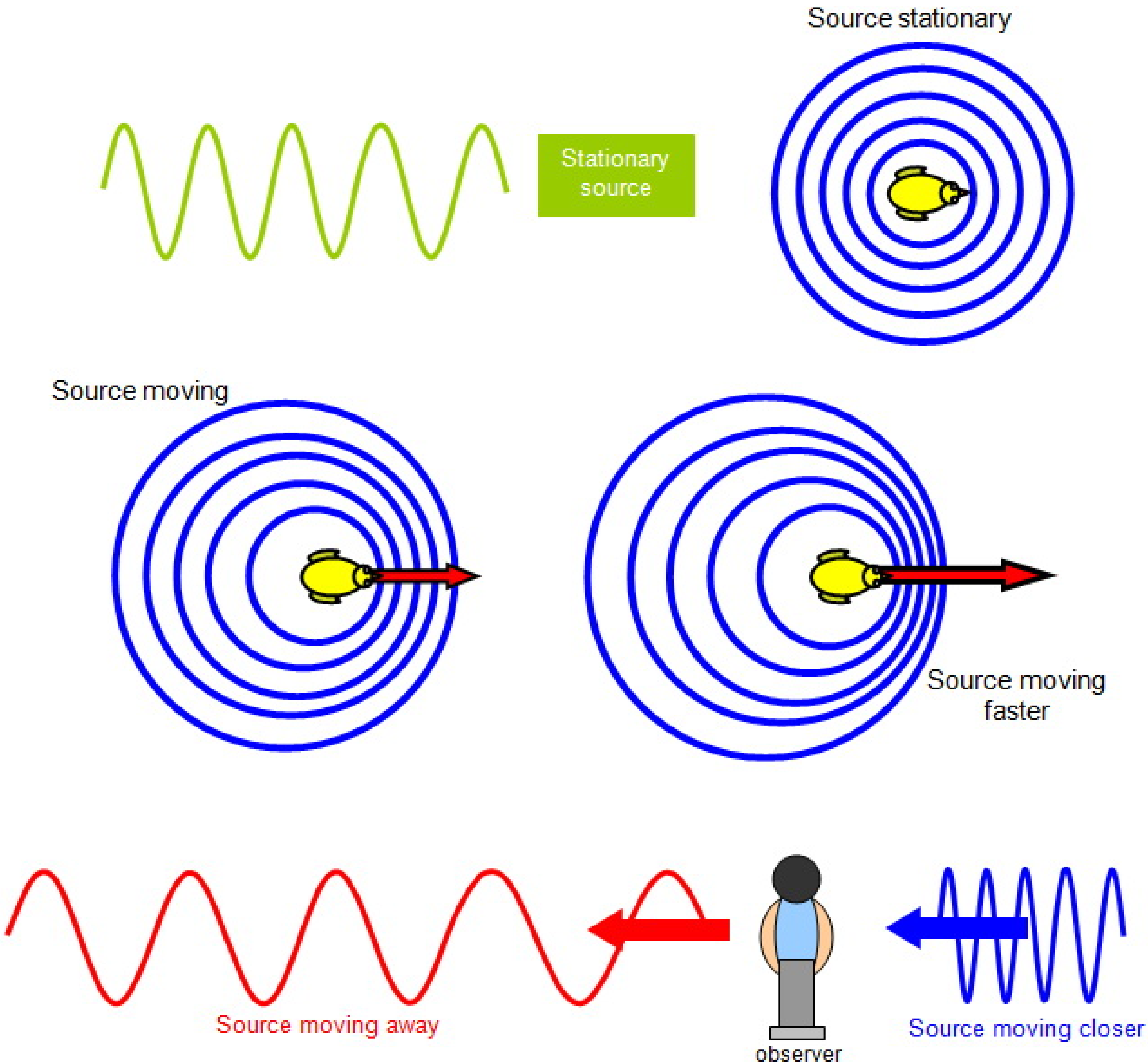
ne može biti testirana niti dokazana

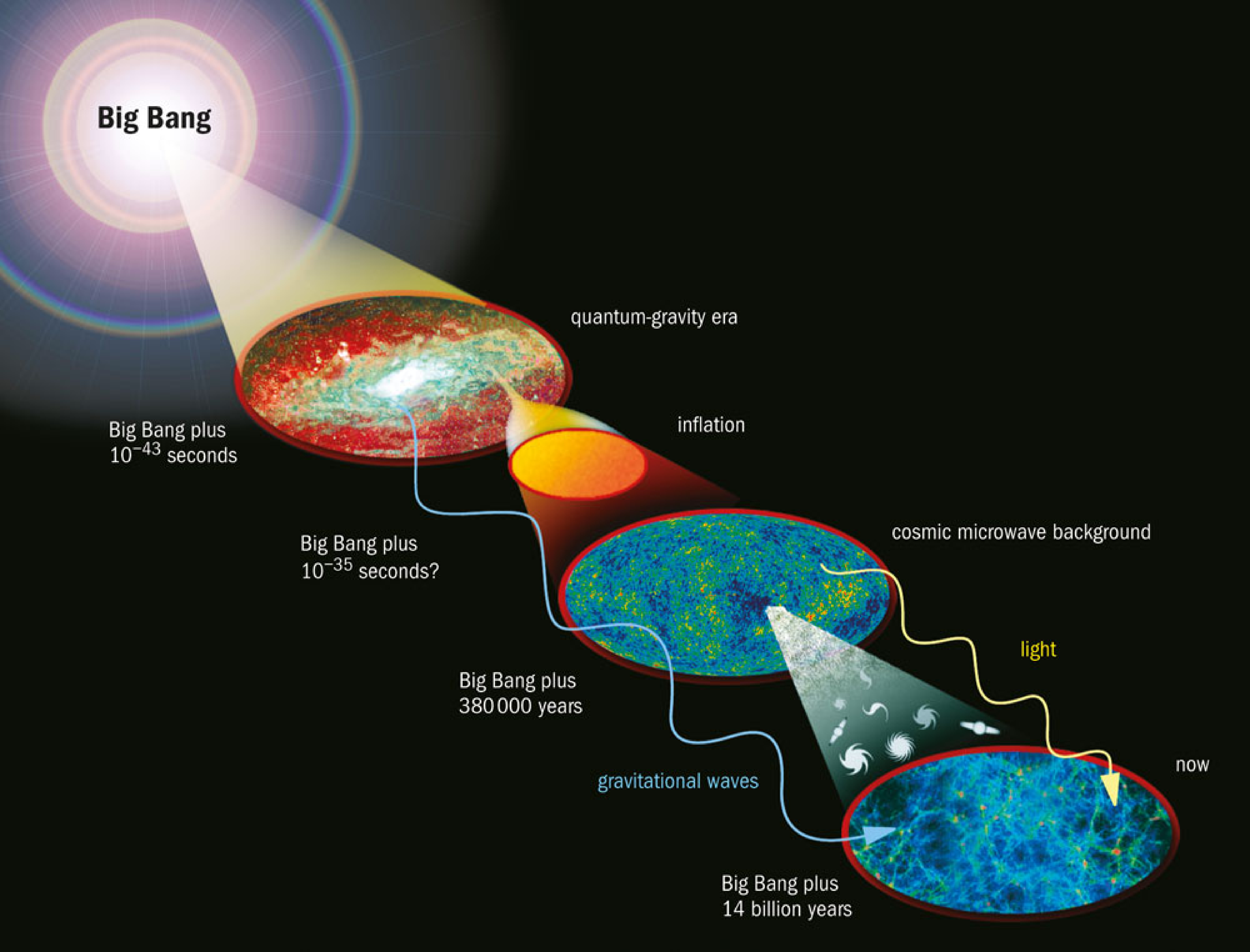
opasno dogme unositi u znanost


Astrobiology
is
multidisciplinary
hence
need to integrate knowledge
from
many disciplines
aided by
concept maps
deals with
Three major questions
i.e.
How did life begin & evolve?
studied on
Earth
has
several methods of study
e.g.
fossil record
life in extreme environments
as in
desert life
desert varnish
studied in
archaebacterial ecology
may define
habitability limits
high or low pH
extended occlusion of sunlight
high or low temperatures −0 C. or 50+ C.
hot springs
high salinity
Mexico salt works
but have
high production rates
similar to
early Earth environments
molecular phylogenetics
e.g., using
DNA analysis
theoretical models
complexity theory
of
molecular structure & function
organic chemistry
creates
variety of organic molecules
need to
develop selection criteria
some may be
precursors to life
may be
obscured by later life
required
time
.5 to 1.5 billion years
hence might expect
many younger biospheres
Does life exist elsewhere?
studied by
planetary science
maybe as
must check for
life requirements
aided by
atmospheric chemists
to
self sustain
for
water
and
water artifacts
suggest
chemical effects
topographic effects
habitable temperatures
to select sites for
Mars
study with
orbiters
with
sensors
help with
site selection
robotic landers
need to
control costs
analytic instruments
ideally
reprogrammable
high reliability
low power requirements
may
return samples
for
analysis on Earth
may offer
planets
studied by
geochemists
can
analyze rocks
What is the future of life?
Big Bang
stars
galaxies
involved
much time
13–15 billion years
Big Mind
studied with
instrumentation
at
observatories
using
light telescopes
radio telescopes
orbiting telescopes
Haley
meteorite information


History of the Universe
Gravitational Waves
Inflation Generates Two Types of Waves
Density Waves
Waves Imprint Characteristic Polarization Signals
Free Electrons Scatter Light
Earliest Time Visible with Light
Radius of the Visible Universe
Quantum Fluctuations
Big Bang
Inflation
Protons Formed
Nuclear Fusion Begins
Nuclear Fusion Ends
Cosmic Microwave Background
Neutral Hydrogen Forms
Modern Universe
0
10 −32 s
1 μs
0.01 s
3 min
380,000 yrs
13.8 Billion yrs
Age of the Universe

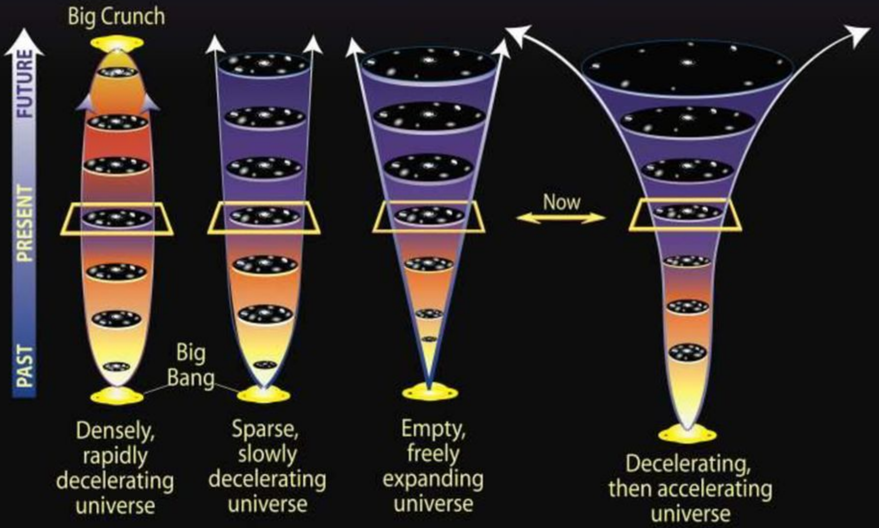

Big bang
Big bang
300,000 years
11 to 15 billion years
1 billion years
10 million years
100,000 years
1,000 years
10 years
250 days
6 hours
4 minutes
2 seconds
TIME
Distant quasars and galaxies
Big bang
Great Wall
Nearby galaxies
Milky Way
Neighbor stars
Nearest stars
Oort cloud and Kuiper belt
Planets and sun
Near-Earth asteroids
Orbit of moon
4,000 miles from center
400,000 miles
40 million miles
4 billion miles
4 trillion miles
10 light-years
1,000 light-years
100,000 light-years
10 million light-years
1 billion light-years
11 to 15 billion light-years
DISTANCE
Big bang
M81
Great Wall
M87
Coma cluster
M101
Arcturus
Alpha Centauri
Procyon
Sirius
Canopus
Large Magellanic Cloud
Betelgeuse
Rigel
Capella
Moon
Earth
Sun
Vega
M33
M31
Big bang
Big bang

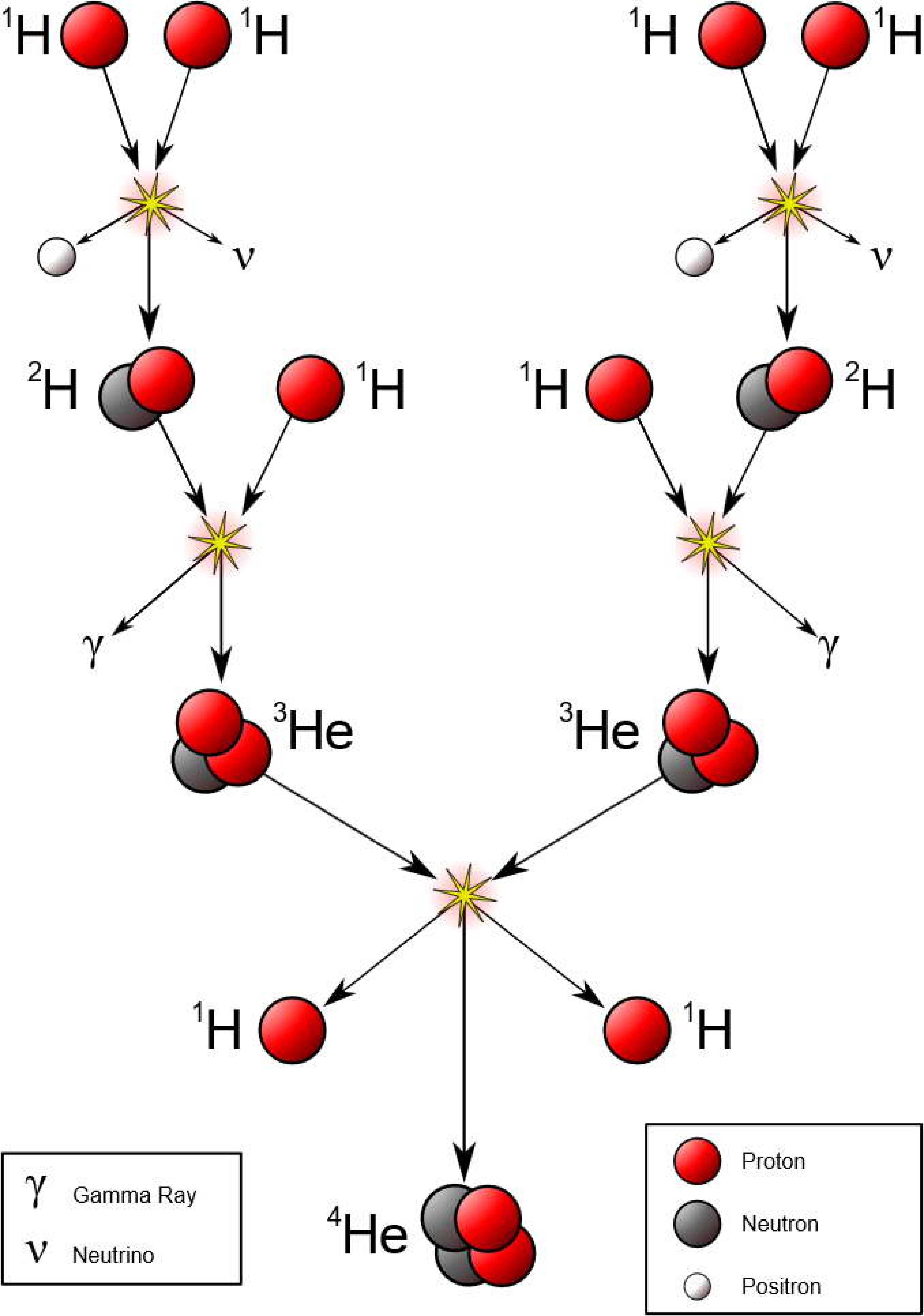

Source stationary
Stationary source
Source moving
Source moving faster
Source moving away
observer
Source moving closer



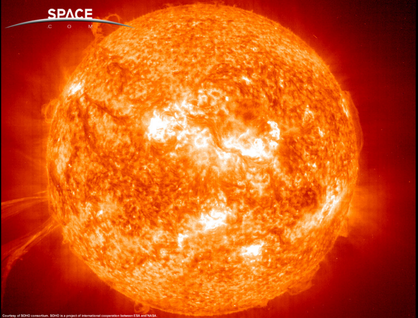
Big Bang
quantum-gravity era
Big Bang plus
10^{-43} seconds
inflation
Big Bang plus
10^{-35} seconds?
cosmic microwave background
light
Big Bang plus
380 000 years
gravitational waves
now
Big Bang plus
14 billion years

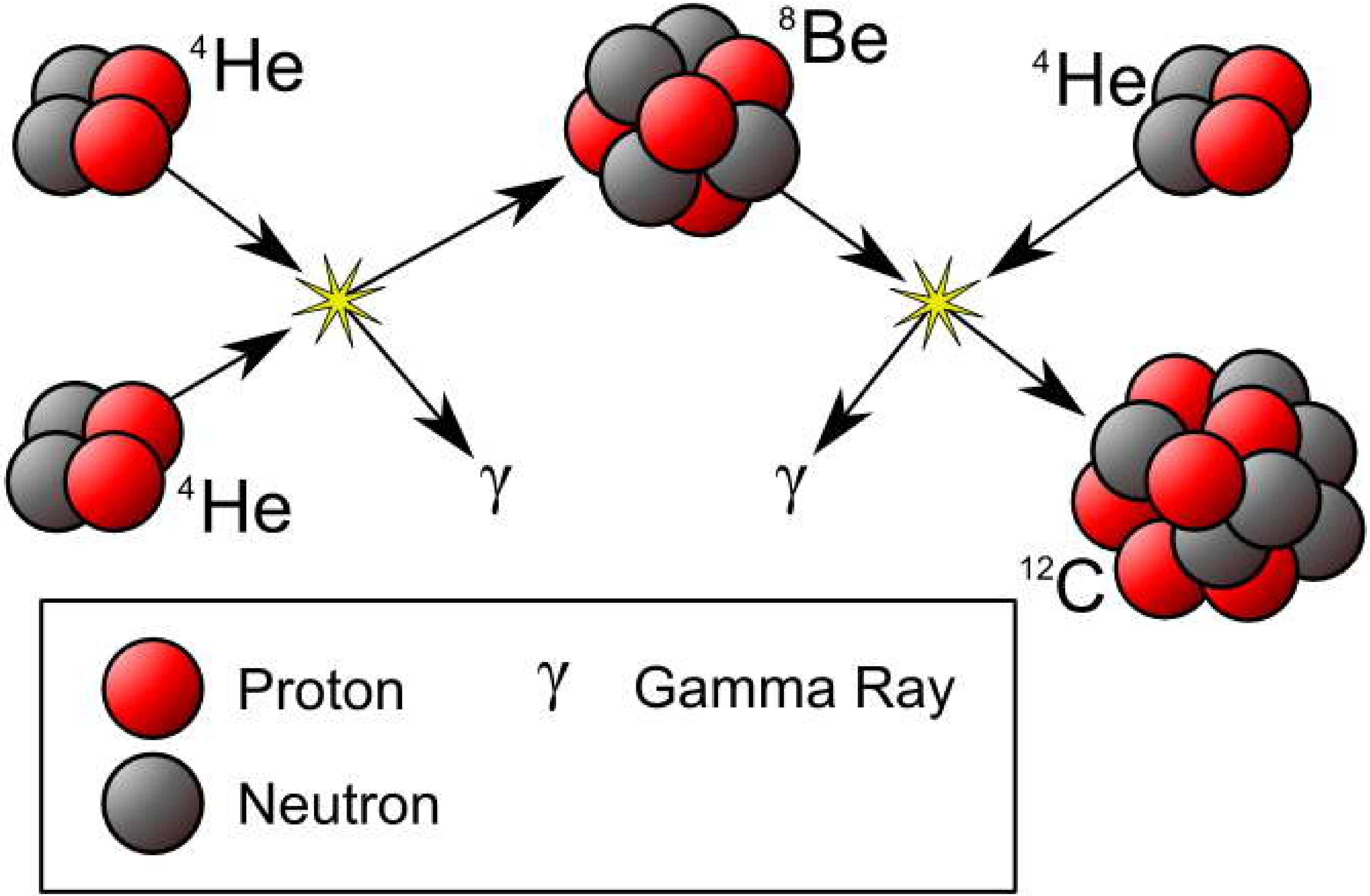
Models of the EXPANDING UNIVERSE





^{1}H
^{1}H
^{1}H
^{1}H
ν
ν
^{2}H
^{1}H
^{1}H
^{2}H
γ
γ
^{3}He
^{3}He
^{1}H
^{1}H
^{4}He
γ Gamma Ray
ν Neutrino
Proton
Neutron
Positron

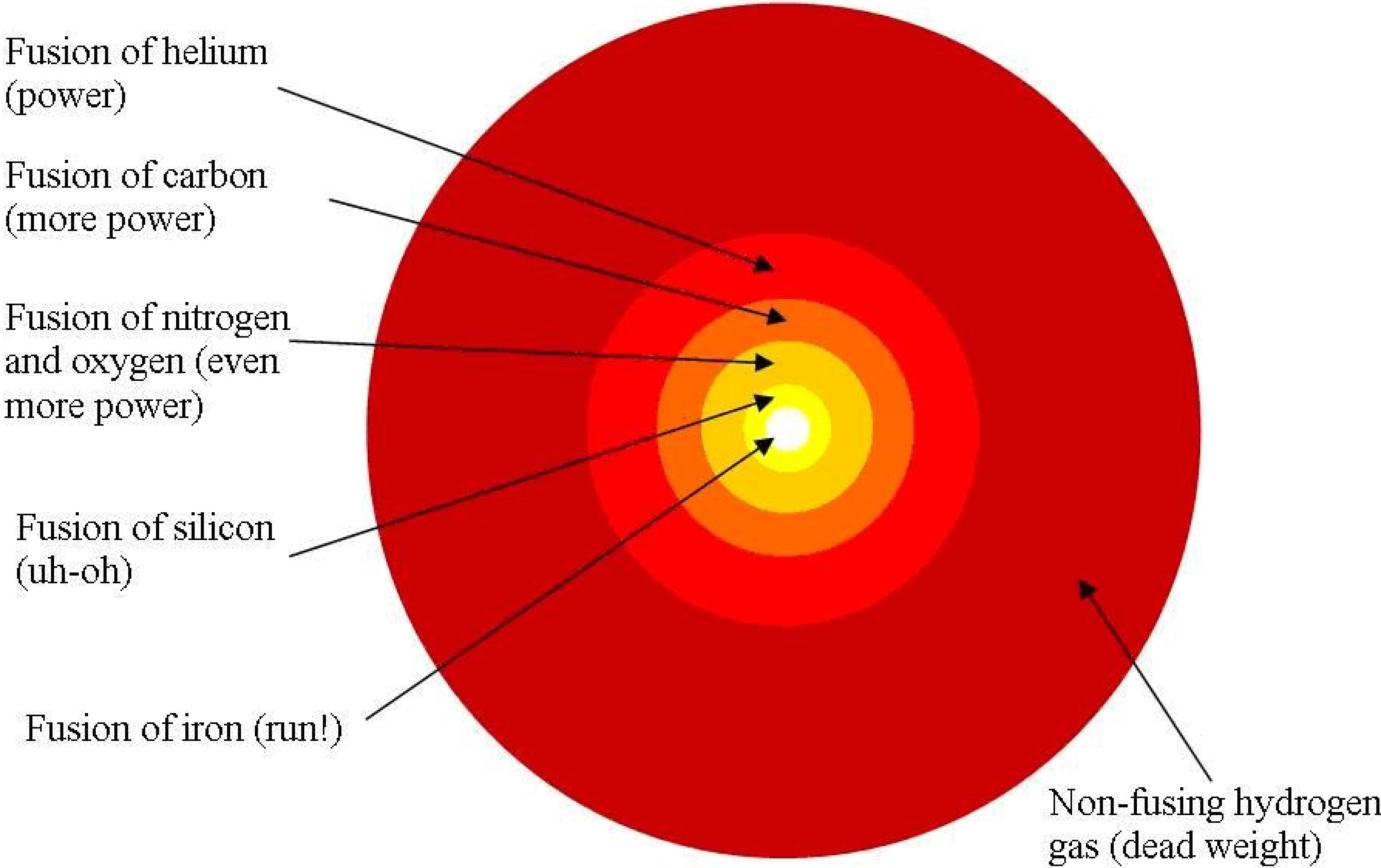

SPACE
.COM
Courtesy of SOHO consortium. SOHO is a project of international cooperation between ESA and NASA.

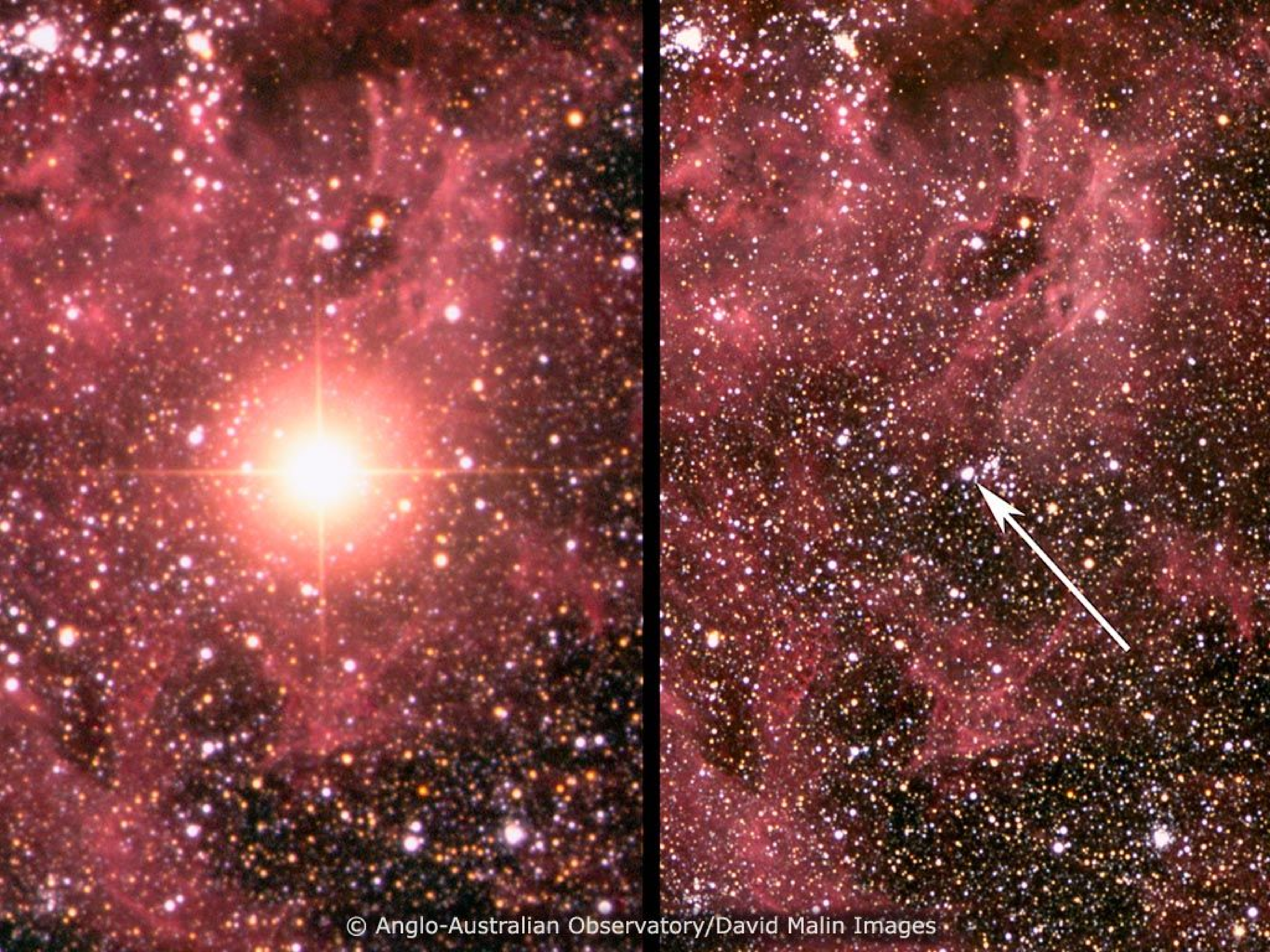


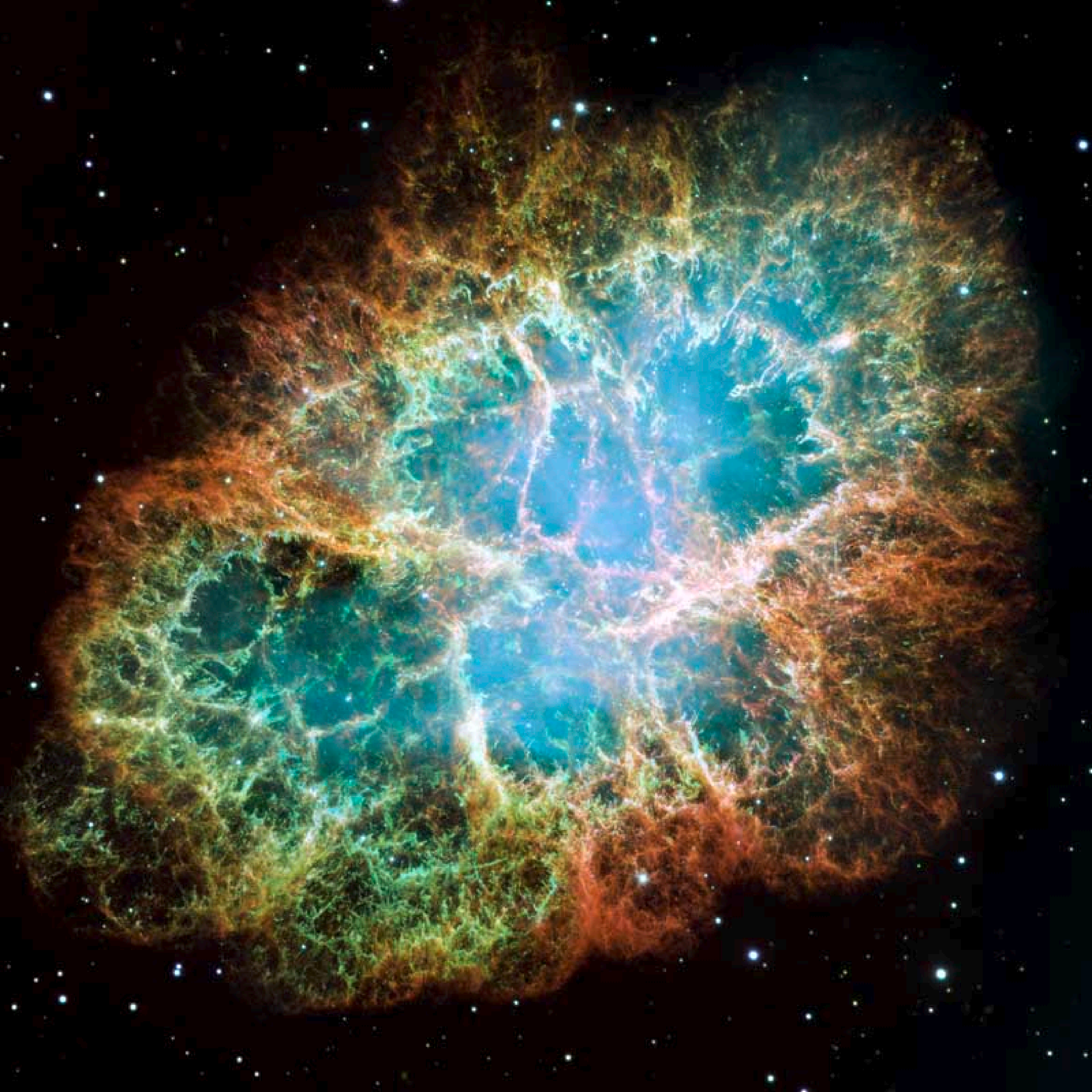
4He
8Be
4He
4He
γ
γ
12C
Proton
γ
Gamma Ray
Neutron

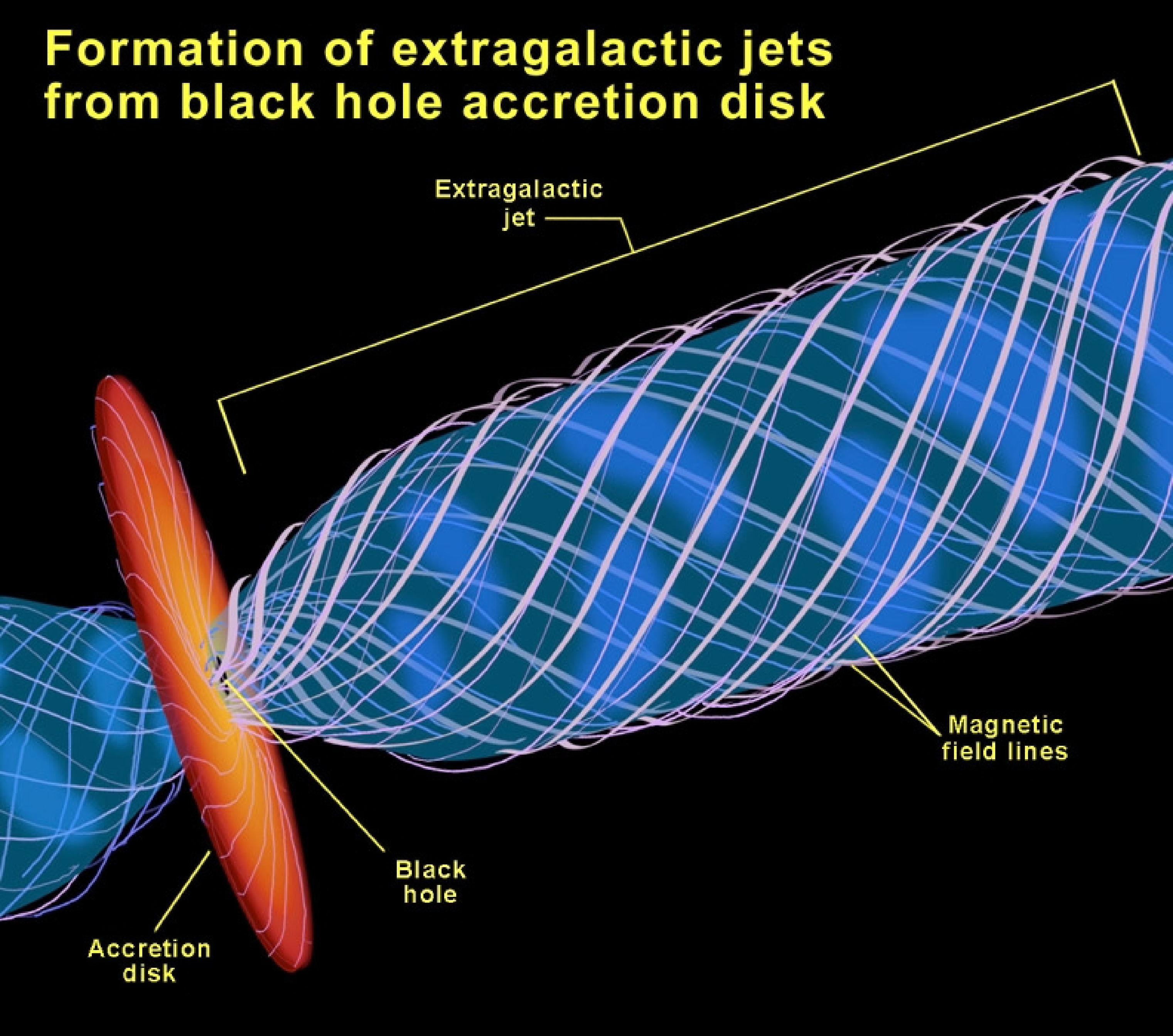

Life Cycle of Our Sun
Nebula
Nebula
Protostar
Main Sequence
Red Giant
Helium and Hydrogen shells burn out and expand into space.
White Dwarf Remains and will fade into a black dwarf over many billions of years.
0
2
4
6
8
10
11
12
13
Billions Of Years

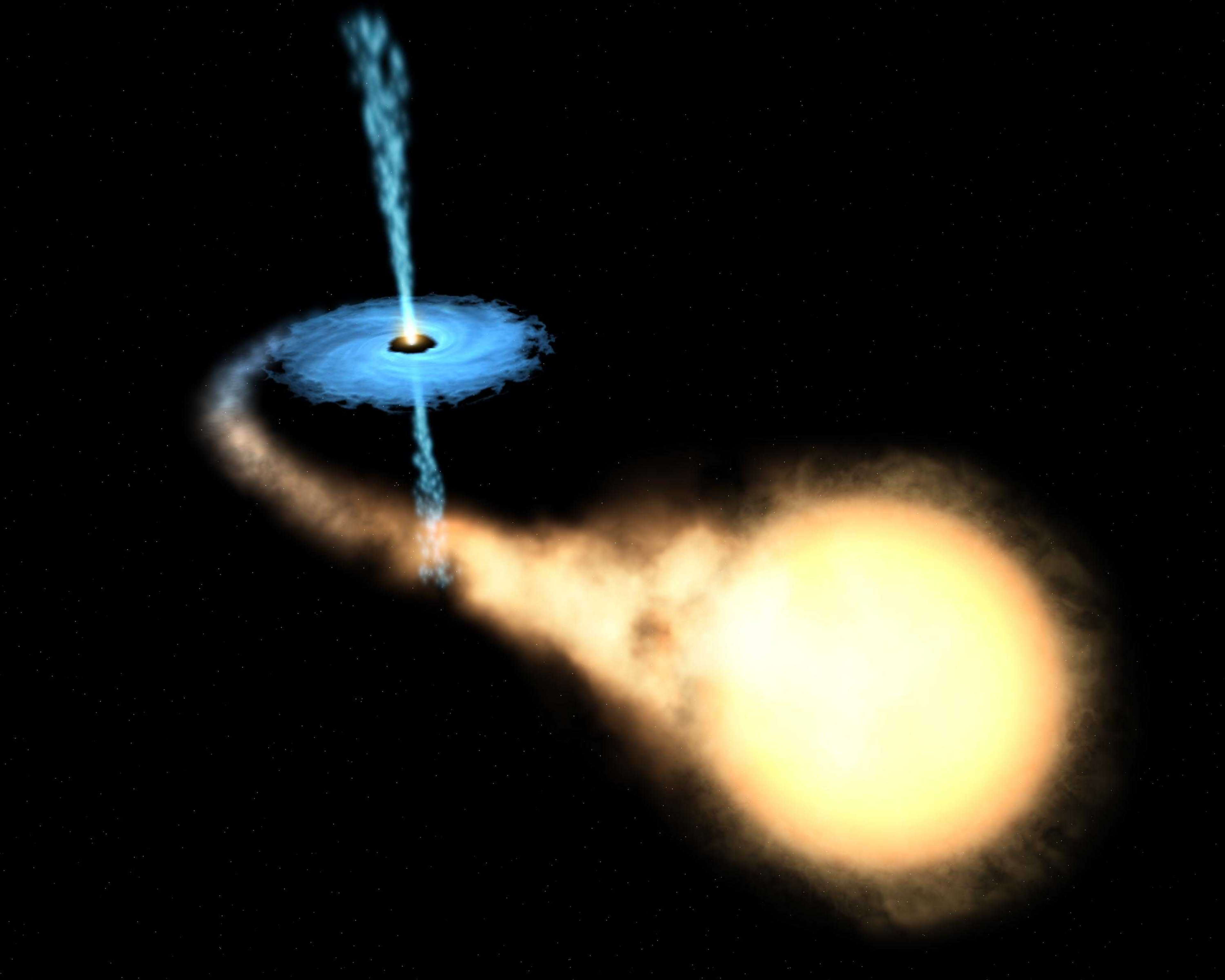
Red Super-Giant Star

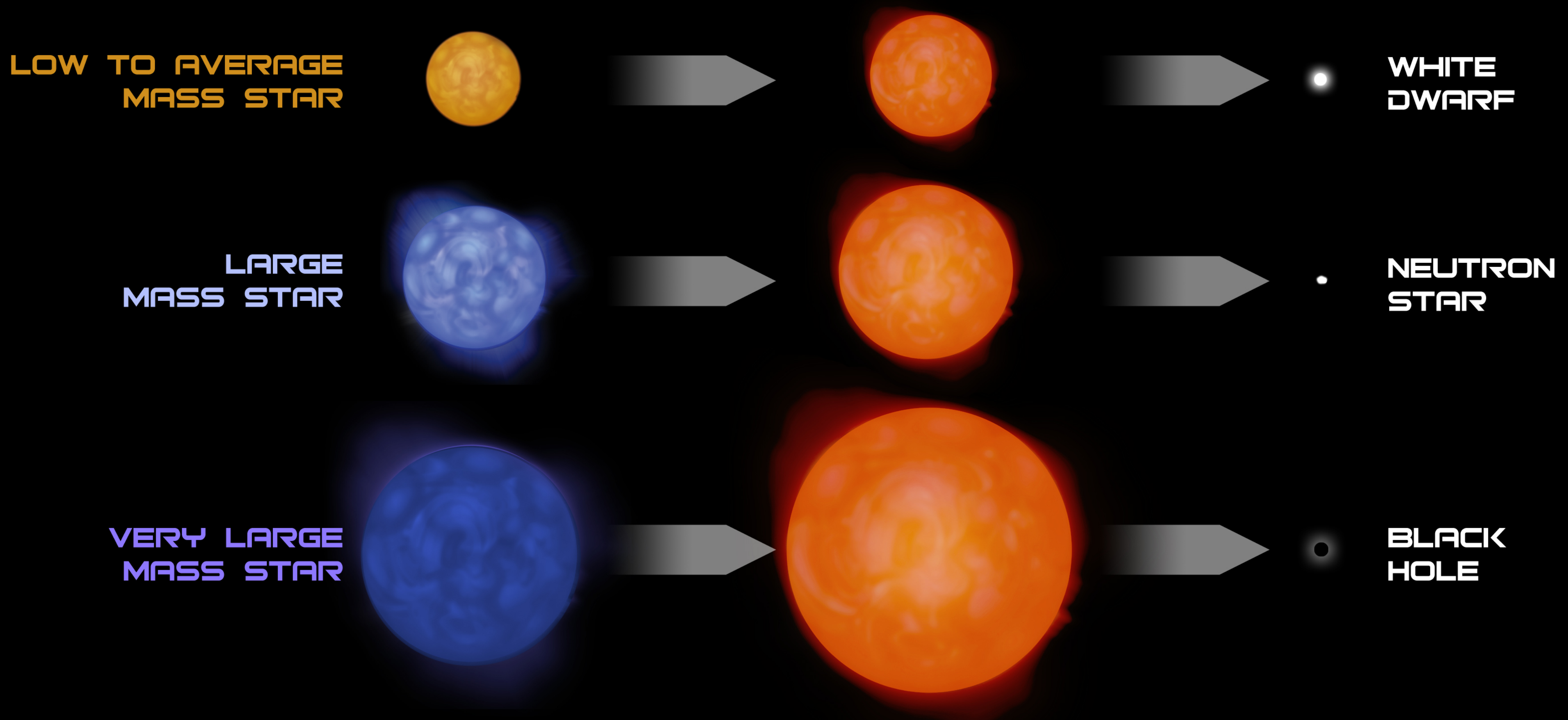



© Anglo-Australian Observatory/David Malin Images

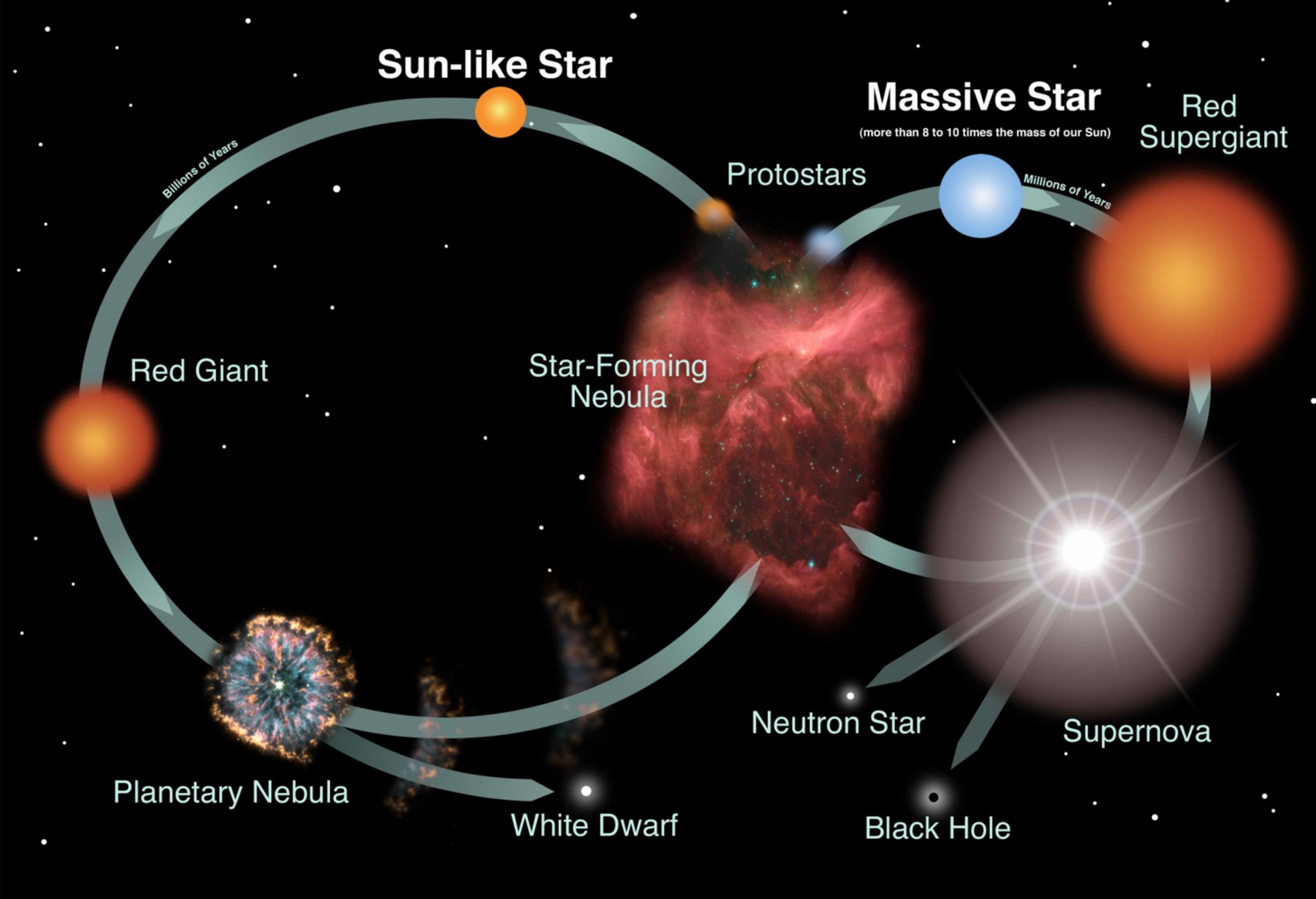



Formation of extragalactic jets
from black hole accretion disk
Extragalactic
jet
Magnetic
field lines
Black
hole
Accretion
disk



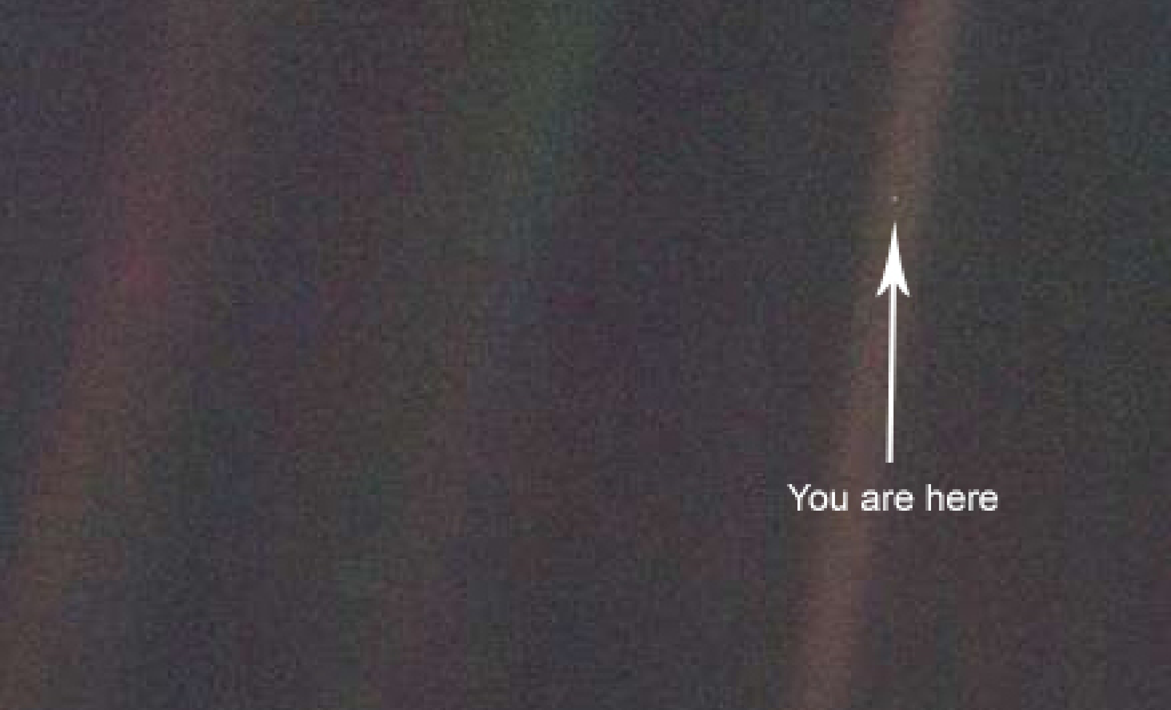


The fate of a star depends on its mass (size not to scale)


Sun-like Star
Massive Star
(more than 8 to 10 times the mass of our Sun)
Red Supergiant
Billions of Years
Protostars
Millions of Years
Red Giant
Star-Forming Nebula
Planetary Nebula
White Dwarf
Neutron Star
Black Hole
Supernova

"Look again at that dot. That's here. That's home. That's us. On it everyone you love, everyone you know, everyone you ever heard of, every human being who ever was, lived out their lives. The aggregate of our joy and suffering, thousands of confident religions, ideologies, and economic doctrines, every hunter and forager, every hero and coward, every creator and destroyer of civilization, every king and peasant, every young couple in love, every mother and father, hopeful child, inventor and explorer, every teacher of morals, every corrupt politician, every "superstar," every "supreme leader," every saint and sinner in the history of our species lived there – on a mote of dust suspended in a sunbeam."

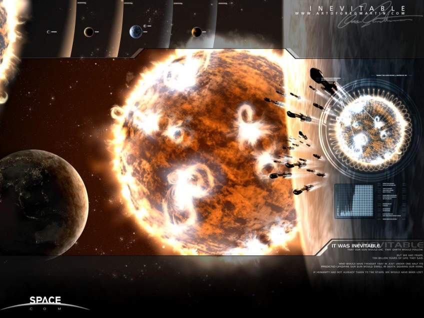
- Carl Sagan, 1934-1996



The Earth as imaged from the the Voyager 1 spacecraft, as it exited the solar system in 1990. Earth is nearly 4 billion miles away in this image.


ORBIT
100,000 years
413,000 years
19-24,000
years
SPIN
TILT
41,000
years
21.5° - 24.5°
Currently 23.5°

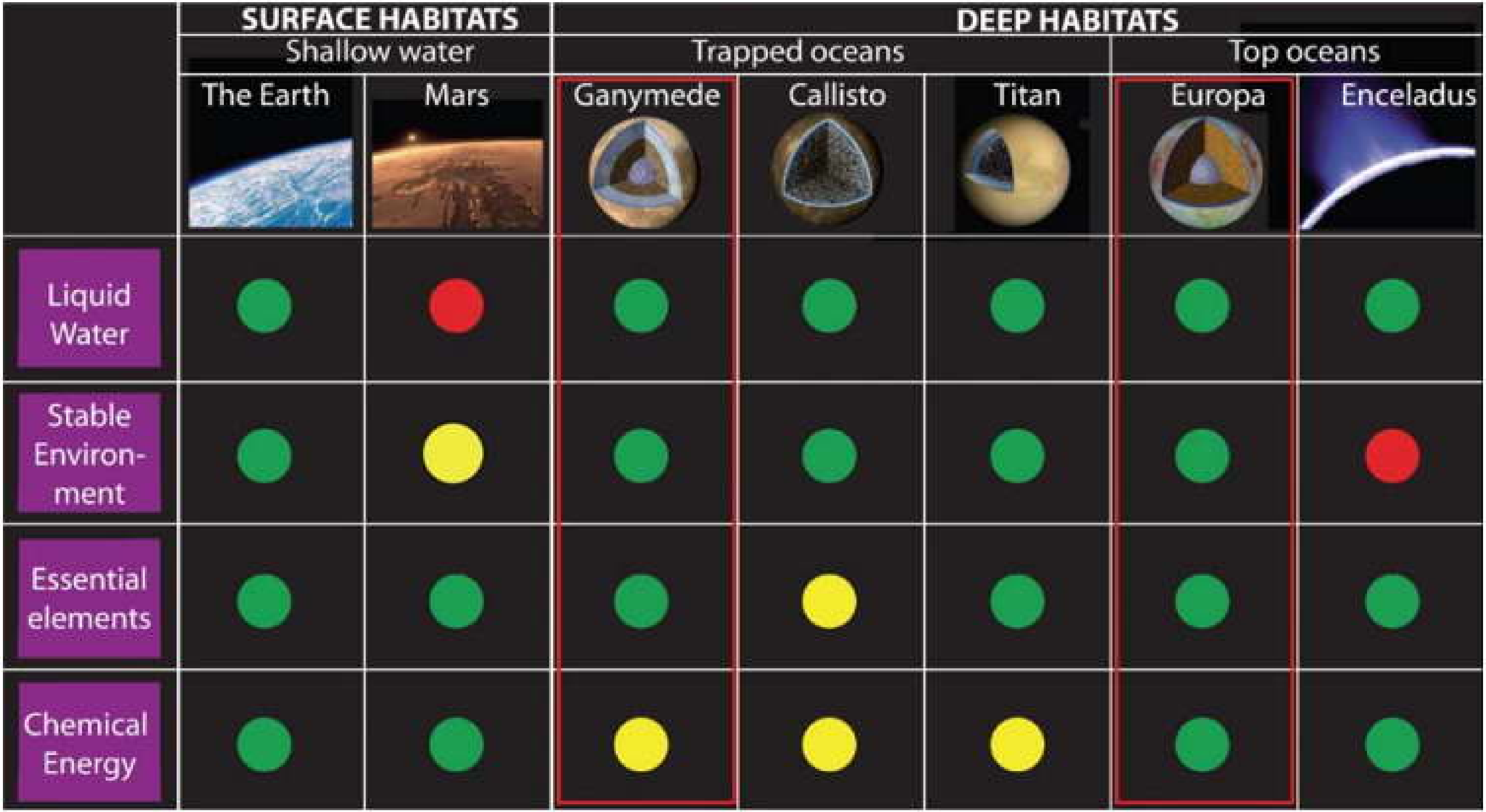

SPACE
CATACLYSM
WWW.ARTOFGREGMARTIN.COM


INEVITABLE
WWW.ARTOFGREGMARTIN.COM
IT WAS INEVITABLE.
INEVITABLE
THAT OUR SUN WOULD DIE. THAT EARTH WOULD FOLLOW.
BUT WE HAD YEARS.
TEN BILLION YEARS OF LIFE, THEY SAID.
WHO WOULD HAVE THOUGHT THAT IN JUST UNDER ONE HALF ITS PREDICTED LIFESPAN, OUR SUN WOULD SWELL IN DEATH, SEARING OUR HOME.
IF HUMANITY HAD NOT ALREADY TAKEN TO THE STARS, WE WOULD HAVE BEEN LOST.
SPACE
.COM

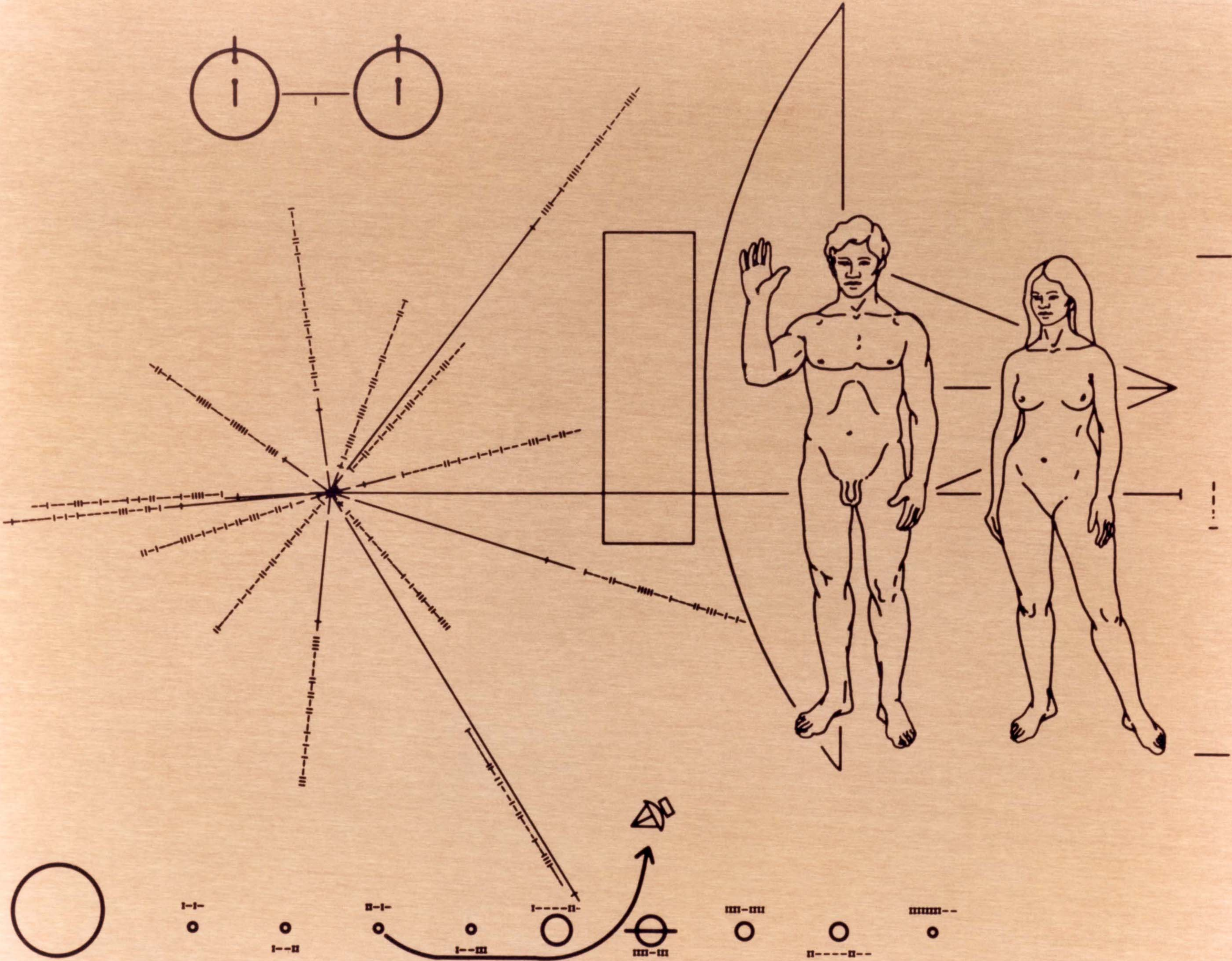

Mercury
Venus
Earth
Mars
Jupiter
Saturn
Uranus
Neptune
"Planets"
HABITABLE ZONE
Ceres
Pluto
2003 UB313
"Dwarf Planets"

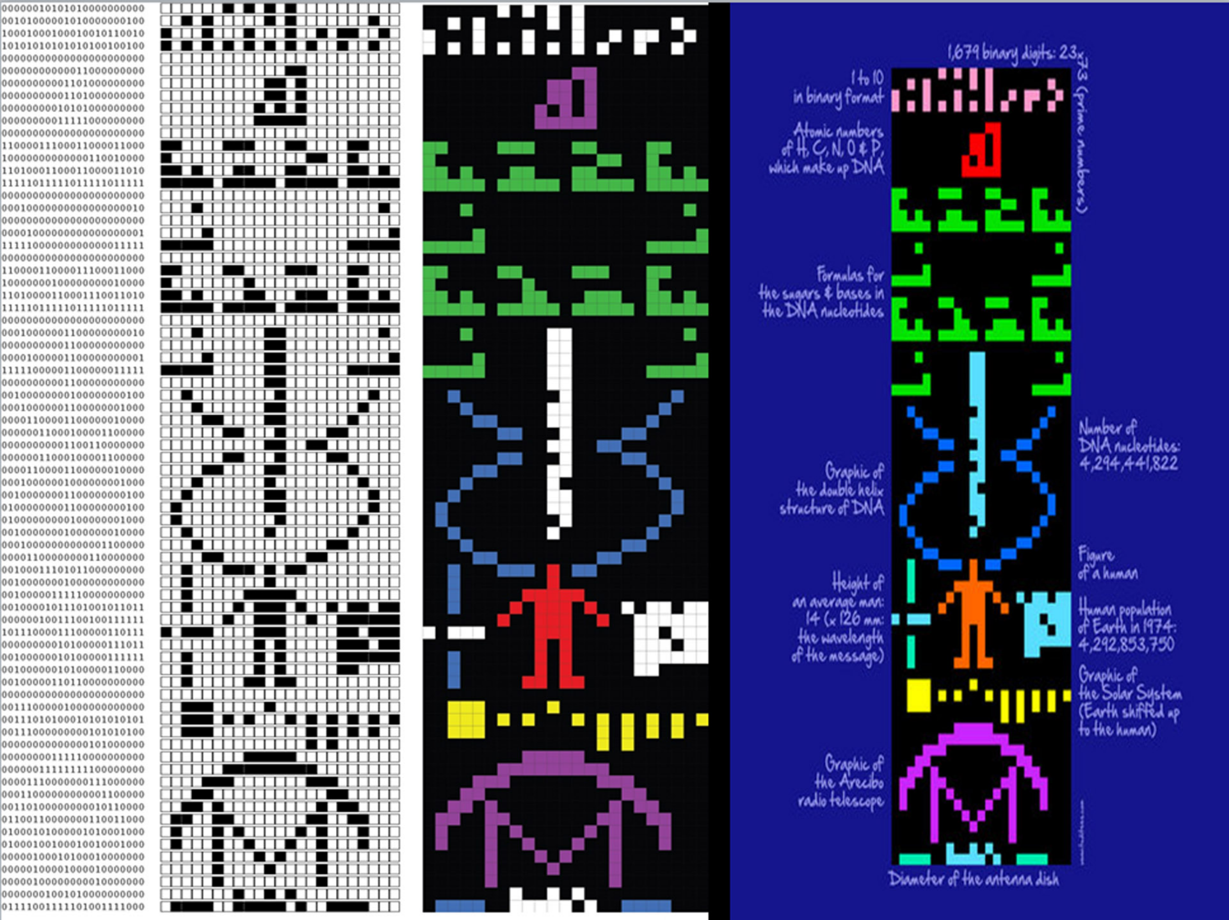

Habitable Zone
Mass of star relative to Sun
2
1
0,5
Mars
Earth
Venus
0
0,1
1
10
40
Radius of orbit relative to Earth's


Current Potentially Habitable Exoplanets
Ranked in Order of Similarity to Earth
01. Gliese 667C c
02. Kepler-62 e
NEW
03. Kepler-283 c
NEW
04. Kepler-296 f
05. Tau Ceti e*
NEW
06. Gliese 180 c*
07. Gliese 667C f
08. Gliese 581 g*
NEW
09. Gliese 180 b*
10. Gliese 163 c
11. HD 40307 g
12. Kepler-61 b
NEW
13. Gliese 422 b*
14. Kepler-22 b
NEW
15. Kepler-298 d
16. Kepler-62 f
NEW
17. Kepler-174 d
18. Gliese 667C e
NEW
19. Gliese 682 b*
20. Gliese 581 d
Earth
Mars
Jupiter
Neptune
*planet candidates
CREDIT: PHL @ UPR Arecibo (phl.upr.edu) March 4, 2014


SURFACE HABITATS
DEEP HABITATS
Shallow water
Trapped oceans
Top oceans
The Earth
Mars
Ganymede
Callisto
Titan
Europa
Enceladus
Liquid Water
Stable Environ-ment
Essential elements
Chemical Energy


THE NUMBER OF CIVILIZATIONS IN OUR GALAXY WITH WHICH COMMUNICATION IS POSSIBLE
N =
THE AVERAGE RATE OF STAR FORMATION PER YEAR IN OUR GALAXY
R*
THE FRACTION OF THOSE STARS WITH PLANETS
fp
THE AVERAGE NUMBER OF THOSE PLANETS THAT MAY DEVELOP AN ECOSYSTEM
Ne
THE FRACTION OF THOSE PLANETS THAT SUCCEED IN DEVELOPING LIFE
fl
THE FRACTION OF THOSE PLANETS WITH LIFE THAT DEVELOP INTELLIGENT LIFE
fi
THE FRACTION OF THOSE PLANETS WITH INTELLIGENT LIFE THAT DEVELOP INTERSTELLAR COMMUNICATION
fc
THE AVERAGE LENGTH OF TIME SUCH CIVILIZATIONS SURVIVE AND CONTINUE TO SEND COMMUNICATIONS
L
SETI INSTITUTE

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00000000001101000000000
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00000000011111000000000
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00010000000000000000010
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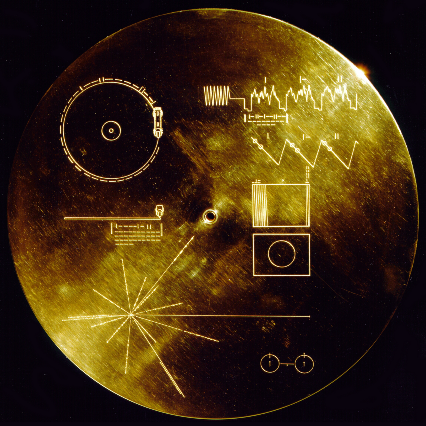
00000011111111100000000
00001110000000111000000
00011000000000001100000
00110100000000010110000
01100110000000110011000
01000101000001010001000
01000100100010010001000
00000100010100010000000
00000100001000010000000
00000100000000010000000
00000001001010000000000
01111001111101001111000
1,679 binary digits: 23 x 73 (prime numbers)
1 to 10 in binary format
Atomic numbers of H, C, N, O & P, which make up DNA
Formulas for the sugars & bases in the DNA nucleotides
Number of DNA nucleotides: 4,294,441,822
Graphic of the double helix structure of DNA
Figure of a human
Height of an average man: 14 (x 126 mm: the wavelength of the message)
Human population of Earth in 1974: 4,292,853,750
Graphic of the Solar System (Earth shifted up to the human)
Graphic of the Arecibo radio telescope
Diameter of the antenna dish


THE SOUNDS OF EARTH
Side 1
NASA
UNITED STATES OF AMERICA
PLANET EARTH

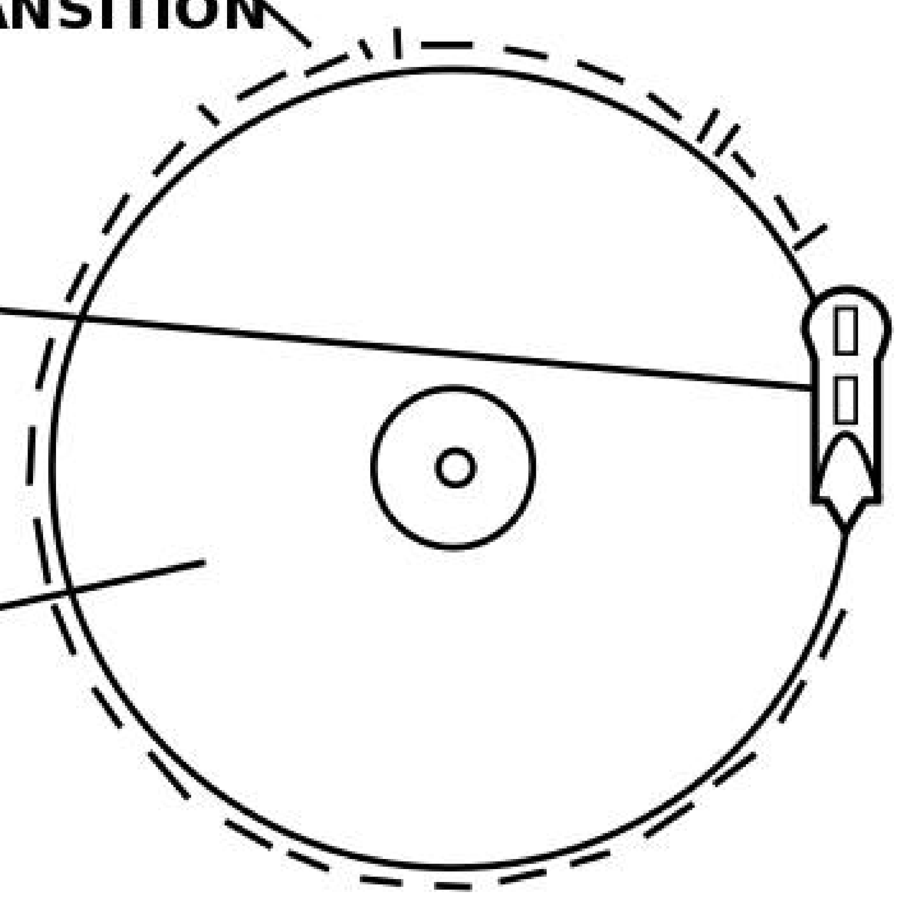


EXPLANATION OF RECORDING COVER DIAGRAM

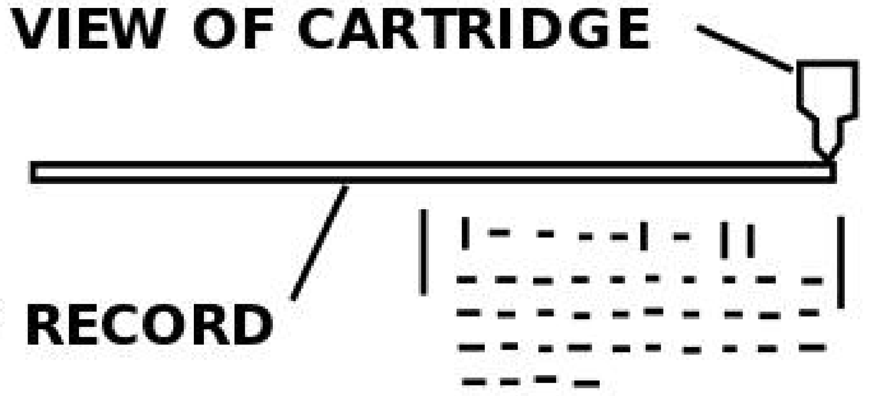
BINARY CODE DEFINING PROPER SPEED (3.6 seconds/ROTATION) TO TURN THE RECORD (|=BINARY 1, —= BINARY 0) EXPRESSED IN 0.70 × 10-9 seconds, THE TIME PERIOD ASSOCIATED WITH THE FUNDAMENTAL TRANSITION OF THE HYDROGEN ATOM

UTLINE OF CARTRIDGE WITH STYLUS TO PLAY RECORD (FURNISHED ON SPACECRAFT)

PICTORIAL PLAN VIEW OF RECORD



ELEVATION VIEW OF CARTRIDGE

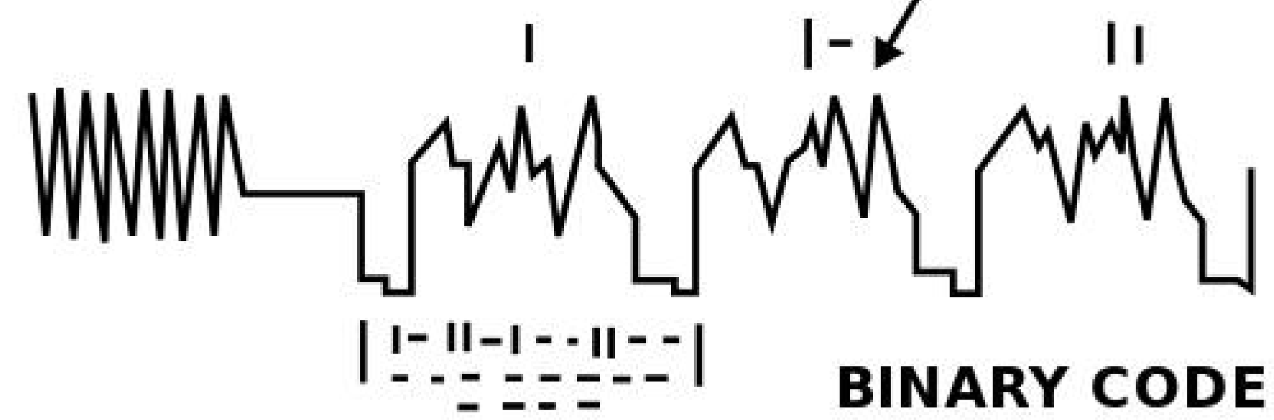


ELEVATION VIEW OF RECORD

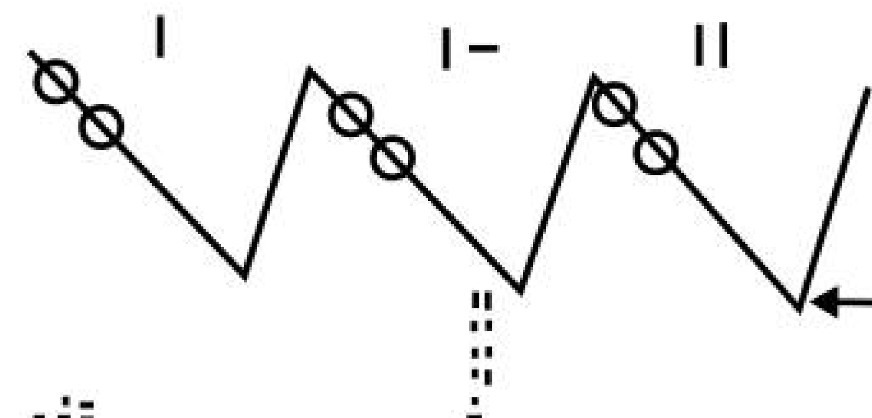
PLAYING TIME, ONE SIDE = ~1 hour

THE DIAGRAMS BELOW DEFINE THE VIDEO PORTION OF THE RECORDING

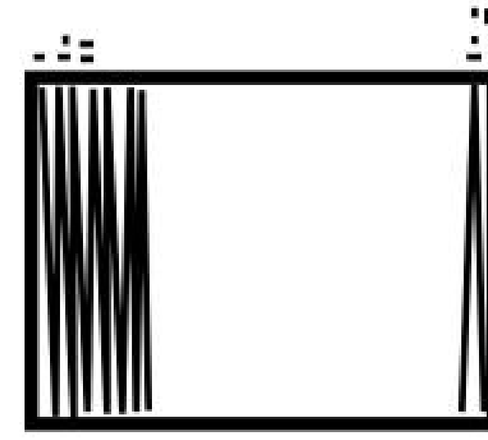
GENERAL APPEARANCE OF WAVE FORM OF VIDEO SIGNALS FOUND ON THE RECORDING



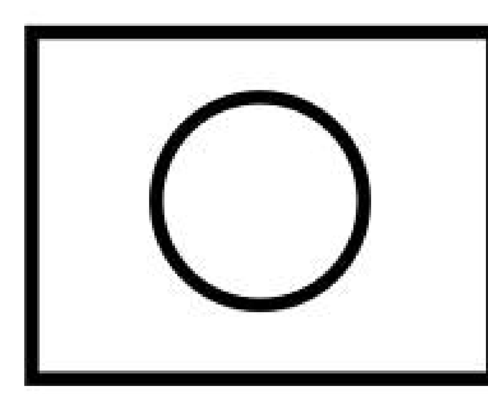
BINARY CODE TELLS TIME OF THE SCAN (~8 msec)



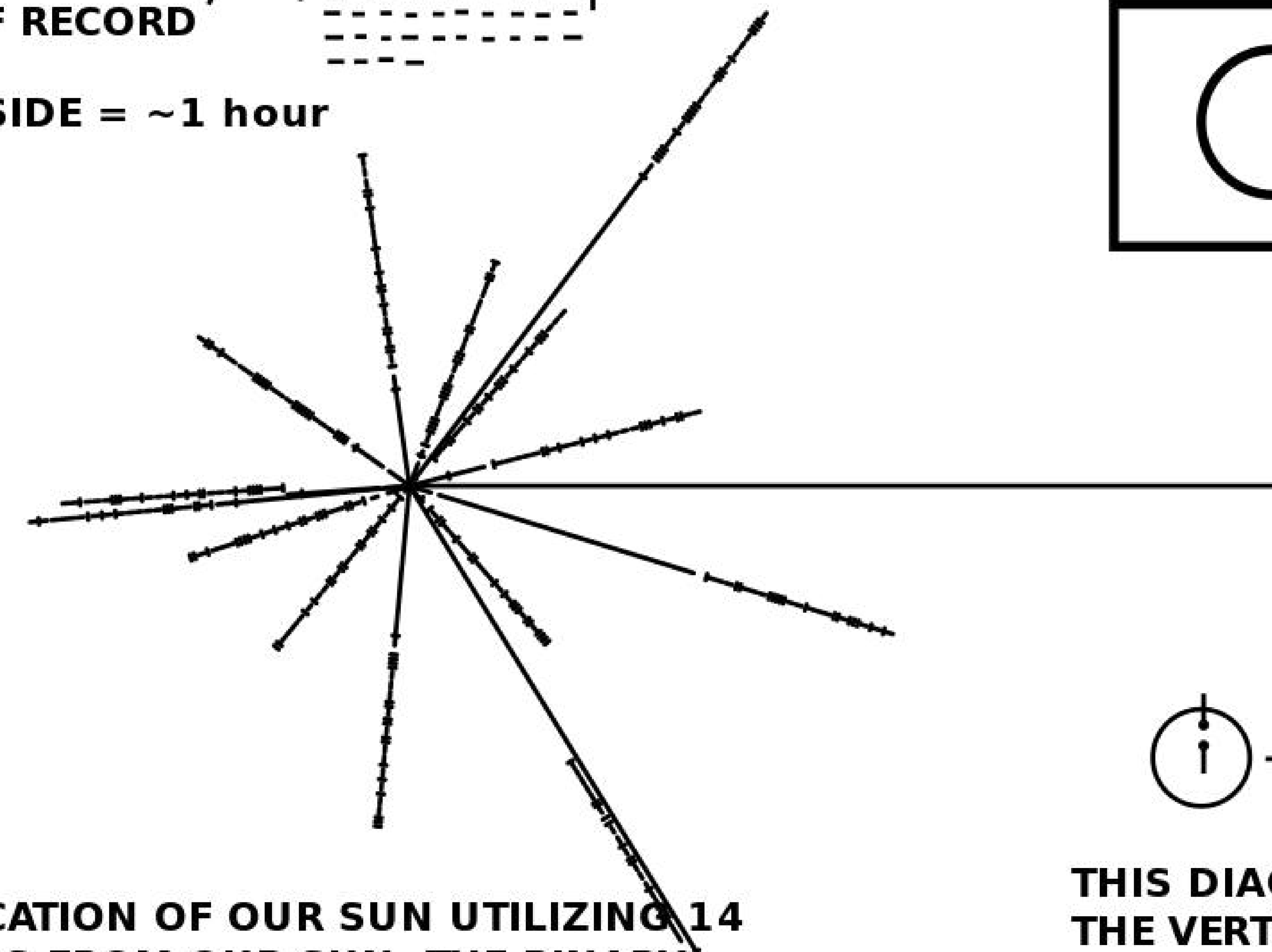
SCAN TRIGGERING



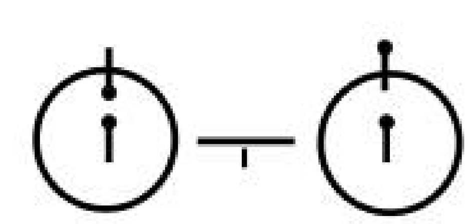
VIDEO IMAGE FRAME SHOWING DIRECTION OF SCAN. BINARY CODE INDICATES TIME OF EACH SCAN SWEEP (512 VERTICAL LINES PER COMPLETE PICTURE)



IF PROPERLY DECODED, THE FIRST IMAGE WHICH WILL APPEAR IS A CIRCLE



THIS DIAGRAM DEFINES THE LOCATION OF OUR SUN UTILIZING 14 PULSARS OF KNOWN DIRECTIONS FROM OUR SUN. THE BINARY CODE DEFINES THE FREQUENCY OF THE PULSES.



THIS DIAGRAM ILLUSTRATES THE TWO LOWEST STATES OF THE HYDROGEN A THE VERTICAL LINES WITH THE DOTS INDICATE THE SPIN MOMENTS OF THE PROTON AND ELECTRON. THE TRANSITION TIME FROM ONE STATE TO THE OTHER PROVIDES THE FUNDAMENTAL CLOCK REFERENCE USED IN ALL THE COVER DIAGRAMS AND DECODED PICTURES.

The Kardashev Scale of Civilizations

Type 1
Uses the energy
of an entire planet.

Type 2
…of an entire star.

Type 3
…of an entire galaxy.

Kardashev Scale	Barrow Scale	
KI – energy consumption at ~ 4×10^{19} erg s^{-1}	BI – manipulates objects of its own scale	~ 1 m
KII – energy consumption at ~ 4×10^{33} erg s^{-1}	BII – manipulates genes	~ 10^{-7} m
KIII – energy consumption at ~ 4×10^{44} erg s^{-1}	BIII – manipulates molecules	~ 10^{-9} m
	BIV – manipulates individual atoms	~ 10^{-11} m
	BV – manipulates atomic nuclei	~ 10^{-15} m
	BVI – manipulates elementary particles	~ 10^{-18} m
	BΩ – manipulates space-time's structure	~ 10^{-35} m

Table 1. Energetic and Inward civilization development

```
CHANNEL NUMBER (TWO DIGITS, WRITTEN VERTICALLY).   C RT. ASCEN.  DECLIN.    2ND LO    GLCTIC   GLCTIC   EASTERN    OBJECT
00000000011111111112222222222333333333344444444445 N  (1950.0)  (1950.0)   FREQ.      LAT      LONG    STD TIME
12345678901234567890123456789012345678901234567890 T  HH MM SS   DD MM    (MHZ.)    (DEG.)   (DEG.)   HH MM SS

   2     1       1        1    21  1 1        1       19 05 22  - 27 02   120.162   -15.39   10.13    22 04 10
   1  21    1     12 1 11 1    11 1  1 1              19 05 37  - 27 02   120.163   -15.44   10.16    22 04 25
   1  1     1  2 1 1 1 1    11 1111   1      1        19 05 49  - 27 02   120.163   -15.48   10.18    22 04 37
  2 1    1        1    1  11 11  1   1                19 06 01  - 27 02   120.164   -15.52   10.19    22 04 49
 12    1   1   1       1      1111   1                19 06 13  - 27 02   120.164   -15.56   10.21    22 05 01
    1  1     1 11 1  1 1   1   111211                 19 06 25  - 27 02   120.164   -15.60   10.23    22 05 13
   12 21    1  21    1 1 1     11 21      2    1      19 06 37  - 27 02   120.165   -15.64   10.25    22 05 25
   2  21    1  2 111   11       1 2 1        1        19 06 49  - 27 02   120.165   -15.68   10.27    22 05 37
      21             11   1    11221  1      1        19 07 01  - 27 02   120.166   -15.72   10.28    22 05 49
    1 2      1   1  1     11     11   1   1           19 07 13  - 27 02   120.166   -15.76   10.30    22 06 01
  11  2       1   2       11 11112     1     1   1    19 07 25  - 27 02   120.166   -15.81   10.32    22 06 13
 1  1 11       111 2  1 1  1    111    1       1      19 07 37  - 27 02   120.167   -15.85   10.34    22 06 25
  2    1    1      1      11  1111   1 1        11    19 07 49  - 27 02   120.167   -15.89   10.36    22 06 37
  12  1                                  1            19 08 01  - 27 02   120.167   -15.93   10.37    22 06 49
    1          1  11             11  1 1  1 11 1 1    19 08 13  - 27 02   120.168   -15.97   10.39    22 07 01
       1     2   113  1               1               19 08 25  - 27 02   120.168   -16.01   10.41    22 07 13
  1  111       111   1 2   1    11  1  1    11 1      19 08 37  - 27 02   120.169   -16.05   10.43    22 07 25
   1 11        1  2              1           1        19 08 49  - 27 02   120.169   -16.09   10.45    22 07 37
   11 21  1 1  1                  1     2  1     1    19 09 01  - 27 02   120.169   -16.13   10.46    22 07 49
12  1  1 41 2  211 1   1  1    1         1  1         19 09 13  - 27 02   120.170   -16.18   10.48    22 08 01
  221        1 11 11  11           1  11 1       1    19 09 25  - 27 02   120.170   -16.22   10.50    22 08 13
  312    1                1        11  1     1        19 09 37  - 27 02   120.170   -16.26   10.52    22 08 25
1  3     1  1    122   1  1   1   1   1     1         19 09 49  - 27 02   120.171   -16.30   10.54    22 08 37
1 31  41     1     2   1      1  1111                 19 10 01  - 27 02   120.171   -16.34   10.55    22 08 49
  12212        1   1    1     1 12                    19 10 13  - 27 02   120.172   -16.38   10.57    22 09 01
   21 23     1 1 1 1     1        21      1  1        19 10 25  - 27 02   120.172   -16.42   10.59    22 09 13
  6 3 1    111       1  11 1    2 1   1 1   2         19 10 37  - 27 02   120.172   -16.46   10.61    22 09 25
   11       1  1   1        11              1   1     19 10 49  - 27 02   120.173   -16.50   10.63    22 09 37
  211          2   2    1 1   1                       19 11 01  - 27 02   120.173   -16.55   10.64    22 09 49
  211 11    2  1 11       1   1111    11              19 11 13  - 27 02   120.173   -16.59   10.66    22 10 01
 12   11 1  2 11  2111 1  1    12 1             1     19 11 25  - 27 02   120.174   -16.63   10.68    22 10 12
 21         1  111        1  1 1      1     1  1      19 11 37  - 27 02   120.174   -16.67   10.70    22 10 24
   1        11 211    111 1   1  112 11  1      1     19 11 49  - 27 02   120.175   -16.71   10.71    22 10 36
   1  1     1  2       11     211 21  1               19 12 01  - 27 02   120.175   -16.75   10.73    22 10 48
   21  1    1  1   2      1   111  11 1               19 12 13  - 27 02   120.175   -16.79   10.75    22 11 00
  1         1  11111            1    1  1             19 12 25  - 27 02   120.176   -16.83   10.77    22 11 12
  212             1              1  2                 19 12 37  - 27 02   120.176   -16.87   10.79    22 11 24
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  1111  111    1   1  1     1      112      11        19 13 24  - 27 02   120.177   -17.04   10.86    22 12 11
               1     1 1 1      22  211 22 111        19 13 36  - 27 02   120.178   -17.08   10.87    22 12 23
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  11  2        1   2            1   11       1        19 14 12  - 27 02   120.179   -17.20   10.93    22 12 59
   11 3        1 15             11  21     1  1       19 14 24  - 27 02   120.179   -17.24   10.94    22 13 11
1 111 11    1                11 11         1          19 14 36  - 27 03   120.180   -17.28   10.96    22 13 23
      1                    2      1   1     11 2      19 14 48  - 27 03   120.180   -17.32   10.98    22 13 35
1  2           1  21 2            1111      1 1  1    19 15 00  - 27 03   120.180   -17.37   11.00    22 13 47
1 12     1        1   11  1   1   1 21   1     1      19 15 12  - 27 03   120.181   -17.41   11.02    22 13 59
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   21 1         121  1 1      1   1   1  22 21  1     19 15 48  - 27 03   120.182   -17.53   11.07    22 14 35
1     2        1  4  32 1    1   2    2 1 1      1    19 16 00  - 27 03   120.182   -17.57   11.09    22 14 47
1 16  1      1     1    11 13  1 11   111   1 1 11    19 16 12  - 27 03   120.183   -17.61   11.10    22 14 59
1 11  1    1      11 1        1  1        1     1     19 16 24  - 27 03   120.183   -17.65   11.12    22 15 11
  1            3   1             1 1       1 2   1    19 16 36  - 27 03   120.183   -17.69   11.14    22 15 23
 6 2           31      1  2 11 1         3111221 1    19 16 48  - 27 03   120.184   -17.74   11.16    22 15 35
1E24  3  12  1 21 1         1 3  1 1     3 1 11 1     19 17 00  - 27 03   120.184   -17.78   11.17    22 15 47
 Q 1 16 1 2  1  1    1               11 11  1 1       19 17 12  - 27 03   120.184   -17.82   11.19    22 15 59
 U31  1      3 7  1              1    2  11   1       19 17 24  - 27 03   120.185   -17.86   11.21    22 16 10
2J1   31 3 111  11 1 12       2 12  2 1 2111 11211    19 17 36  - 27 03   120.185   -17.90   11.23    22 16 22
 51            1  1           1 1   1   121   1 1     19 17 48  - 27 03   120.185   -17.94   11.24    22 16 34
  14   1   113   2  111        11   1   1111111       19 18 00  - 27 03   120.186   -17.98   11.26    22 16 46
 1 3  1   1    1       11 1        1  1 12 112  1     19 18 12  - 27 03   120.186   -18.03   11.28    22 16 58
 1 4      1  1 1  11  2       11  1   1 111 11        19 18 23  - 27 03   120.186   -18.06   11.30    22 17 09
   4  1 1  1 11   111         12 1    1  1211 1       19 18 35  - 27 03   120.187   -18.10   11.31    22 17 21
   1        1    2 1               11    1   2 11     19 18 47  - 27 03   120.187   -18.15   11.33    22 17 33
 1 1  1        11  1      1    1 1      3 2           19 18 59  - 27 03   120.187   -18.19   11.35    22 17 45
   1      1       14    11        1 1     3 1 21 1    19 19 11  - 27 03   120.188   -18.23   11.37    22 17 57
1  1  1        2    1   1 1       11   11112  1 1     19 19 23  - 27 03   120.188   -18.27   11.38    22 18 09
   11 2    1 1 3   1    1    1   1 11   2 11    1     19 19 35  - 27 03   120.188   -18.31   11.40    22 18 21
1  1           1 1   1    11  1  1111 2     11        19 19 47  - 27 03   120.189   -18.35   11.42    22 18 33
2     3      1 3 11              1111   11   11       19 19 59  - 27 03   120.189   -18.39   11.44    22 18 45
2  3  4 1  1   1        1 1   1     1   1 2 111 1     19 20 11  - 27 03   120.190   -18.44   11.45    22 18 57
      1           11            1  112    1   11      19 20 23  - 27 03   120.190   -18.48   11.47    22 19 09
     12 1 1       111     1 21 2   111     1   211    19 20 35  - 27 03   120.190   -18.52   11.49    22 19 21
 2    51   1 1  1     2      1    1 11  1 2 1    1    19 20 47  - 27 03   120.191   -18.56   11.51    22 19 33
 1 2  1        1   1   1    1  1  112     1 1         19 20 59  - 27 03   120.191   -18.60   11.52    22 19 45
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```
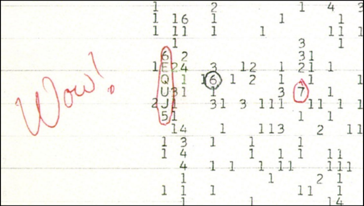

Aug 15, 1977

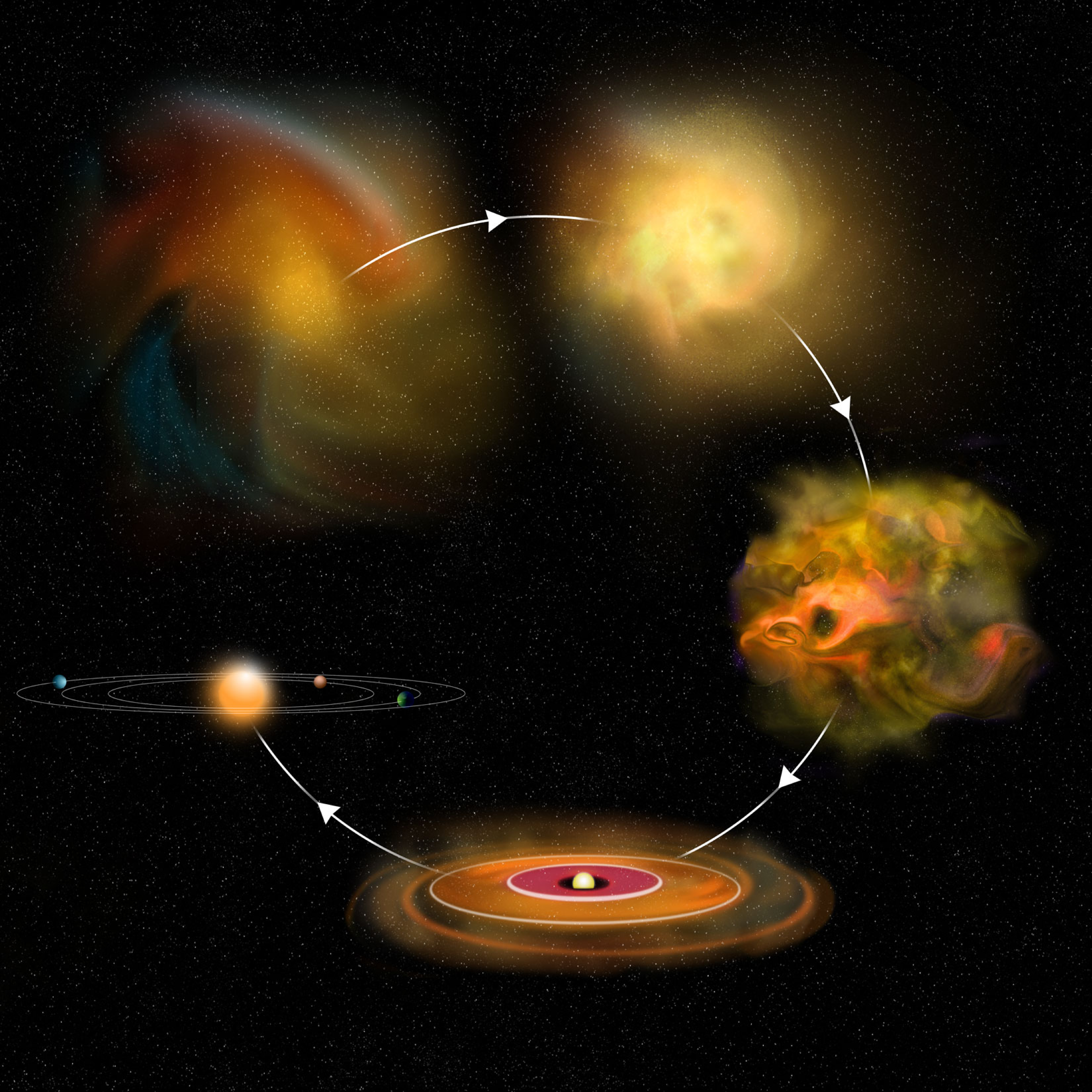
Wow!

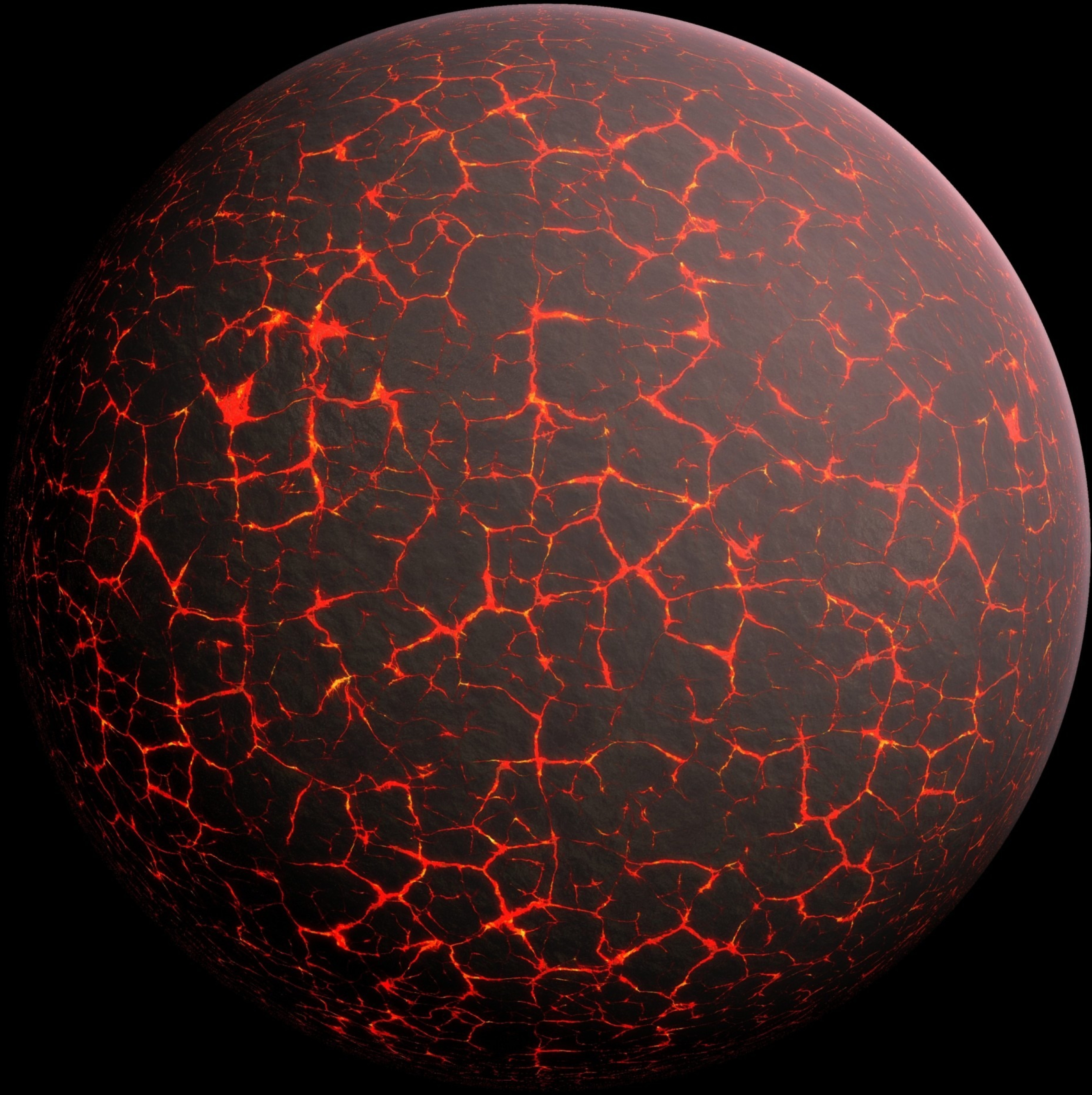


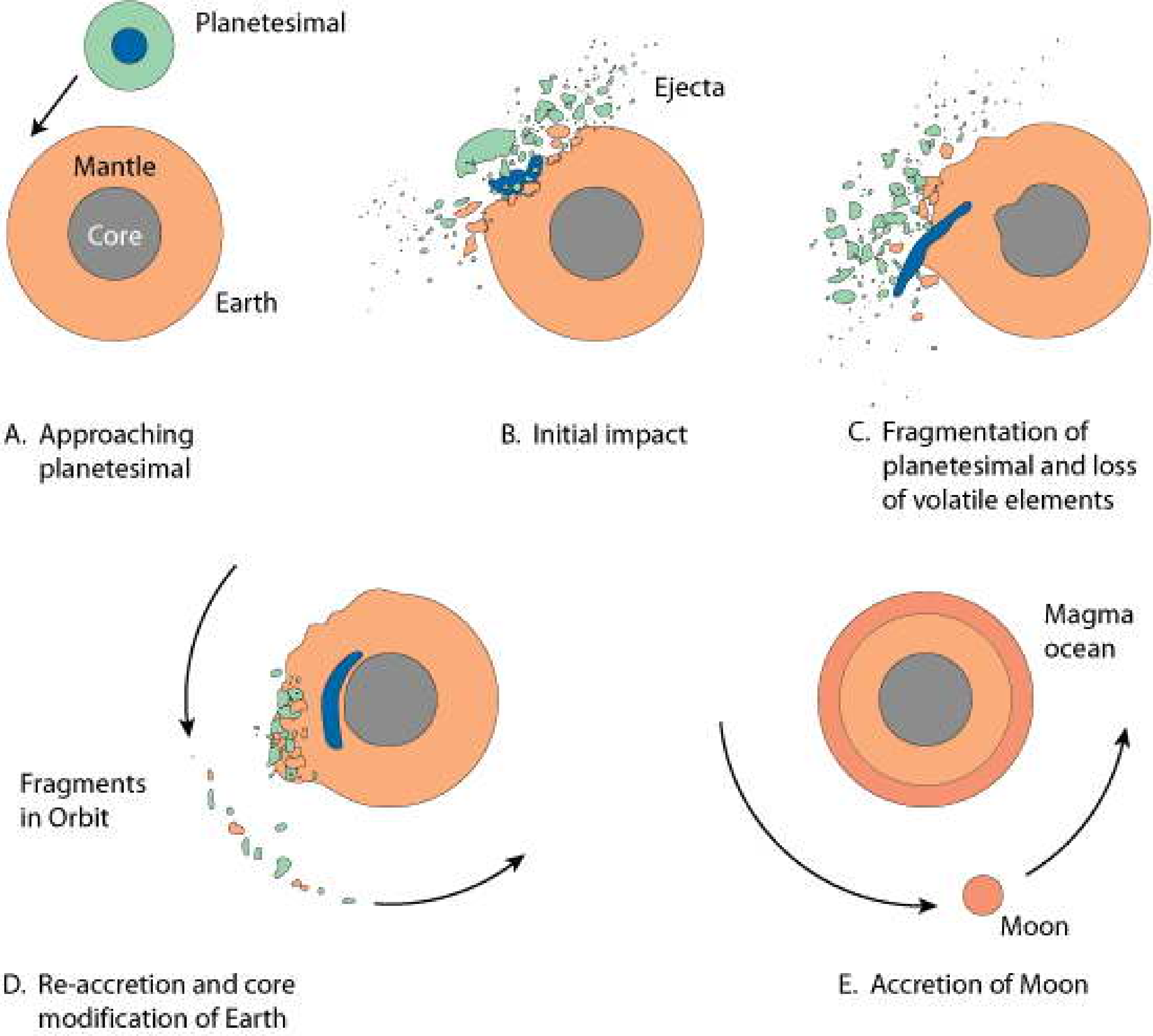
Jerry R. Ehman on August 15, 1977 with Big Ear telescope @ Ohio State University

30X from constellation Sagittarius near the Chi Sagittarii star group
72 sec @ 1420.4556 MHz

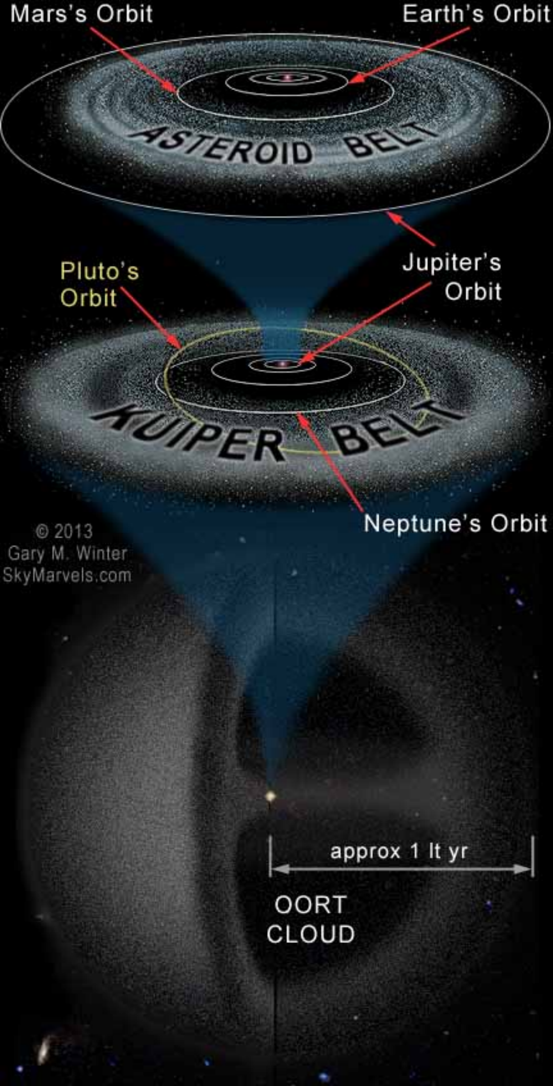
15.8.2012. +10 000 & videos from celebrities



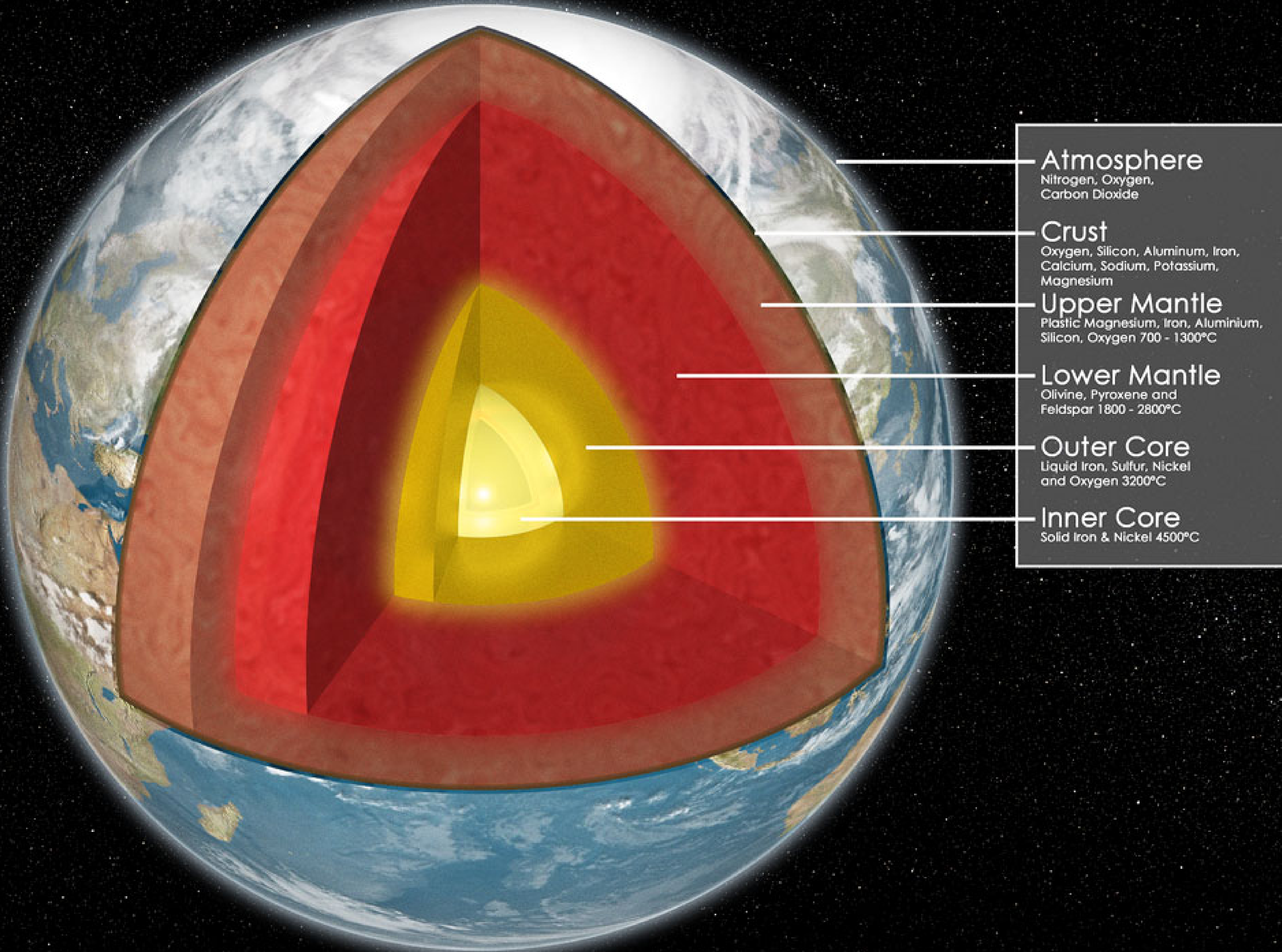


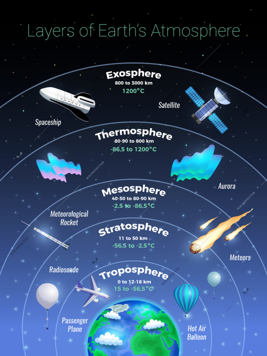


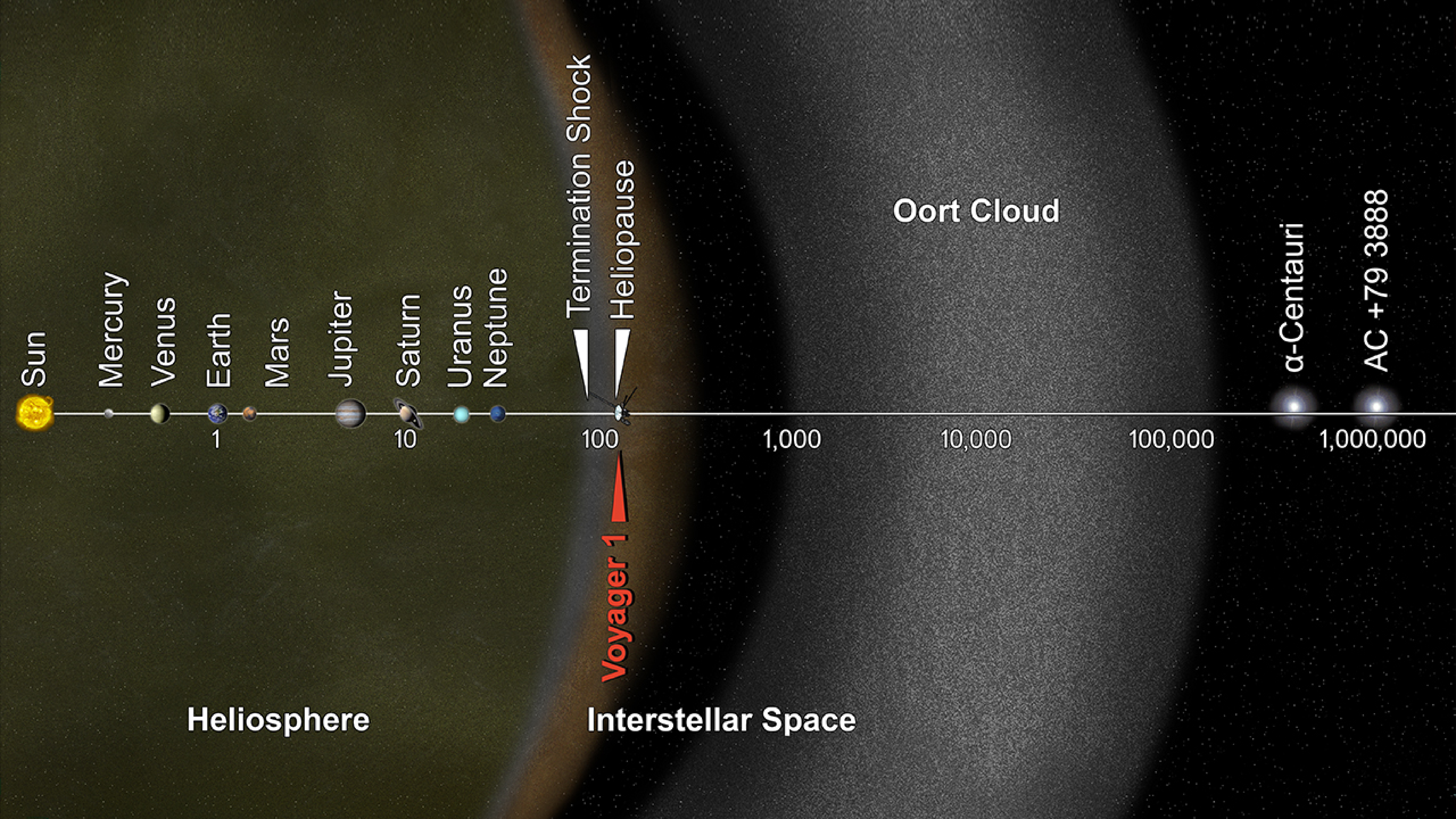
Planetesimal
Mantle
Core
Earth
A. Approaching planetesimal
Ejecta
B. Initial impact
C. Fragmentation of planetesimal and loss of volatile elements
Fragments in Orbit
D. Re-accretion and core modification of Earth
Magma ocean
Moon
E. Accretion of Moon


Mars's Orbit
Earth's Orbit
ASTEROID BELT
Jupiter's Orbit
Pluto's Orbit
KUIPER BELT
Neptune's Orbit
© 2013 Gary M. Winter SkyMarvels.com
approx 1 lt yr
OORT CLOUD

Earth: Cross Section




Layers of Earth's Atmosphere
Exosphere
800 to 3000 km
1200°C
Spaceship
Satellite
Thermosphere
80-90 to 800 km
-86,5 to 1200°C
Aurora
Mesosphere
40-50 to 80-90 km
-2,5 to -86,5°C
Meteorological Rocket
Stratosphere
11 to 50 km
-56,5 to -2,5°C
Meteors
Radiosonde
Troposphere
0 to 12-18 km
15 to -56,5°C
Passenger Plane
Hot Air Balloon


Sun
Mercury
Venus
Earth
Mars
Jupiter
Saturn
Uranus
Neptune
Termination Shock
Heliopause
Oort Cloud
α-Centauri
AC +79 3888
1
10
100
1,000
10,000
100,000
1,000,000
Voyager 1
Heliosphere
Interstellar Space

By ERWIN SCHRÖDINGER

WHAT IS LIFE ?

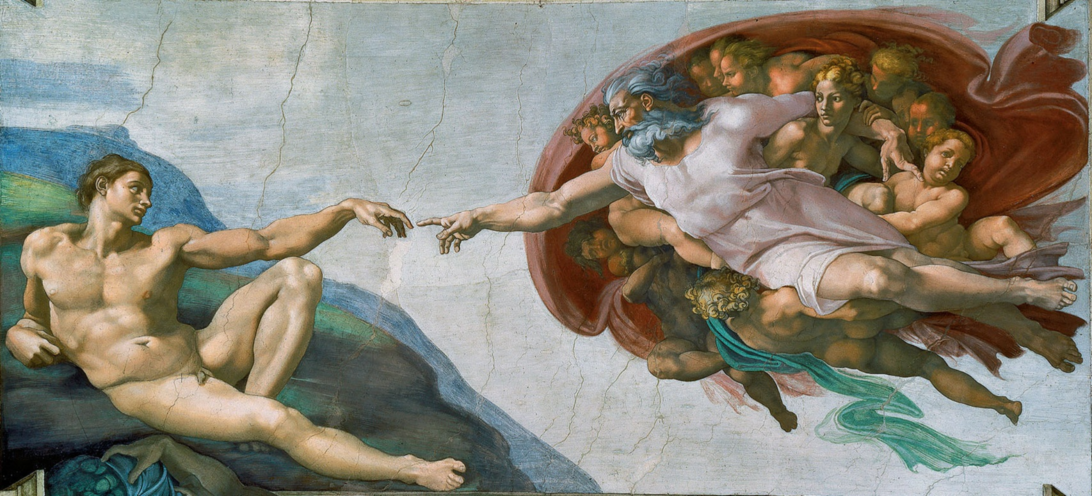
The Physicist's approach to the Subject—With an Epilogue on Determinism and Free Will

CAMBRIDGE UNIVERSITY PRESS

SCHRÖDINGER: What is Life?

CITROËN

Complex **I**nformation-producing **T**ransforming **O**bjects, that **E**volve by **N**atural **S**election



KREACIONIZAM

- Flat Earthers (International Flat Earth Society, Box 2533, Lancaster, CA.)
  - Geocentristi
    - Kreacionisti mlade Zemlje
      - Kreacionisti stare Zemlje
        - (Krecionizam ponovne uspostave)
        - (Dan-Vrijeme Kreacionizam)
        - (Progresivni Kreacionizam)
        - (ID)
      - Evolucioni Kreacionisti
    - Teistički Evolucionisti
  - Metodološki Materijalistički Evolucionisti
- Filozofski Materialistički Evolucionisti

EVOLUCIJA

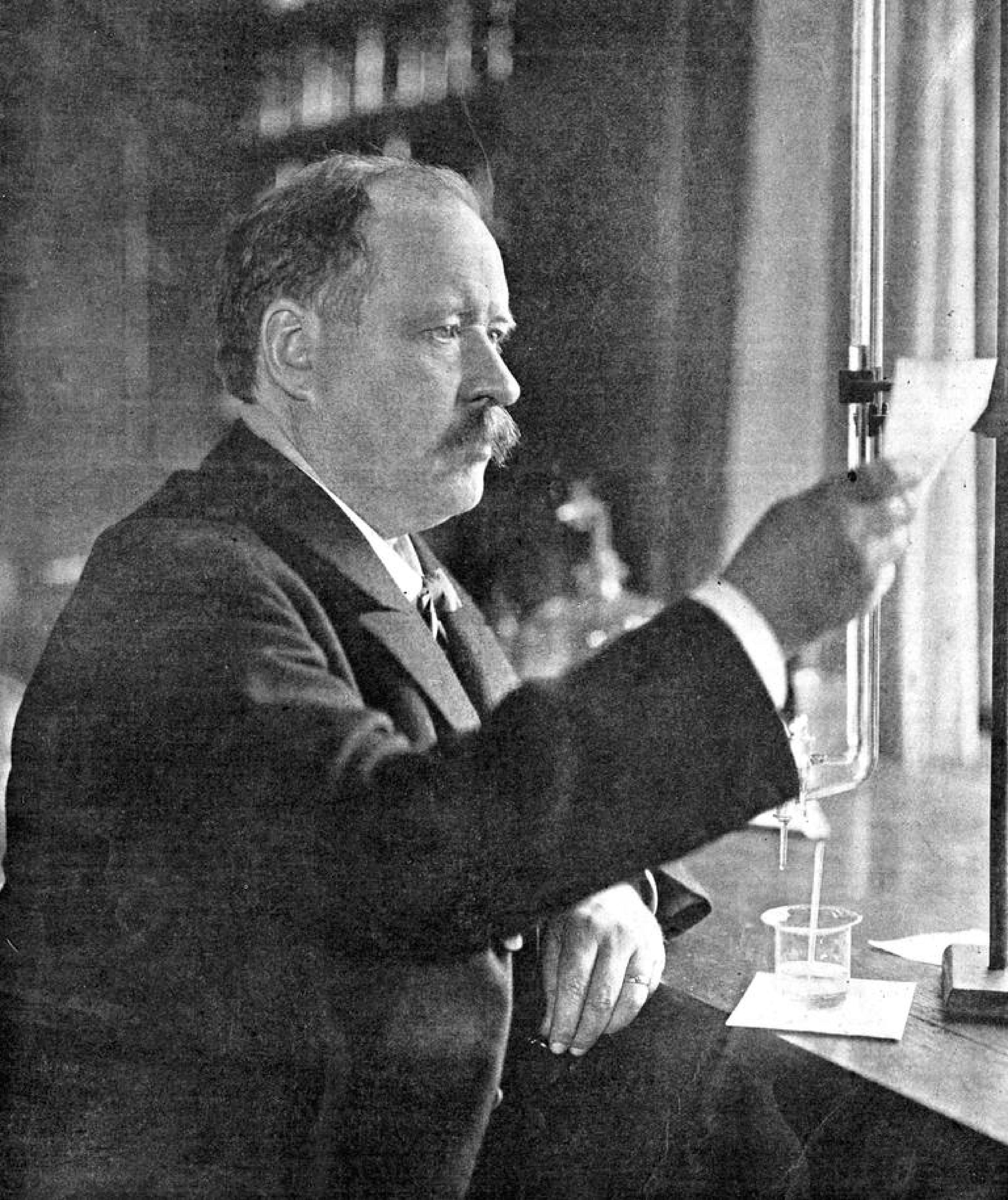
Raelianci

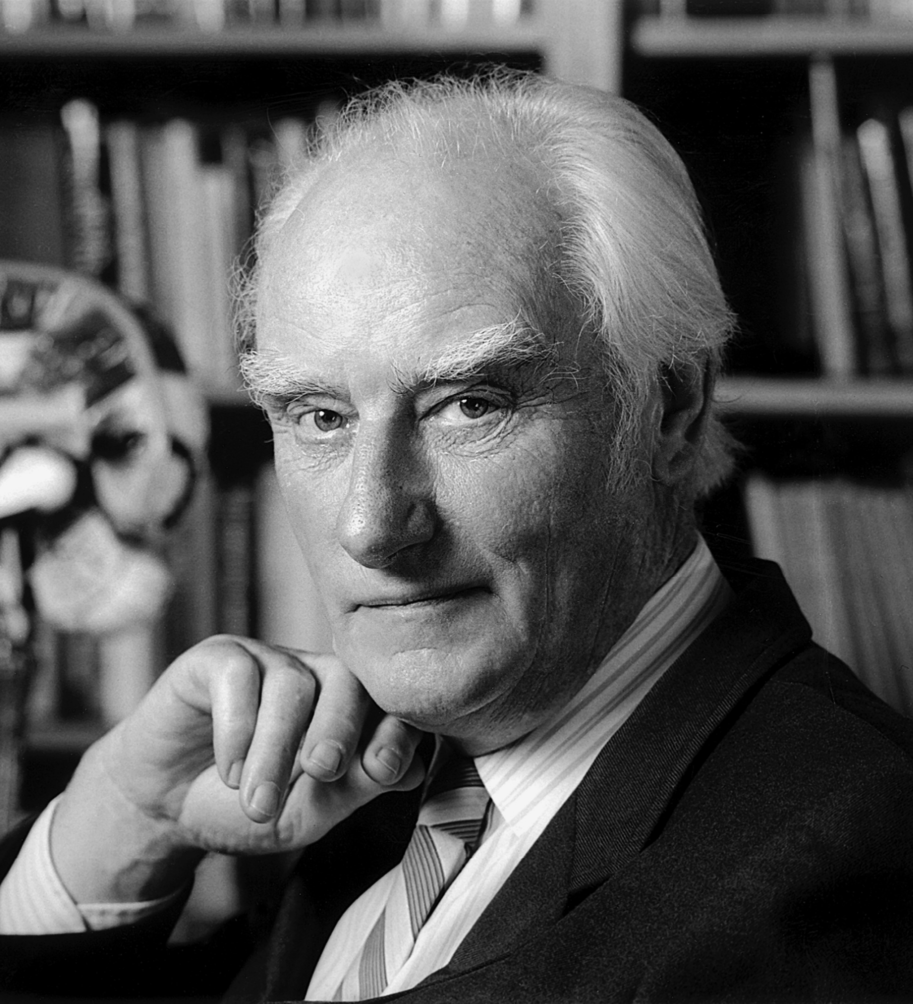
Panspermia

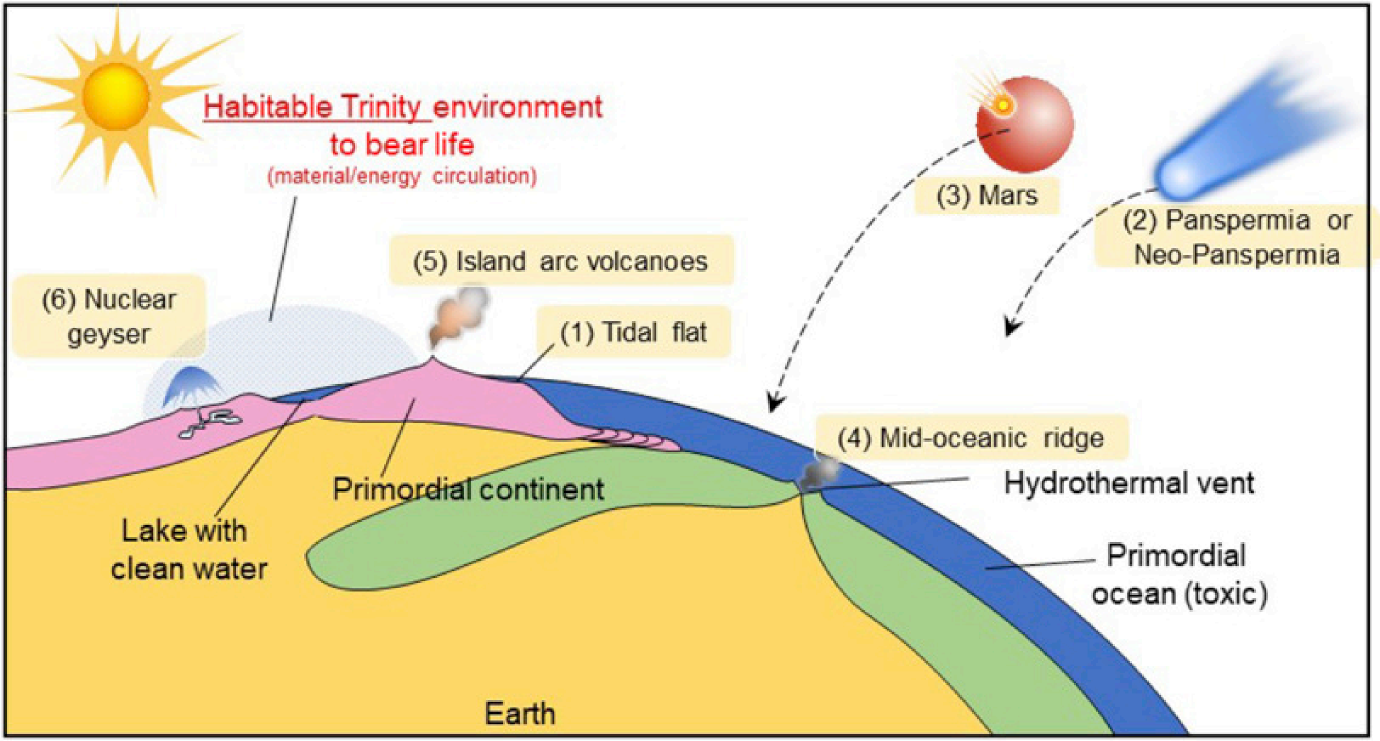
Evolucija putem katastrofa

Islamski kreacionizam

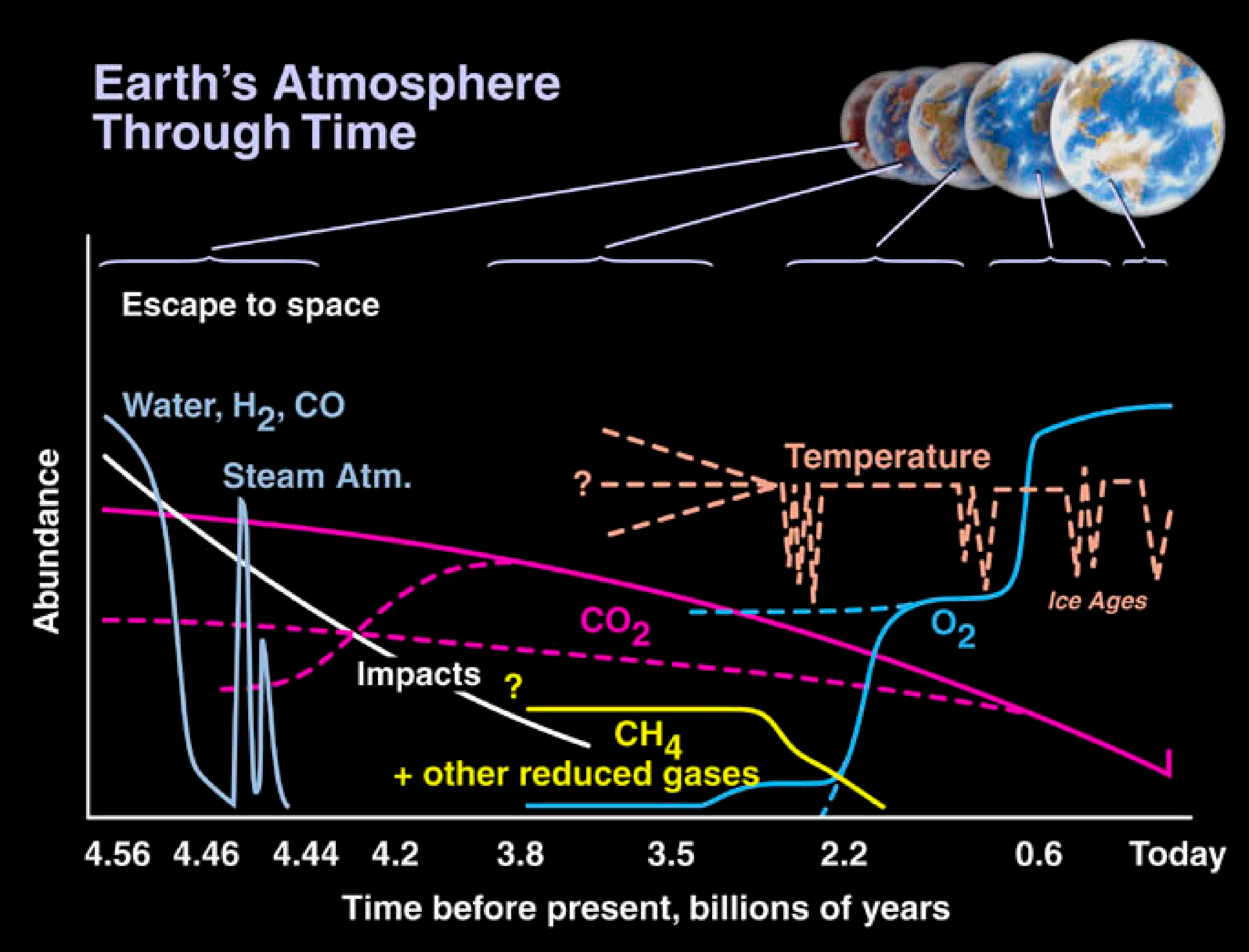
Vedski kreacionizam

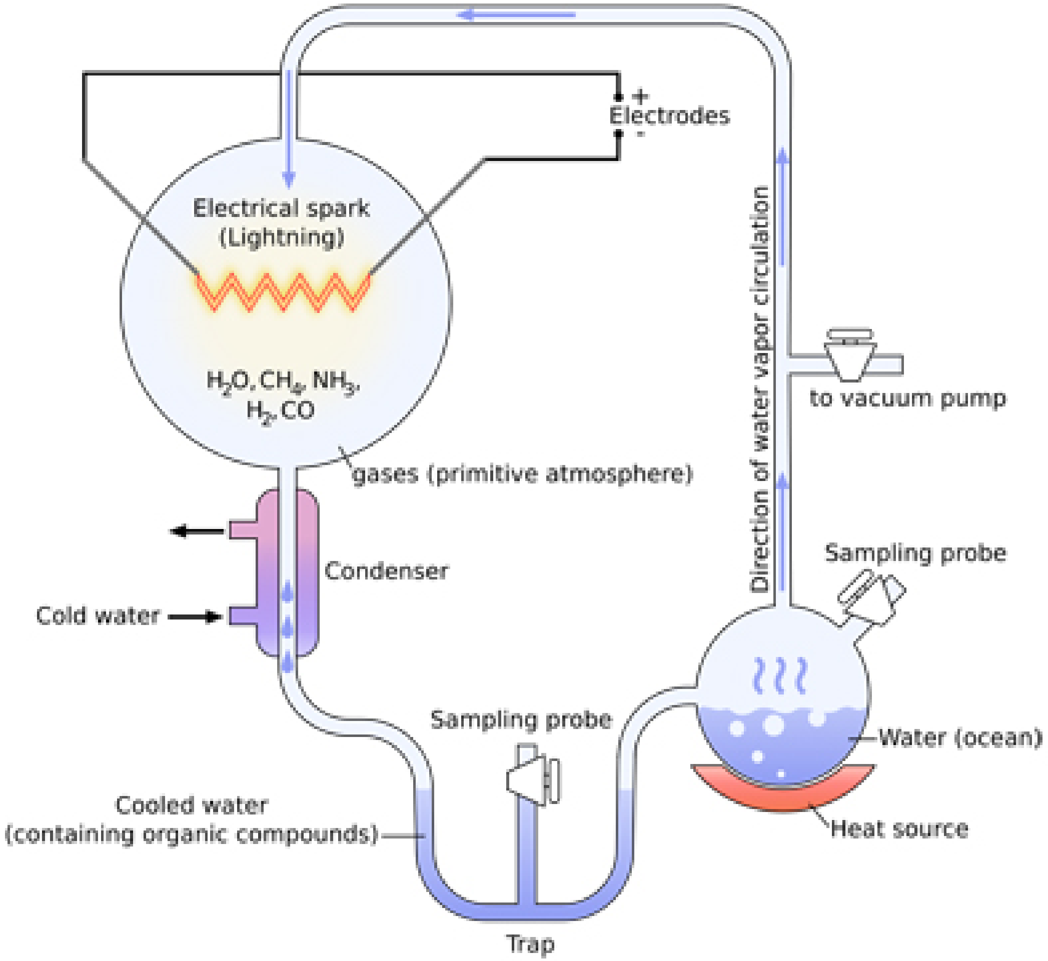






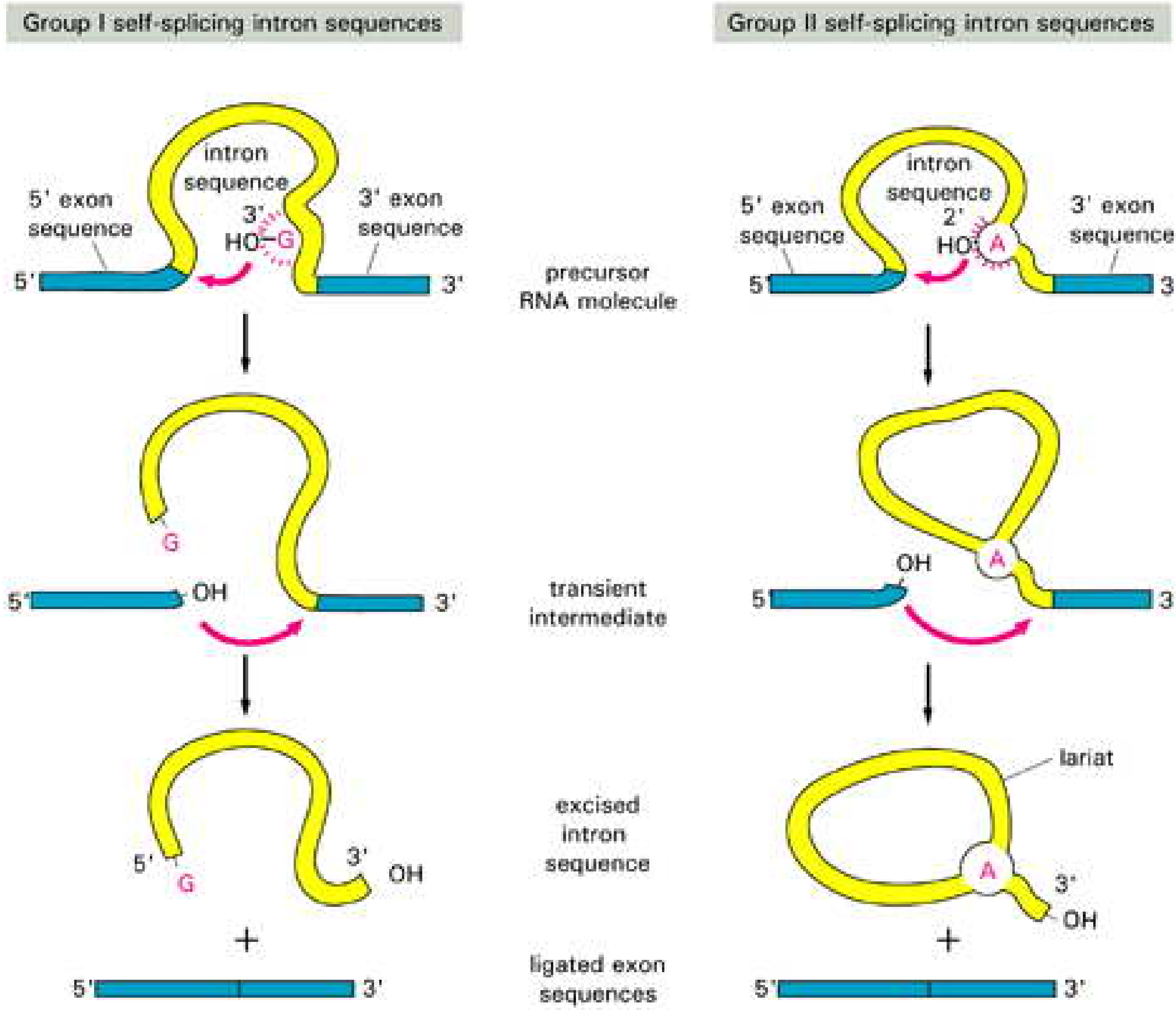
Habitable Trinity environment
to bear life
(material/energy circulation)
(3) Mars
(2) Panspermia or
Neo-Panspermia
(5) Island arc volcanoes
(6) Nuclear
geyser
(1) Tidal flat
(4) Mid-oceanic ridge
Hydrothermal vent
Primordial continent
Lake with
clean water
Primordial
ocean (toxic)
Earth


Earth's Atmosphere
Through Time
Escape to space
Water, H_2, CO
Steam Atm.
Temperature
?
Ice Ages
CO_2
O_2
Impacts
?
CH_4
+ other reduced gases
Abundance
4.56
4.46
4.44
4.2
3.8
3.5
2.2
0.6
Today
Time before present, billions of years



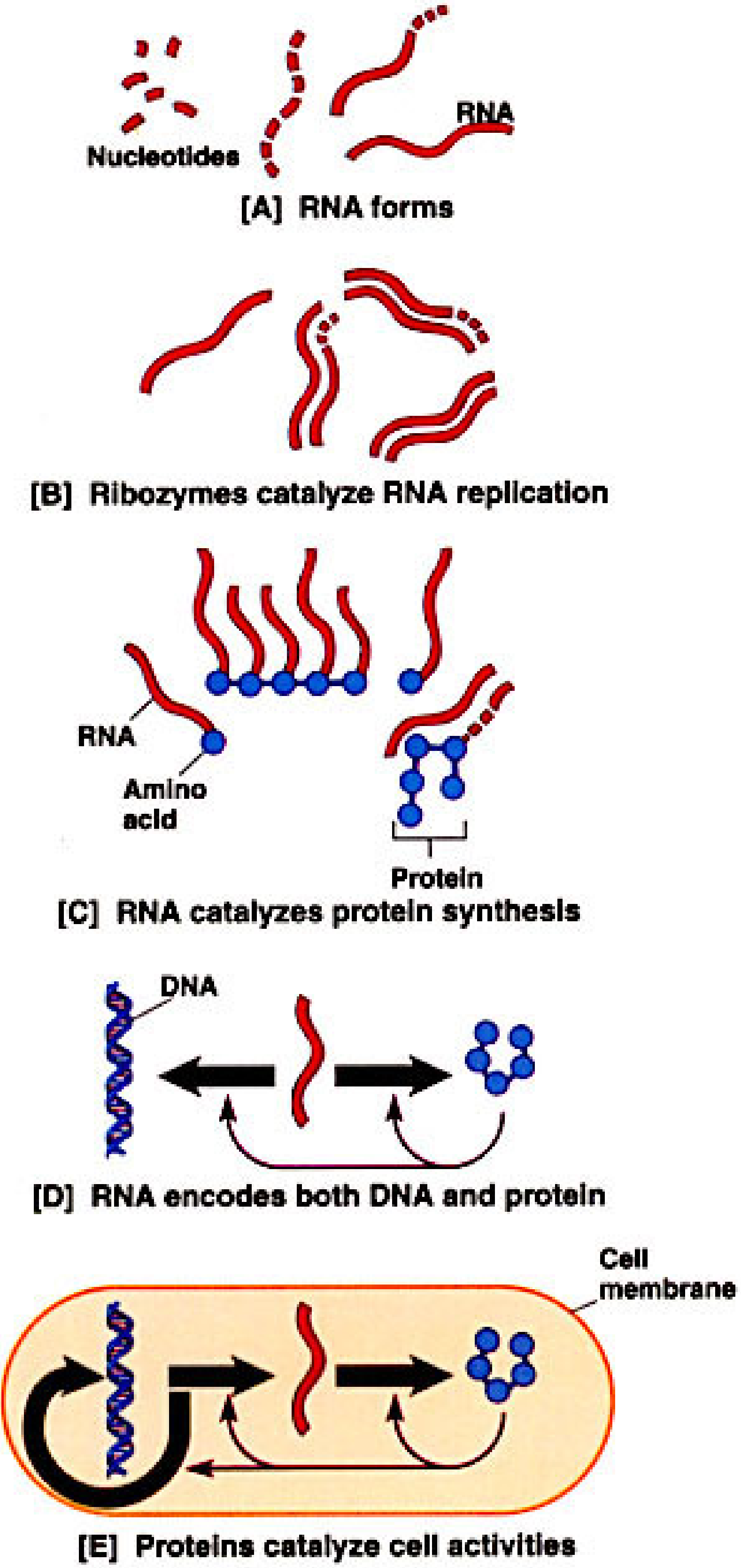
Electrodes
+
-
Electrical spark
(Lightning)
H_2O, CH_4, NH_3,
H_2, CO
gases (primitive atmosphere)
Direction of water vapor circulation
to vacuum pump
Condenser
Cold water
Sampling probe
Sampling probe
Water (ocean)
Heat source
Cooled water
(containing organic compounds)
Trap

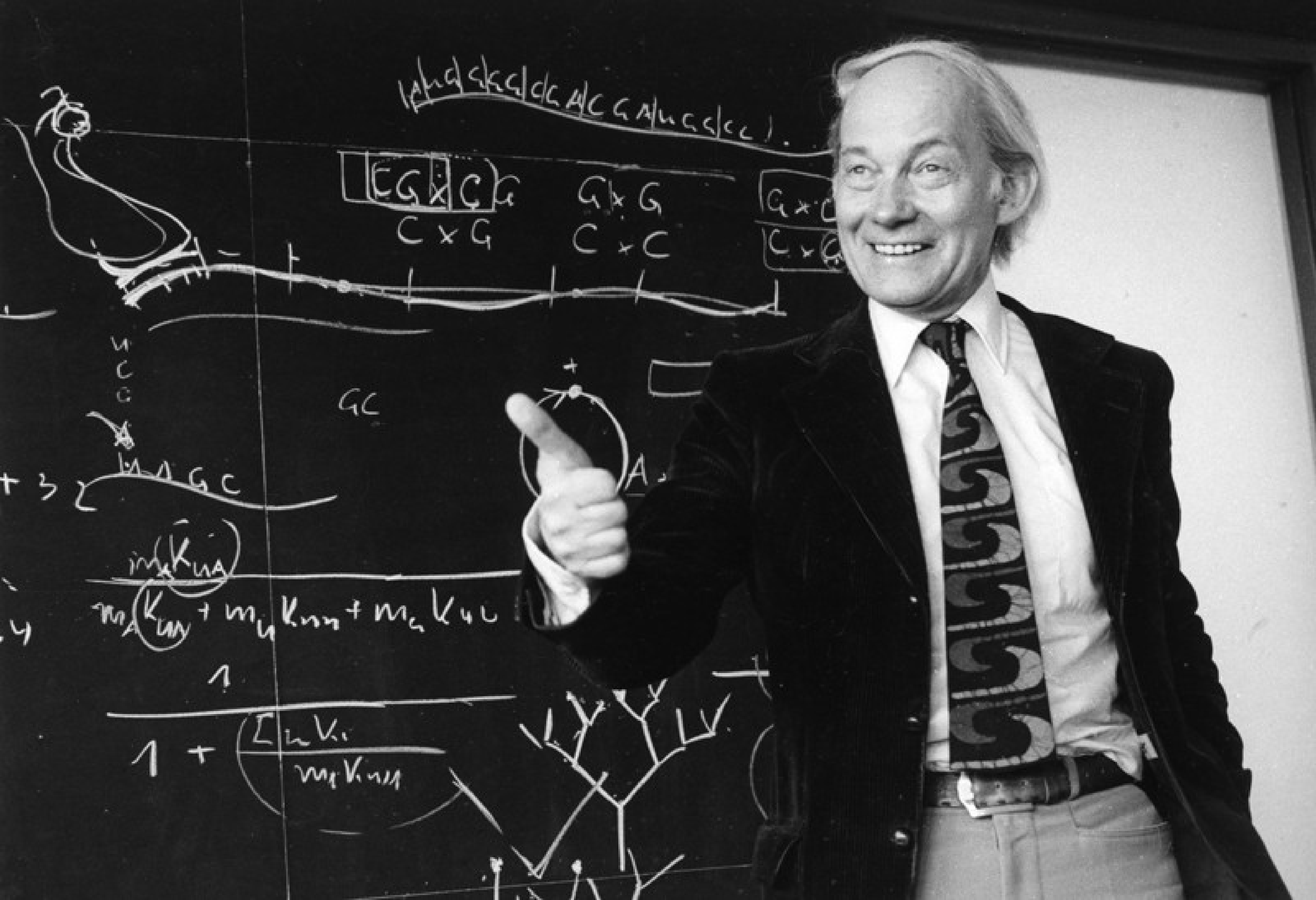

Ribozyme
RNA message
Ribozyme-mediated cut
introduced into RNA message
Cut (cleaved) RNA messages

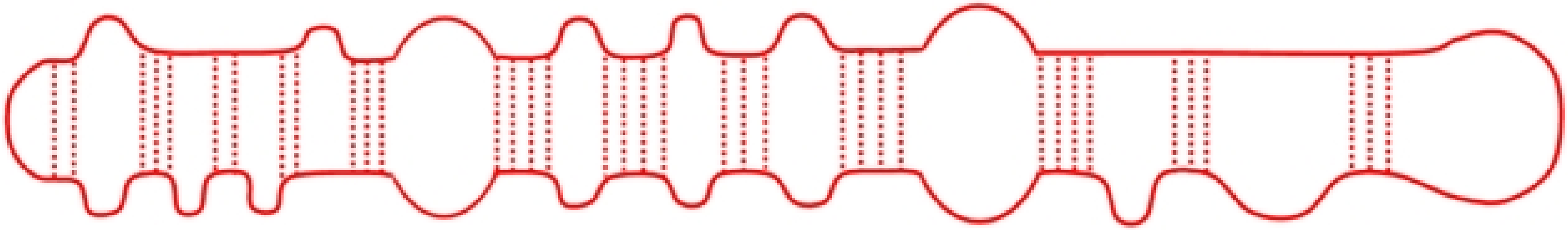


Group I self-splicing intron sequences
Group II self-splicing intron sequences
intron sequence
5' exon sequence
3' exon sequence
3'
HO
G
5'
3'
precursor RNA molecule
intron sequence
5' exon sequence
3' exon sequence
2'
HO
A
5'
3'
G
OH
5'
3'
transient intermediate
A
OH
5
3'
5'
G
3'
OH
excised intron sequence
lariat
A
3'
OH
+
ligated exon sequences
5'
3'
+
5'
3'

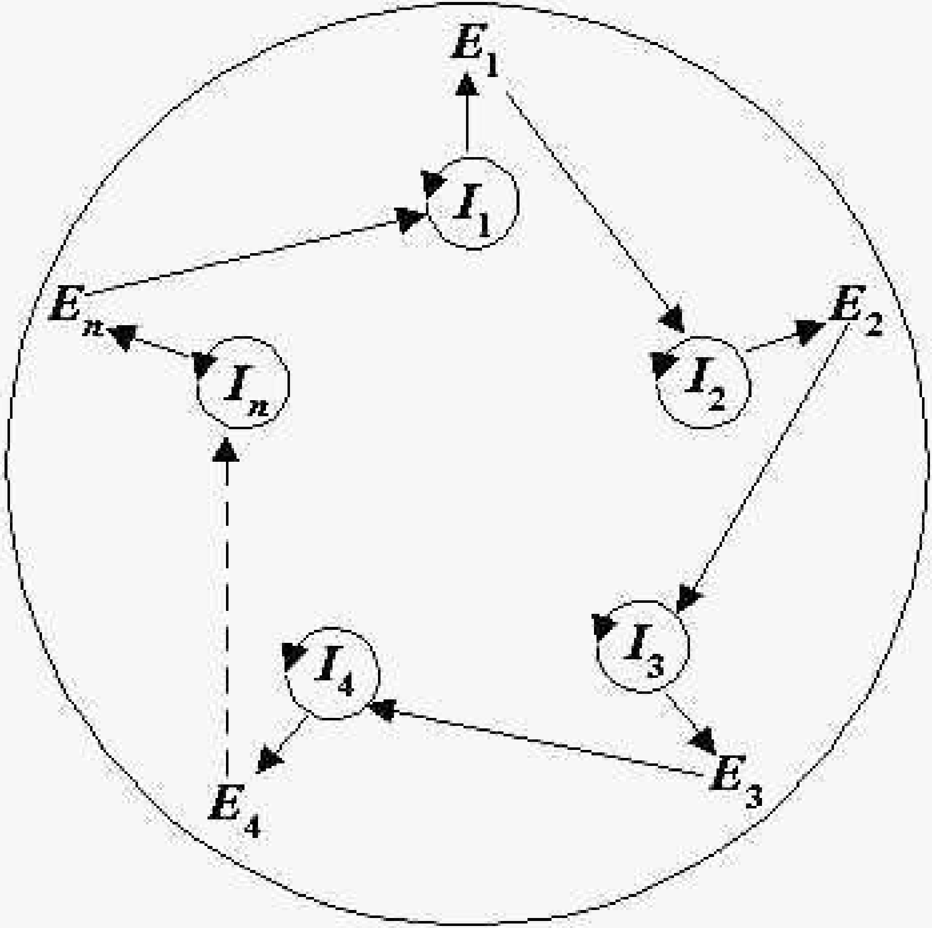
154 Proposed RNA world origins

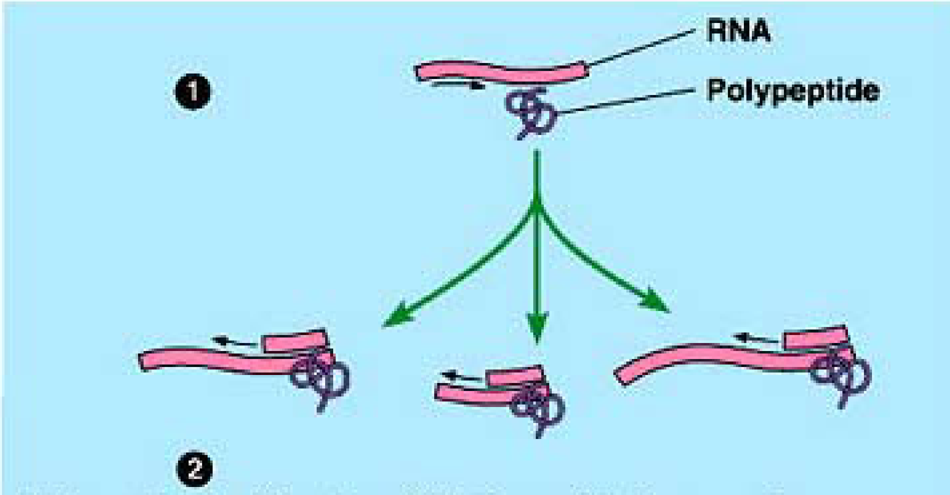



G x G
C x G
C x C
GC

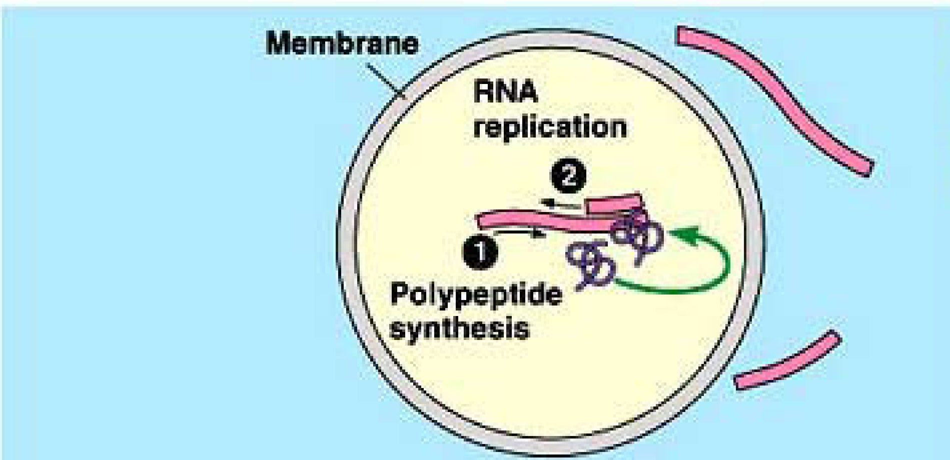


Structure of a viroid – circular single-stranded RNA with some pairing between complementary bases and loops where no such pairing occurs


E_1
I_1
E_2
I_2
E_3
I_3
E_4
I_4
E_n
I_n



(a) A molecular "free-for-all" in the prebiotic soup of organic molecules.

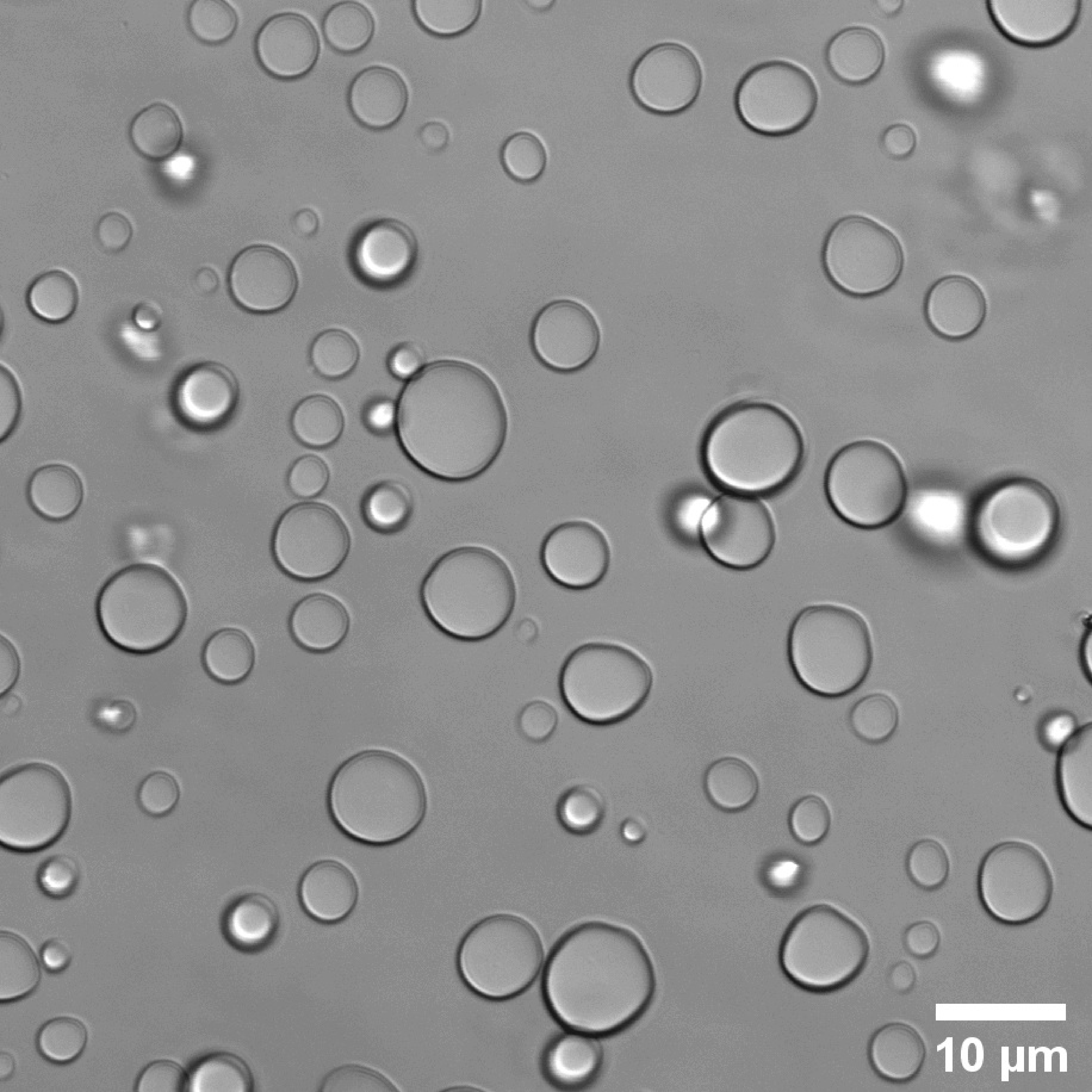


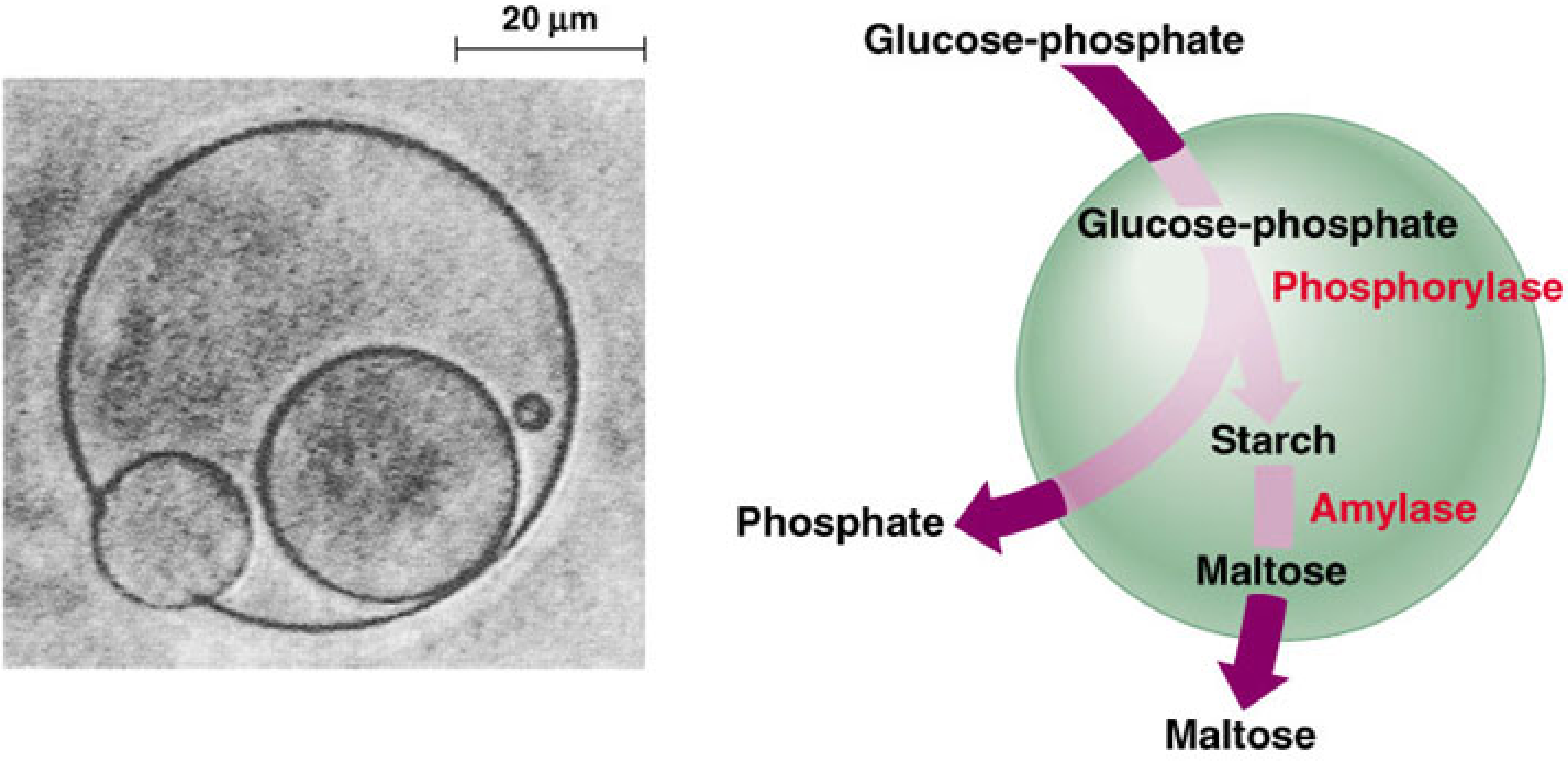
(b) Exclusive cooperation among membrane-enclosed molecules.

Encapsulation:

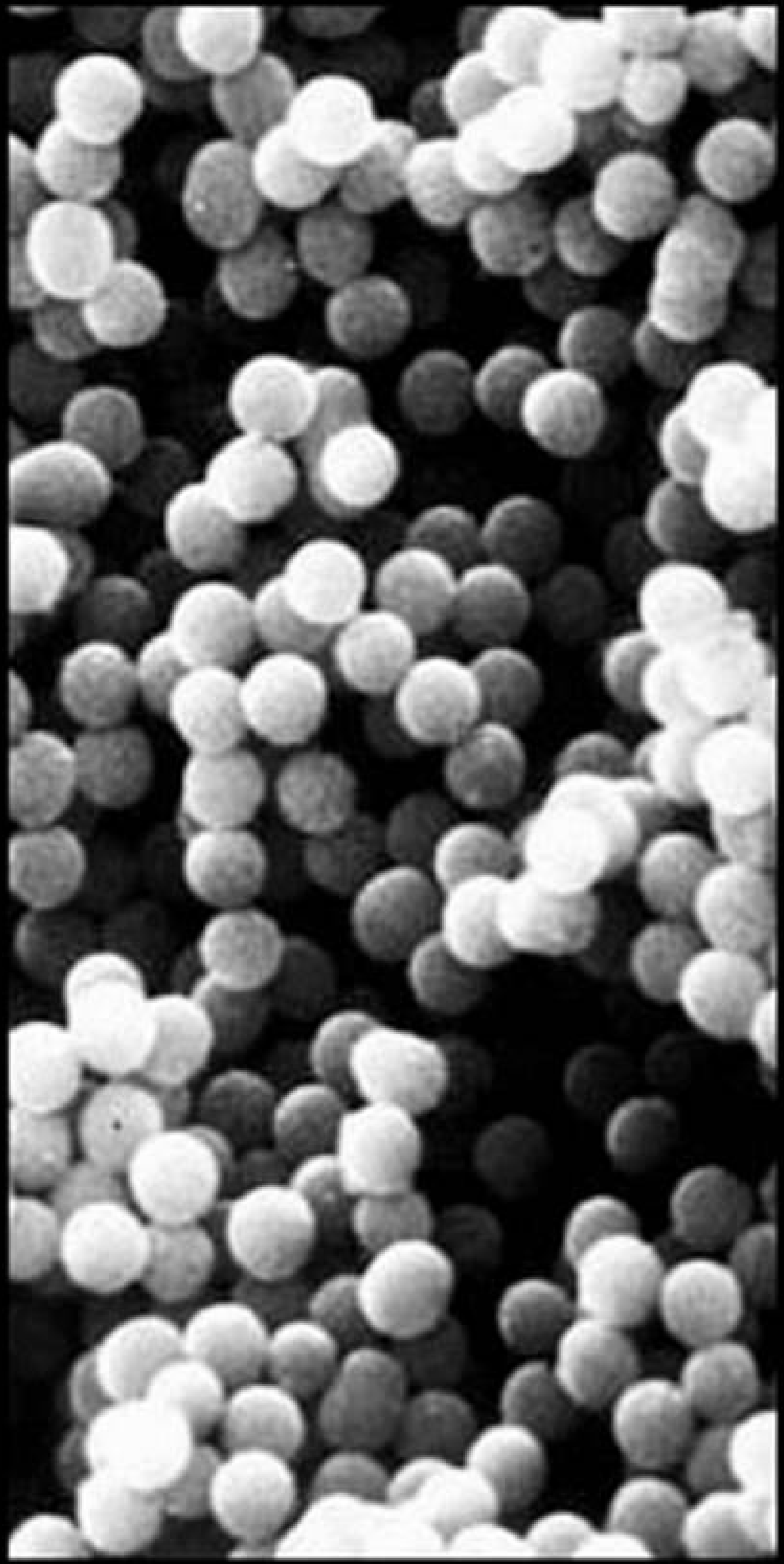
akin to lipid drops
self-coaleasing
without energy

allows concentration
higher reactivity, &
molecular selection


10 µm

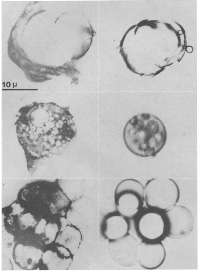


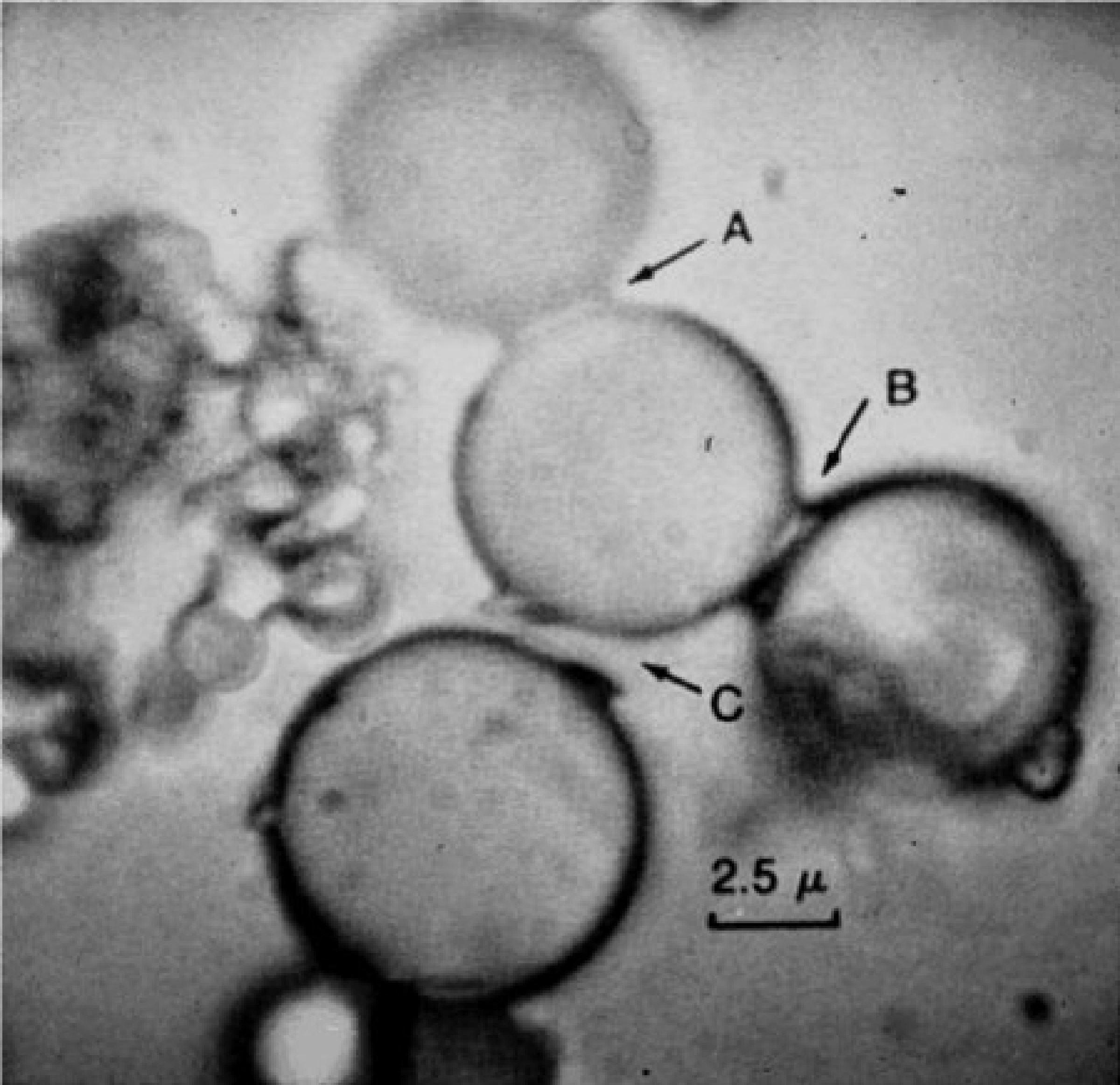
(a) Simple reproduction (b) Simple metabolism



Sidney W. Fox

1912-1998


10 μ

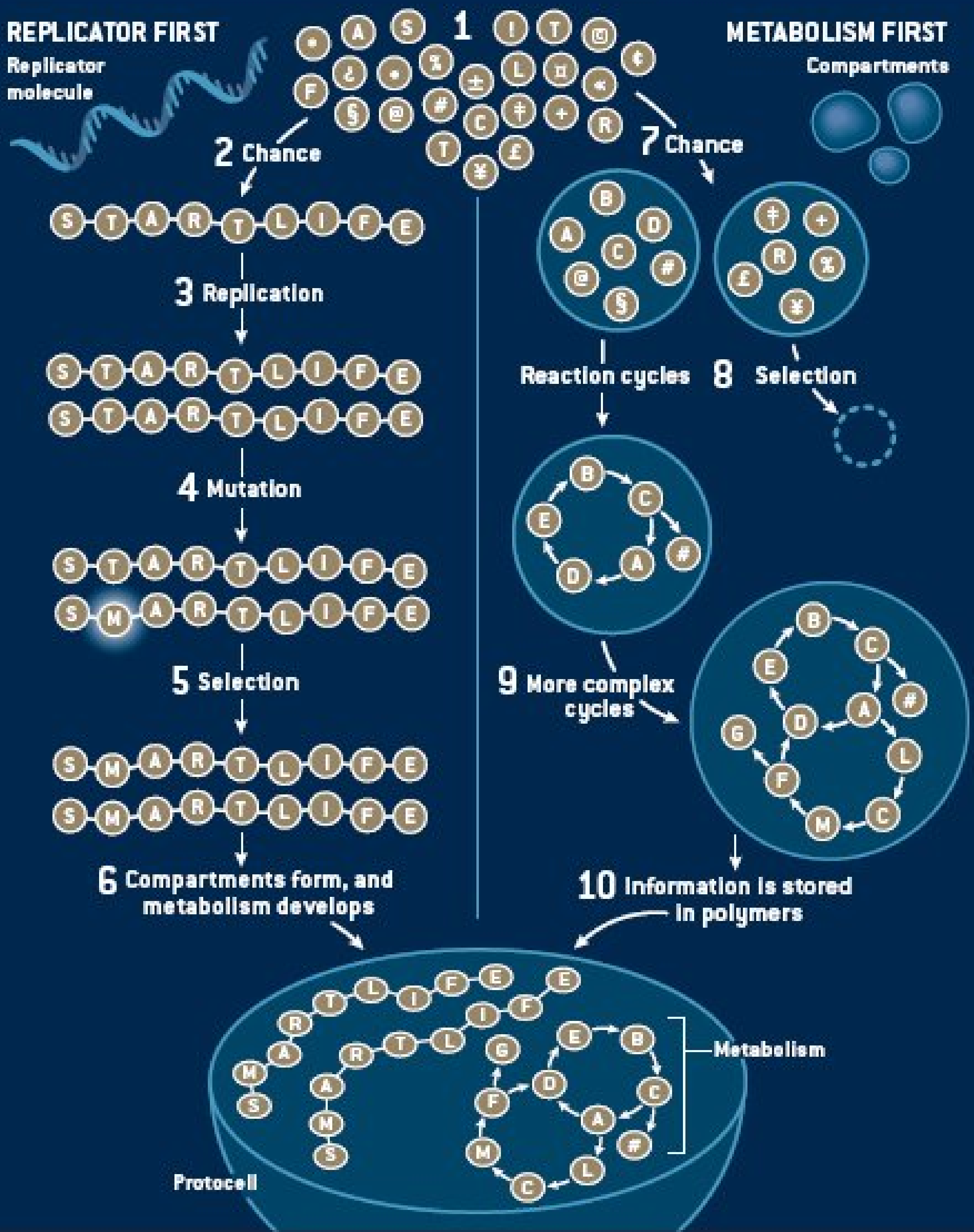

A
B
C
2.5 µ

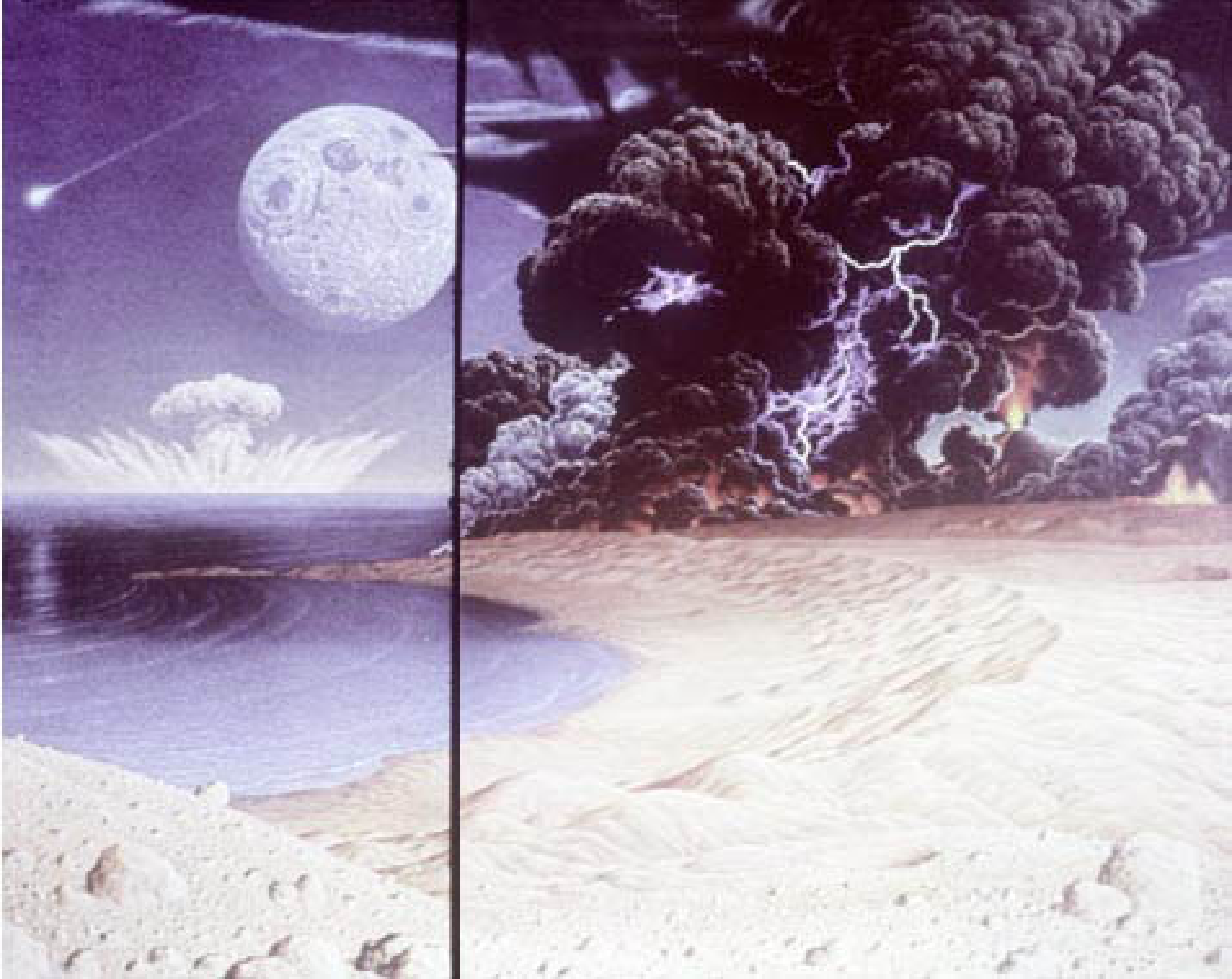
REPLICATOR VS. METABOLISM

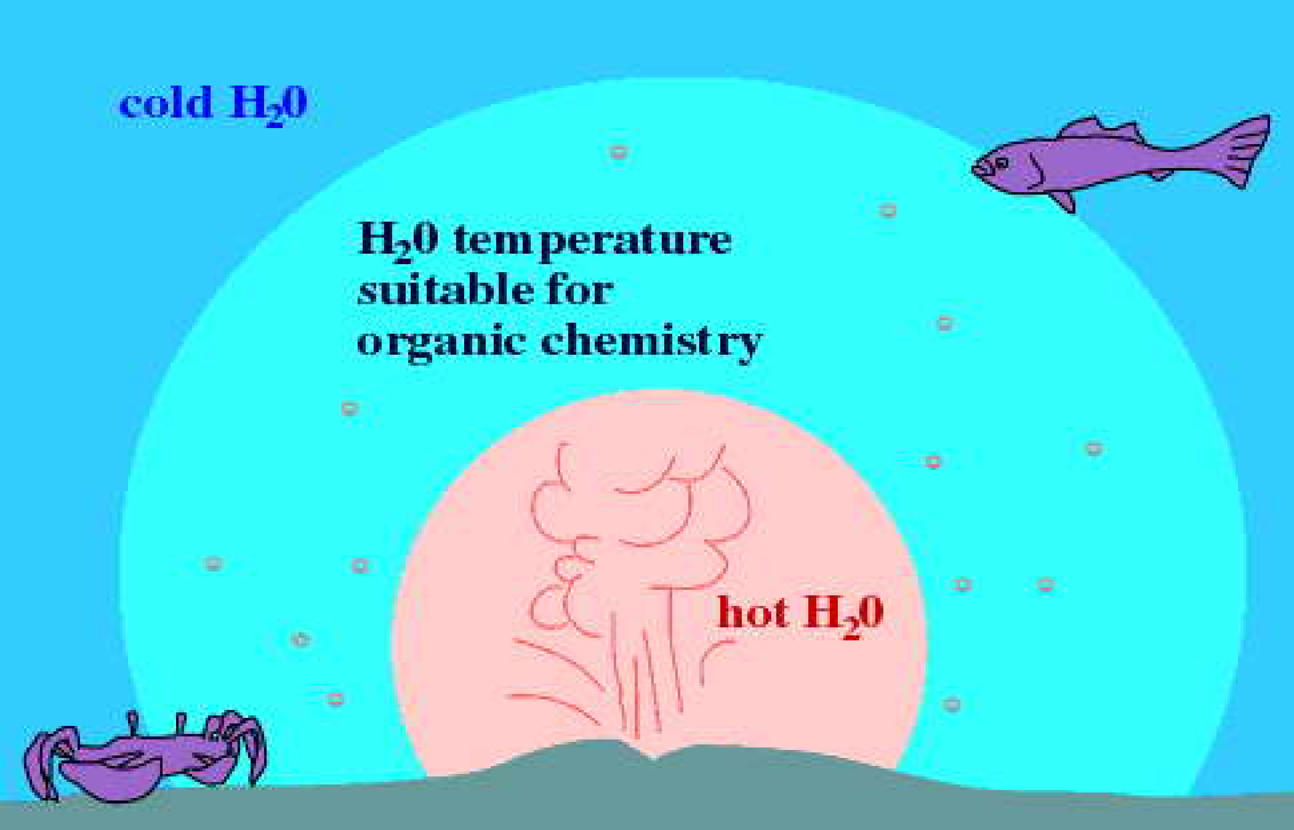
Scientific theories of the origin of life largely fall into two rival camps: replicator first and metabolism first. Both models must start from molecules formed by nonbiological chemical processes, represented here by balls labeled with symbols (*1*).

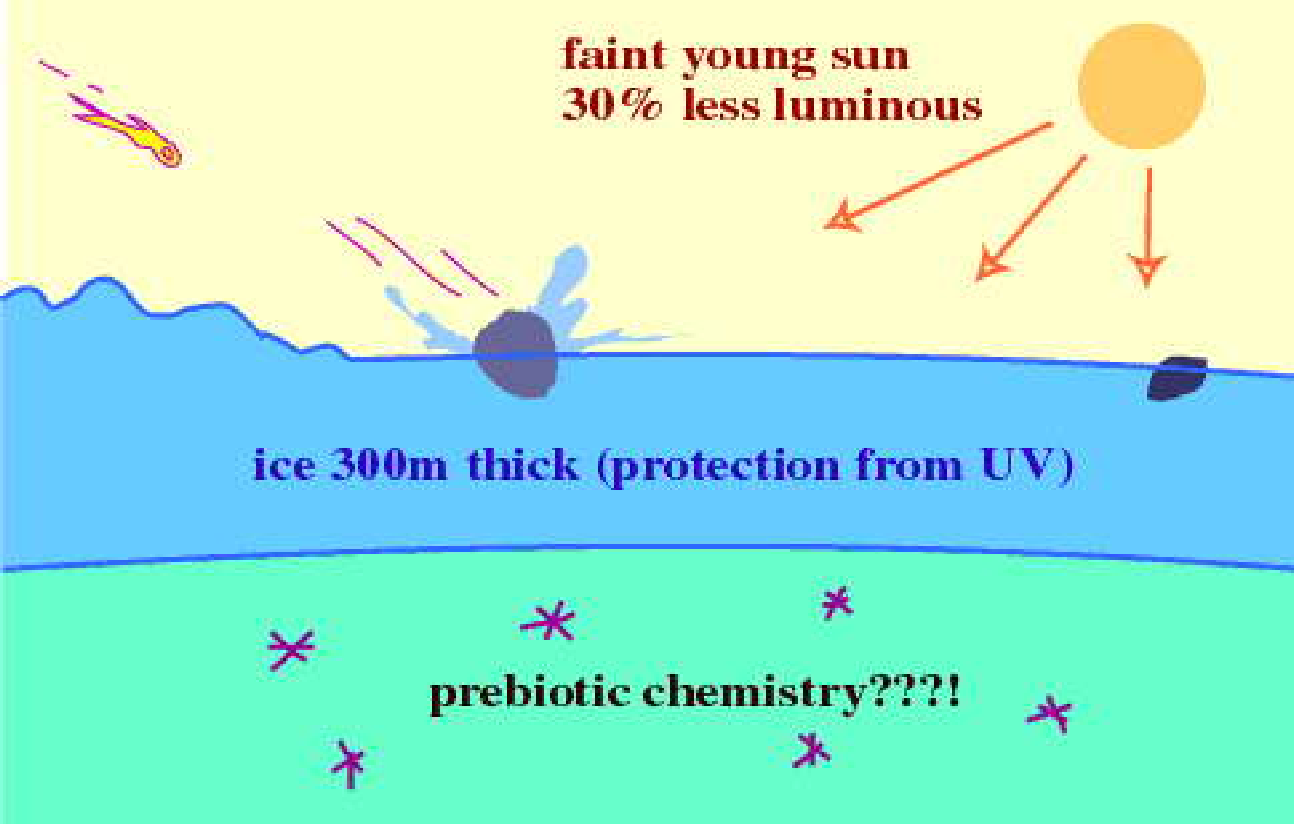
In the replicator-first model, some of these compounds join together in a chain, by chance forming a molecule—perhaps some kind of RNA—capable of reproducing itself (*2*). The molecule makes many copies of itself (*3*), sometimes forming mutant versions that are also capable of replicating (*4*). Mutant replicators that are better adapted to the conditions supplant earlier versions (*5*). Eventually this evolutionary process must lead to the development of compartments (like cells) and metabolism, in which smaller molecules use energy to perform useful processes (*6*).

Metabolism first starts off with the spontaneous formation of compartments (*7*). Some compartments contain mixtures of the starting compounds that undergo cycles of reactions (*8*), which over time become more complicated (*9*). Finally, the system must make the leap to storing information in polymers (*10*).



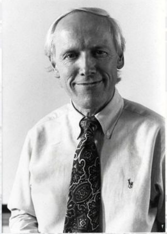



cold H_2O
H_2O temperature suitable for organic chemistry
hot H_2O


faint young sun
30% less luminous
ice 300m thick (protection from UV)
prebiotic chemistry???!

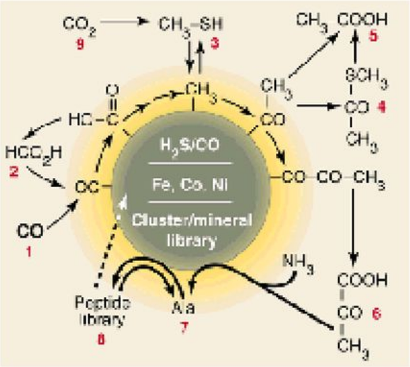
Gunter Wachtershauser

- Iron-Sulfur world provided an inorganic form of metabolism



1938-
German Chemist

Wächtershäuser's hypothesis

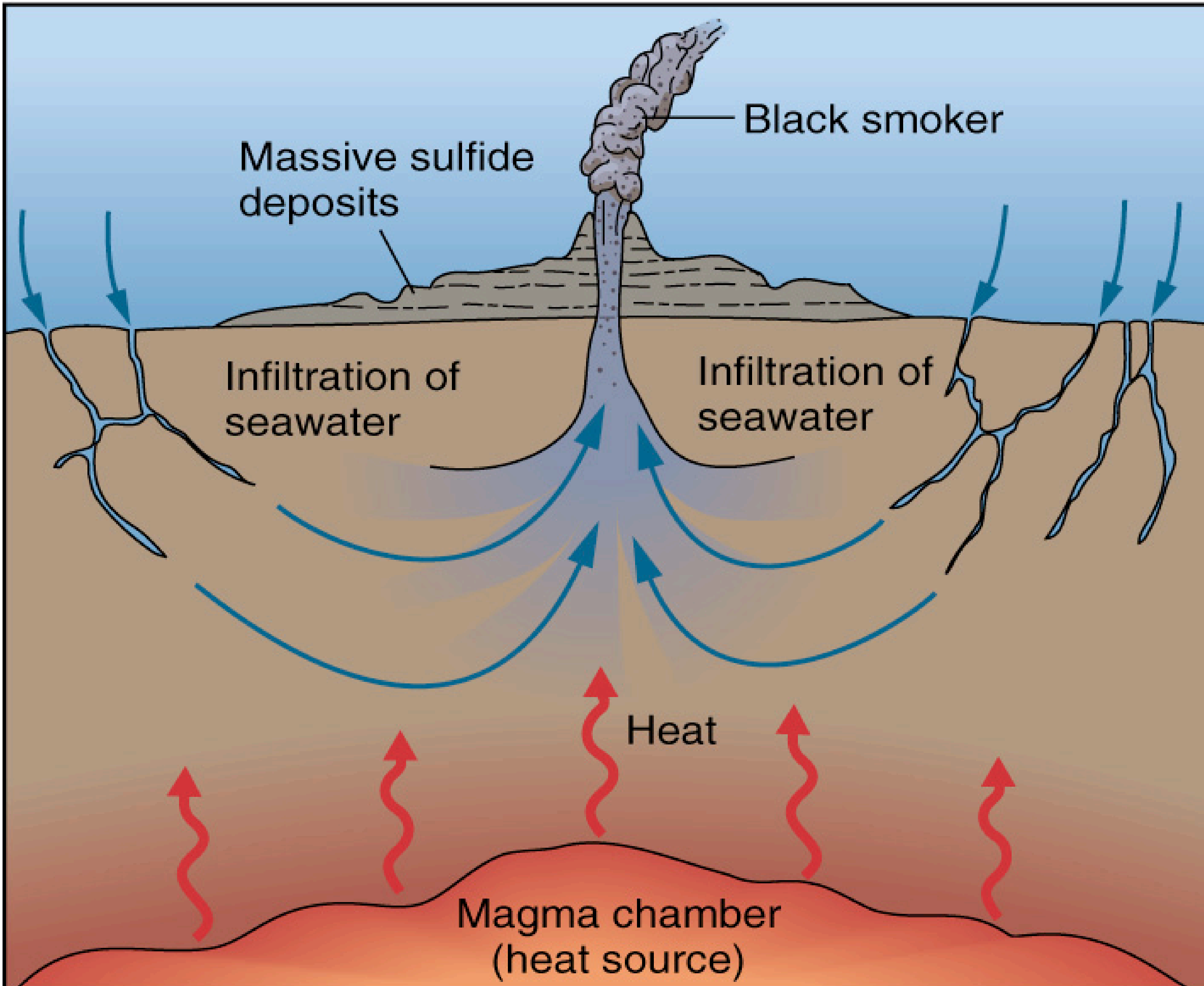


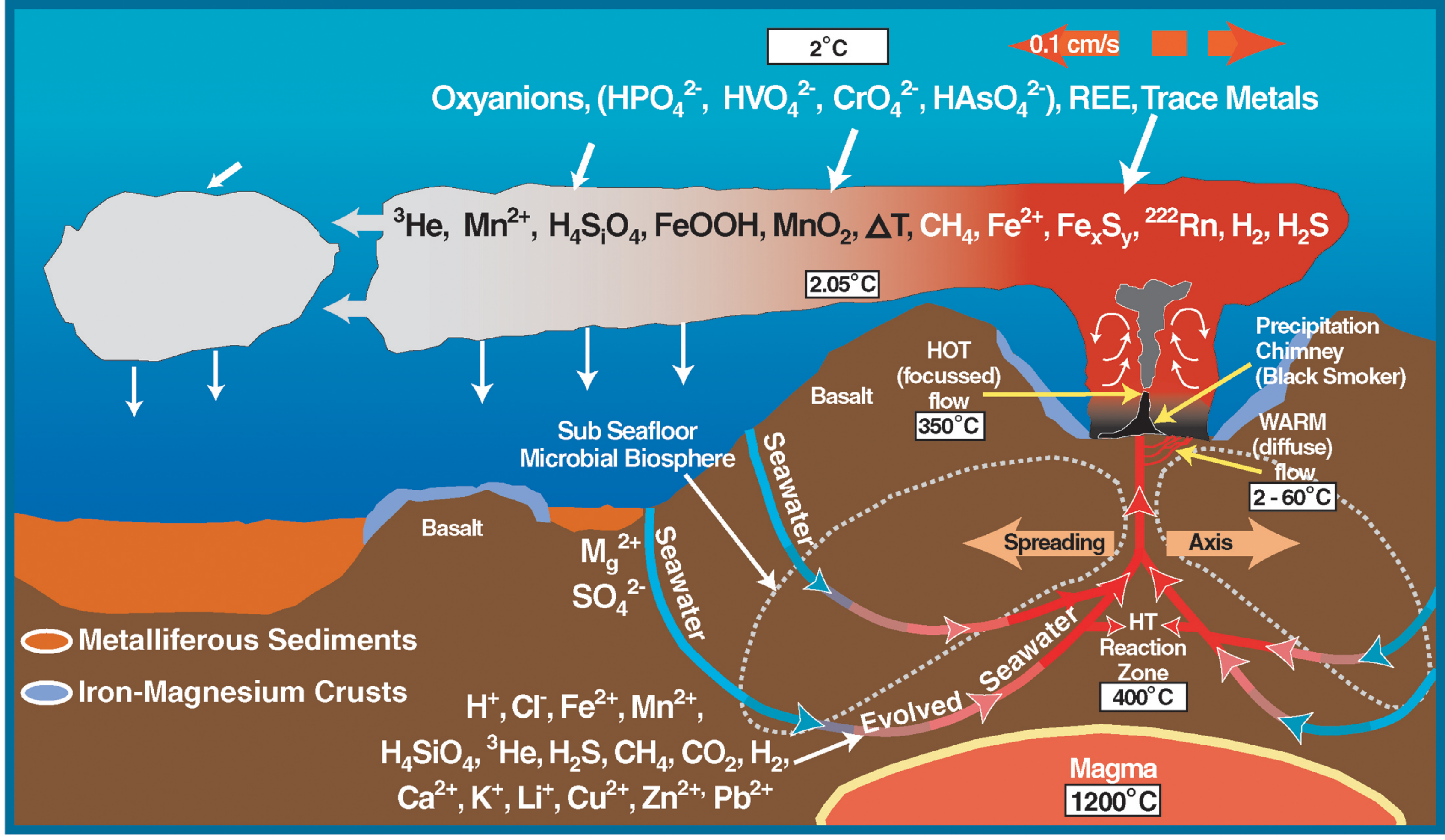
ajdubre.tripod.com/…/OriginLifeSci-82500.html

- Early chemistry of life starting on mineral surfaces (e.g. iron pyrites) near deep hydrothermal vents
- Bubbles on the mineral surfaces acting as the first 'cell'
- Demonstrating amino acids and peptide could be formed by mixing carbon, monoxide, hydrogen sulfide, nickel sulfide and iron sulfide by Wächtershäuser and Claudia Huber, in 1997 and 1998

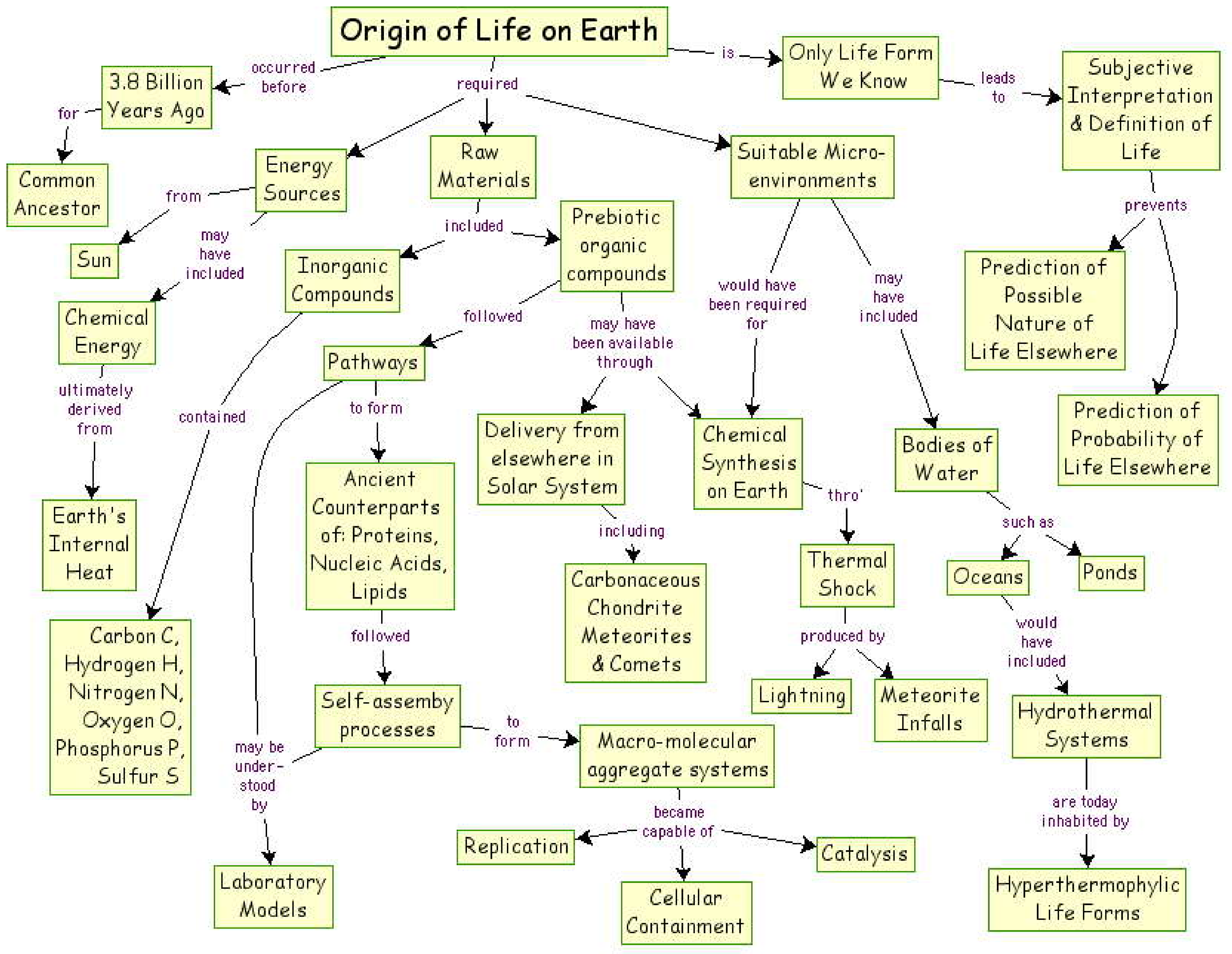
Huber, C. and Wächterhäuser, G. , *Science*, 1998

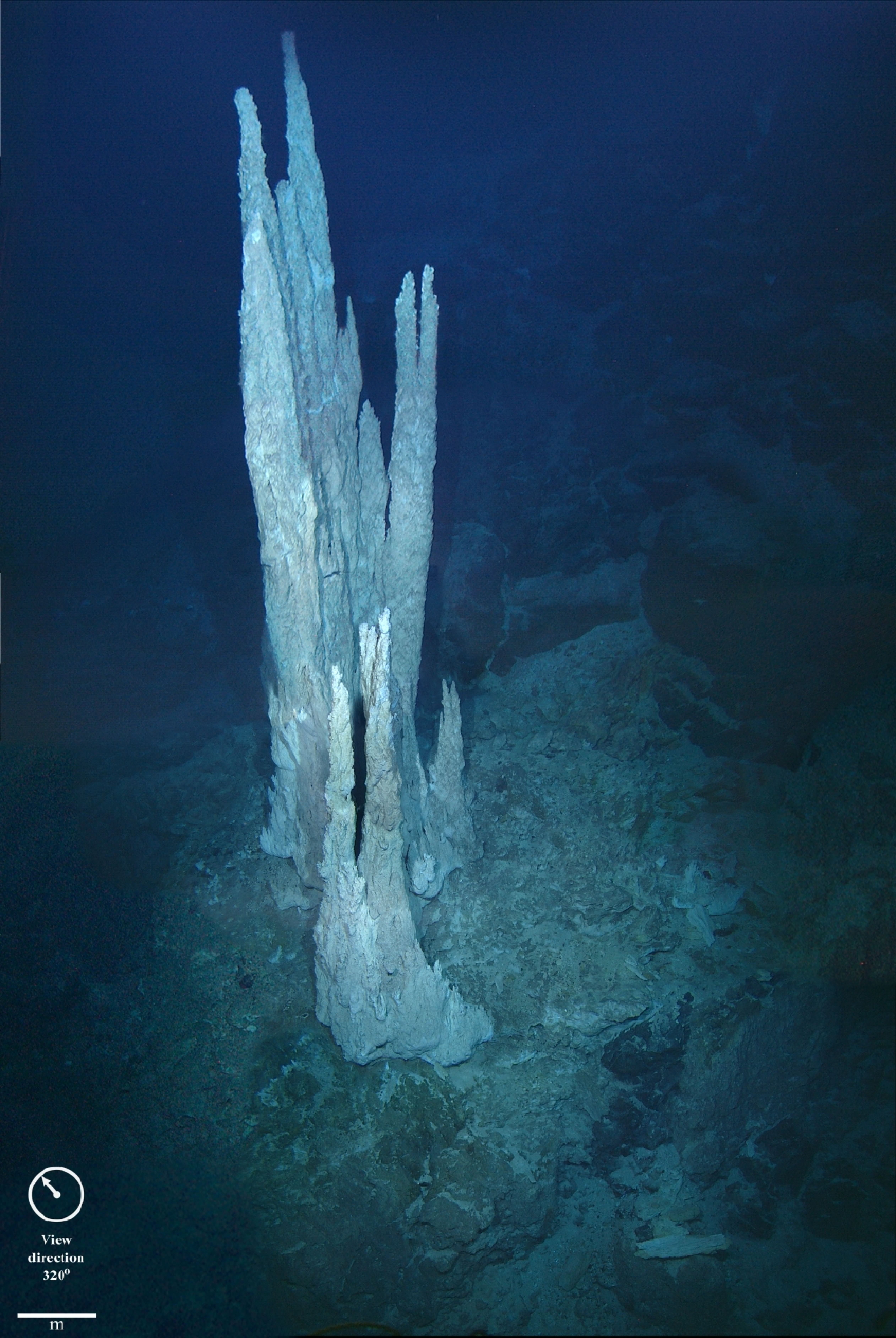
Wächtershäuser, G. , *Science* 2000.

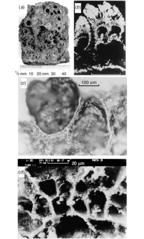

Black smoker
Massive sulfide
deposits
Infiltration of
seawater
Infiltration of
seawater
Heat
Magma chamber
(heat source)



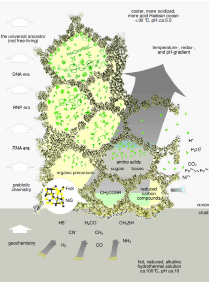
2°C
0.1 cm/s
Oxyanions, (HPO4 2-, HVO4 2-, CrO4 2-, HAsO4 2-), REE, Trace Metals
3He, Mn2+, H4SiO4, FeOOH, MnO2, ΔT, CH4, Fe2+, FexSy, 222Rn, H2, H2S
2.05°C
Precipitation Chimney (Black Smoker)
HOT (focussed) flow
350°C
Basalt
WARM (diffuse) flow
2 - 60°C
Sub Seafloor Microbial Biosphere
Seawater
Spreading
Axis
Basalt
Mg 2+
SO4 2-
Seawater
HT Reaction Zone
400°C
Evolved Seawater
Metalliferous Sediments
Iron-Magnesium Crusts
H+, Cl-, Fe2+, Mn2+,
H4SiO4, 3He, H2S, CH4, CO2, H2,
Ca2+, K+, Li+, Cu2+, Zn2+, Pb2+
Magma
1200°C


Origin of Life on Earth
occurred before
3.8 Billion Years Ago
for
Common Ancestor
required
is
Only Life Form We Know
leads to
Subjective Interpretation & Definition of Life
prevents
Prediction of Possible Nature of Life Elsewhere
Prediction of Probability of Life Elsewhere
Energy Sources
from
Sun
may have included
Chemical Energy
ultimately derived from
Earth's Internal Heat
Raw Materials
included
Inorganic Compounds
contained
Carbon C, Hydrogen H, Nitrogen N, Oxygen O, Phosphorus P, Sulfur S
Prebiotic organic compounds
followed
Pathways
to form
Ancient Counterparts of: Proteins, Nucleic Acids, Lipids
followed
Self-assemby processes
to form
Macro-molecular aggregate systems
became capable of
Replication
Cellular Containment
Catalysis
may be under-stood by
Laboratory Models
may have been available through
Delivery from elsewhere in Solar System
including
Carbonaceous Chondrite Meteorites & Comets
Chemical Synthesis on Earth
thro'
Thermal Shock
produced by
Lightning
Meteorite Infalls
Suitable Micro-environments
would have been required for
may have included
Bodies of Water
such as
Oceans
Ponds
would have included
Hydrothermal Systems
are today inhabited by
Hyperthermophylic Life Forms

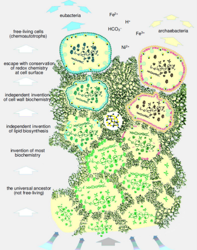

View
direction
320°
m



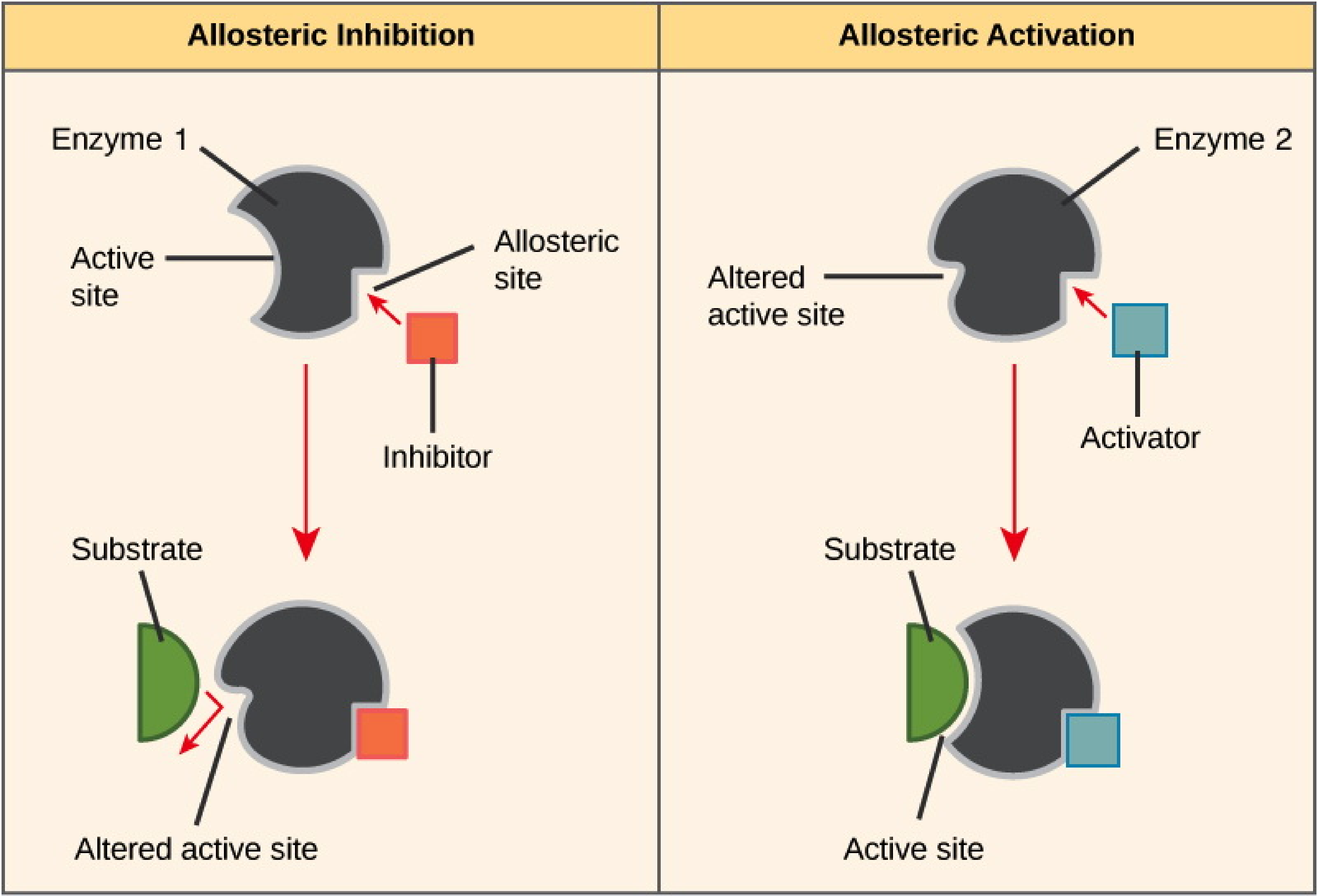
(a)
(b)
½ mm 10 20 mm 30 40
(c)
100 μm
(d)
20 μm



cooler, more oxidized, more acid Hadean ocean <30 ℃, pH ca.5.5
the universal ancestor (not free-living)
temperature-, redox-, and pH-gradient
DNA era
RNP era
RNA era
prebiotic chemistry
geochemistry
H^+
$P_2O_7^{4-}$
CO_2
$Fe^{2+} >> Fe^{3+}$
Ni^{2+}
amino acids
sugars bases
organic precursors
FeS
NiS
CH_3COSR
reduced carbon compounds
ocean
crust
HS^-
CN^-
H_2
H_2CO
CH_4
CO
CH_3SH
NH_3
hot, reduced, alkaline hydrothermal solution ca.100 ℃, pH ca.10



eubacteria
Fe^{2+}
H^+
HCO_3^-
Fe^{3+}
archaebacteria
Ni^{2+}
free-living cells
(chemoautotrophs)
escape with conservation
of redox chemistry
at cell surface
independent invention
of cell wall biochemistry
independent invention
of lipid biosynthesis
invention of most
biochemistry
the universal ancestor
(not free-living)


Allosteric Inhibition
Allosteric Activation
Enzyme 1
Active
site
Allosteric
site
Inhibitor
Substrate
Altered active site
Enzyme 2
Altered
active site
Activator
Substrate
Active site

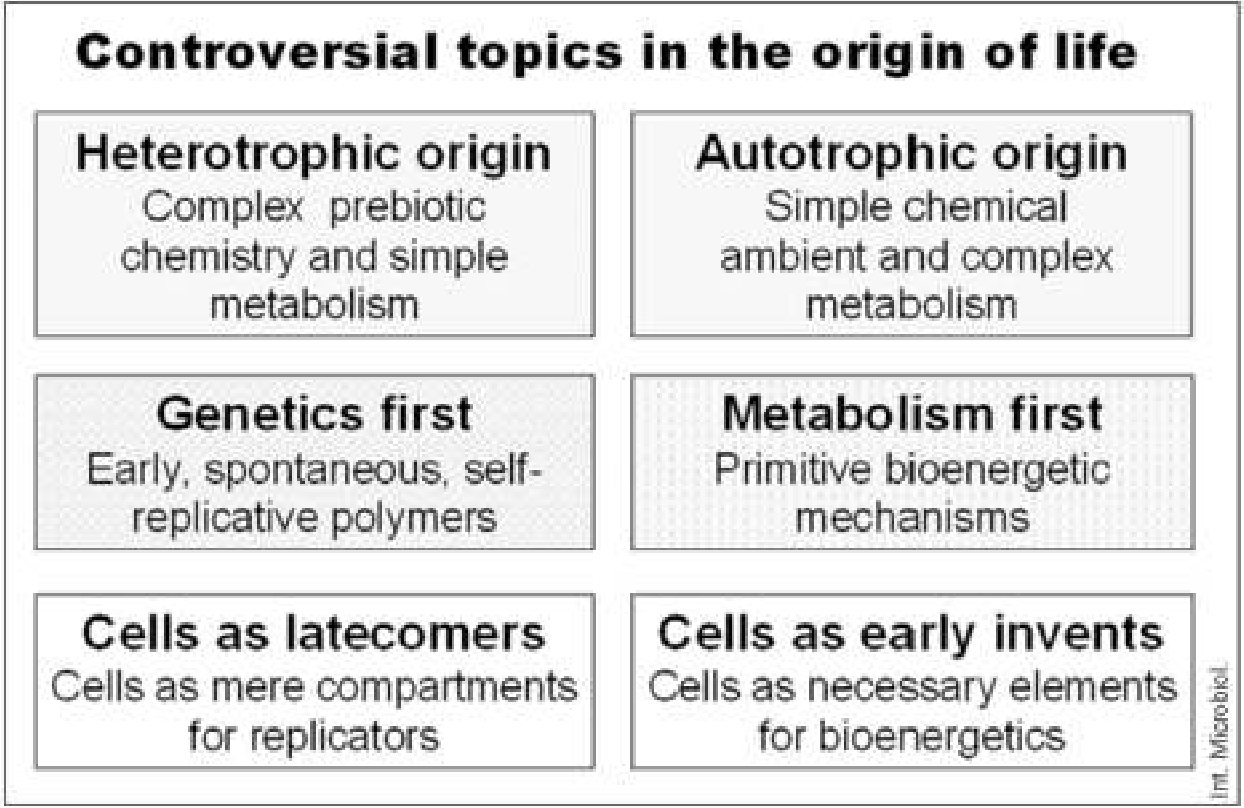
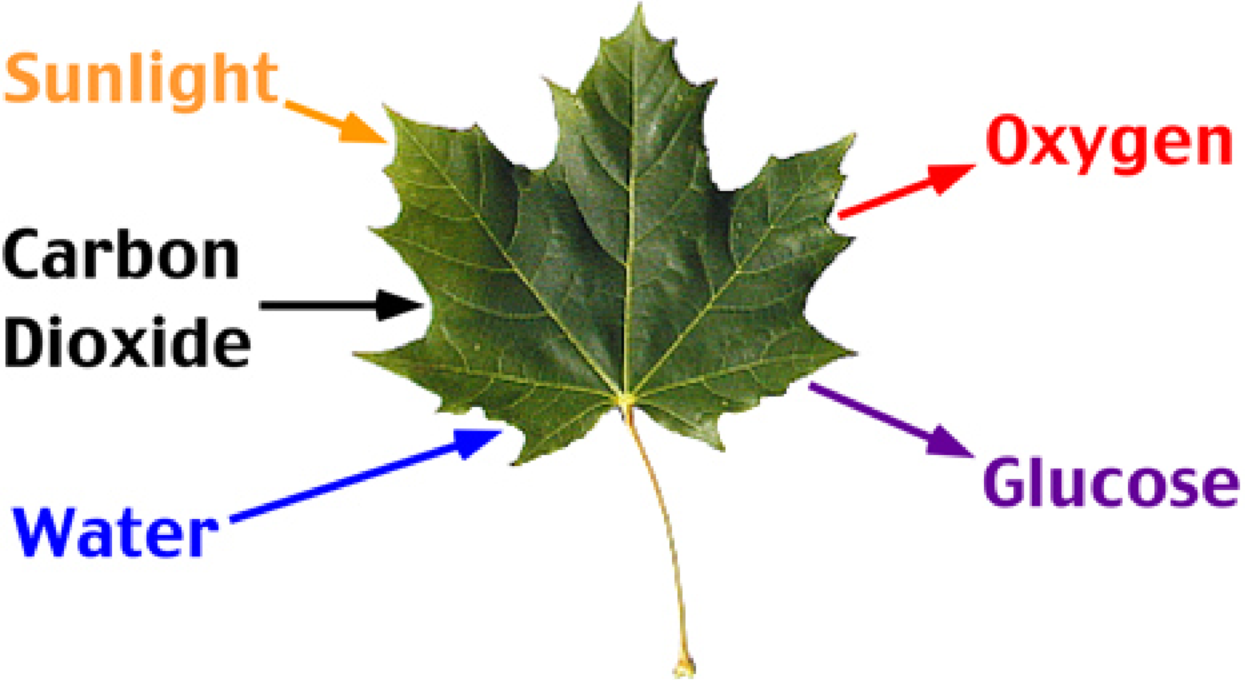
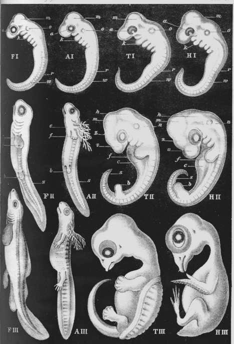


Fig. 1. Main controversial research topics in the origin of life.


Sunlight
Oxygen
Carbon Dioxide
Glucose
Water

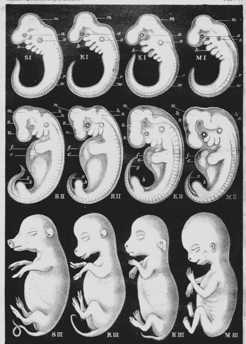
Haeckel. Entwickelungsgeschichte. Taf. IV.



F. Fisch. A. Salamander. T. Schildkröte. H. Huhn.

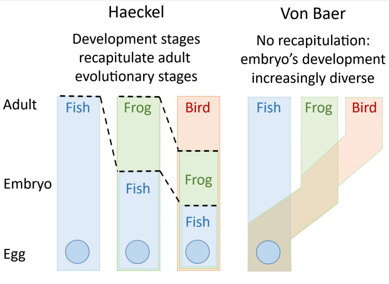
Haeckel del. Lith. Anst. v. J. G. Bach, Leipzig

Haeckel. Entwickelungsgeschichte. Taf. V.

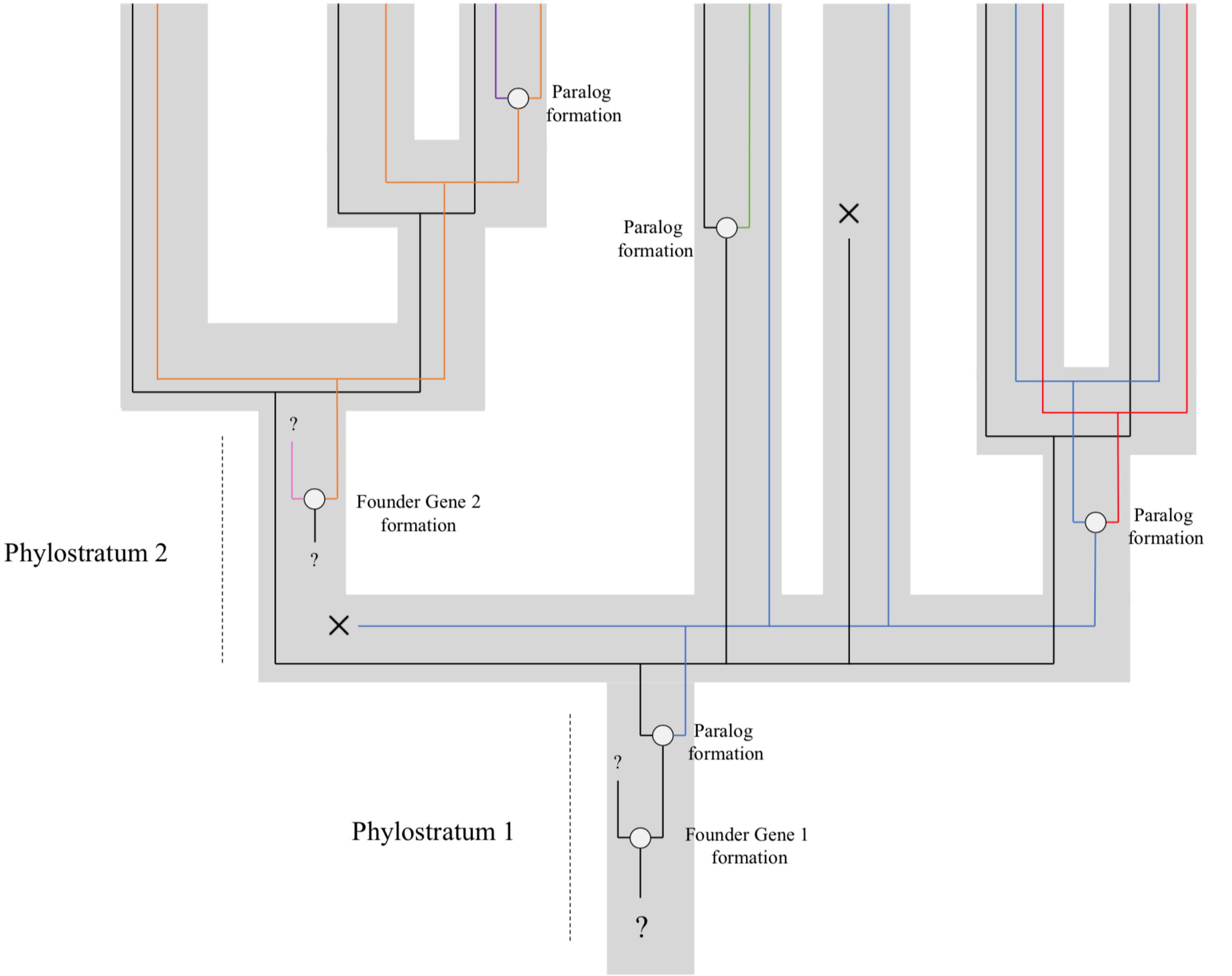


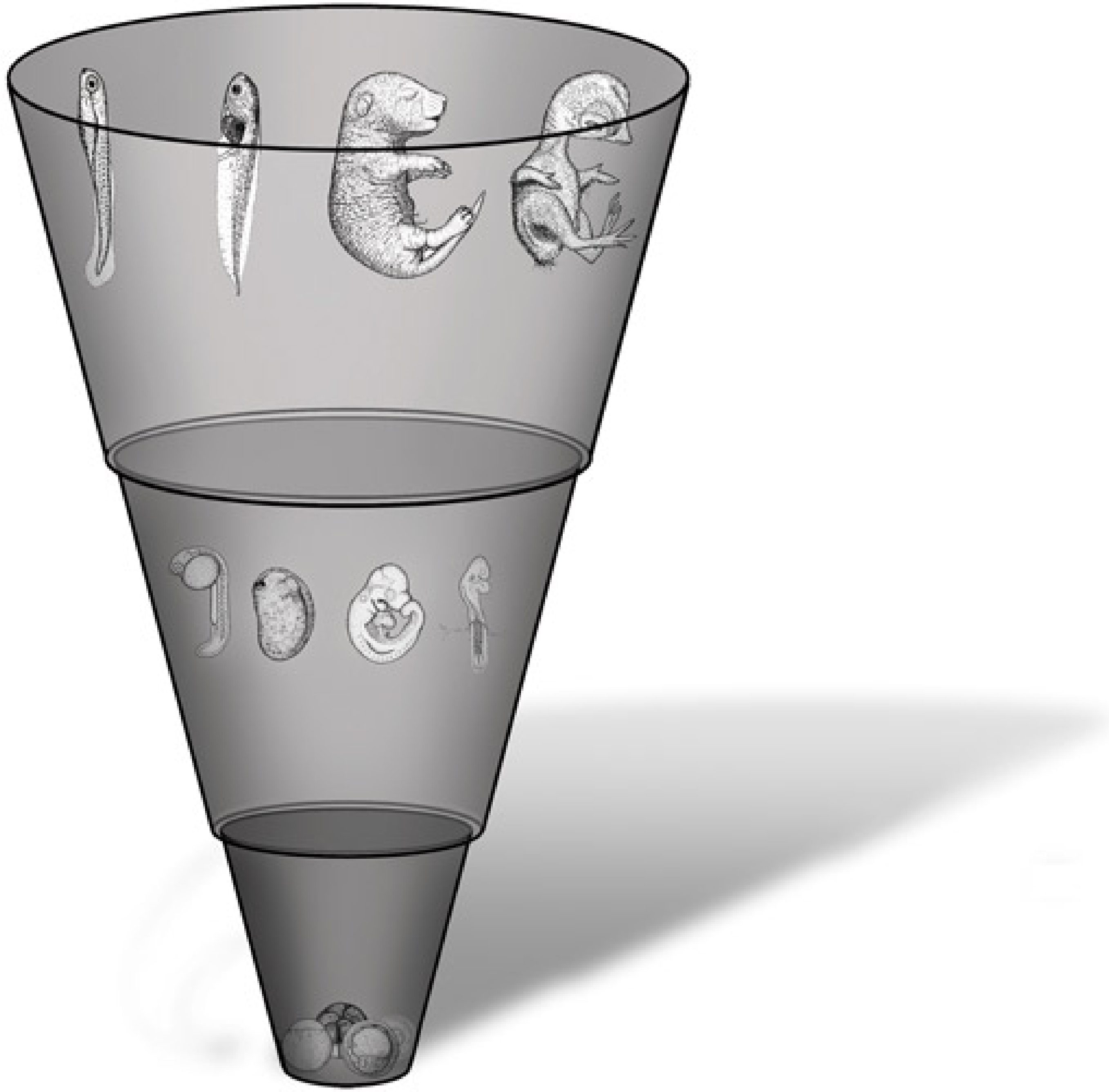
S. Schwein. R. Rind. K. Kaninchen. M. Mensch.

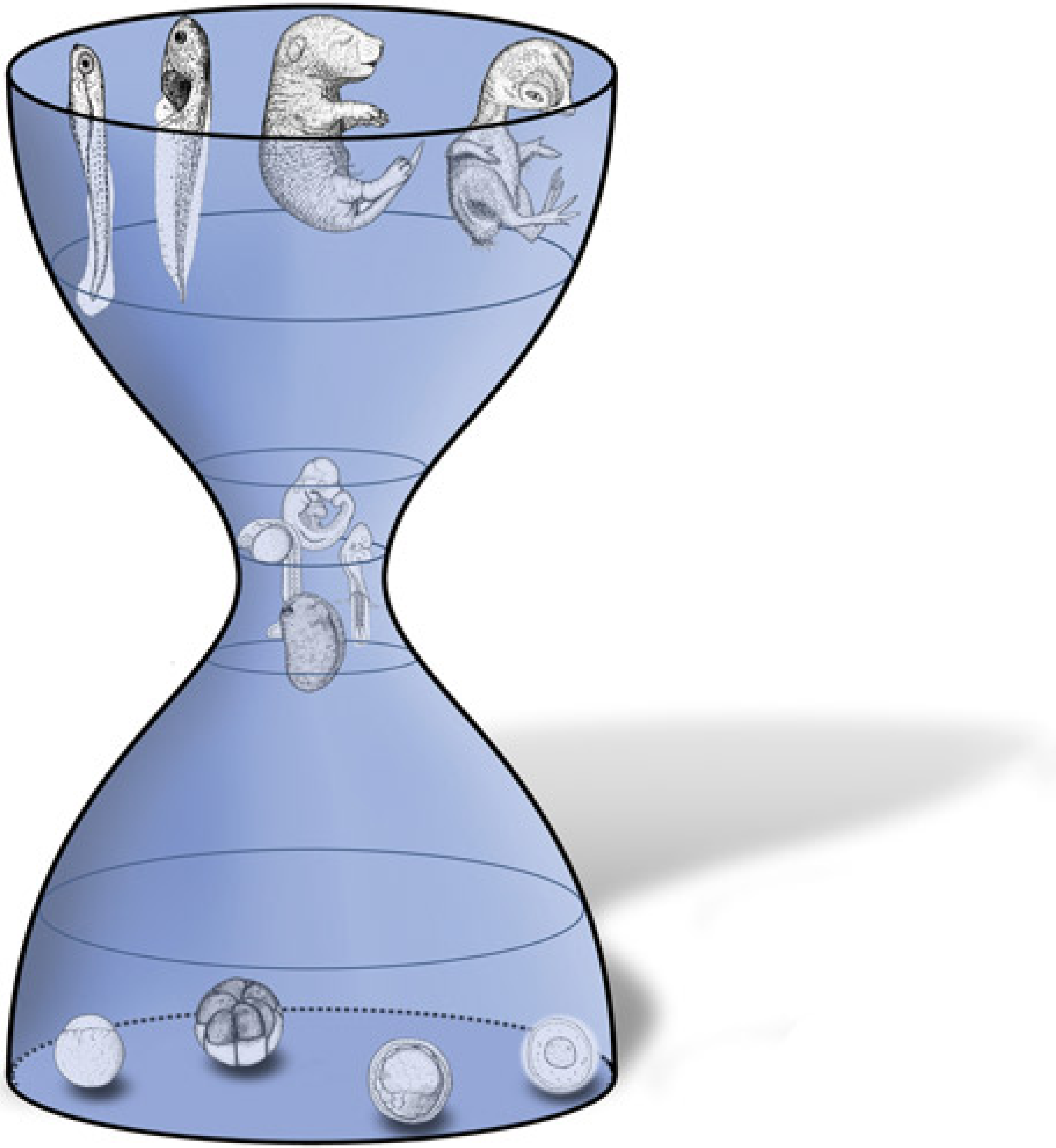
E. Haeckel del. Lith. Anst. v. J. G. Bach, Leipzig



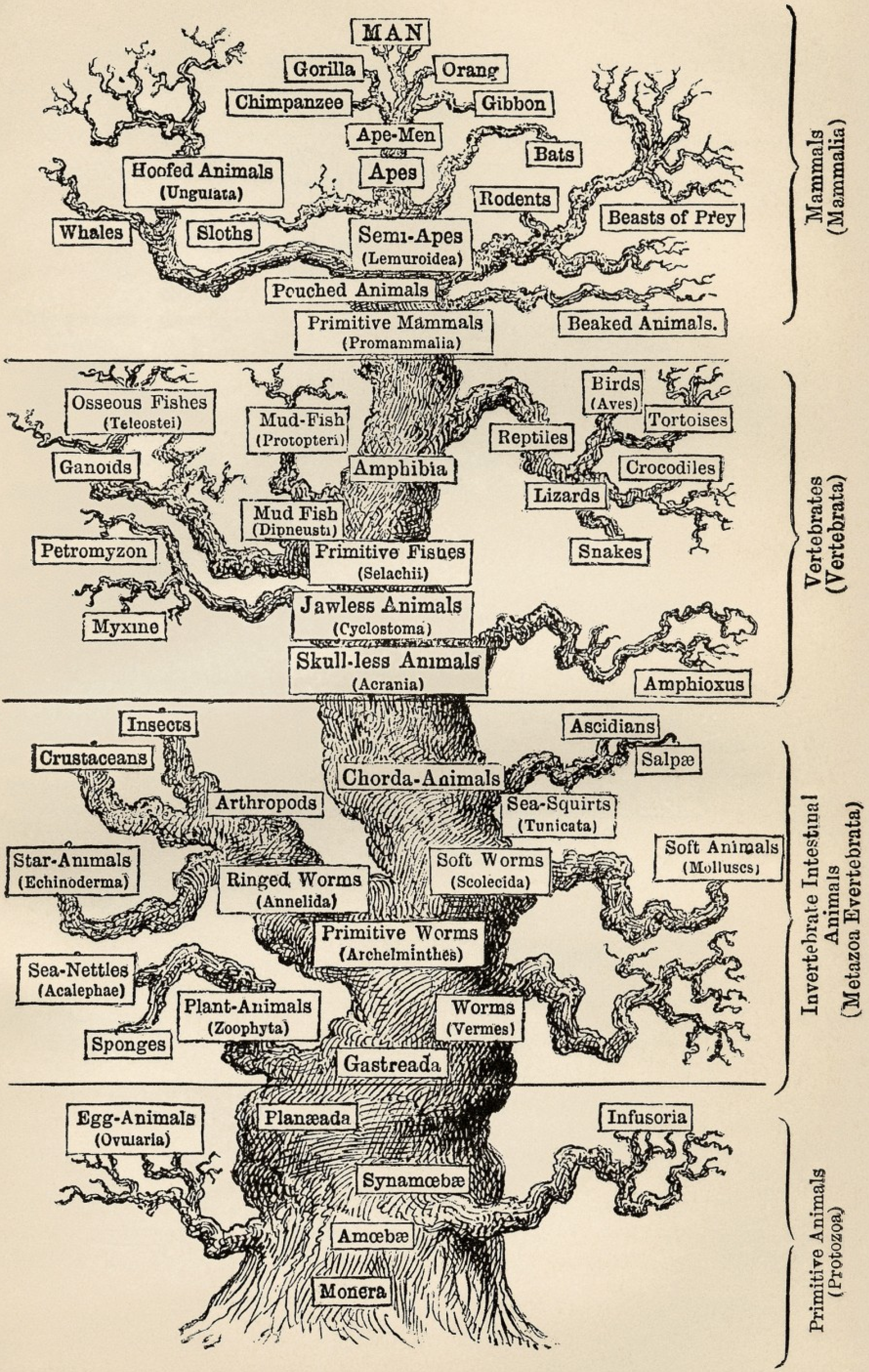
Haeckel
Development stages recapitulate adult evolutionary stages
Von Baer
No recapitulation: embryo's development increasingly diverse
Adult
Embryo
Egg
Fish
Frog
Bird
Fish
Frog
Fish
Fish
Frog
Bird

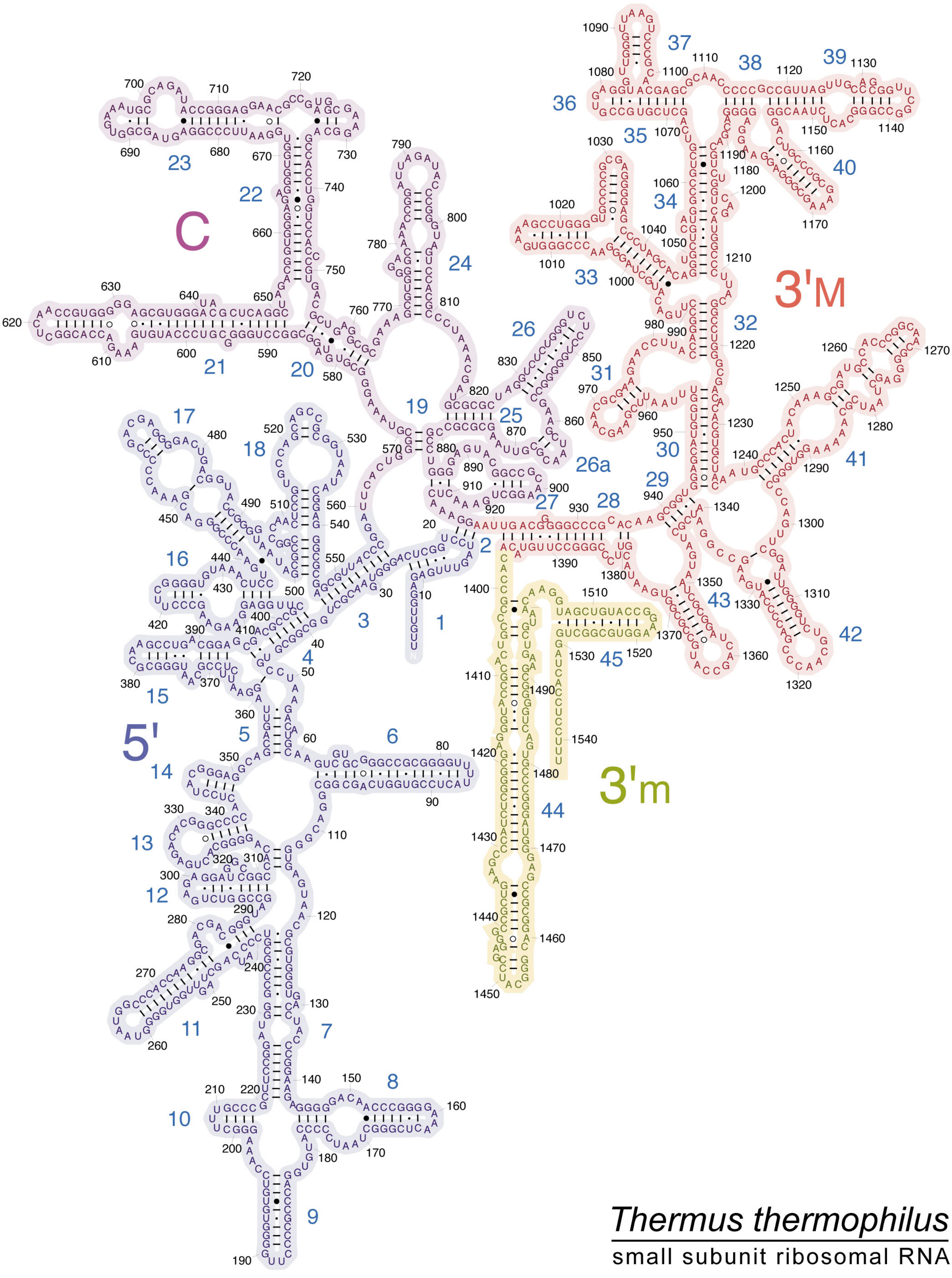

Paralog formation
Paralog formation
?
Founder Gene 2 formation
?
Phylostratum 2
Paralog formation
Paralog formation
?
Phylostratum 1
Founder Gene 1 formation
?





PEDIGREE OF MAN.

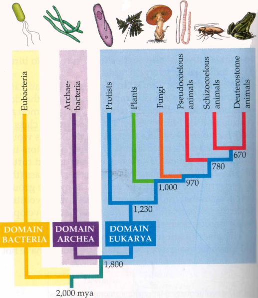




Thermus thermophilus

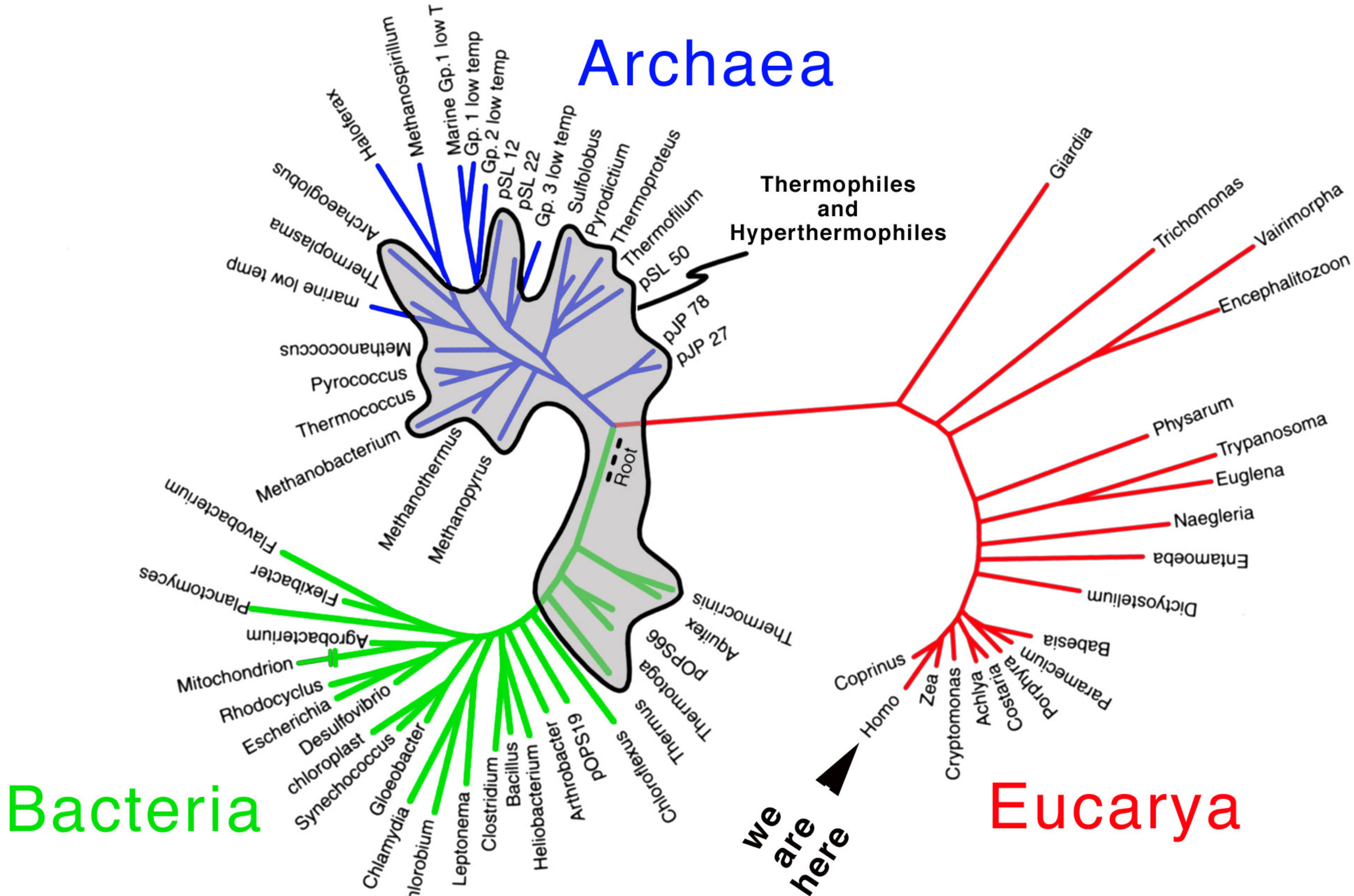
small subunit ribosomal RNA

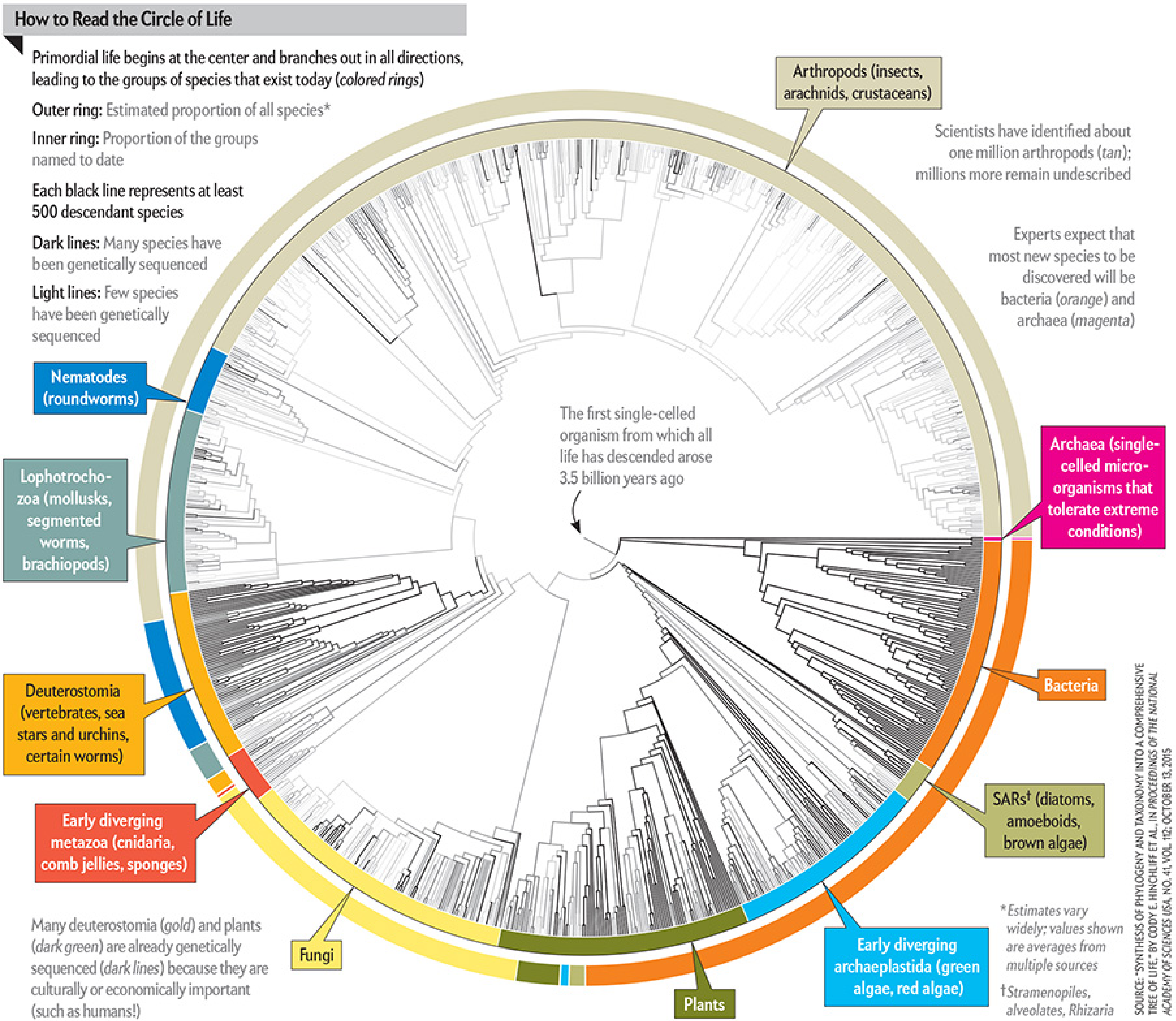
Shared with Bacteria	**Shared with Eukarya**	**Unique to Archaea**
No nucleus or membrane-bound organelles	No **peptidoglycan**	Cell wall structure (for example, some archaeal cell walls contain **pseudomurein**)
Circular genome	DNA associated with **histones**	Cell membrane containing ether-linked lipids
Genes grouped in **operons**	Translation initiated with **methionine**	**Flagellin** protein structure
No introns or **RNA processing**	Similar **RNA polymerase, promoters**, other transcriptional machinery	Ribosomal structure (characteristics shared with both Bacteria and Eukarya)
Polycistronic mRNA	Similar DNA replication and repair	tRNA sequence and metabolism
Cellular size (>100-fold smaller than eukaryotes)	Similar **ATPase (Type V)**	No **fatty acid synthetase** enzyme

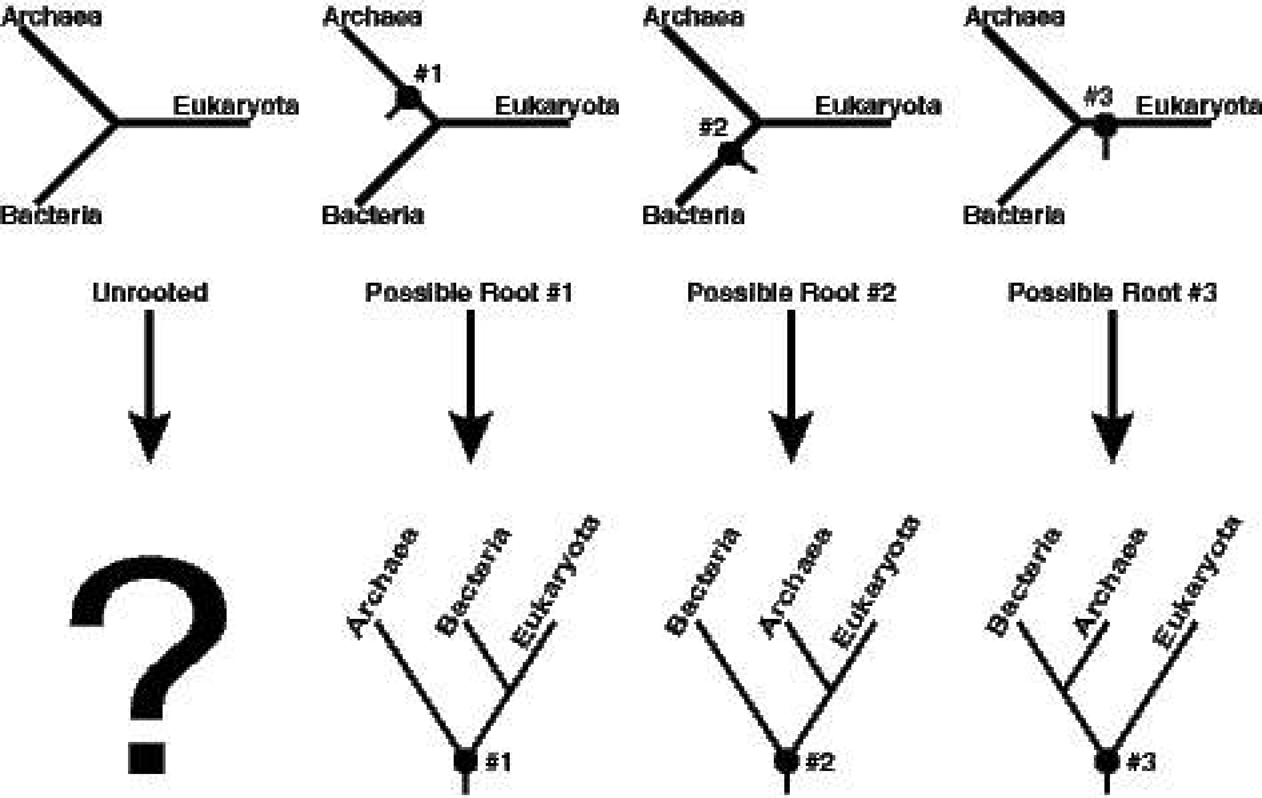


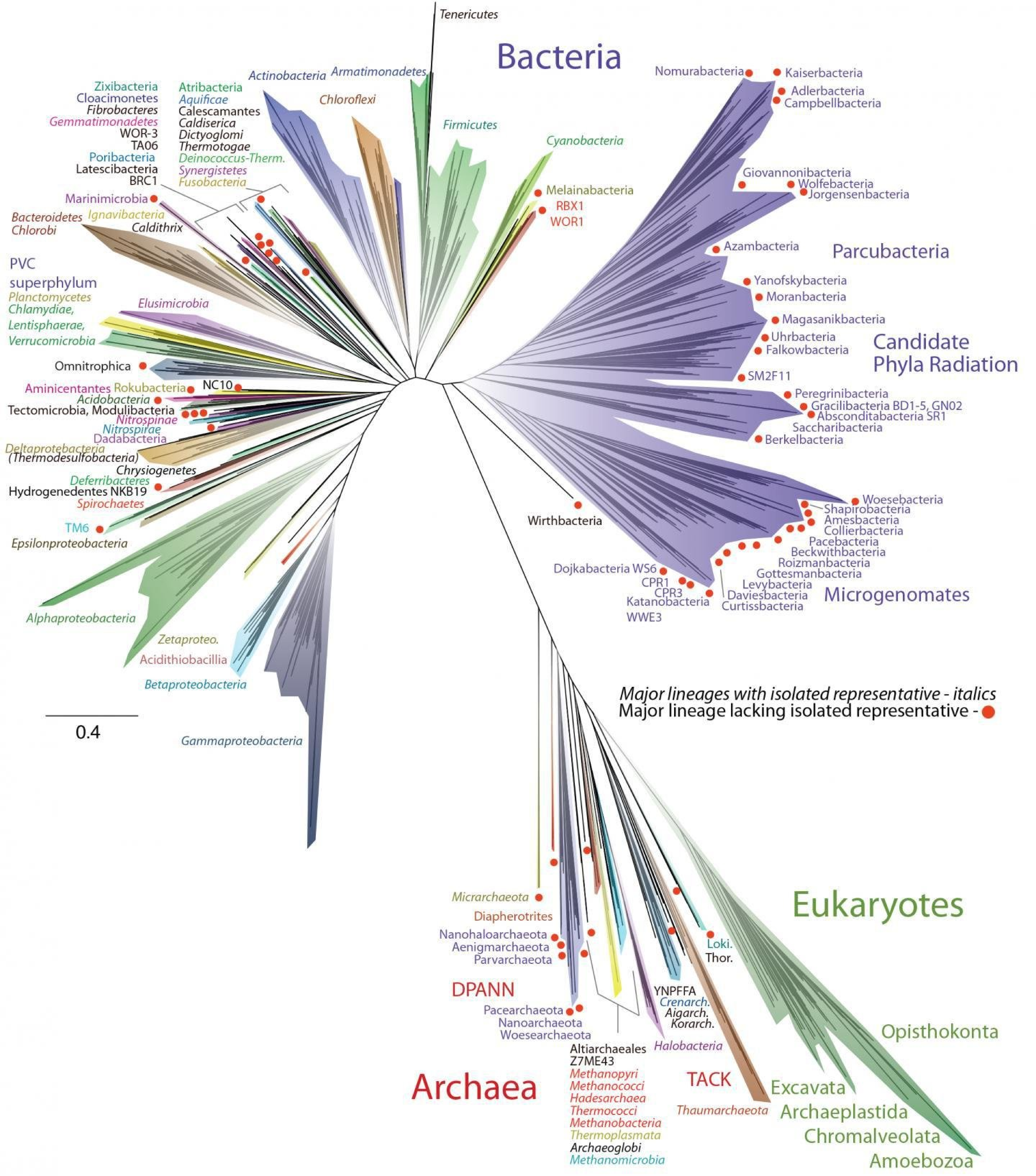
Eubacteria
Archae-bacteria
Protists
Plants
Fungi
Pseudocoelous animals
Schizocoelous animals
Deuterostome animals
670
780
970
1,000
1,230
DOMAIN BACTERIA
DOMAIN ARCHEA
DOMAIN EUKARYA
1,800
2,000 mya

The Tree of Life



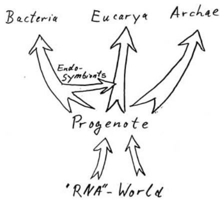

How to Read the Circle of Life
Primordial life begins at the center and branches out in all directions, leading to the groups of species that exist today (*colored rings*)
Outer ring: Estimated proportion of all species*
Inner ring: Proportion of the groups named to date
Each black line represents at least 500 descendant species
Dark lines: Many species have been genetically sequenced
Light lines: Few species have been genetically sequenced
Arthropods (insects, arachnids, crustaceans)
Scientists have identified about one million arthropods (*tan*); millions more remain undescribed
Experts expect that most new species to be discovered will be bacteria (*orange*) and archaea (*magenta*)
The first single-celled organism from which all life has descended arose 3.5 billion years ago
Nematodes (roundworms)
Lophotrochozoa (mollusks, segmented worms, brachiopods)
Archaea (single-celled micro-organisms that tolerate extreme conditions)
Bacteria
Deuterostomia (vertebrates, sea stars and urchins, certain worms)
Early diverging metazoa (cnidaria, comb jellies, sponges)
SARs† (diatoms, amoeboids, brown algae)
Fungi
Plants
Early diverging archaeplastida (green algae, red algae)
Many deuterostomia (*gold*) and plants (*dark green*) are already genetically sequenced (*dark lines*) because they are culturally or economically important (such as humans!)
*Estimates vary widely; values shown are averages from multiple sources
†Stramenopiles, alveolates, Rhizaria
SOURCE: "SYNTHESIS OF PHYLOGENY AND TAXONOMY INTO A COMPREHENSIVE TREE OF LIFE," BY CODY E. HINCHLIFF ET AL., IN *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES USA*, NO. 41, VOL. 112; OCTOBER 13, 2015


Archaea
Eukaryota
Bacteria
Unrooted
Archaea
#1
Eukaryota
Bacteria
Possible Root #1
Archaea
Eukaryota
#2
Bacteria
Possible Root #2
Archaea
#3
Eukaryota
Bacteria
Possible Root #3
?
Archaea
Bacteria
Eukaryota
#1
Bacteria
Archaea
Eukaryota
#2
Bacteria
Archaea
Eukaryota
#3

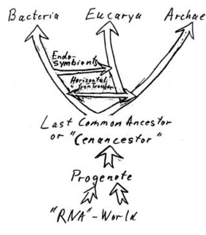


Tenericutes
Bacteria
Actinobacteria
Armatimonadetes
Chloroflexi
Firmicutes
Cyanobacteria
Zixibacteria
Cloacimonetes
Fibrobacteres
Gemmatimonadetes
WOR-3
TA06
Poribacteria
Latescibacteria
BRC1
Atribacteria
Aquificae
Calescamantes
Caldiserica
Dictyoglomi
Thermotogae
Deinococcus-Therm.
Synergistetes
Fusobacteria
Marinimicrobia
Bacteroidetes
Chlorobi
Ignavibacteria
Caldithrix
PVC
superphylum
Planctomycetes
Chlamydiae,
Lentisphaerae,
Verrucomicrobia
Elusimicrobia
Omnitrophica
Aminicentantes
Rokubacteria
NC10
Acidobacteria
Tectomicrobia, Modulibacteria
Nitrospinae
Nitrospirae
Dadabacteria
Deltaprotebacteria
(Thermodesulfobacteria)
Chrysiogenetes
Deferribacteres
Hydrogenedentes NKB19
Spirochaetes
TM6
Epsilonproteobacteria
Alphaproteobacteria
Zetaproteo.
Acidithiobacillia
Betaproteobacteria
Gammaproteobacteria
0.4
Melainabacteria
RBX1
WOR1
Nomurabacteria
Kaiserbacteria
Adlerbacteria
Campbellbacteria
Giovannonibacteria
Wolfebacteria
Jorgensenbacteria
Azambacteria
Parcubacteria
Yanofskybacteria
Moranbacteria
Magasanikbacteria
Uhrbacteria
Falkowbacteria
Candidate
Phyla Radiation
SM2F11
Peregrinibacteria
Gracilibacteria BD1-5, GN02
Absconditabacteria SR1
Saccharibacteria
Berkelbacteria
Woesebacteria
Shapirobacteria
Amesbacteria
Collierbacteria
Pacebacteria
Beckwithbacteria
Roizmanbacteria
Gottesmanbacteria
Levybacteria
Daviesbacteria
Curtissbacteria
Microgenomates
Wirthbacteria
Dojkabacteria WS6
CPR1
CPR3
Katanobacteria
WWE3
Major lineages with isolated representative - italics
Major lineage lacking isolated representative -
Micrarchaeota
Diapherotrites
Nanohaloarchaeota
Aenigmarchaeota
Parvarchaeota
DPANN
Pacearchaeota
Nanoarchaeota
Woesearchaeota
Altiarchaeales
Z7ME43
Methanopyri
Methanococci
Hadesarchaea
Thermococci
Methanobacteria
Thermoplasmata
Archaeoglobi
Methanomicrobia
Archaea
YNPFFA
Crenarch.
Aigarch.
Korarch.
Halobacteria
Loki.
Thor.
TACK
Thaumarchaeota
Eukaryotes
Opisthokonta
Excavata
Archaeplastida
Chromalveolata
Amoebozoa

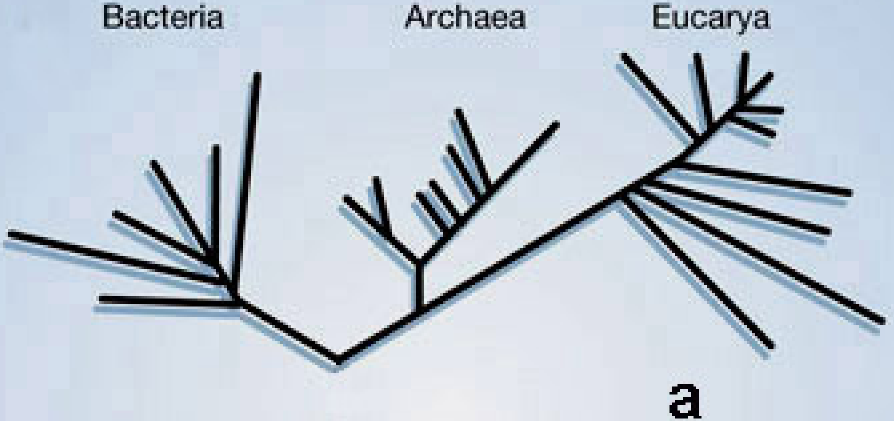
A) Old Paradigm

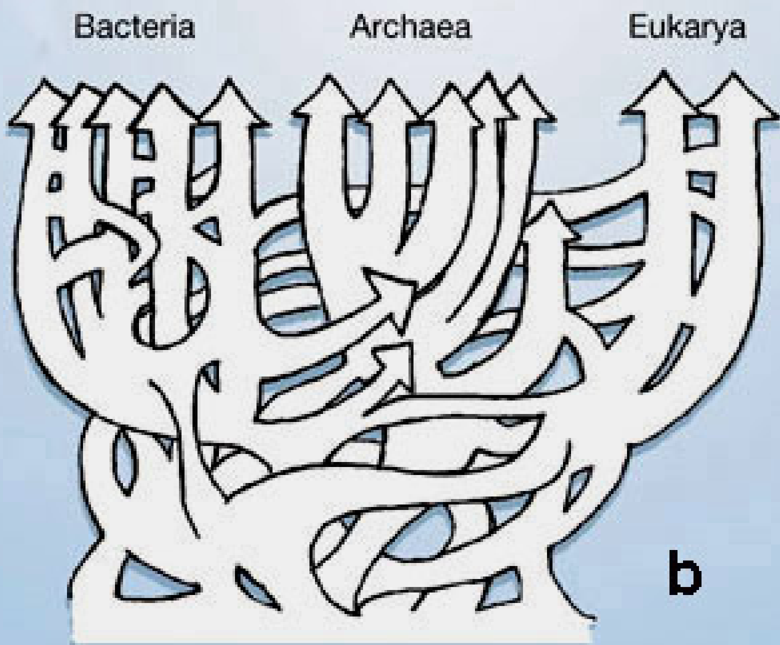


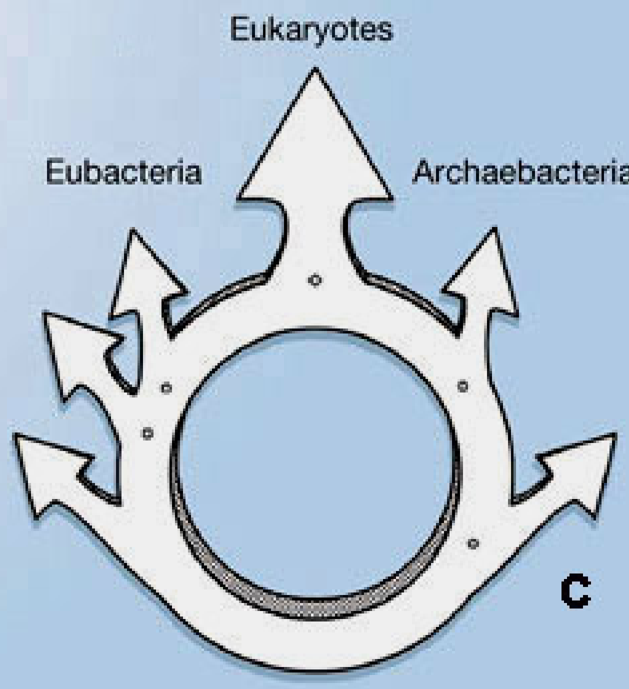
B) New Paradigm

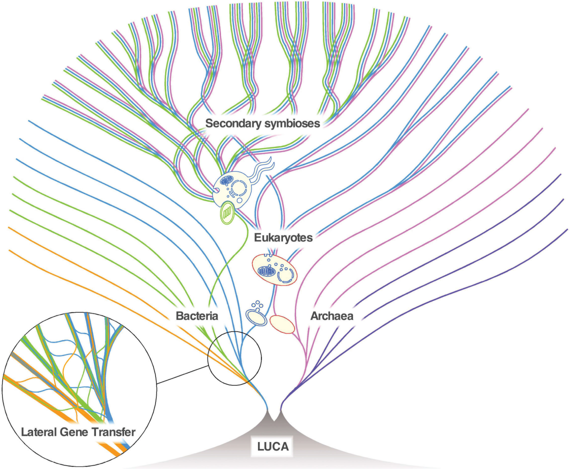


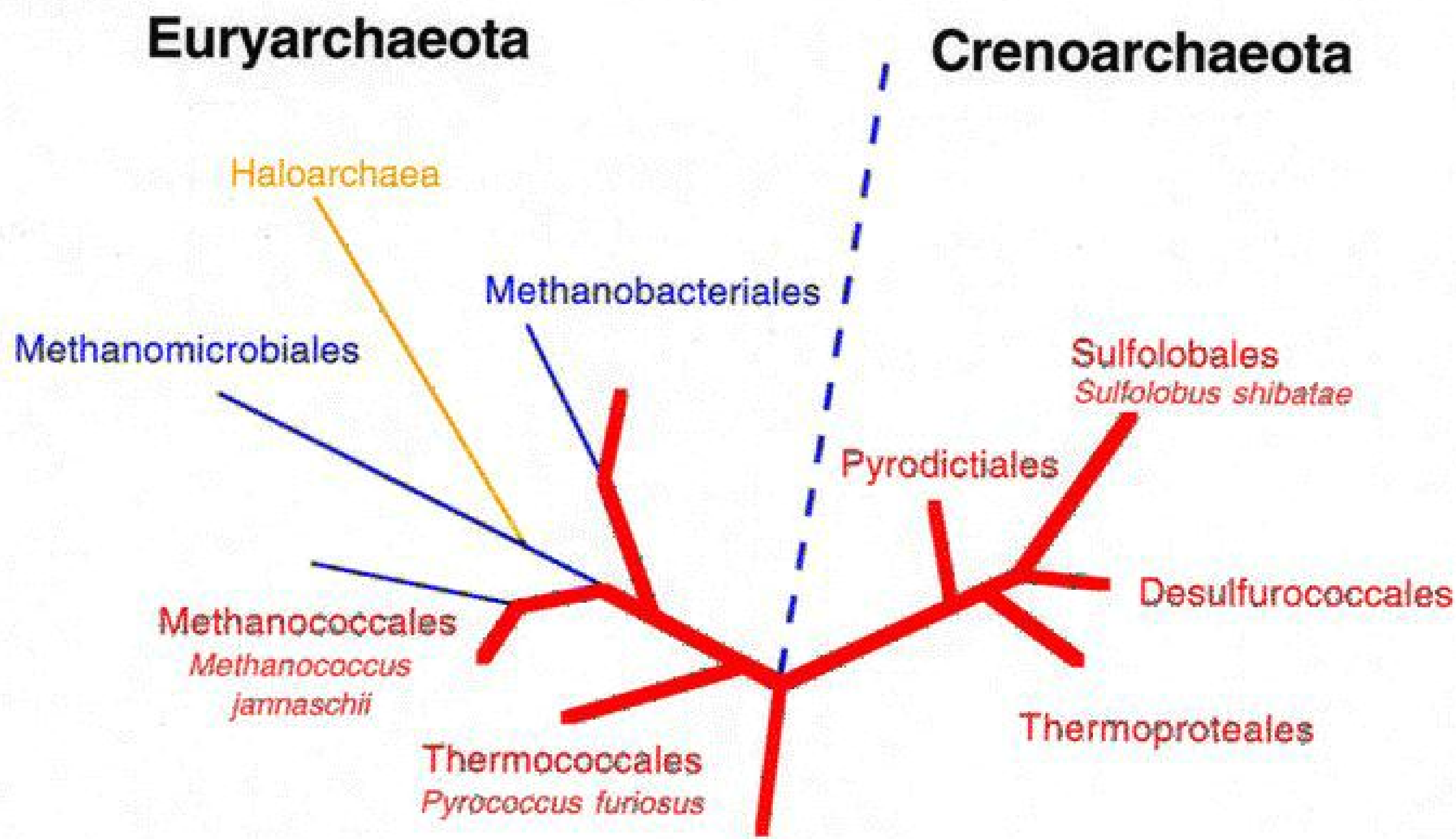
What tree?
What root?

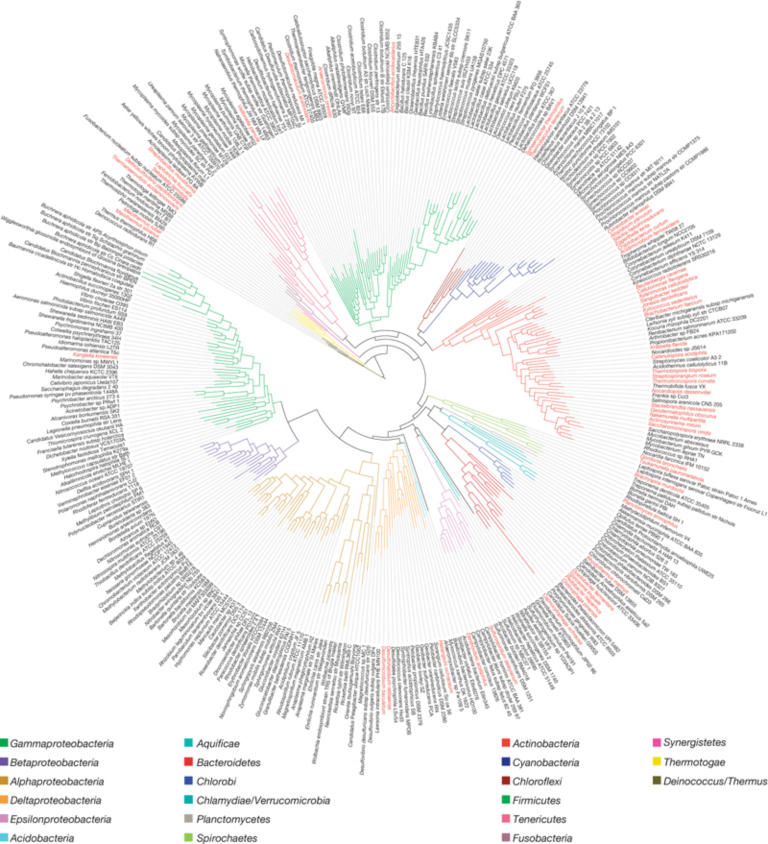


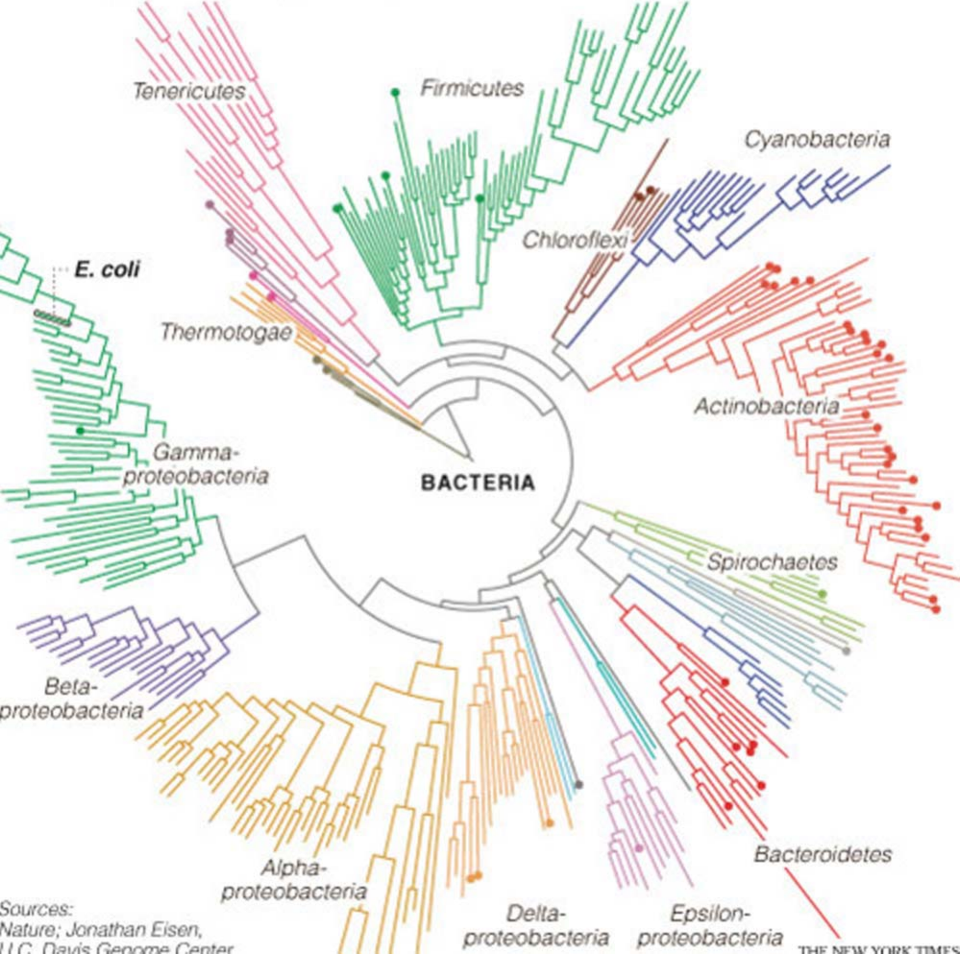





Secondary symbioses
Eukaryotes
Bacteria
Archaea
Lateral Gene Transfer
LUCA

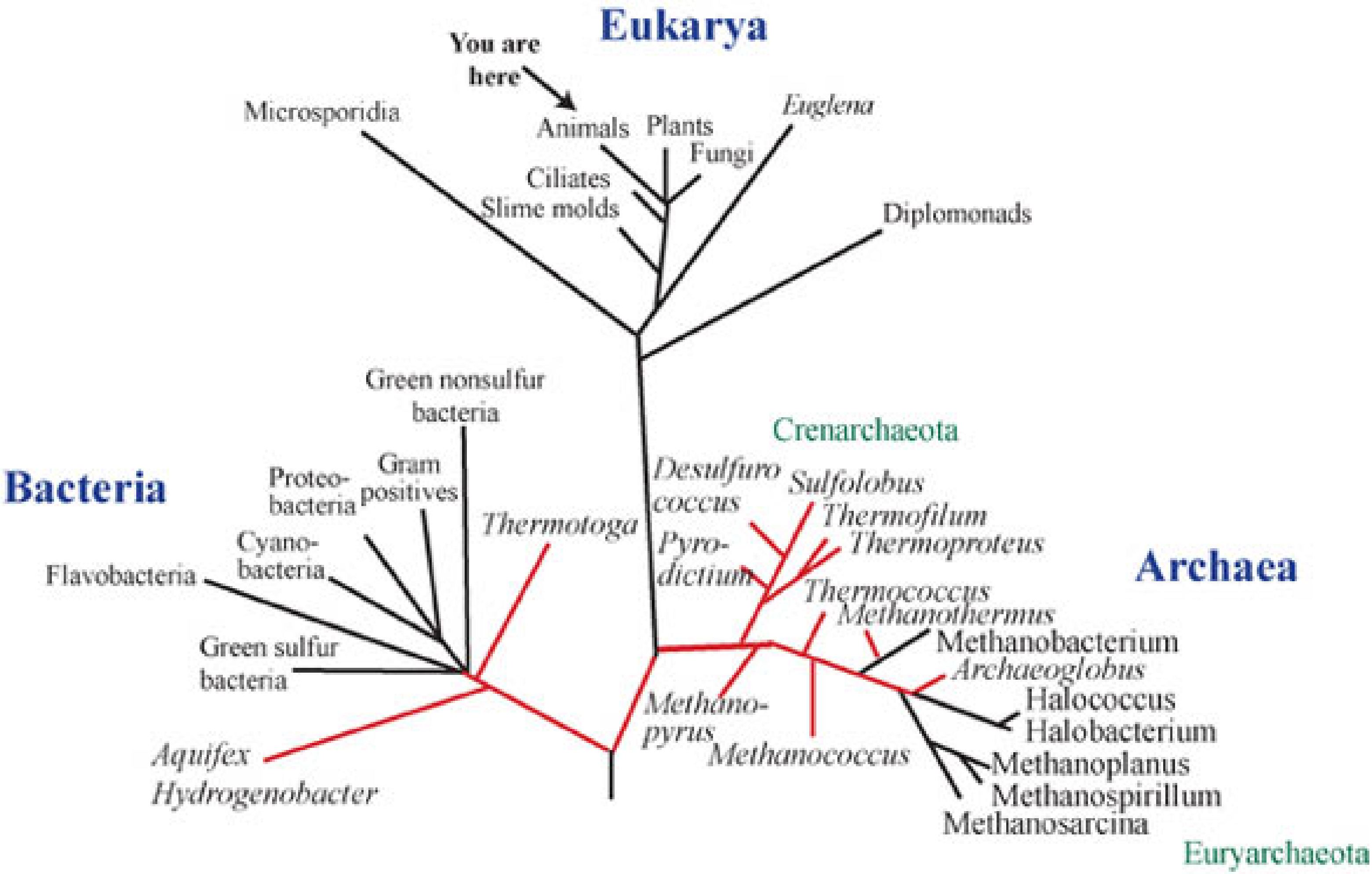

Euryarchaeota
Crenoarchaeota
Haloarchaea
Methanobacteriales
Methanomicrobiales
Sulfolobales
Sulfolobus shibatae
Pyrodictiales
Desulfurococcales
Methanococcales
Methanococcus
jannaschii
Thermoproteales
Thermococcales
Pyrococcus furiosus


Gammaproteobacteria
Betaproteobacteria
Alphaproteobacteria
Deltaproteobacteria
Epsilonproteobacteria
Acidobacteria
Aquificae
Bacteroidetes
Chlorobi
Chlamydiae/Verrucomicrobia
Planctomycetes
Spirochaetes
Actinobacteria
Cyanobacteria
Chloroflexi
Firmicutes
Tenericutes
Fusobacteria
Synergistetes
Thermotogae
Deinococcus/Thermus

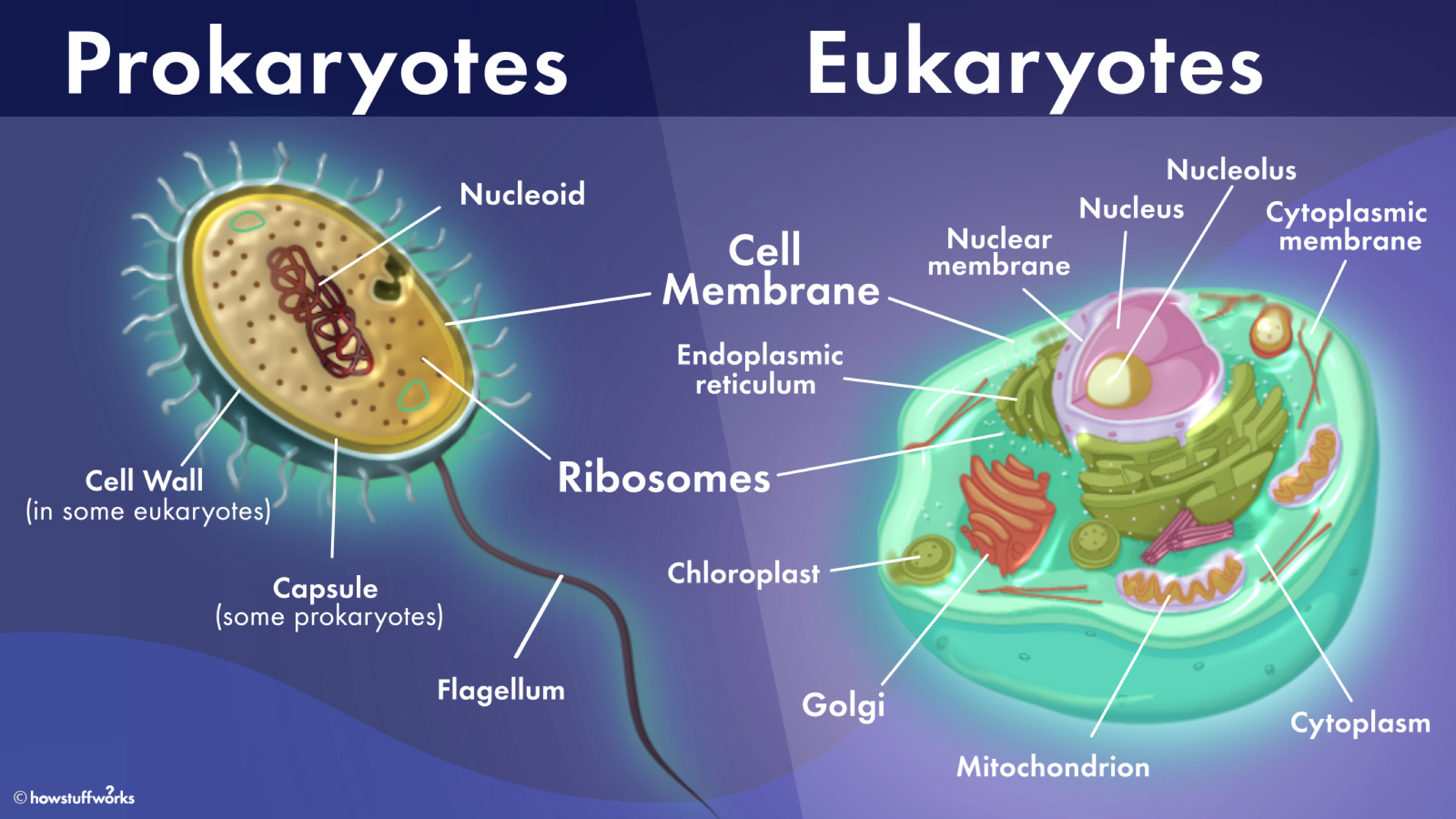


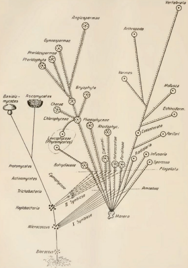
Sources:
Nature; Jonathan Eisen,
U.C. Davis Genome Center

THE NEW YORK TIMES

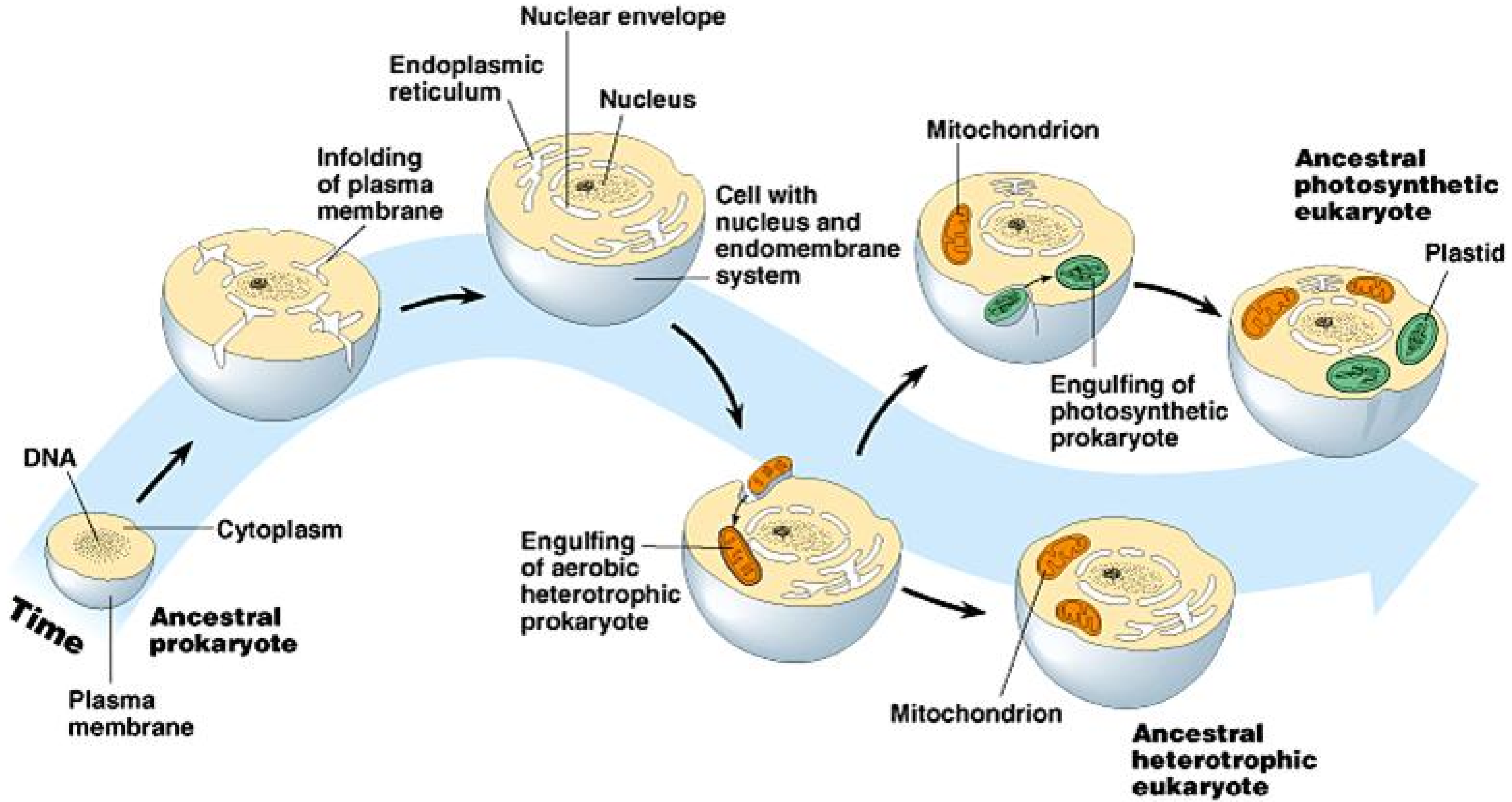


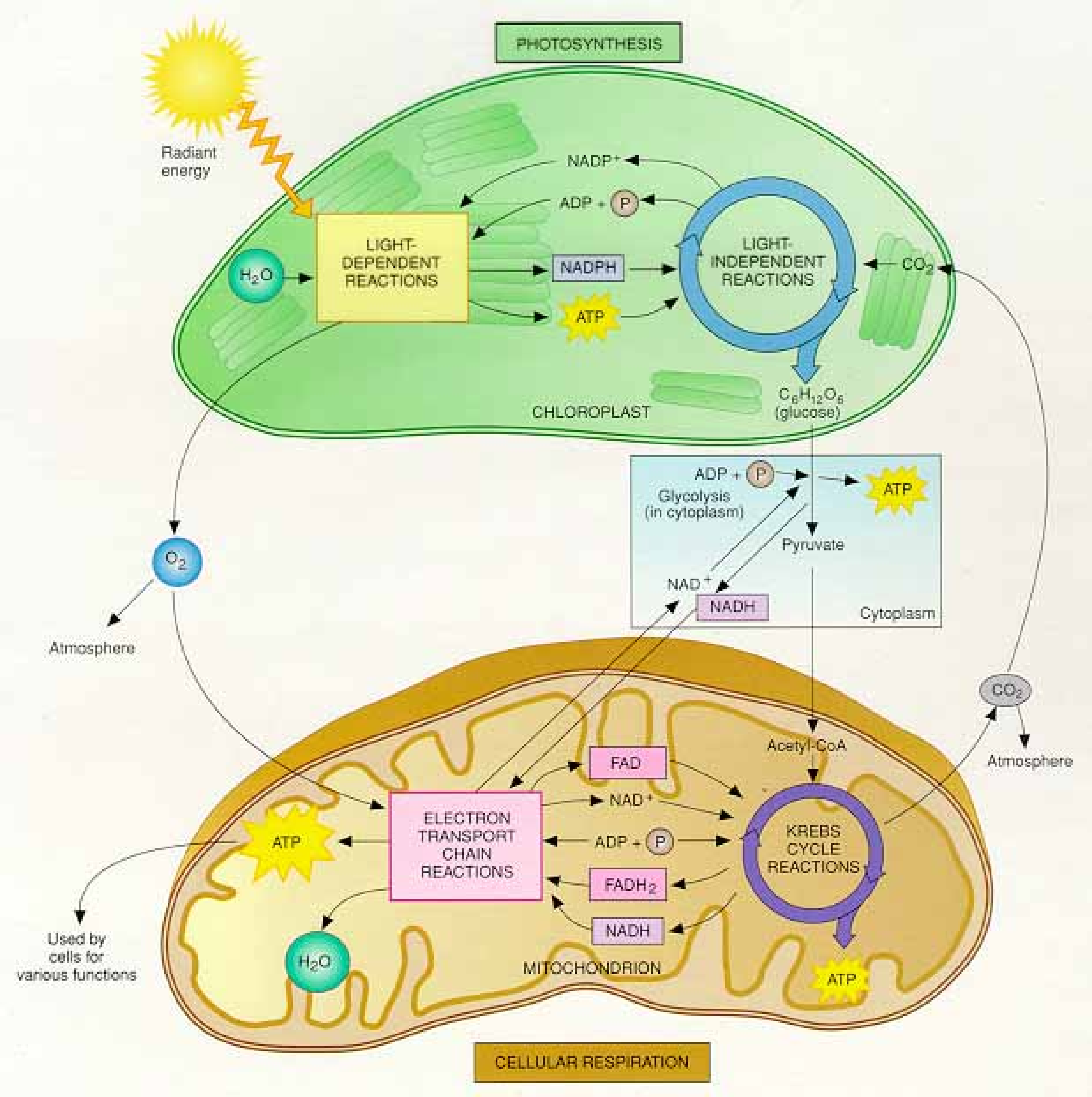
Eukarya
You are here
Microsporidia
Animals
Plants
Fungi
Euglena
Ciliates
Slime molds
Diplomonads
Green nonsulfur bacteria
Crenarchaeota
Bacteria
Proteo-bacteria
Gram positives
Desulfuro coccus
Sulfolobus
Thermofilum
Thermoproteus
Thermotoga
Cyano-bacteria
Pyro-dictium
Archaea
Flavobacteria
Thermococcus
Methanothermus
Methanobacterium
Green sulfur bacteria
Archaeoglobus
Halococcus
Halobacterium
Methano-pyrus
Methanococcus
Aquifex
Hydrogenobacter
Methanoplanus
Methanospirillum
Methanosarcina
Euryarchaeota

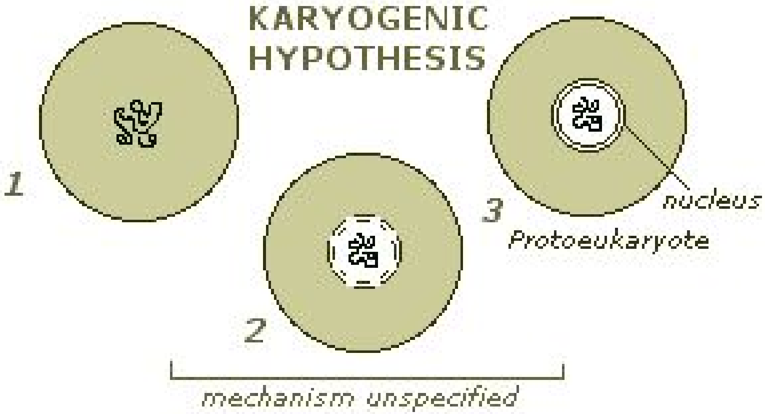

Prokaryotes
Eukaryotes
Nucleoid
Cell Membrane
Ribosomes
Cell Wall
(in some eukaryotes)
Capsule
(some prokaryotes)
Flagellum
Nucleolus
Nucleus
Nuclear membrane
Cytoplasmic membrane
Endoplasmic reticulum
Chloroplast
Golgi
Mitochondrion
Cytoplasm
© howstuffworks

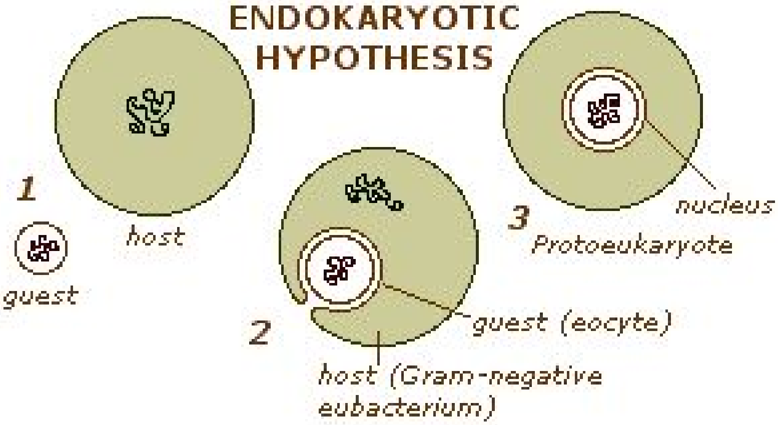


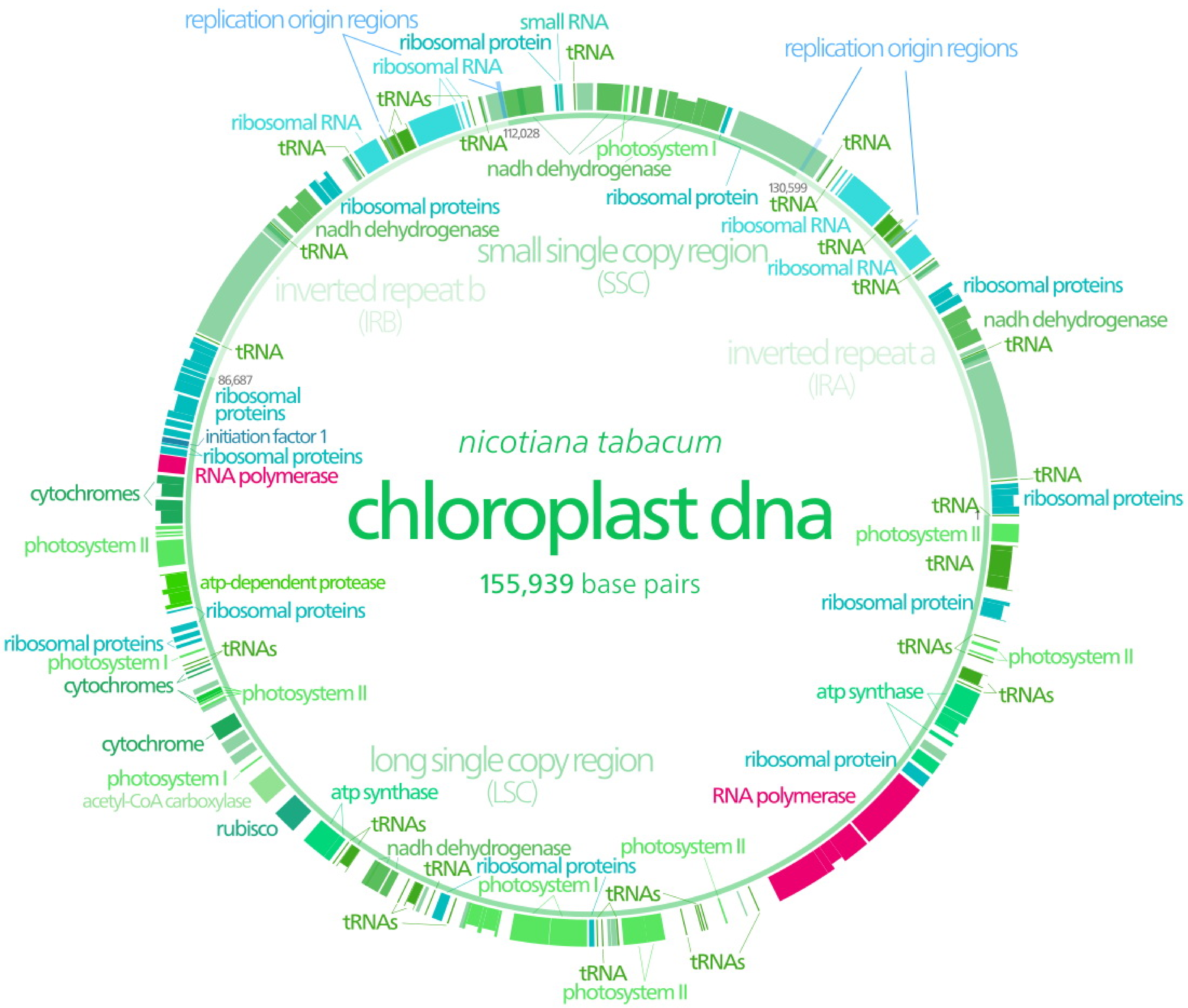
Vertebrata
Angiospermae
Arthropoda
Gymnospermae
Pteridospermae
Pteridophyta
Vermes
Mollusca
Basidiomycetes
Ascomycetes
Bryophyta
Charae
Echinoderm.
Chlorophyceae
Phaeophyceae
Rhodophyc.
Coelenterata
Poriferi
Leucophyceae (Phycomycetes)
Diatomac.
Heterocontae
Peridineae
Radiolaria
Infusoria
Sporozoa
Botrydiaceae
Protomycetes
Flagellata
Actinomycetes
Cyanophyceae
Trichobacteria
Amoebae
II Symbiose
Haplobacteria
Monera
I Symbiose
Micrococcus
Biococcus


Nuclear envelope
Endoplasmic reticulum
Nucleus
Infolding of plasma membrane
Cell with nucleus and endomembrane system
Mitochondrion
Ancestral photosynthetic eukaryote
Plastid
DNA
Cytoplasm
Engulfing of photosynthetic prokaryote
Engulfing of aerobic heterotrophic prokaryote
Time
Ancestral prokaryote
Plasma membrane
Mitochondrion
Ancestral heterotrophic eukaryote

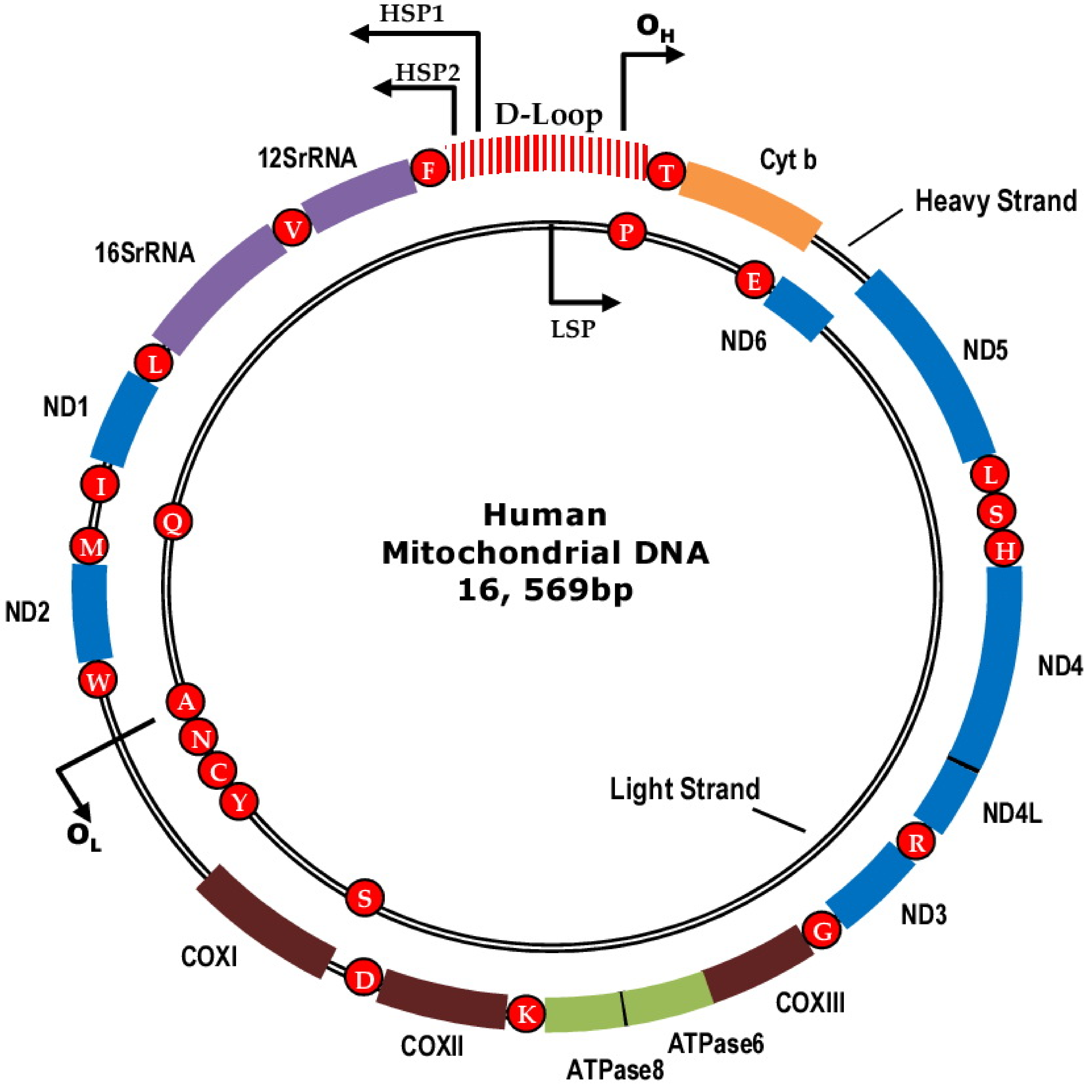

PHOTOSYNTHESIS
Radiant energy
$NADP^+$
ADP + P
LIGHT-DEPENDENT REACTIONS
H_2O
NADPH
ATP
LIGHT-INDEPENDENT REACTIONS
CO_2
$C_6H_{12}O_6$ (glucose)
CHLOROPLAST
ADP + P
ATP
Glycolysis (in cytoplasm)
Pyruvate
NAD^+
NADH
Cytoplasm
O_2
Atmosphere
CO_2
Atmosphere
Acetyl-CoA
FAD
NAD^+
ELECTRON TRANSPORT CHAIN REACTIONS
ADP + P
KREBS CYCLE REACTIONS
ATP
$FADH_2$
NADH
Used by cells for various functions
H_2O
MITOCHONDRION
ATP
CELLULAR RESPIRATION


KARYOGENIC HYPOTHESIS
1
2
3
nucleus
Protoeukaryote
mechanism unspecified

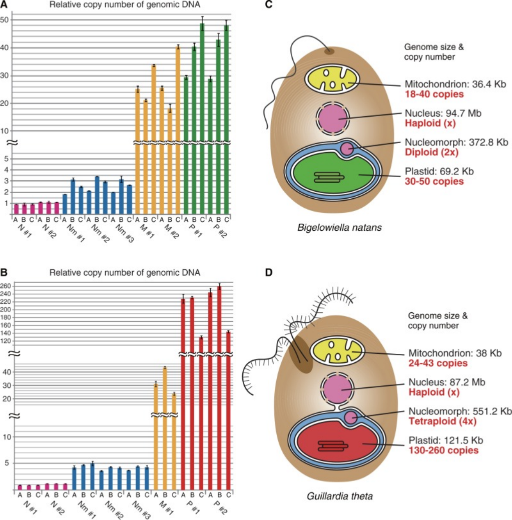

ENDOKARYOTIC HYPOTHESIS
1
host
guest
2
guest (eocyte)
host (Gram-negative eubacterium)
3
nucleus
Protoeukaryote

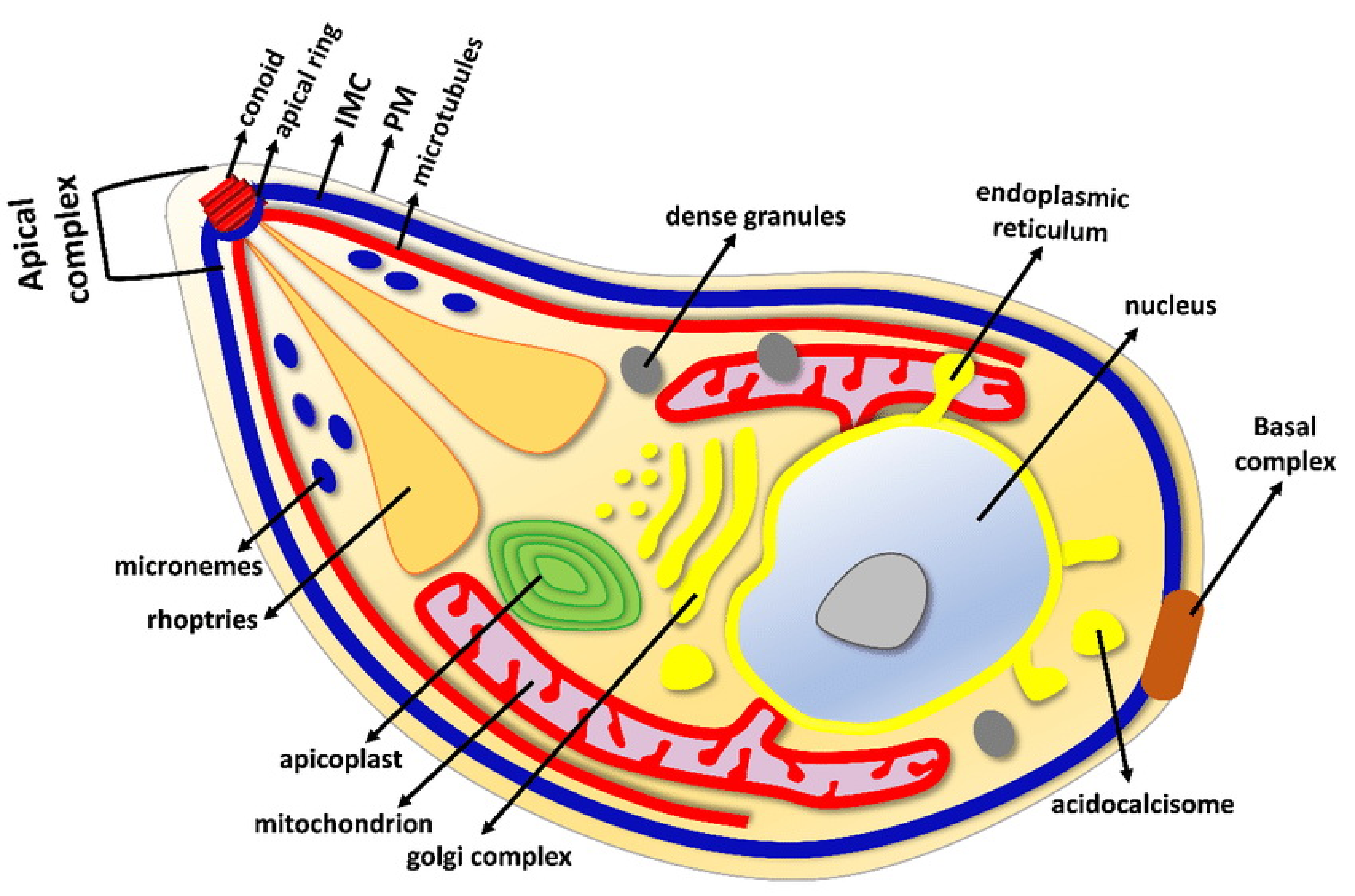


chloroplast dna
nicotiana tabacum
155,939 base pairs
small single copy region
(SSC)
inverted repeat b
(IRB)
inverted repeat a
(IRA)
long single copy region
(LSC)
replication origin regions
replication origin regions
small RNA
ribosomal protein
ribosomal RNA
tRNA
tRNAs
ribosomal RNA
tRNA
tRNA
112,028
photosystem I
nadh dehydrogenase
ribosomal protein
130,599
tRNA
tRNA
ribosomal RNA
tRNA
ribosomal RNA
tRNA
ribosomal proteins
nadh dehydrogenase
tRNA
ribosomal proteins
nadh dehydrogenase
tRNA
tRNA
86,687
ribosomal
proteins
initiation factor 1
ribosomal proteins
RNA polymerase
cytochromes
tRNA
ribosomal proteins
tRNA
1
photosystem II
photosystem II
tRNA
atp-dependent protease
ribosomal protein
ribosomal proteins
ribosomal proteins
tRNAs
photosystem II
photosystem I
tRNAs
cytochromes
photosystem II
atp synthase
tRNAs
cytochrome
ribosomal protein
photosystem I
RNA polymerase
acetyl-CoA carboxylase
atp synthase
rubisco
tRNAs
nadh dehydrogenase
photosystem II
tRNA
ribosomal proteins
photosystem I
tRNAs
tRNAs
tRNA
tRNAs
photosystem II


HSP1
HSP2
O_H
D-Loop
12SrRNA
Cyt b
Heavy Strand
16SrRNA
LSP
ND6
ND5
ND1
Human
Mitochondrial DNA
16, 569bp
ND2
ND4
Light Strand
O_L
ND4L
ND3
COXI
COXIII
COXII
ATPase6
ATPase8
F
T
V
P
E
L
I
Q
M
W
A
N
C
Y
S
D
K
G
R
H


primary endosymbiosis
secondary endosymbiosis
Eukaryotic cell
Nucleus
Phagosomal membrane
Free cyanobacterium
Eukaryotic
cell membrane
Eukaryotic cell
(secondary endosymbiont)
Nuclei
Double-membraned chloroplast
(primary endosymbiont)
Quadruple-membraned
chloroplast
(secondary endosymbiont)
Nucleomorph
(Secondary endosymbiont's
nucleus)
Periplastid membrane
(secondary endosymbiont's
cell membrane)
Epiplastid membrane
(phagosomal membrane)
Cyanobacterial
cell membranes
Phagosomal membrane
Peptidoglycan wall
Intermembrane space
Chloroplast
membranes
Thylakoids
Stroma
Chloroplast
inner membrane
Intermembrane
space
Chloroplast
outer membrane
Nucleomorph
Periplastid space
Periplastid
membrane
Epiplastid space
Epiplastid
membrane
Periplastid
membrane
Epiplastid membrane
Triple-membraned
chloroplast


A
Relative copy number of genomic DNA
N #1
N #2
Nm #1
Nm #2
Nm #3
M #1
M #2
P #1
P #2
B
Relative copy number of genomic DNA
N #1
N #2
Nm #1
Nm #2
Nm #3
M #1
P #1
P #2
C
Genome size & copy number
Mitochondrion: 36.4 Kb
18-40 copies
Nucleus: 94.7 Mb
Haploid (x)
Nucleomorph: 372.8 Kb
Diploid (2x)
Plastid: 69.2 Kb
30-50 copies
Bigelowiella natans
D
Genome size & copy number
Mitochondrion: 38 Kb
24-43 copies
Nucleus: 87.2 Mb
Haploid (x)
Nucleomorph: 551.2 Kb
Tetraploid (4x)
Plastid: 121.5 Kb
130-260 copies
Guillardia theta


conoid
apical ring
IMC
PM
microtubules
Apical complex
dense granules
endoplasmic reticulum
nucleus
Basal complex
micronemes
rhoptries
apicoplast
mitochondrion
golgi complex
acidocalcisome

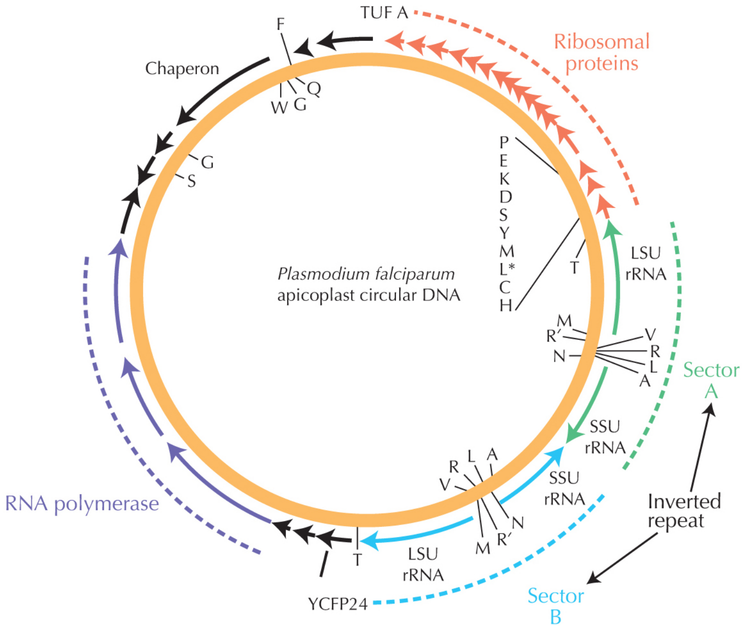
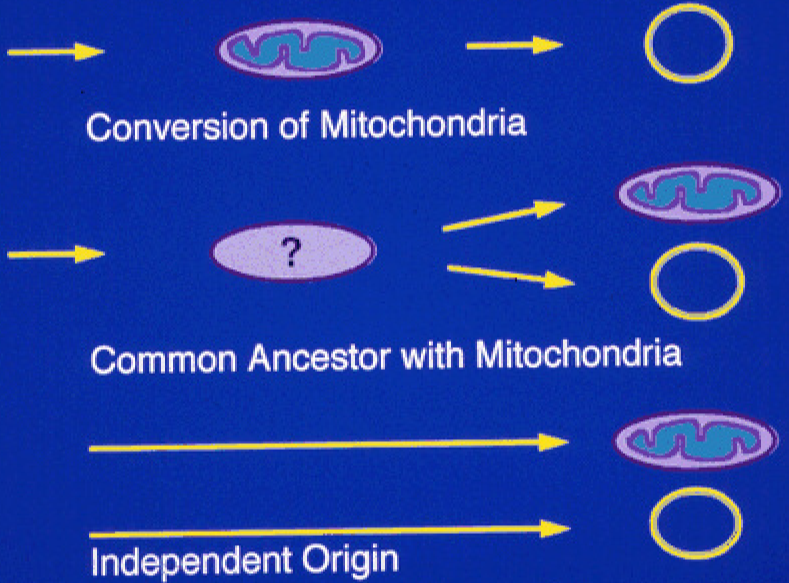
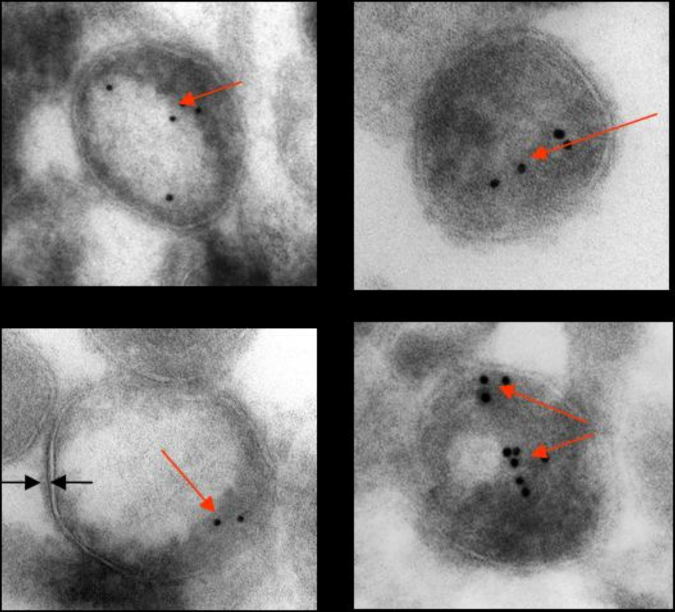


FIGURE 8.8. Apicoplast genome from *Plasmodium falciparum*. Recall from Aim and Scope that the apicoplast is related to chloroplasts. Genes are indicated by *arrows*, which show the direction of transcription. *Broken lines* highlight functional regions. Ribosomal RNA genes are indicated by LSU (large subunit) and SSU (small subunit). Each tRNA is labeled with the single-letter abbreviation of the corresponding amino acid.

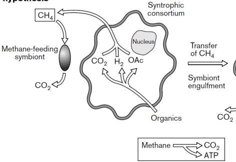
8.8, redrawn from Marechal E. et al., *Trends Plant Sci.* **6:** 200–205, © 2001 Elsevier

Origin of Hydrogenosomes





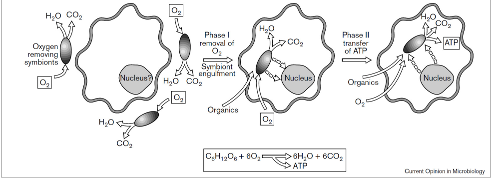
The syntrophy hypothesis



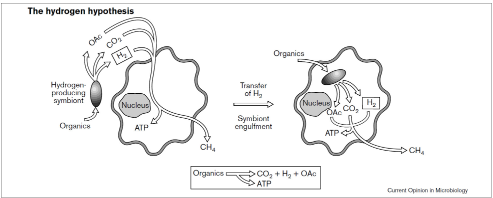
Current Opinion in Microbiology

A schematic view of the syntrophy hypothesis for the origin of aerobic respiration in eukaryotes [42•]. In this model, the host is a syntrophic consortium consisting of hydrogen-producing bacteria and anaerobic, hydrogen-dependent methanotrophs. The symbiont that ultimately becomes the mitochondrion is initially an anaerobic methanotroph that depends on the methane produced by the syntrophic consortium. Here, it is proposed that the mitochondrion originated subsequent to the establishment of the eukaryotic cell. See the text for further details.

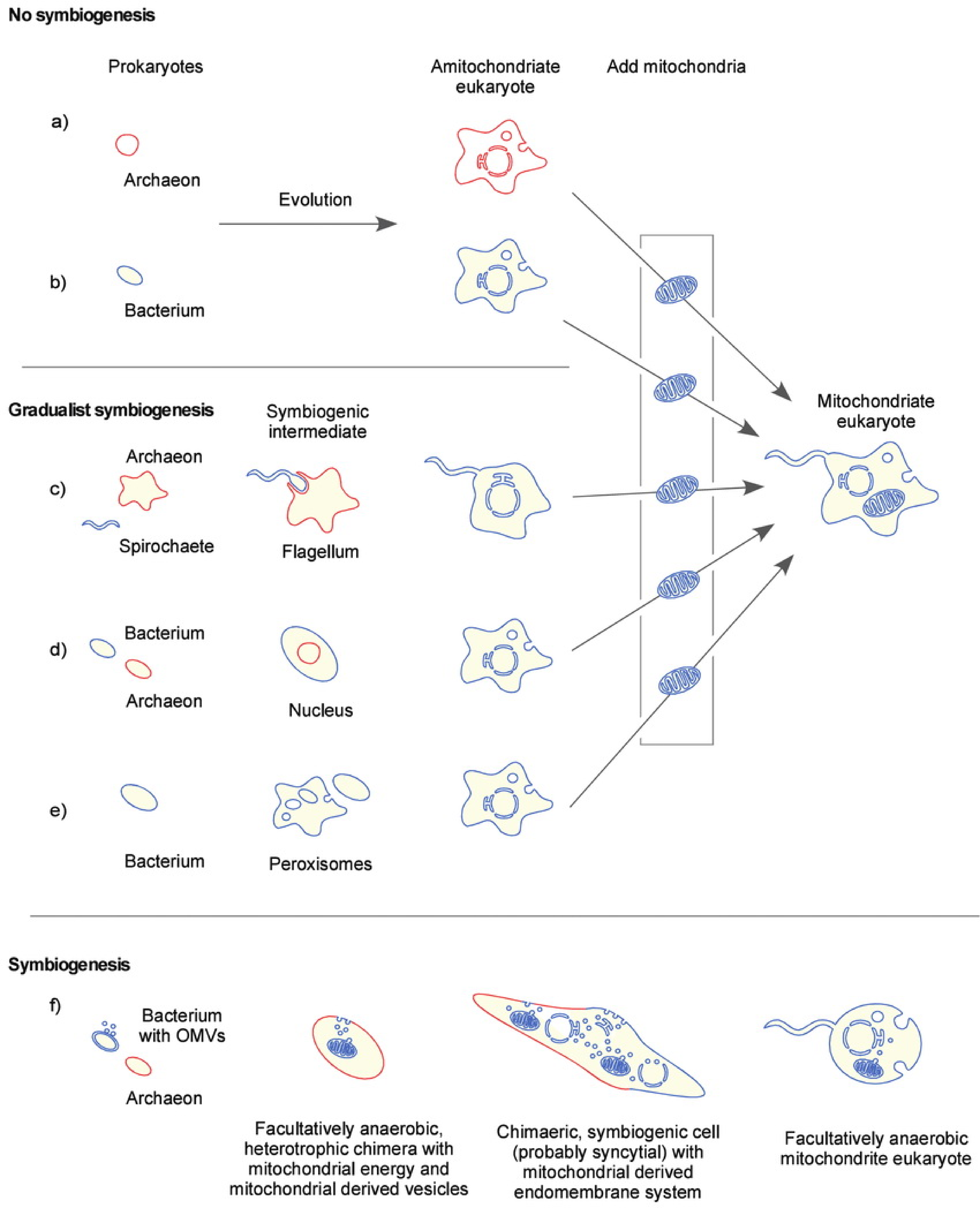
The ox-tox hypothesis

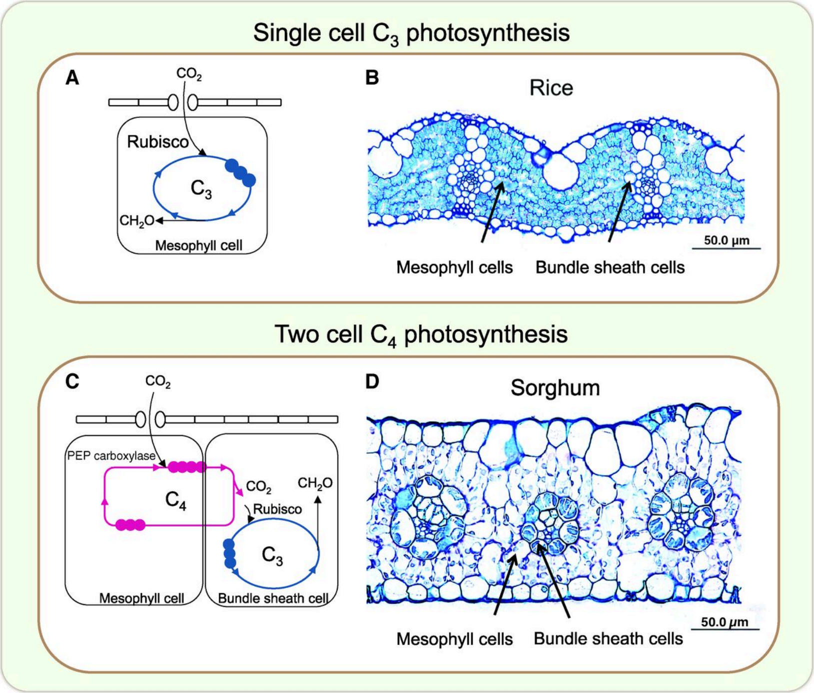


A schematic view of the ox-tox hypothesis for the origin of aerobic respiration in eukaryotes. Here, the acquisition of mitochondria is based on the symbiosis established by a bacterium in two phases. In phase I, the symbiont detoxifies the host cytoplasm by consuming oxygen. During phase II, the transport of ATP from the mitochondrion to the host cell is implemented by the acquisition of appropriate proteins encoded by the host nuclear genome. The dashed arrows represent the transfer of bioenergetic and information genes from the proto-mitochondrion to the nuclear genome (phase I) and the evolution of novel genes in the nuclear genome for mitochondrial functions (phase II). See the text for further details.



A schematic view of the hydrogen hypothesis for the origin of aerobic respiration in eukaryotes [10•]. It is suggested that the initial symbiobitic relation leading to mitochondria was supported by the transfer of hydrogen from a hydrogen-producing bacterium to an anaerobic, hydrogen-dependent host. Here, mitochondria are thought to have been acquired simultaneously with the origin of the eukaryotic lineage. See the text for further details. OAc, acetyl CoA.

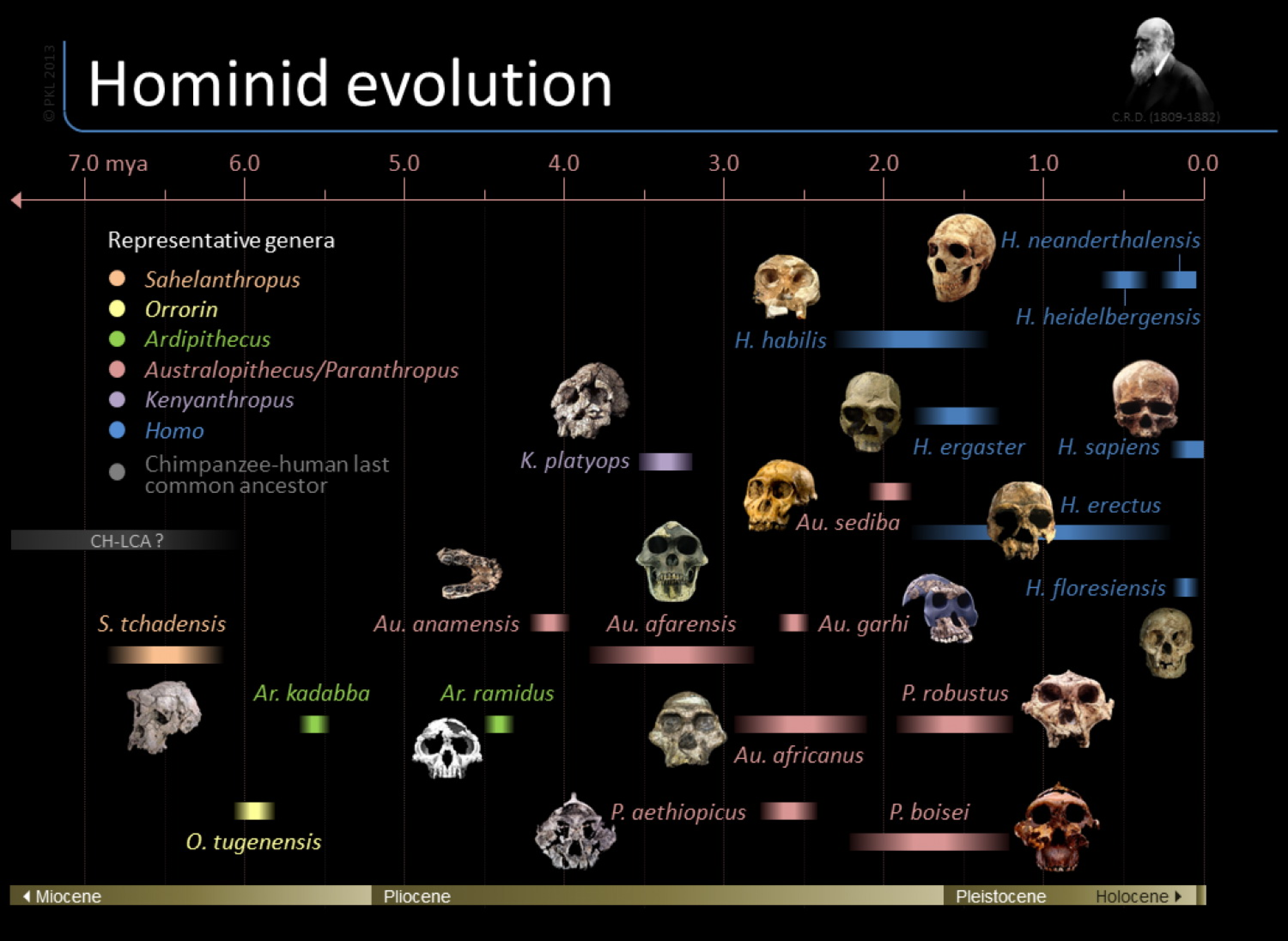

No symbiogenesis
Prokaryotes
Amitochondriate eukaryote
Add mitochondria
a)
Archaeon
Evolution
b)
Bacterium
Mitochondriate eukaryote
Gradualist symbiogenesis
Symbiogenic intermediate
Archaeon
c)
Spirochaete
Flagellum
Bacterium
d)
Archaeon
Nucleus
e)
Bacterium
Peroxisomes
Symbiogenesis
f)
Bacterium with OMVs
Archaeon
Facultatively anaerobic, heterotrophic chimera with mitochondrial energy and mitochondrial derived vesicles
Chimaeric, symbiogenic cell (probably syncytial) with mitochondrial derived endomembrane system
Facultatively anaerobic mitochondrite eukaryote



Single cell C_3 photosynthesis
A
CO_2
Rubisco
C_3
CH_2O
Mesophyll cell
B
Rice
50.0 µm
Mesophyll cells
Bundle sheath cells
Two cell C_4 photosynthesis
C
CO_2
PEP carboxylase
C_4
CO_2
CH_2O
Rubisco
C_3
Mesophyll cell
Bundle sheath cell
D
Sorghum
50.0 µm
Mesophyll cells
Bundle sheath cells

S.N.	Calvin cycle (C_3 cycle)	Hatch and Slack cycle (C_4 cycle)
1.	The primary acceptor of CO_2 is a 5-carbon compound, Ribulose-1, 5- biphosphate.	The primary acceptor of CO_2 is a 3-carbon compound, phosphoenol pyruvic acid.
2.	The first stable compound is a 3-carbon compound, phosphoglyceric acid.	The first stable compound is a 4-carbon compound, oxaloacetic acid.
3.	Chloroplasts are monomorphic (only one type).	Chloroplasts are dimorphic (two types of chloroplasts); the mesophyll chloroplasts perform C_4 cycle and bundle sheath chloroplasts perform C_3 cycle.
4.	Leaves don't show Kranz anatomy.	Leaves show Kranz anatomy.
5.	Photorespiration occurs in C_3 plants.	Photorespiration rarely occurs.
6.	It is less efficient in utilizing atmospheric carbon dioxide.	It is much efficient in utilizing atmospheric carbon dioxide (even when stomata are nearly closed.)
7.	Plants are adapted to all climates except for saline conditions (salty conditions).	Plants are adapted to tropical climates and can also tolerate halophytic (salty) conditions.
8.	It is less energy expensive (requires only 18 ATP for the synthesis of one molecule of glucose).	It is more energy expensive and requires 30 ATP for the synthesis of one molecule of glucose.

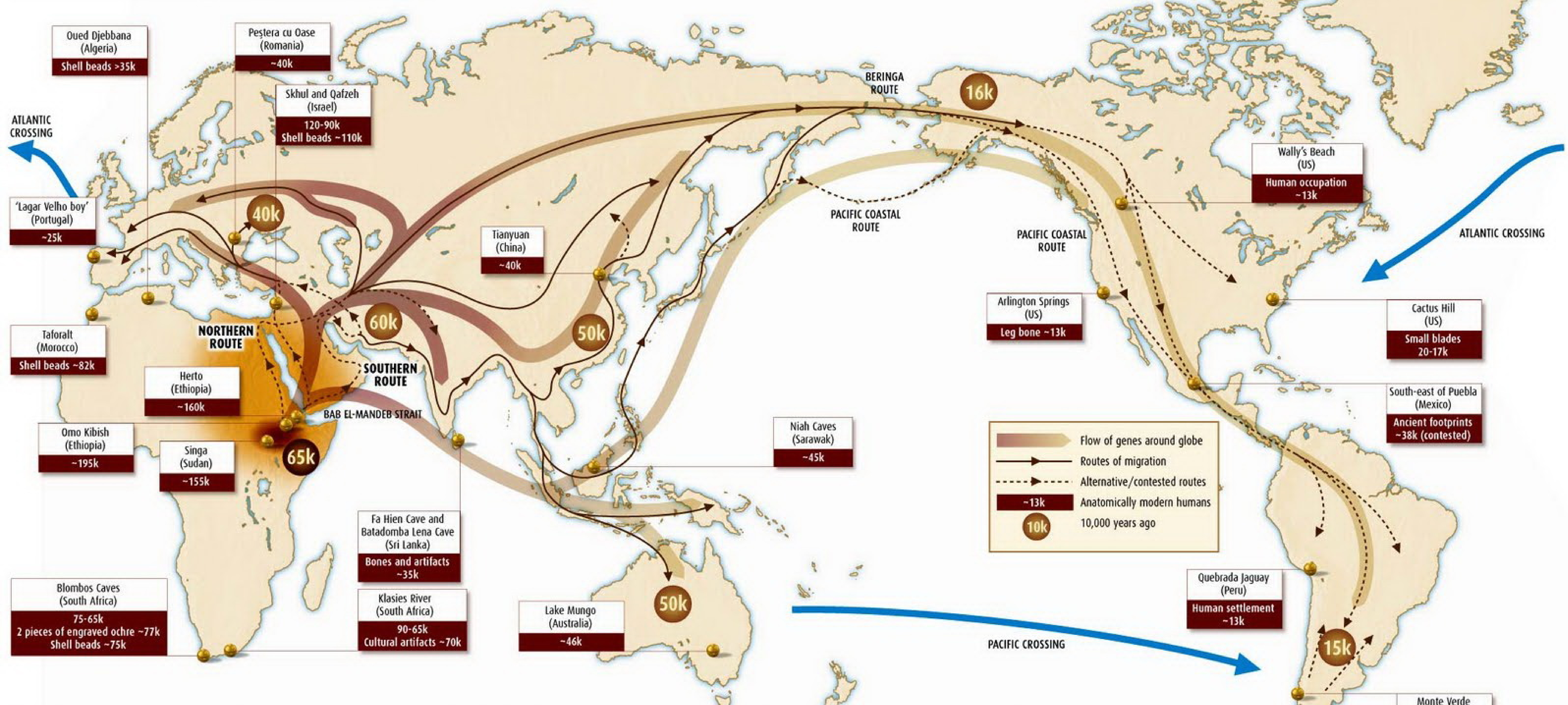
Differences between C3 and C4 cycle



© PKL 2013
Hominid evolution
C.R.D. (1809-1882)
7.0 mya
6.0
5.0
4.0
3.0
2.0
1.0
0.0
Representative genera
Sahelanthropus
Orrorin
Ardipithecus
Australopithecus/Paranthropus
Kenyanthropus
Homo
Chimpanzee-human last common ancestor
CH-LCA ?
H. neanderthalensis
H. heidelbergensis
H. habilis
K. platyops
H. ergaster
H. sapiens
Au. sediba
H. erectus
H. floresiensis
S. tchadensis
Au. anamensis
Au. afarensis
Au. garhi
Ar. kadabba
Ar. ramidus
P. robustus
Au. africanus
P. aethiopicus
P. boisei
O. tugenensis
Miocene
Pliocene
Pleistocene
Holocene

THE MIGRATION OF ANATOMICALLY MODERN HUMANS

Evidence from fossils, ancient artefacts and genetic analyses combine to tell a compelling story

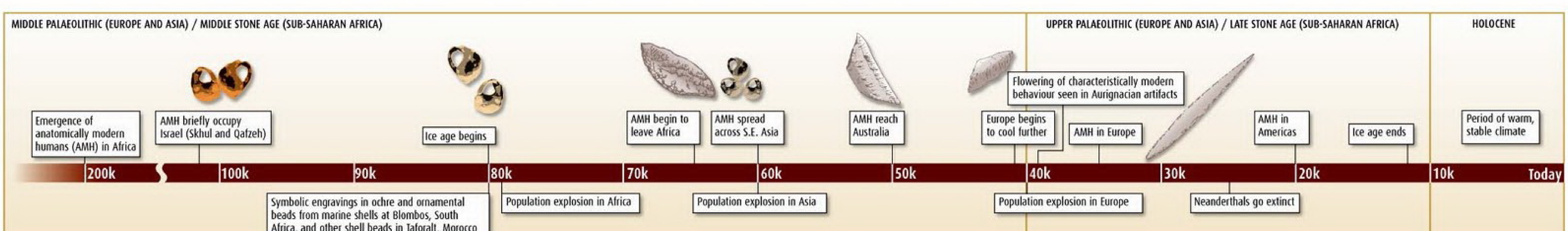


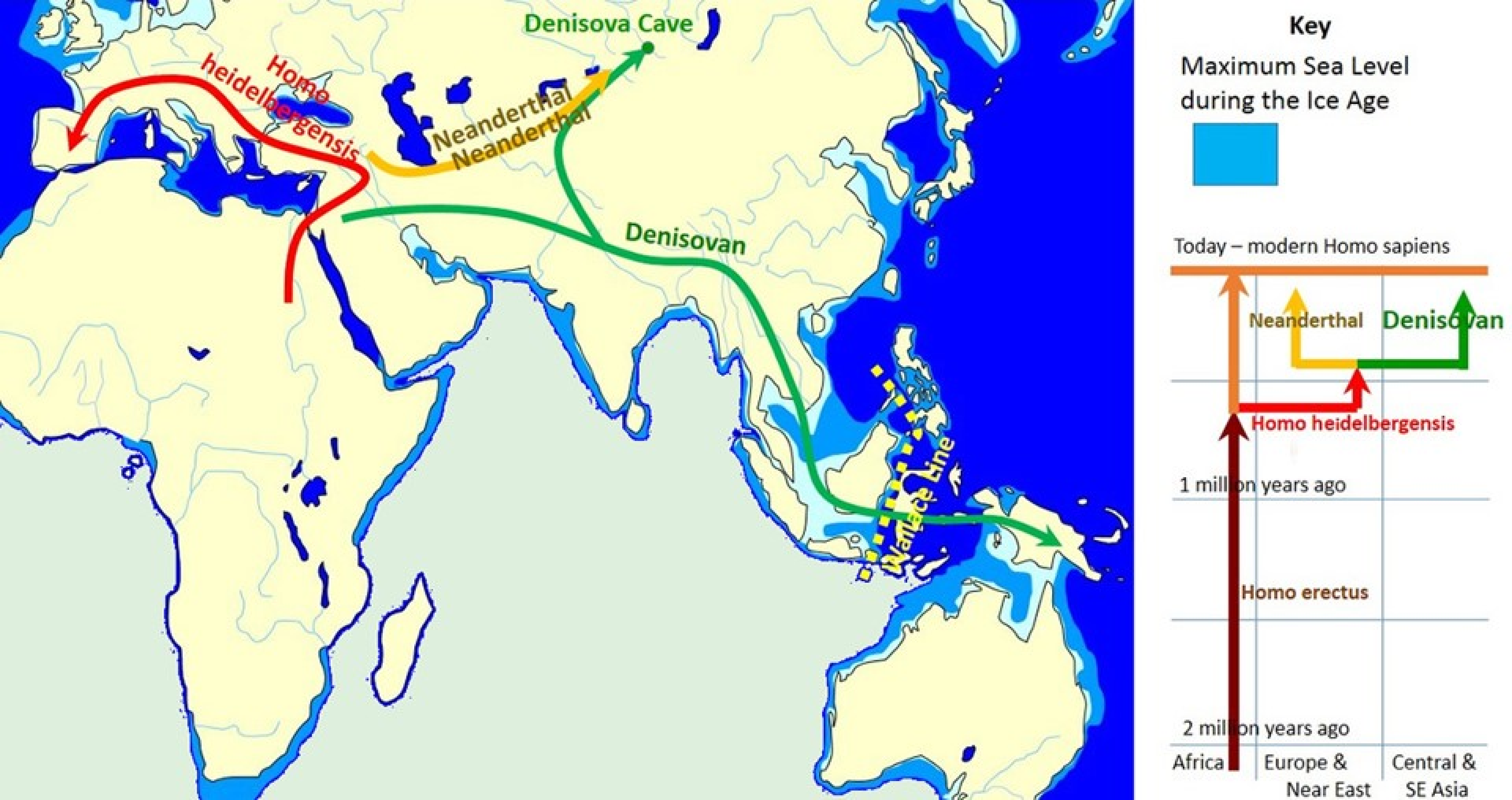
Two routes jump out as prime candidates for the human exodus out of Africa. A northern route would have taken our ancestors from their base in eastern sub-Saharan Africa across the Sahara desert, then through Sinai and into the Levant. An alternative southern route may have charted a path from Djibouti or Eritrea in the Horn of Africa across the Bab el-Mandeb strait and into Yemen and around the Arabian peninsula. The plausibility of these two routes as gateways out of Africa has been studied as part of the UK's Natural Environment Research Council's programme "Environmental Factors in the Chronology of Human Evolution & Dispersal" (EFCHED).

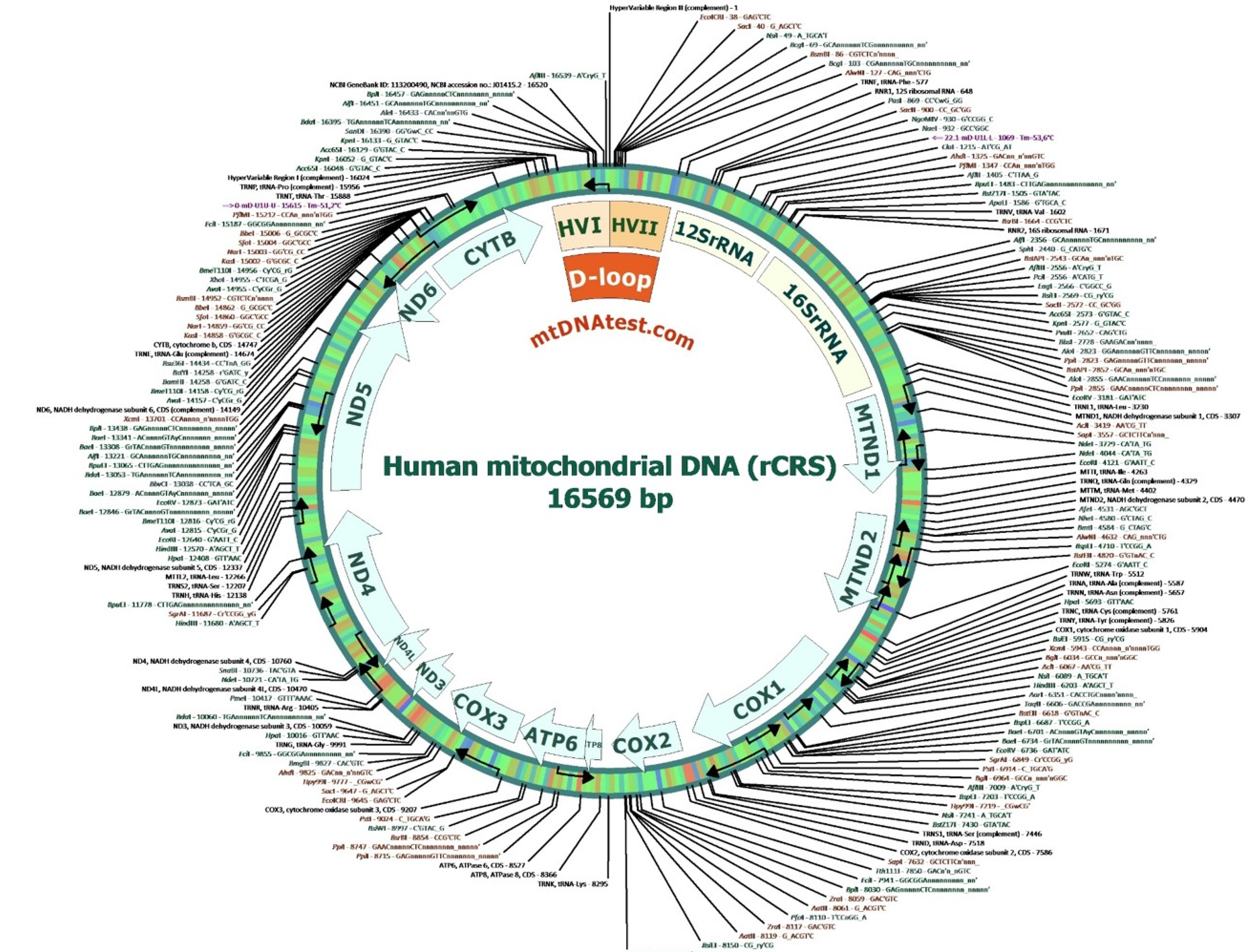
During the last ice age, from about 80,000 to 11,000 years ago, sea levels dropped as the ice sheets grew, exposing large swathes of land now submerged under water and connecting regions now separated by the sea. By reconstructing ancient shorelines, the EFCHED team found that the Bab el-Mandeb strait, now around 30 kilometres wide and one of the world's busiest shipping lanes, was then a narrow, shallow channel.

Early humans may have taken this southern route out of Africa. The northern route appears easier, especially given the team's finding that the Suez basin was dry during the last ice age. But crossing the Sahara desert is no small matter. EFCHED scientist Simon Armitage of the Royal Holloway University of London has found some clues as to how this might have been possible. During the past 150,000 years, North Africa has experienced abrupt switches between dry, arid conditions and a humid climate. During the longer wetter periods huge lakes existed in both Chad and Libya, which would have provided a "humid corridor" across the Sahara.

Armitage has discovered that these lakes were present around 10,000 years ago, when there is abundant evidence for human occupation of the Sahara, as well as around 115,000 years ago, when our ancestors first made forays into Israel. It is unknown whether another humid corridor appeared between about 65,000 and 50,000 years ago, the most likely time frame for the human exodus. Moreover, accumulating evidence is pointing to the southern route as the most likely jumping-off point.

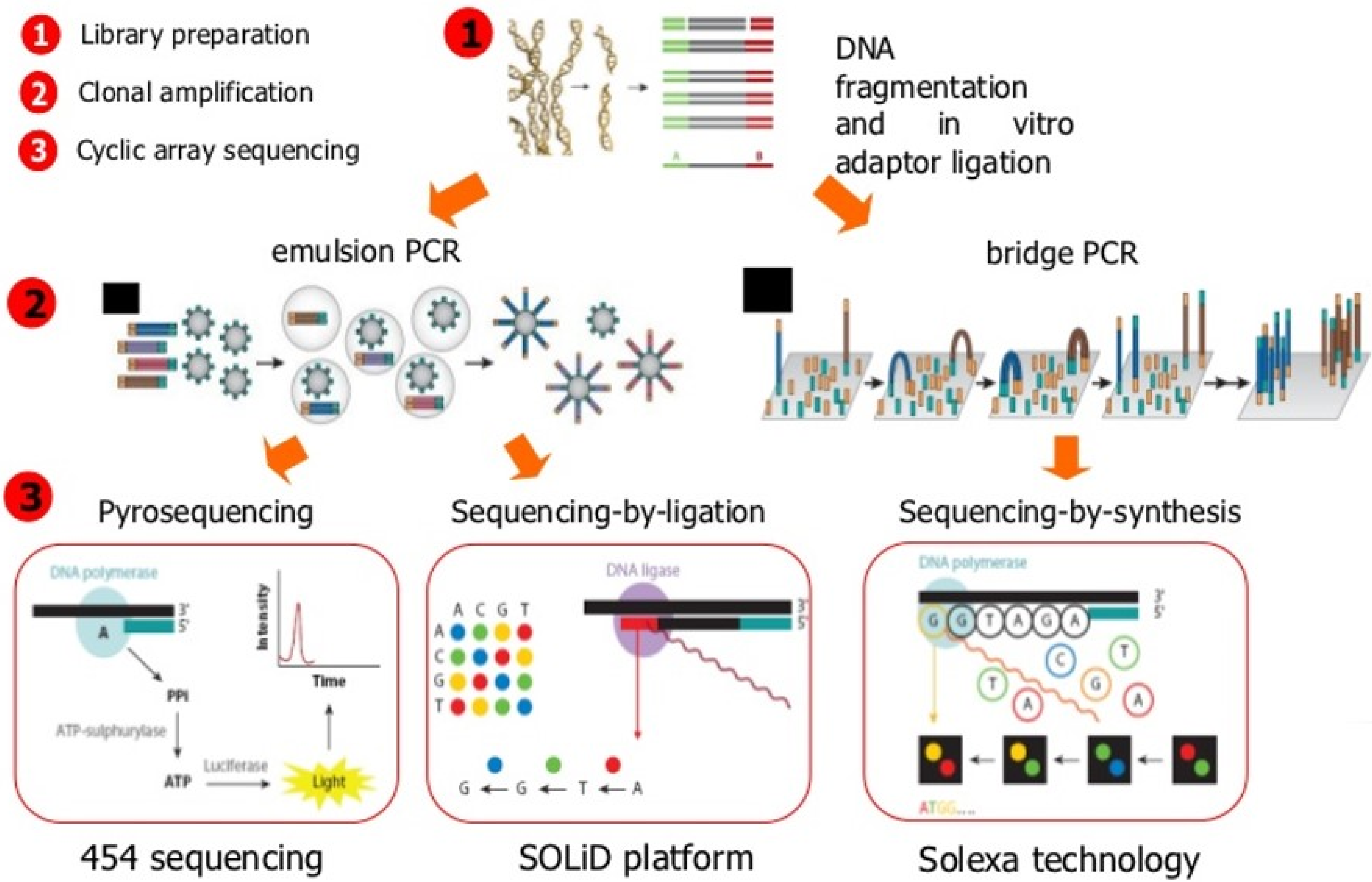


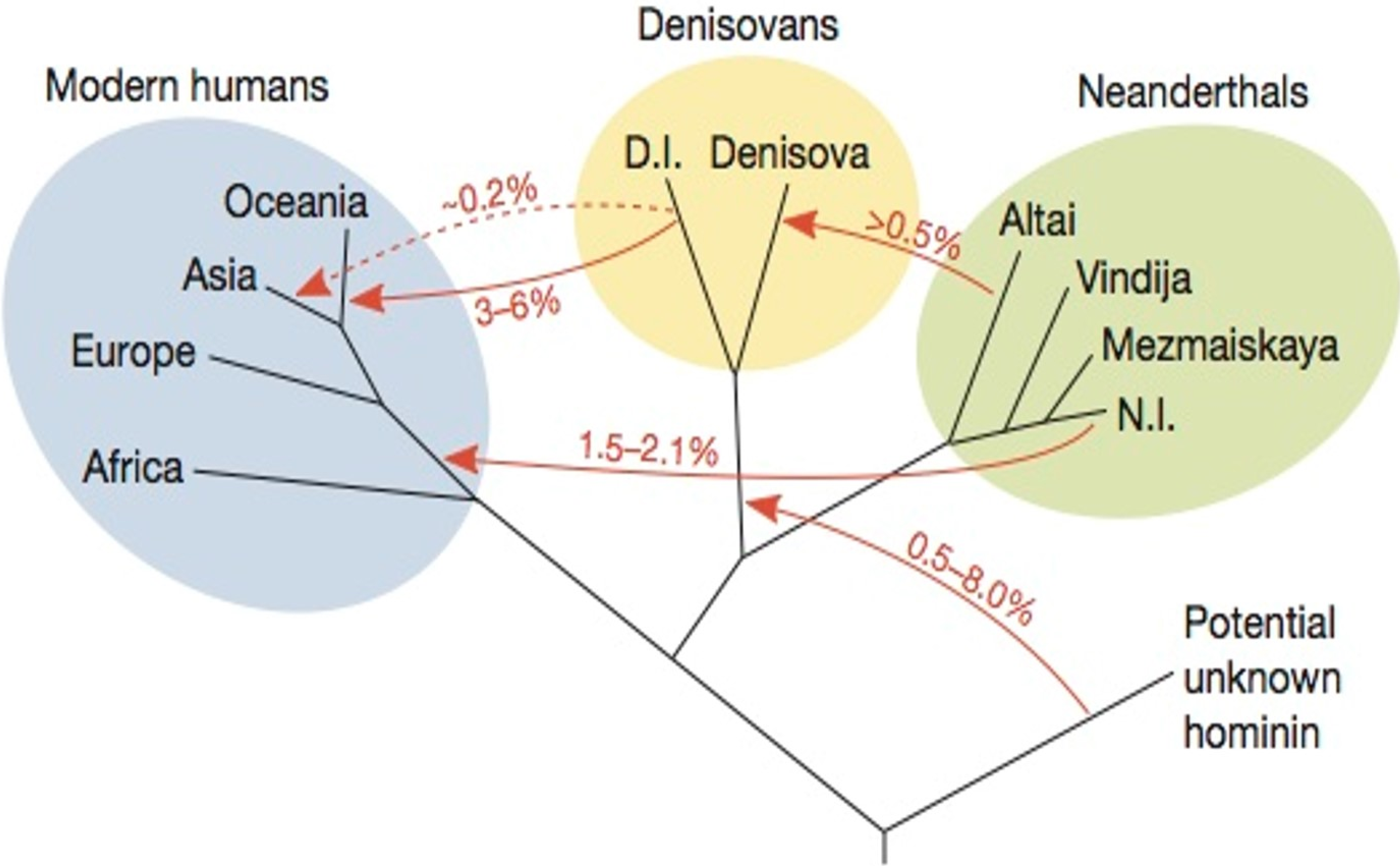

Denisova Cave
Homo heidelbergensis
Neanderthal
Neanderthal
Denisovan
Wallace Line
Key
Maximum Sea Level during the Ice Age
Today – modern Homo sapiens
Neanderthal
Denisovan
Homo heidelbergensis
1 million years ago
Homo erectus
2 million years ago
Africa
Europe & Near East
Central & SE Asia



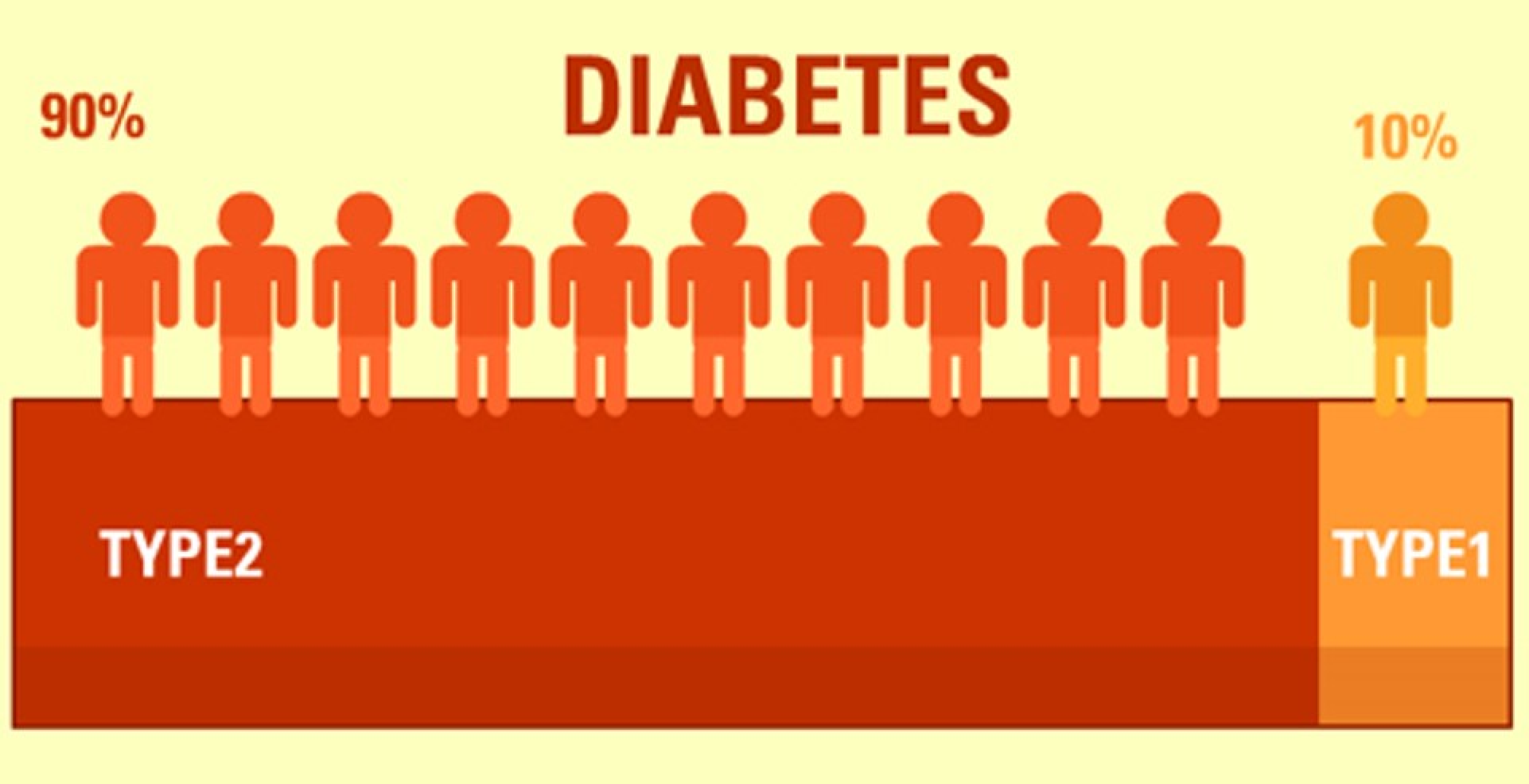
Human mitochondrial DNA (rCRS)
16569 bp
mtDNAtest.com
HVI
HVII
D-loop
12SrRNA
16SrRNA
MTND1
MTND2
COX1
COX2
TP8
ATP6
COX3
ND3
ND4L
ND4
ND5
ND6
CYTB
HyperVariable Region II (complement) - 1
NCBI GeneBank ID: 113200490, NCBI accession no.: J01415.2 - 16520
HyperVariable Region I (complement) - 16024
TRNP, tRNA-Pro (complement) - 15956
TRNT, tRNA-Thr - 15888
TRNF, tRNA-Phe - 577
RNR1, 12S ribosomal RNA - 648
TRNV, tRNA-Val - 1602
RNR2, 16S ribosomal RNA - 1671
TRNL1, tRNA-Leu - 3230
MTND1, NADH dehydrogenase subunit 1, CDS - 3307
MTTI, tRNA-Ile - 4263
TRNQ, tRNA-Gln (complement) - 4329
MTTM, tRNA-Met - 4402
MTND2, NADH dehydrogenase subunit 2, CDS - 4470
TRNW, tRNA-Trp - 5512
TRNA, tRNA-Ala (complement) - 5587
TRNN, tRNA-Asn (complement) - 5657
TRNC, tRNA-Cys (complement) - 5761
TRNY, tRNA-Tyr (complement) - 5826
COX1, cytochrome oxidase subunit 1, CDS - 5904
TRNS1, tRNA-Ser (complement) - 7446
TRND, tRNA-Asp - 7518
COX2, cytochrome oxidase subunit 2, CDS - 7586
TRNK, tRNA-Lys - 8295
ATP8, ATPase 8, CDS - 8366
ATP6, ATPase 6, CDS - 8527
COX3, cytochrome oxidase subunit 3, CDS - 9207
TRNG, tRNA-Gly - 9991
ND3, NADH dehydrogenase subunit 3, CDS - 10059
TRNR, tRNA-Arg - 10405
ND4L, NADH dehydrogenase subunit 4L, CDS - 10470
ND4, NADH dehydrogenase subunit 4, CDS - 10760
TRNH, tRNA-His - 12138
TRNS2, tRNA-Ser - 12207
MTTL2, tRNA-Leu - 12266
ND5, NADH dehydrogenase subunit 5, CDS - 12337
ND6, NADH dehydrogenase subunit 6, CDS (complement) - 14149
TRNE, tRNA-Glu (complement) - 14674
CYTB, cytochrome b, CDS - 14747

Next-generation DNA sequencing

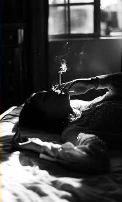


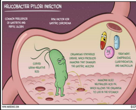


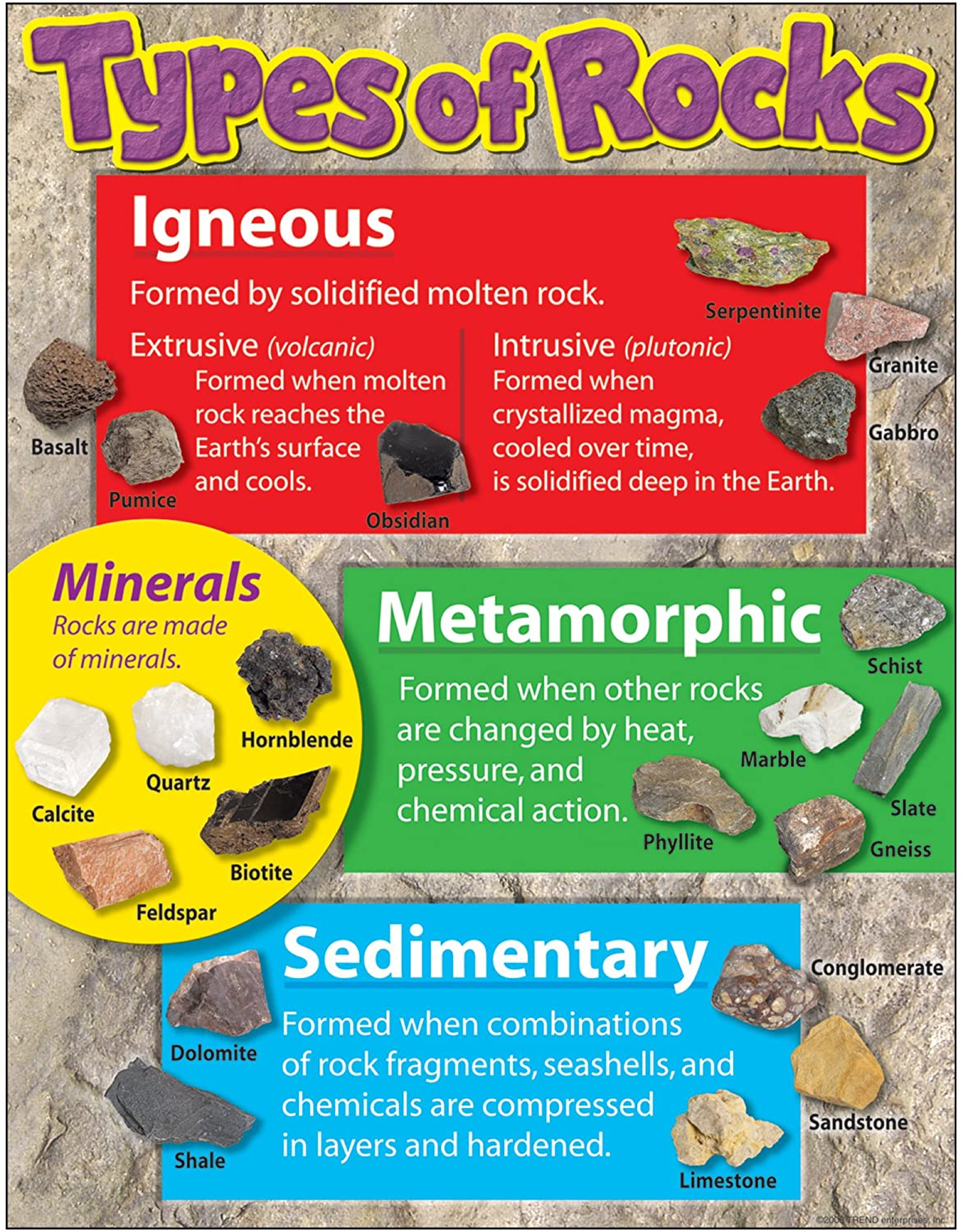
Denisovans
Modern humans
Neanderthals
D.I.
Denisova
Oceania
Asia
Europe
Africa
Altai
Vindija
Mezmaiskaya
N.I.
~0.2%
3–6%
>0.5%
1.5–2.1%
0.5–8.0%
Potential
unknown
hominin


DIABETES
90%
10%
TYPE2
TYPE1

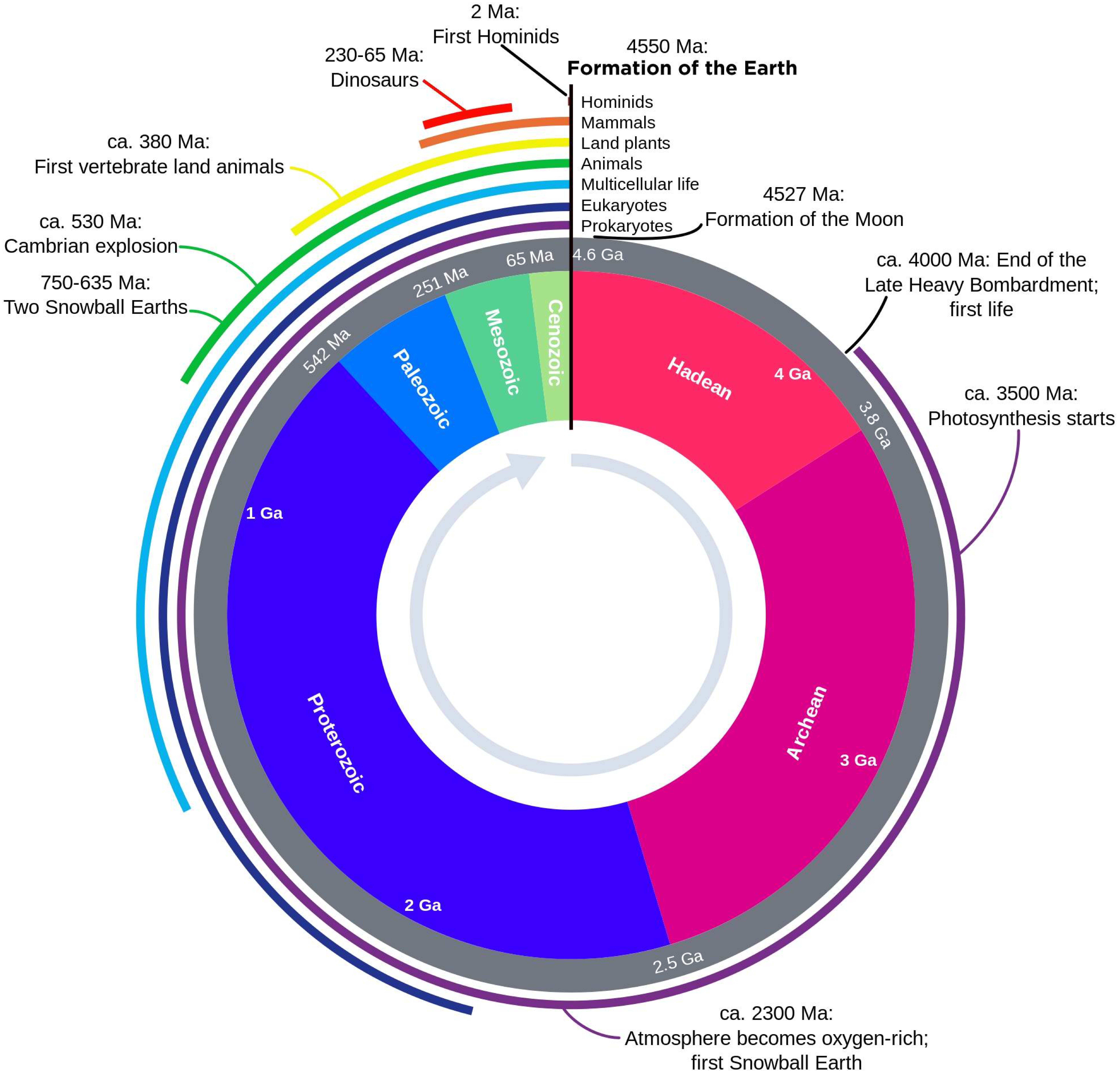




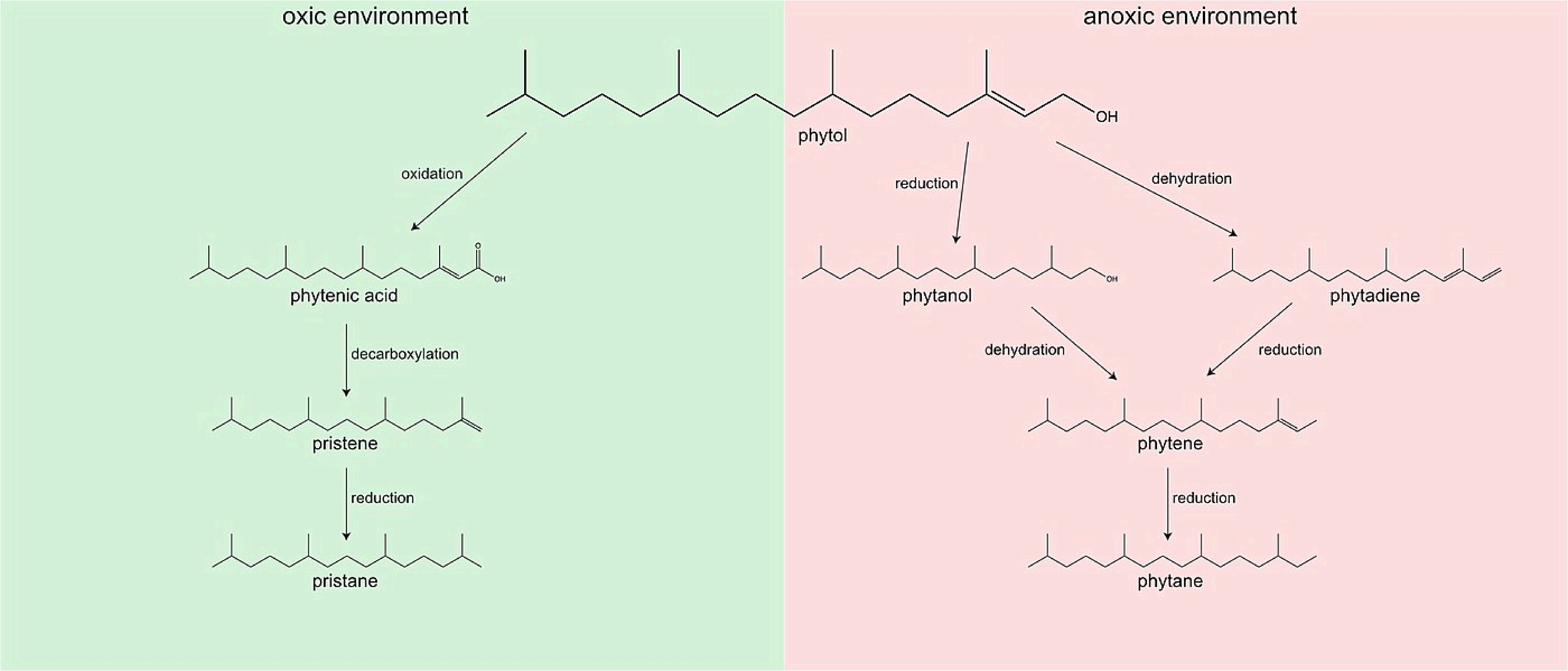

HELICOBACTER PYLORI INFECTION
COMMON PRECURSOR OF GASTRITIS AND PEPTIC ULCERS
RISK FACTOR FOR GASTRIC CARCINOMA
CURVED GRAM-NEGATIVE ROD
ORGANISMS SYNTHESIZE UREASE, WHICH PRODUCES AMMONIA THAT DAMAGES THE GASTRIC MUCOSA
TREATMENT: OMEPRAZOLE, CLARITHROMYCIN, AND AMOXICILLIN
AMMONIA ALSO NEUTRALIZES ACID PH, WHICH ALLOWS THE ORGANISM TO LIVE IN THE STOMACH



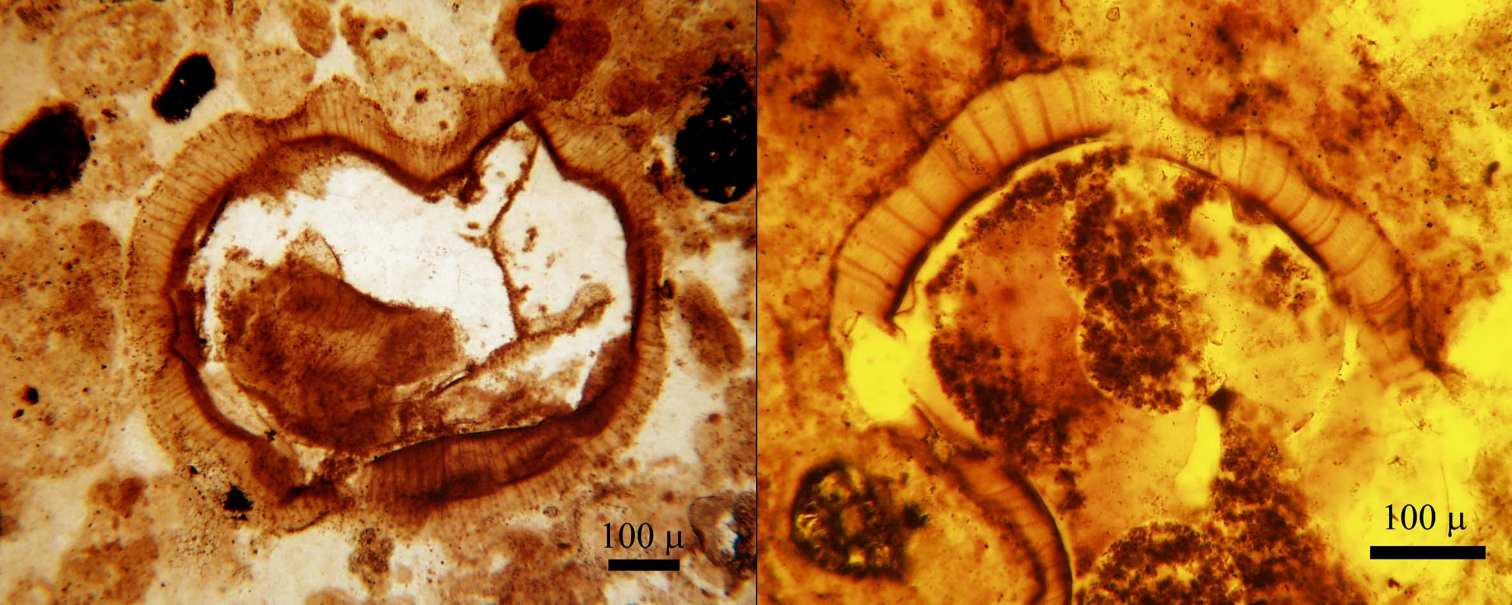
Types of Rocks
Igneous
Formed by solidified molten rock.
Extrusive (volcanic)
Formed when molten rock reaches the Earth's surface and cools.
Intrusive (plutonic)
Formed when crystallized magma, cooled over time, is solidified deep in the Earth.
Serpentinite
Granite
Gabbro
Basalt
Pumice
Obsidian
Minerals
Rocks are made of minerals.
Hornblende
Quartz
Calcite
Biotite
Feldspar
Metamorphic
Formed when other rocks are changed by heat, pressure, and chemical action.
Schist
Marble
Slate
Phyllite
Gneiss
Sedimentary
Formed when combinations of rock fragments, seashells, and chemicals are compressed in layers and hardened.
Conglomerate
Dolomite
Sandstone
Shale
Limestone
TREND enterprises, Inc.

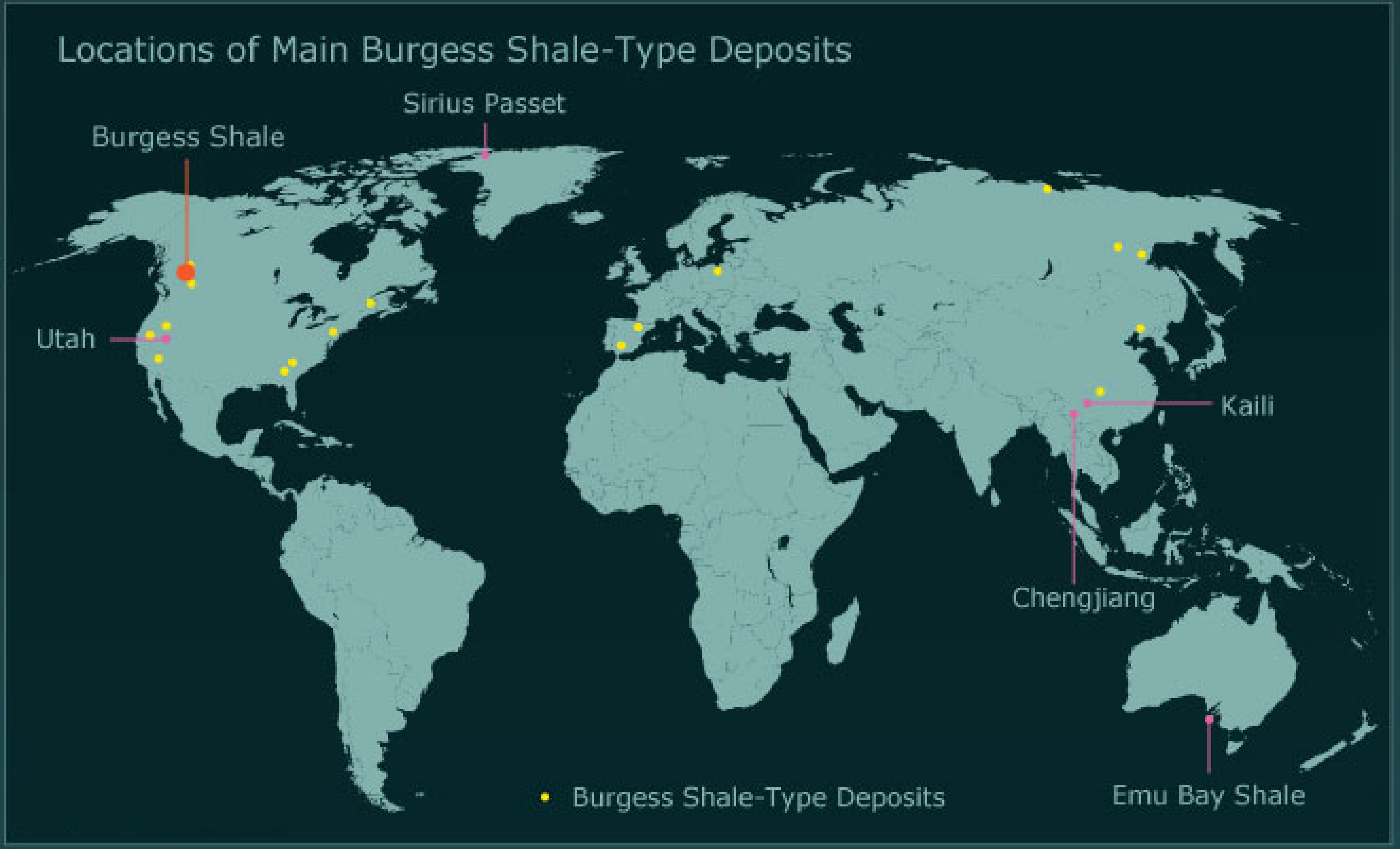


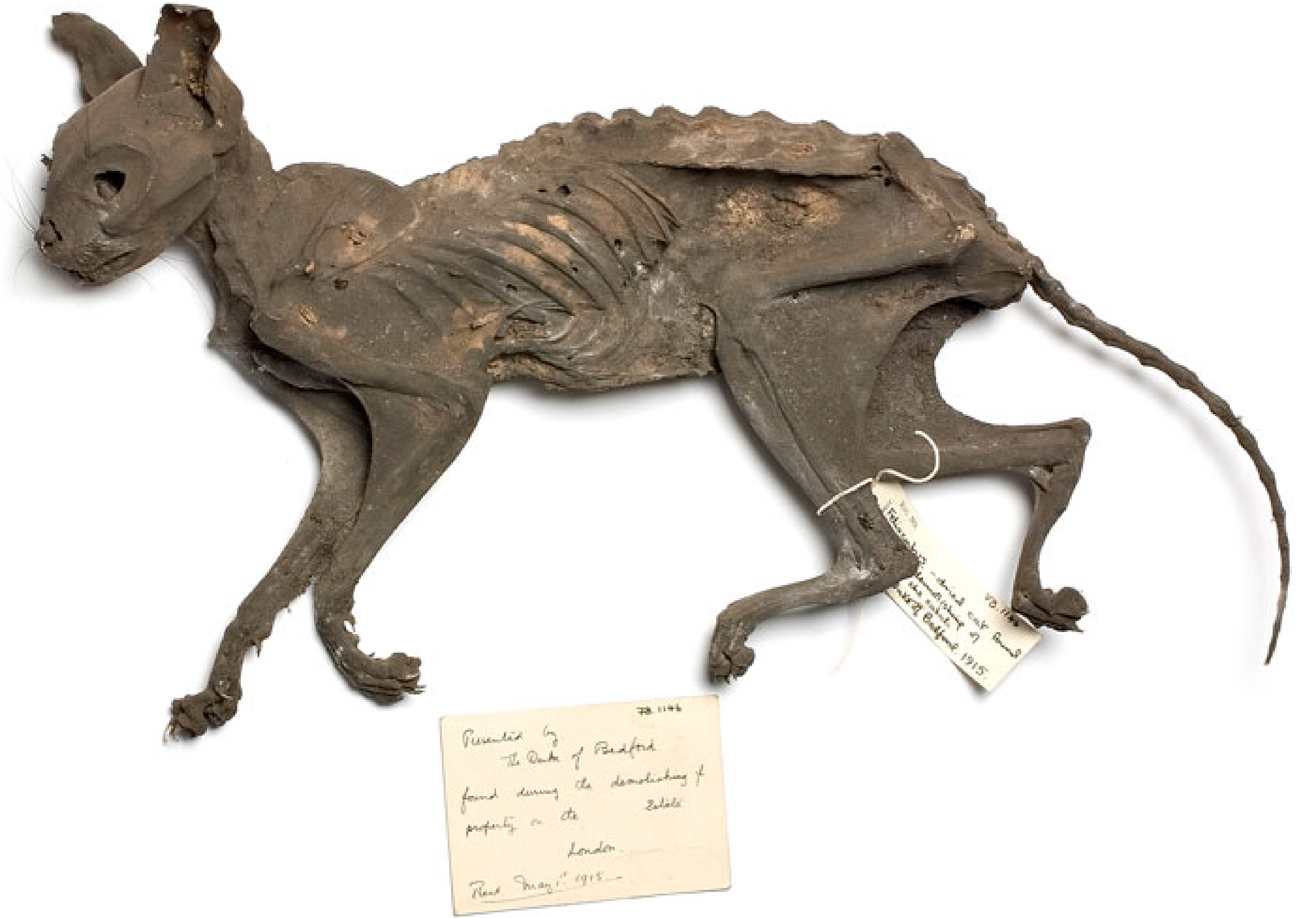
2 Ma:
First Hominids
4550 Ma:
Formation of the Earth
230-65 Ma:
Dinosaurs
Hominids
Mammals
Land plants
Animals
Multicellular life
Eukaryotes
Prokaryotes
ca. 380 Ma:
First vertebrate land animals
4527 Ma:
Formation of the Moon
ca. 530 Ma:
Cambrian explosion
750-635 Ma:
Two Snowball Earths
ca. 4000 Ma: End of the
Late Heavy Bombardment;
first life
4.6 Ga
65 Ma
251 Ma
542 Ma
Cenozoic
Mesozoic
Paleozoic
Hadean
4 Ga
3.8 Ga
ca. 3500 Ma:
Photosynthesis starts
1 Ga
Proterozoic
Archean
3 Ga
2 Ga
2.5 Ga
ca. 2300 Ma:
Atmosphere becomes oxygen-rich;
first Snowball Earth

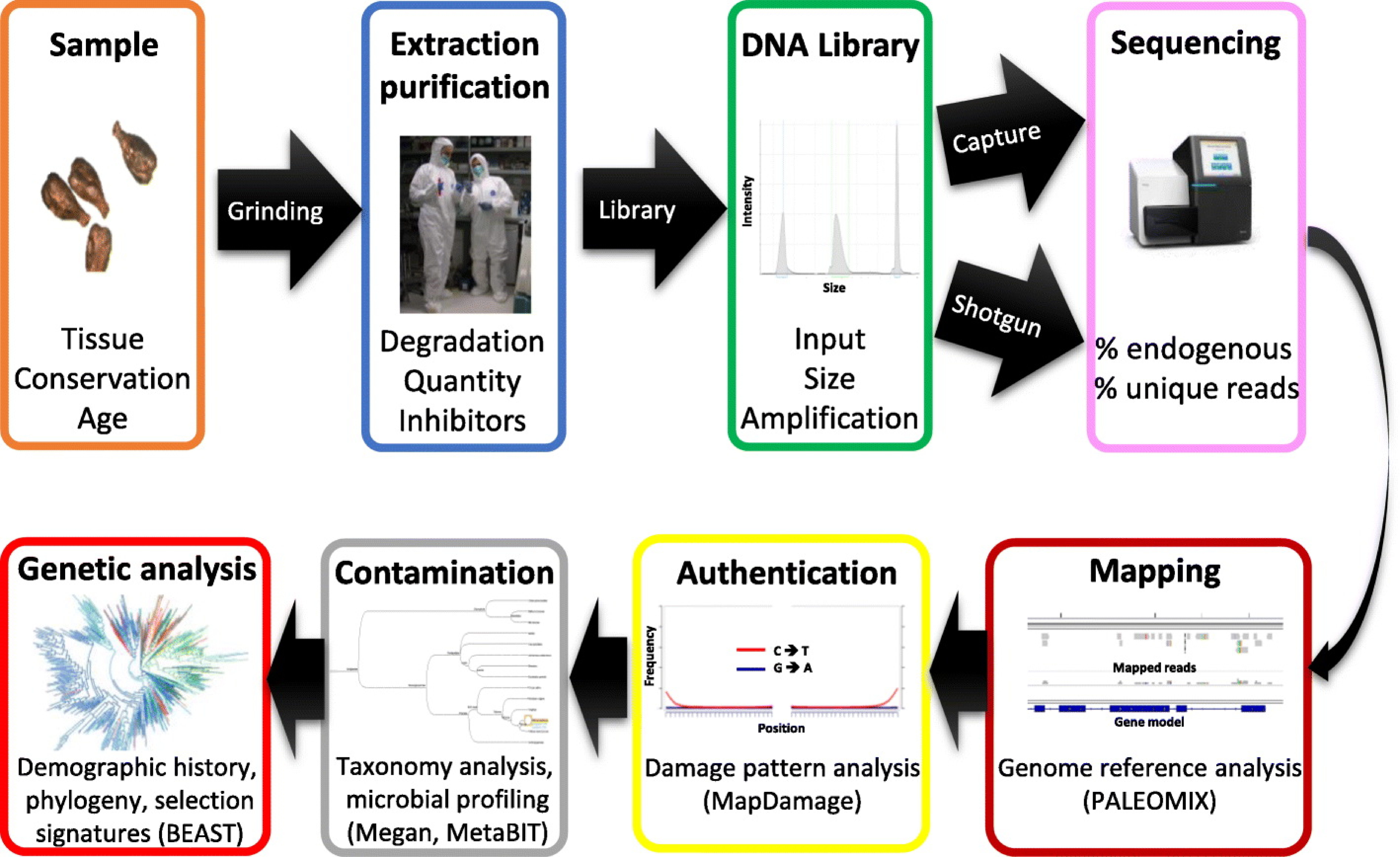


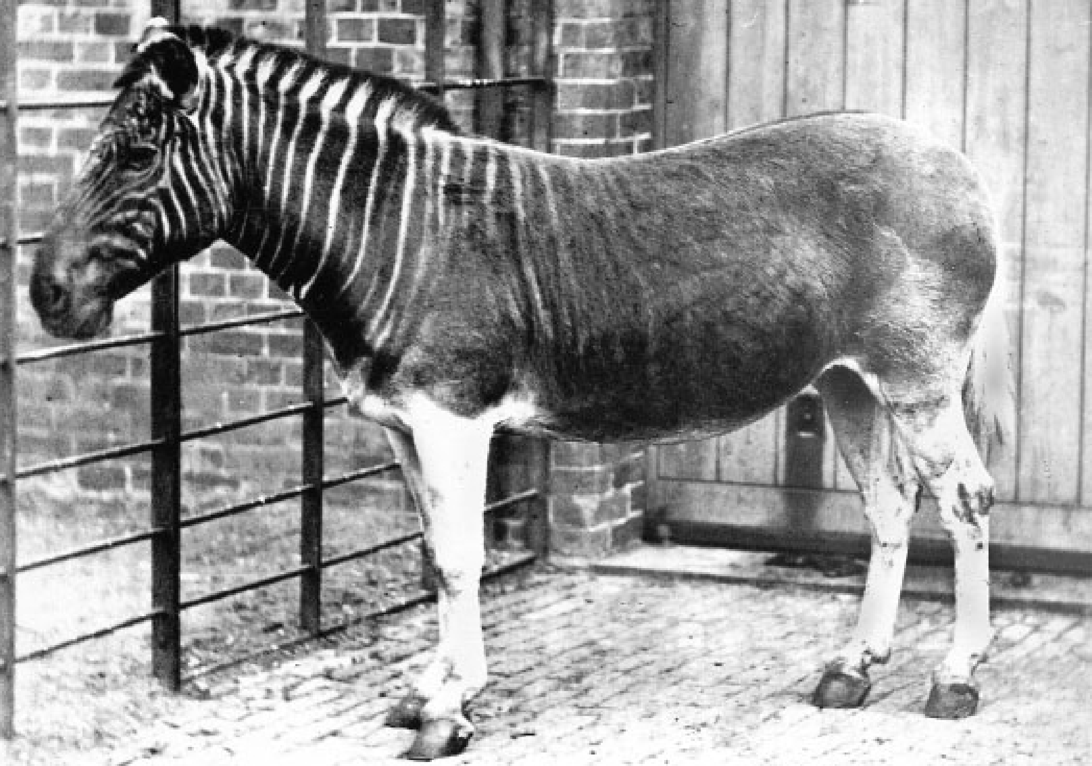
oxic environment
anoxic environment
OH
phytol
oxidation
reduction
dehydration
phytenic acid
phytanol
phytadiene
decarboxylation
dehydration
reduction
pristene
phytene
reduction
reduction
pristane
phytane

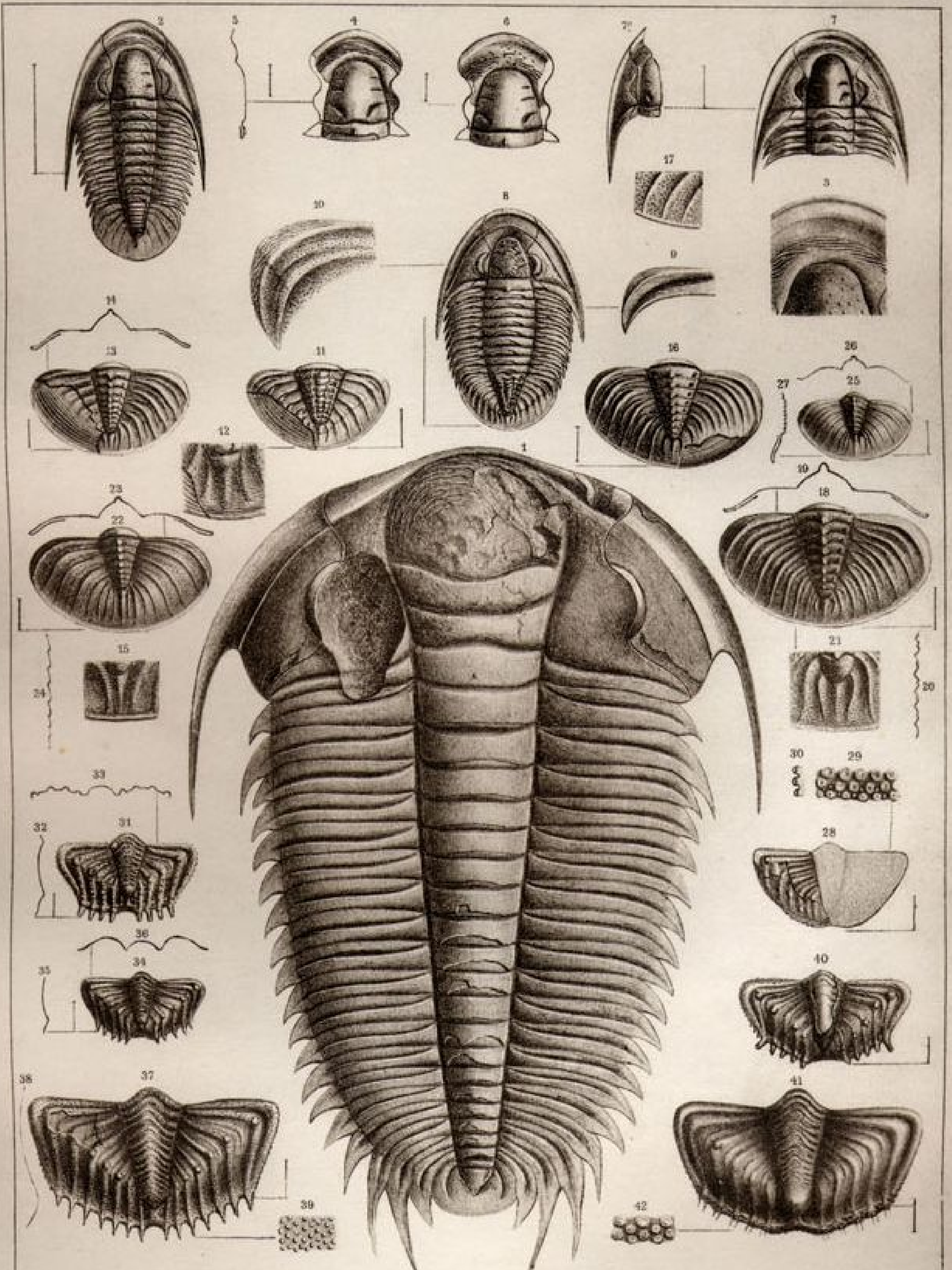

100 μ
100 μ


Locations of Main Burgess Shale-Type Deposits
Sirius Passet
Burgess Shale
Utah
Kaili
Chengjiang
Emu Bay Shale
Burgess Shale-Type Deposits


Presented by
The Duke of Bedford
found during the demolishing of
property on the Estate
London
May 1915


Sample
Tissue
Conservation
Age
Grinding
Extraction
purification
Degradation
Quantity
Inhibitors
Library
DNA Library
Intensity
Size
Input
Size
Amplification
Capture
Shotgun
Sequencing
% endogenous
% unique reads
Mapping
Mapped reads
Gene model
Genome reference analysis
(PALEOMIX)
Authentication
Frequency
C → T
G → A
Position
Damage pattern analysis
(MapDamage)
Contamination
Taxonomy analysis,
microbial profiling
(Megan, MetaBIT)
Genetic analysis
Demographic history,
phylogeny, selection
signatures (BEAST)

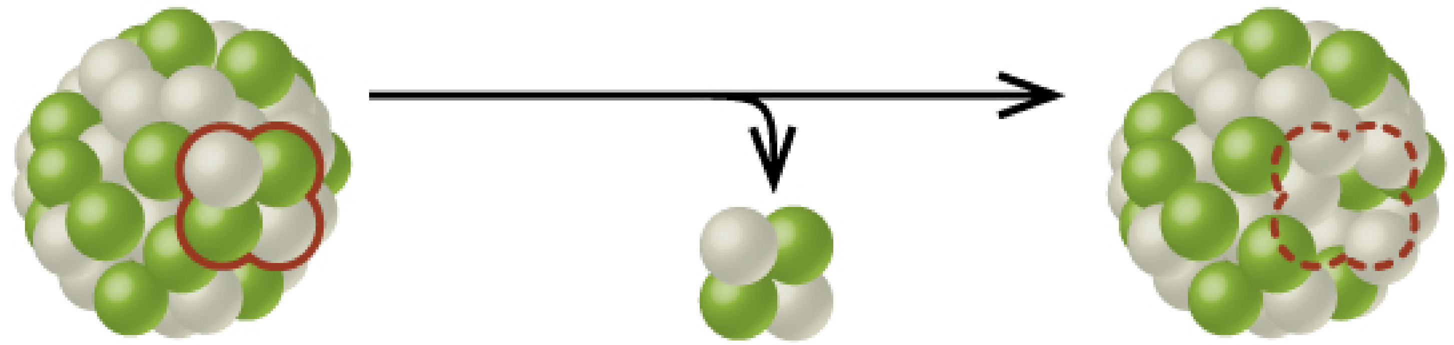
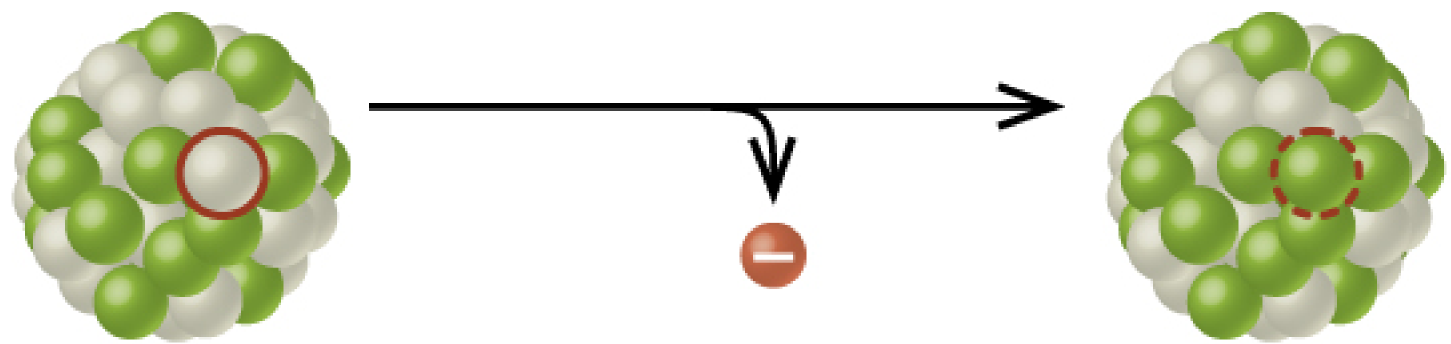
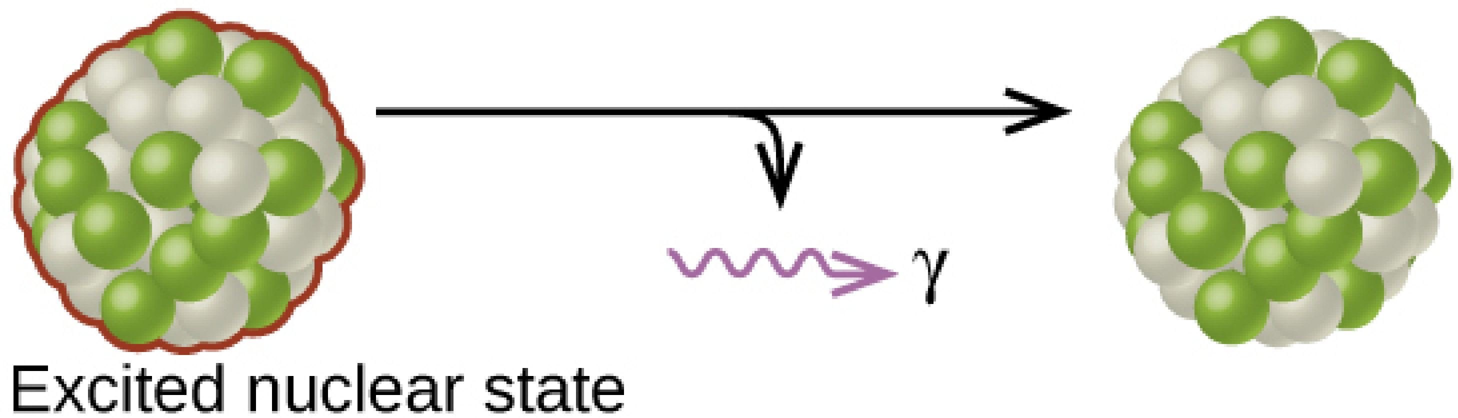
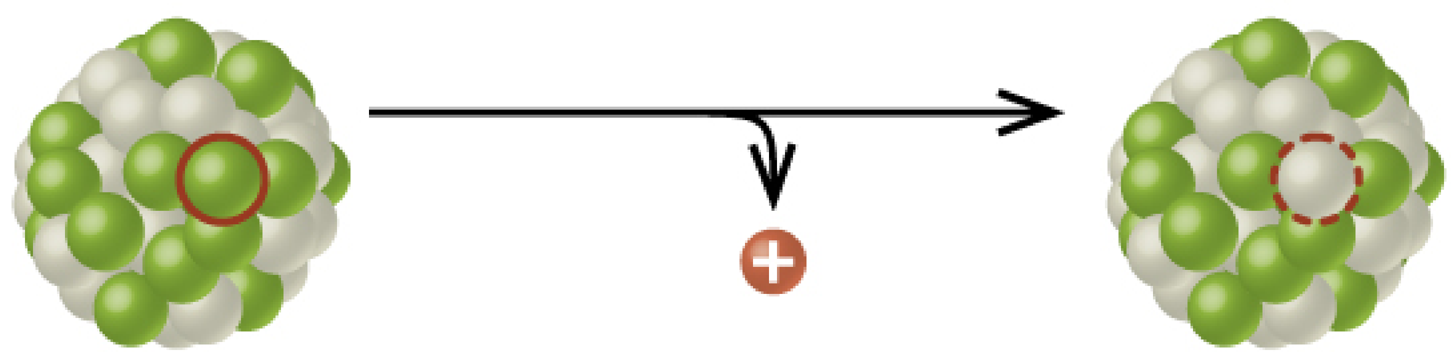
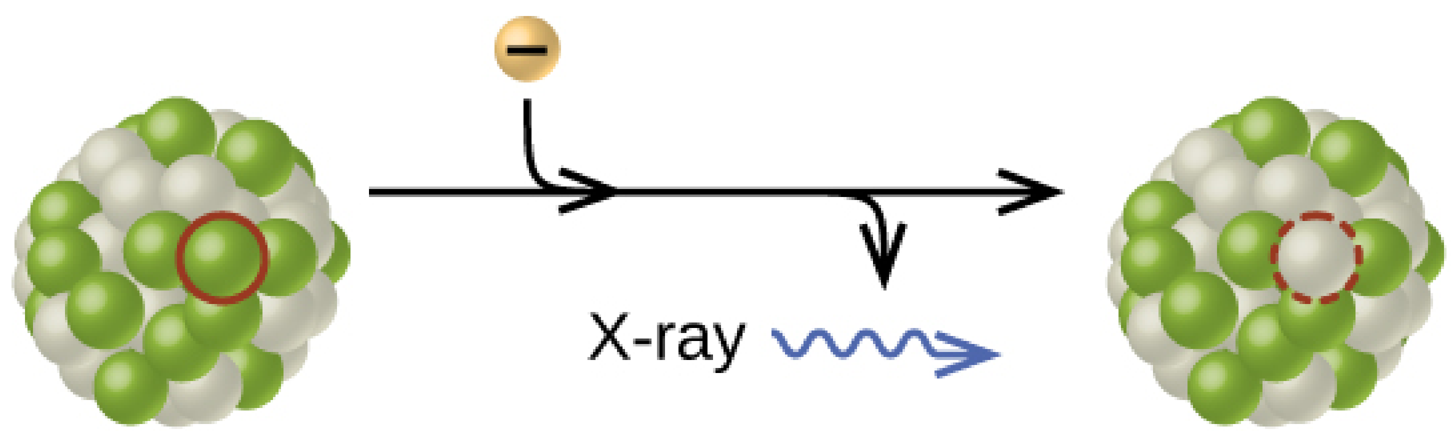




O. Novák ad nat. delin. et lith. 1885

Jmp. Farský Prague


5
6
7
8
9
10
11
12
13
14
15
16

Type	Nuclear equation	Representation	Change in mass/atomic numbers
Alpha decay	${}^{A}_{Z}X \quad {}^{4}_{2}He + {}^{A-4}_{Z-2}Y$		A: decrease by 4 Z: decrease by 2
Beta decay	${}^{A}_{Z}X \quad {}^{0}_{-1}e + {}_{Z+1}^{A}Y$		A: unchanged Z: increase by 1
Gamma decay	${}^{A}_{Z}X \quad {}^{0}_{0}\gamma + {}^{A}_{Z}Y$		A: unchanged Z: unchanged
Positron emission	${}^{A}_{Z}X \quad {}^{0}_{+1}e + {}_{Y-1}^{A}Y$		A: unchanged Z: decrease by 1
Electron capture	${}^{A}_{Z}X \quad {}^{0}_{-1}e + {}_{Y-1}^{A}Y$		A: unchanged Z: decrease by 1

Radiometric Dating

Radiometric Dating — is commonly applied to — Organic Materials

Organic Materials — examples — Trees, Bones, Seeds, Food, Wooden Artifacts

Organic Materials — contain — Carbon 12, Carbon 14

Carbon 12 — is — Stable

Carbon 12 — is — Common in Environment

Common in Environment — is — Known Quantity

Carbon 14 — is — Trace in Environment

Trace in Environment — is created by — Cosmic Ray Interactions with Nitrogen in Upper Atmosphere

Trace in Environment — is — Known Proportion

Carbon 14 — is incorporated into — Tissues

Tissues — of — Live Organisms

Live Organisms — eventually beomes — Dead Organism

Dead Organism — ceases to incorporate — Carbon 14

Carbon 14 — is — Radioactive with Half Life of 5730 Years

Dead Organism — has — Known Fraction of C 14 Atoms at Time of Death

Dead Organism — has — Measured Fraction of C14 Atoms in Laboratory

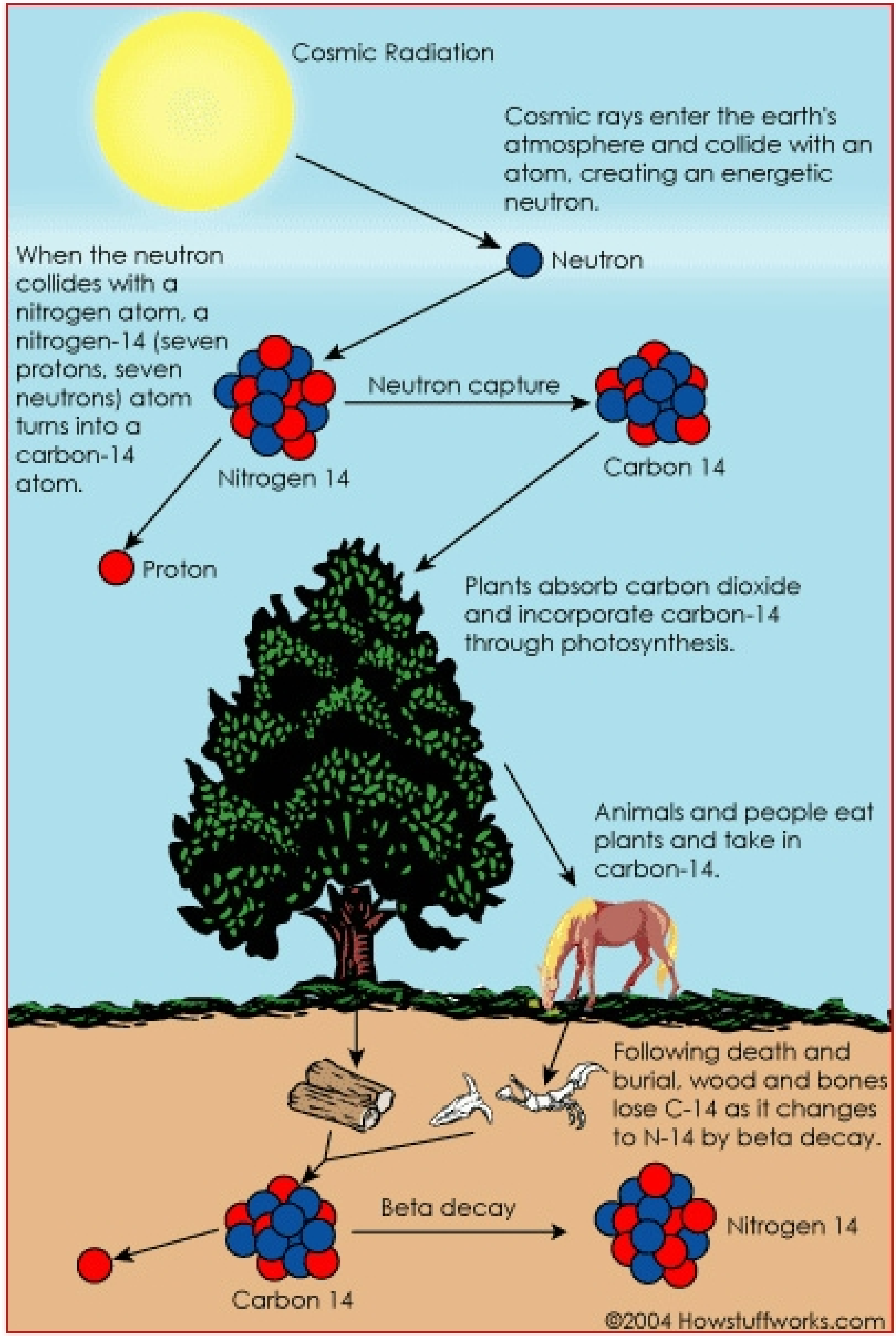
Known Fraction of C 14 Atoms at Time of Death — begins — Radioactive Decay

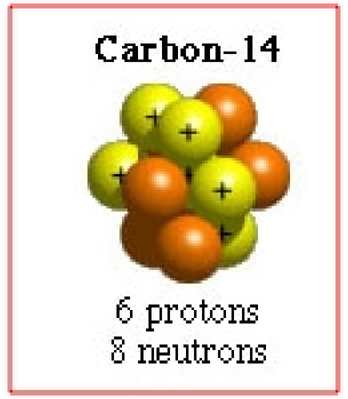
Radioactive Decay — has — Radioactive with Half Life of 5730 Years

Measured Fraction of C14 Atoms in Laboratory — provides — Accurate Estimate of Time of Death

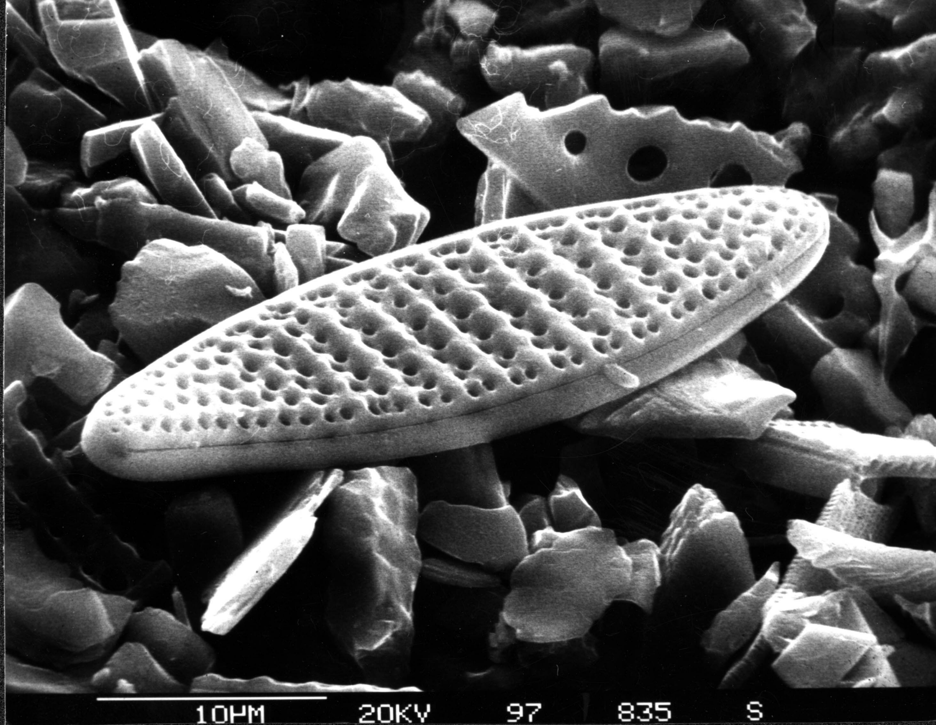
Science Matters pp 119-120

http://static.howstuffworks.com/gif/carbon-14.gif

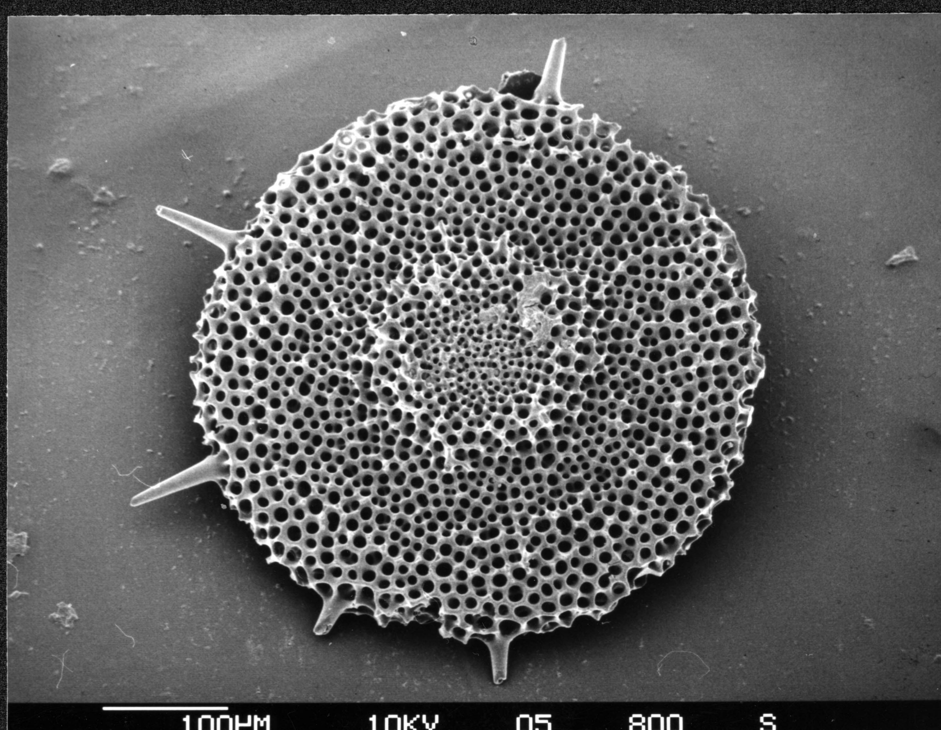


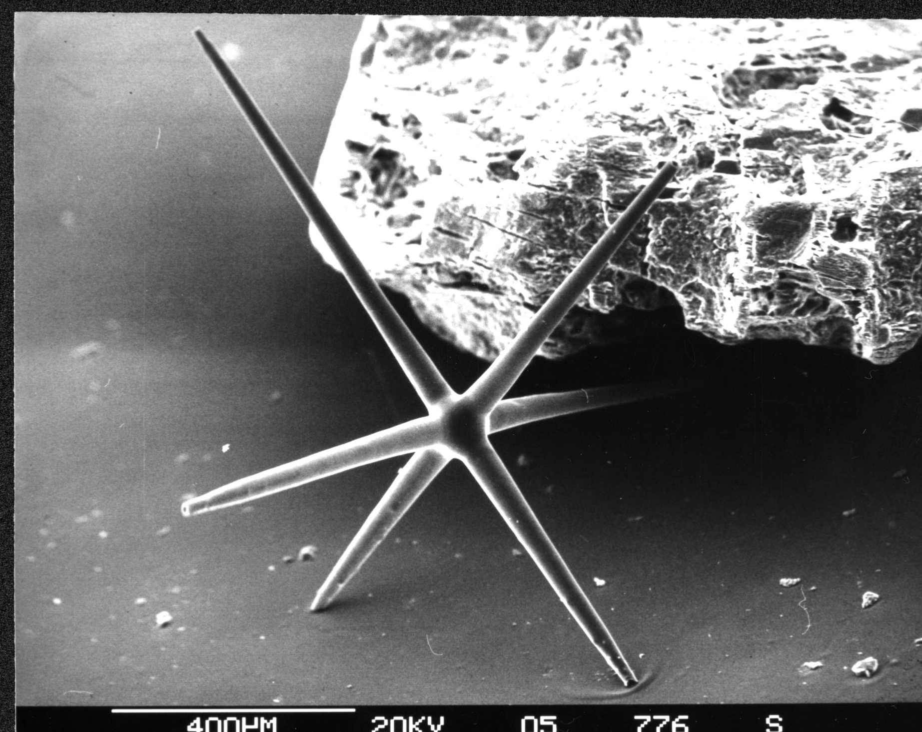


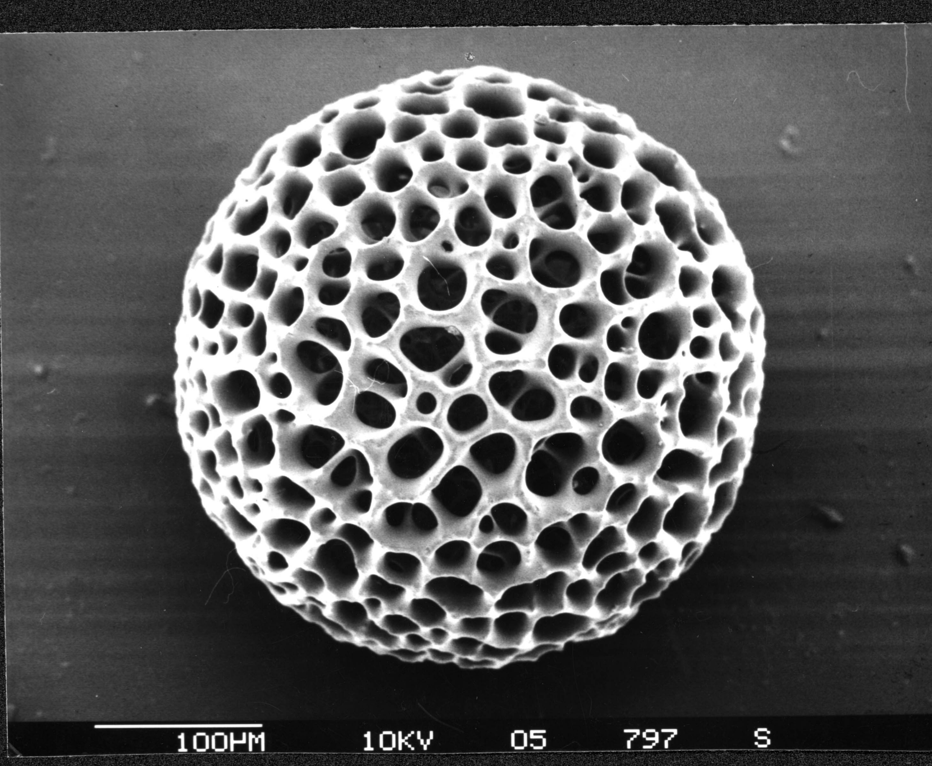
Radiometric dating is also applied to rocks and meteorites by measuring the content of minute quantities of mother and daughter radioisotopes

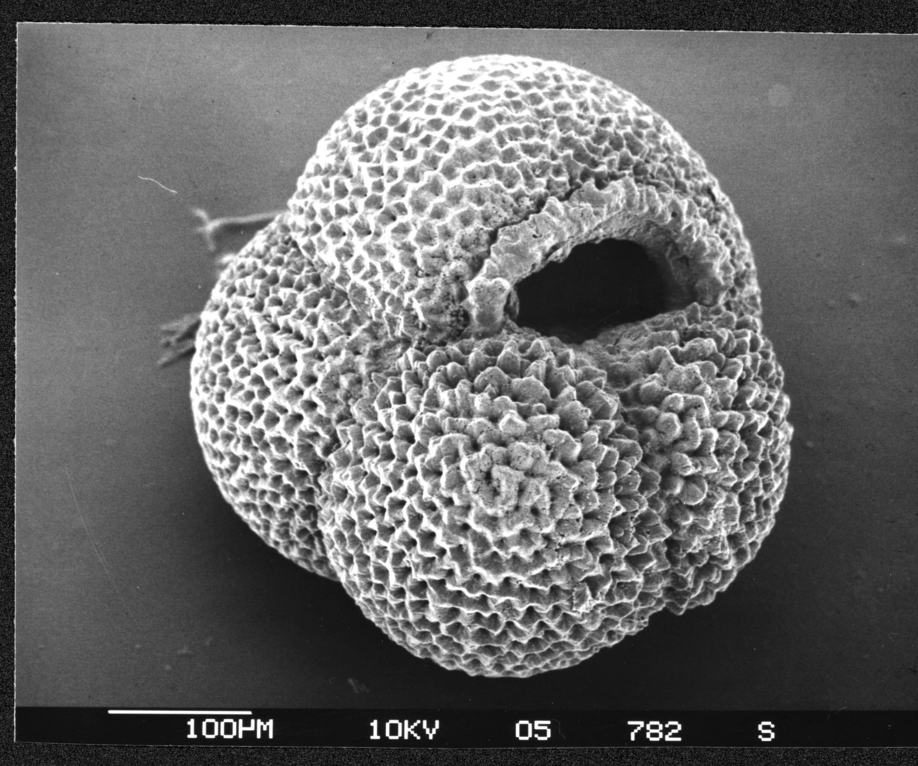

10µM 20KV 97 835 S

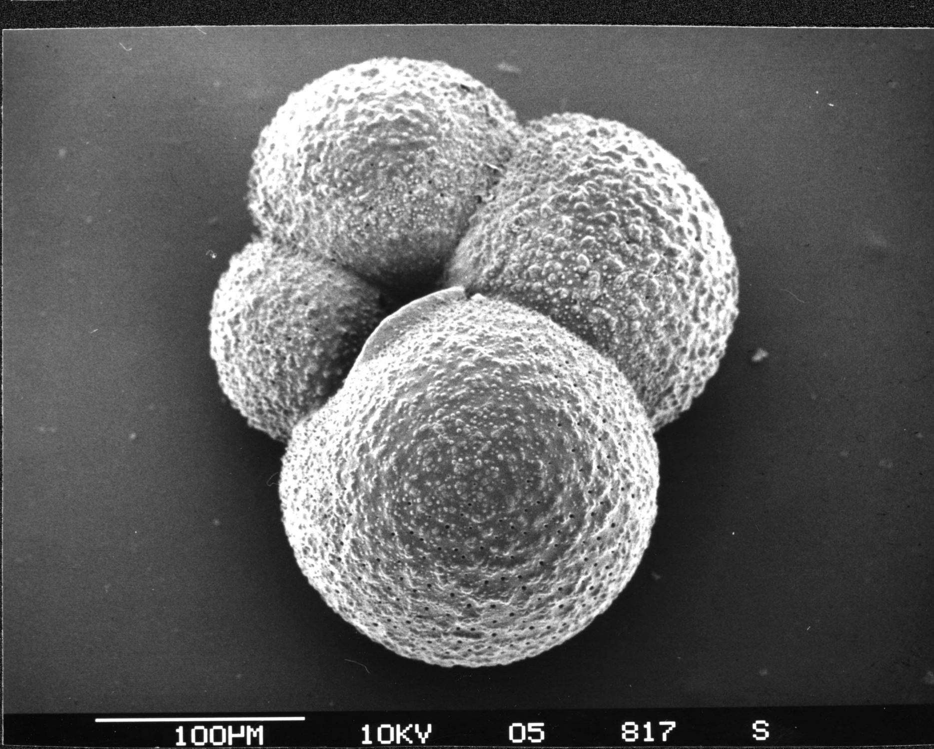

200µM 10KV 78 822 S

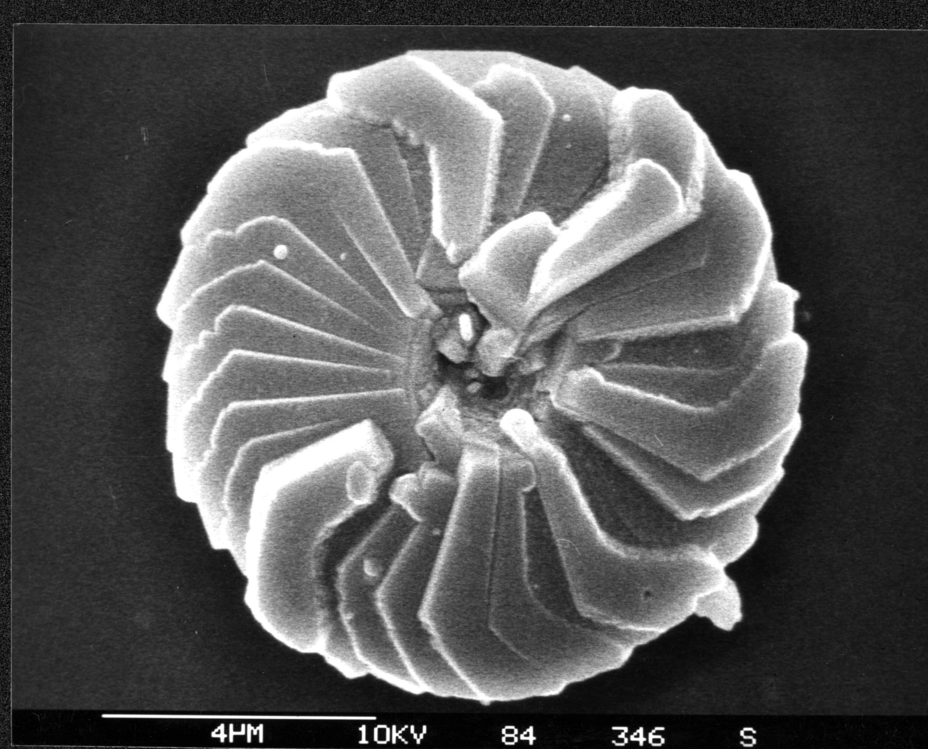

100µM 10KV 05 800 S

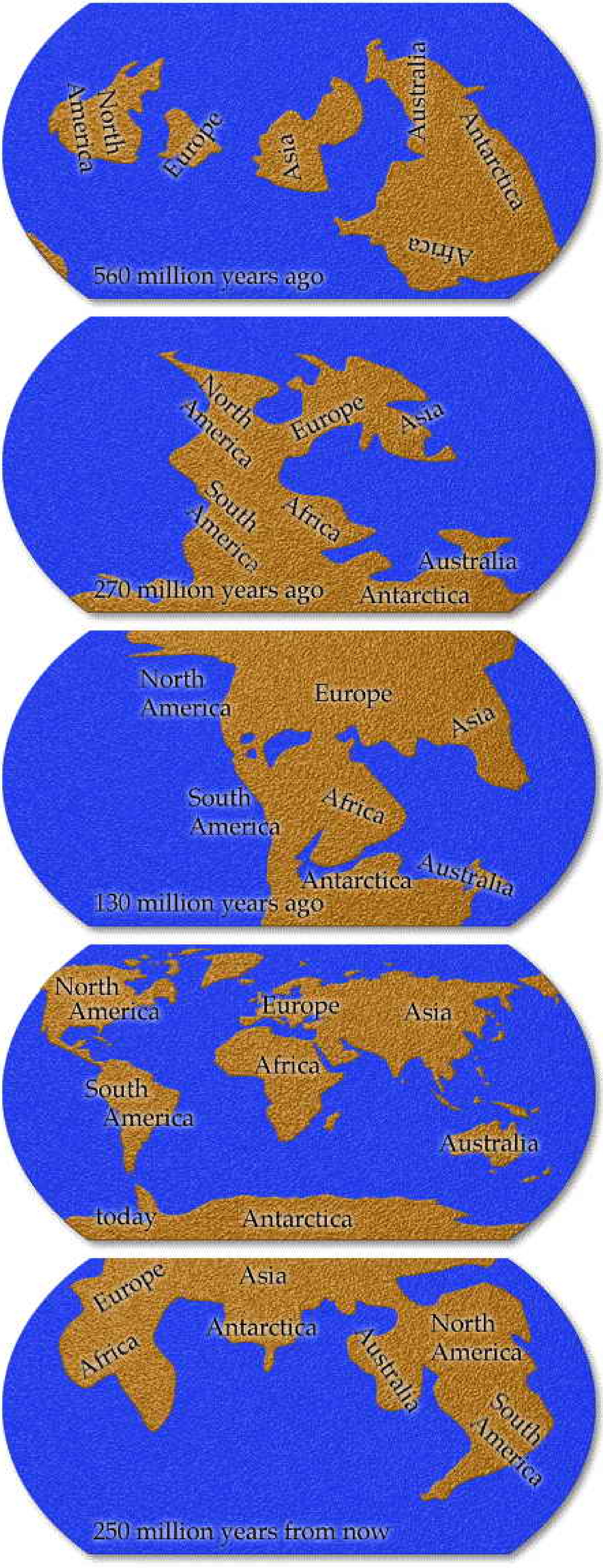

400µM 20KV 05 776 S


100µM 10KV 05 797 S

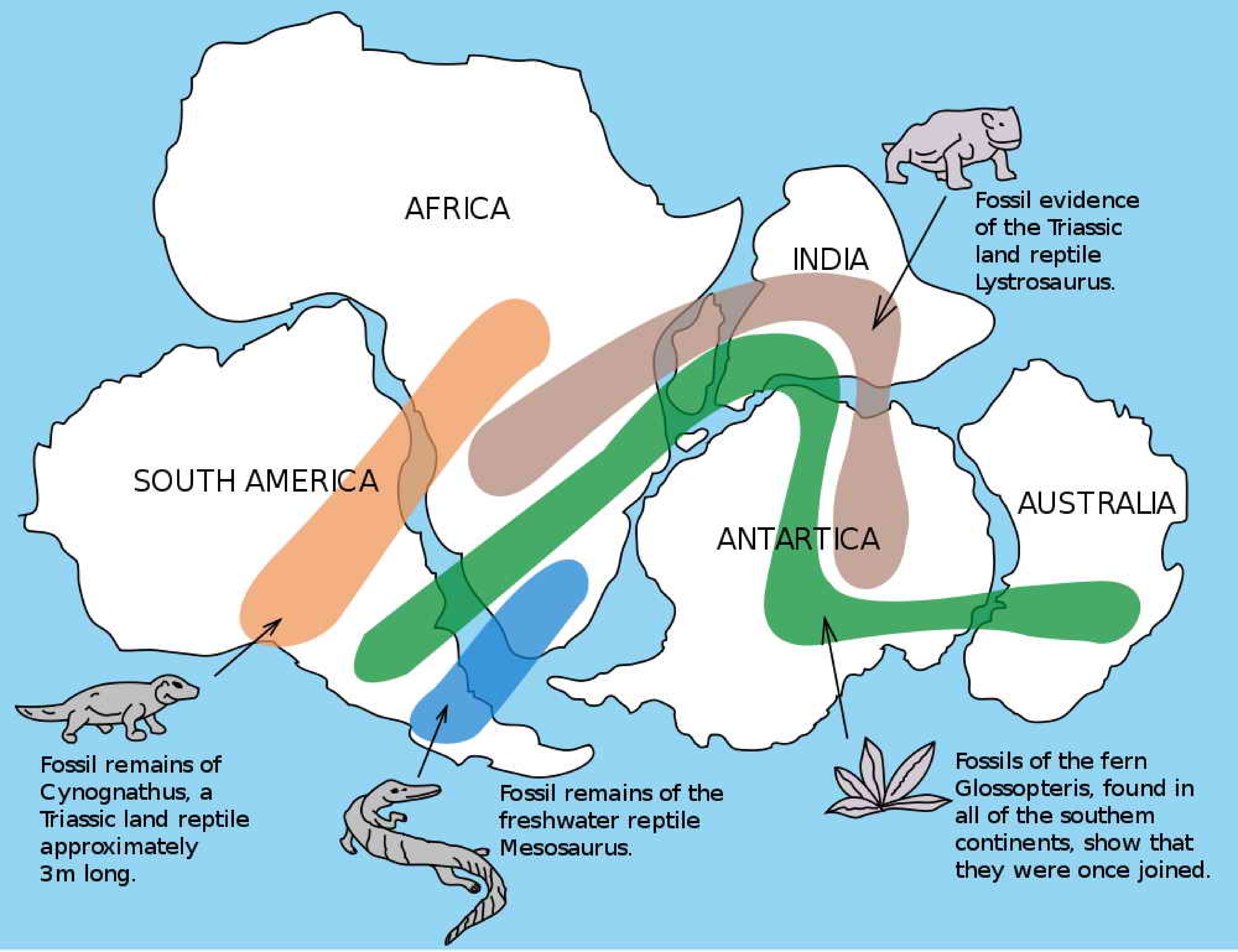

100µM 10KV 05 782 S

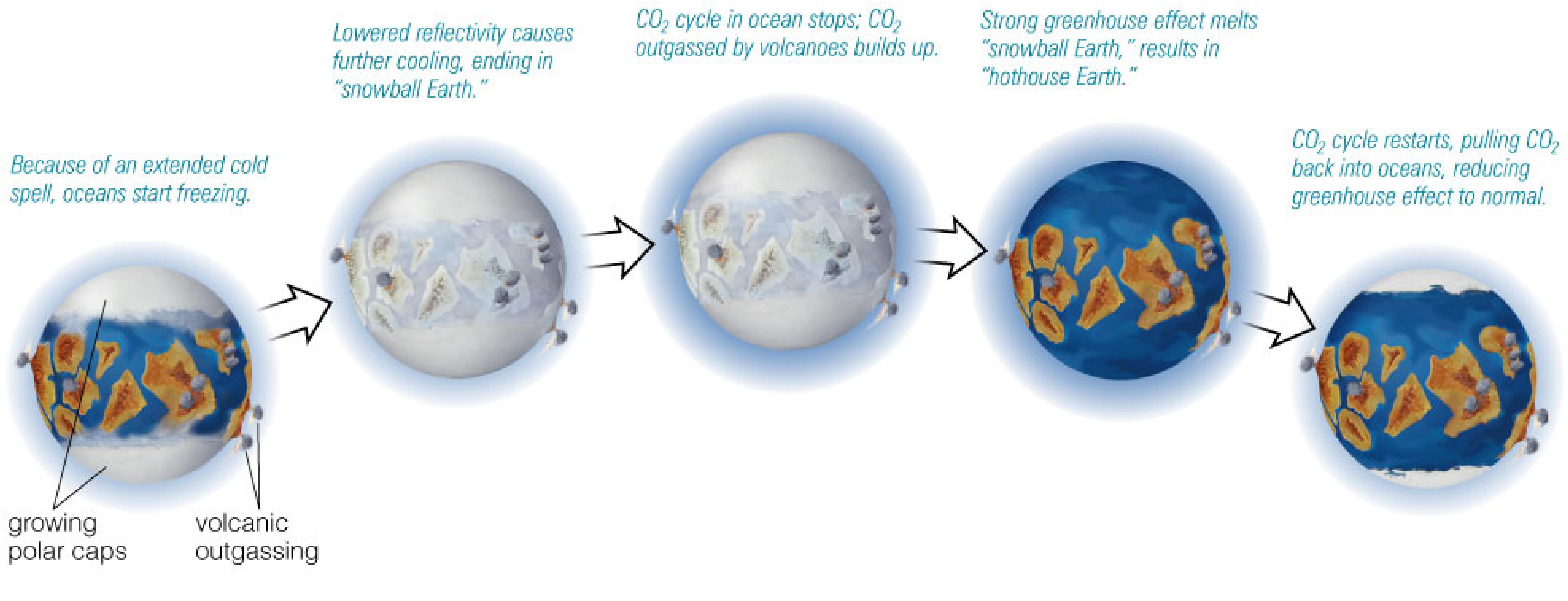

100µM 10KV 05 817 S


4µM 10KV 84 346 S



North America
Europe
Asia
Australia
Antarctica
Africa
560 million years ago
North America
Europe
Asia
South America
Africa
Australia
Antarctica
270 million years ago
North America
Europe
Asia
South America
Africa
Antarctica
Australia
130 million years ago
North America
Europe
Asia
Africa
South America
Australia
today
Antarctica
Europe
Asia
Antarctica
Africa
Australia
North America
South America
250 million years from now


AFRICA
INDIA
Fossil evidence of the Triassic land reptile Lystrosaurus.
SOUTH AMERICA
AUSTRALIA
ANTARTICA
Fossil remains of Cynognathus, a Triassic land reptile approximately 3m long.
Fossil remains of the freshwater reptile Mesosaurus.
Fossils of the fern Glossopteris, found in all of the southem continents, show that they were once joined.


Because of an extended cold spell, oceans start freezing.
Lowered reflectivity causes further cooling, ending in "snowball Earth."
CO_2 cycle in ocean stops; CO_2 outgassed by volcanoes builds up.
Strong greenhouse effect melts "snowball Earth," results in "hothouse Earth."
CO_2 cycle restarts, pulling CO_2 back into oceans, reducing greenhouse effect to normal.
growing polar caps
volcanic outgassing

DAISYWORLD

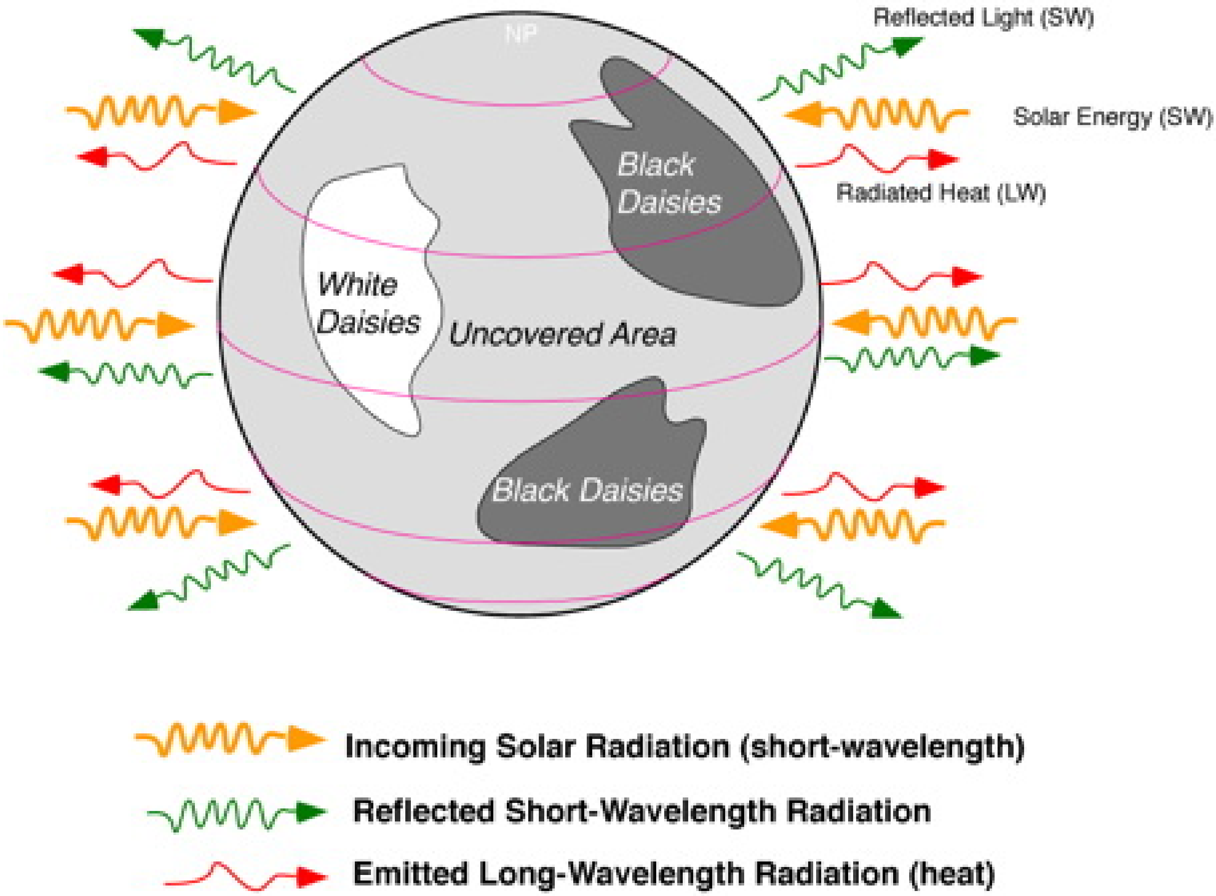
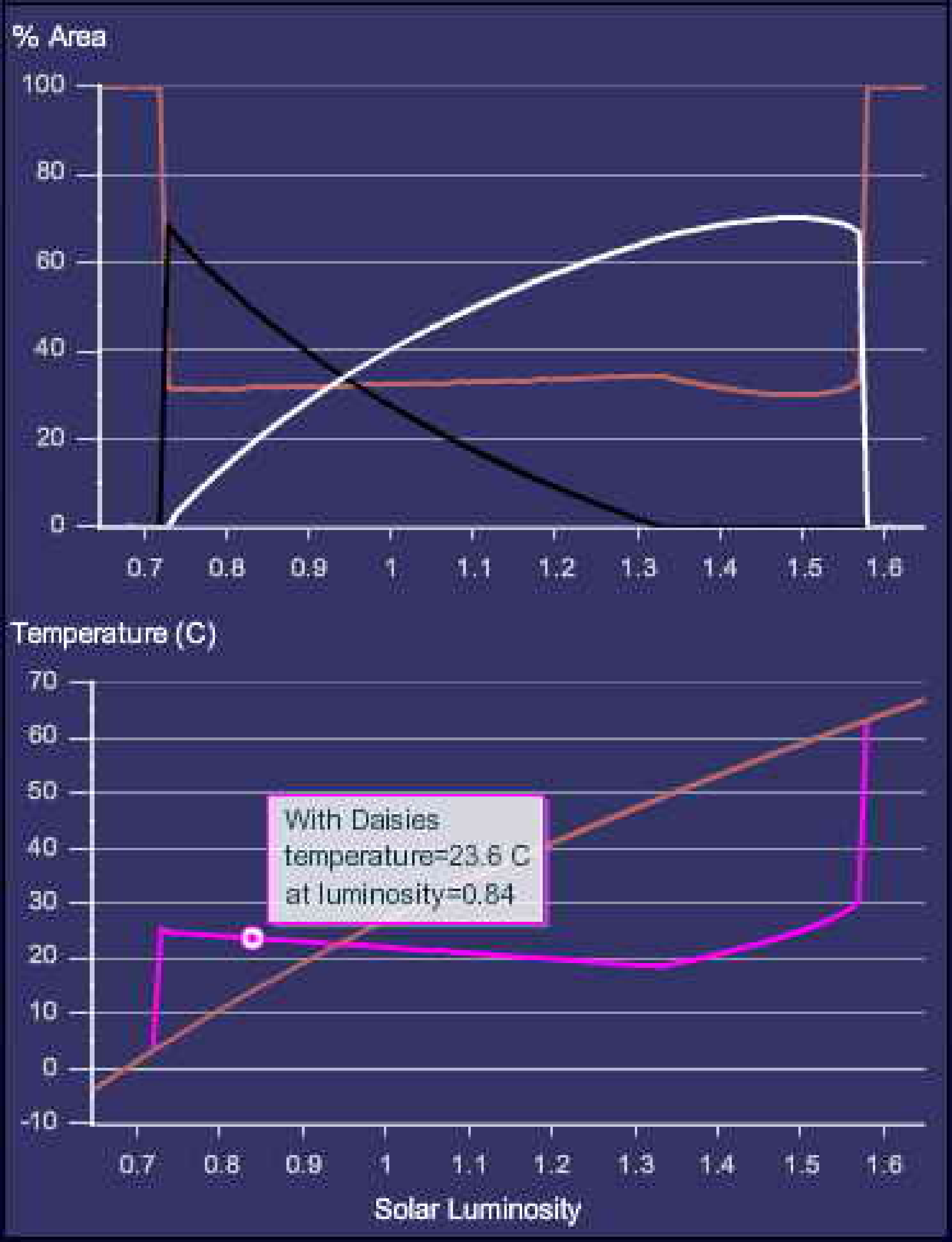
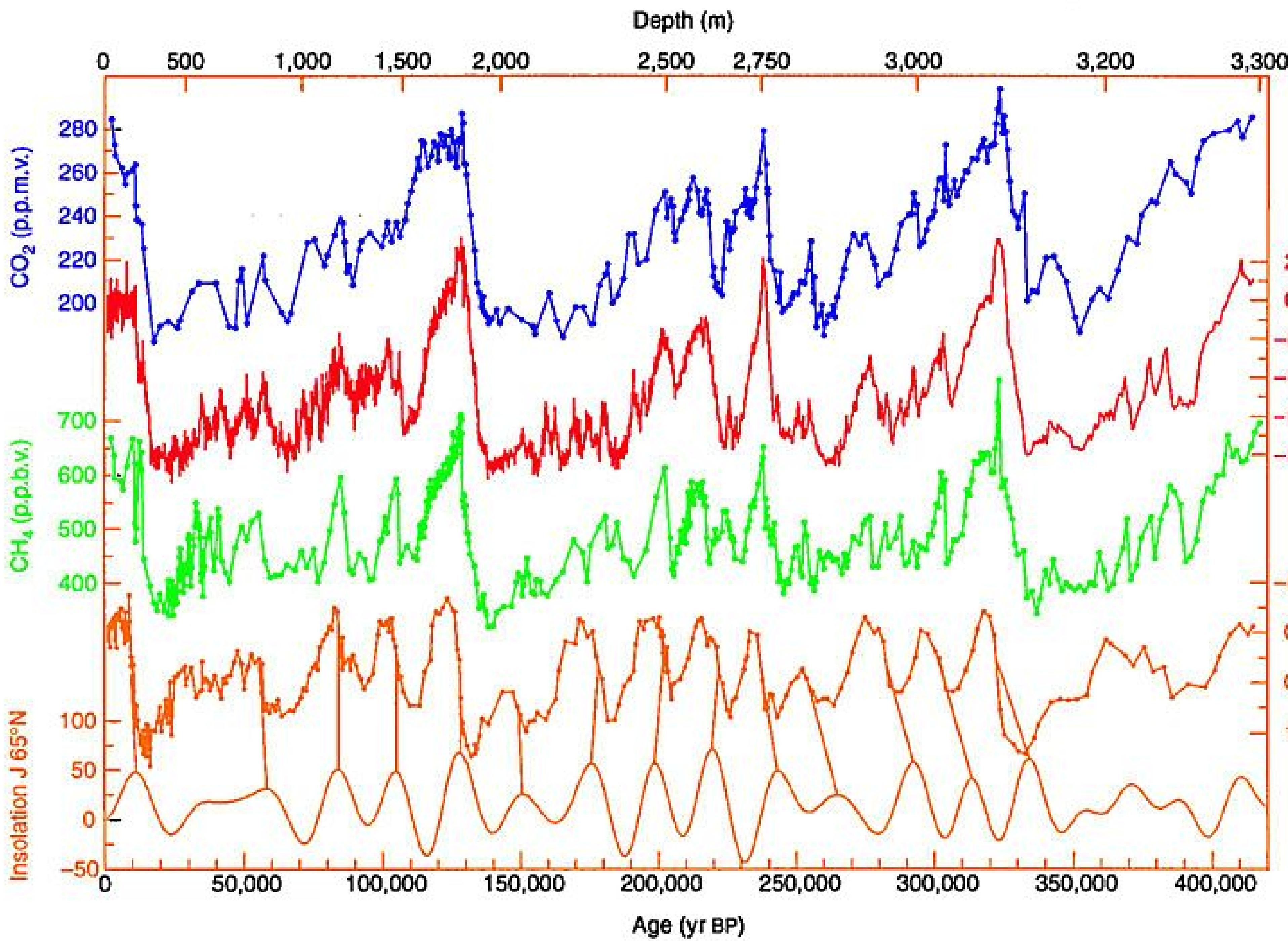


Figure 8.01 Schematic model of Daisyworld, whose surface is covered by black and white daisies and empty area. The temperature of Daisyworld is related to how much energy is received and how much is reflected; the difference is the amount of solar energy absorbed. The amount of energy reflected back to space depends on the planet's albedo (the fraction of light energy that is reflected). The albedo in turn depends on the coverage of white and black daisies. The heat radiated to space is a function of how much energy is absorbed.


% Area
100
80
60
40
20
0
0.7
0.8
0.9
1
1.1
1.2
1.3
1.4
1.5
1.6
Temperature (C)
70
60
50
40
30
20
10
0
-10
With Daisies
temperature=23.6 C
at luminosity=0.84
0.7
0.8
0.9
1
1.1
1.2
1.3
1.4
1.5
1.6
Solar Luminosity


cored
2.2 miles
ANTARCTICA
South Pole
Lake Vostok

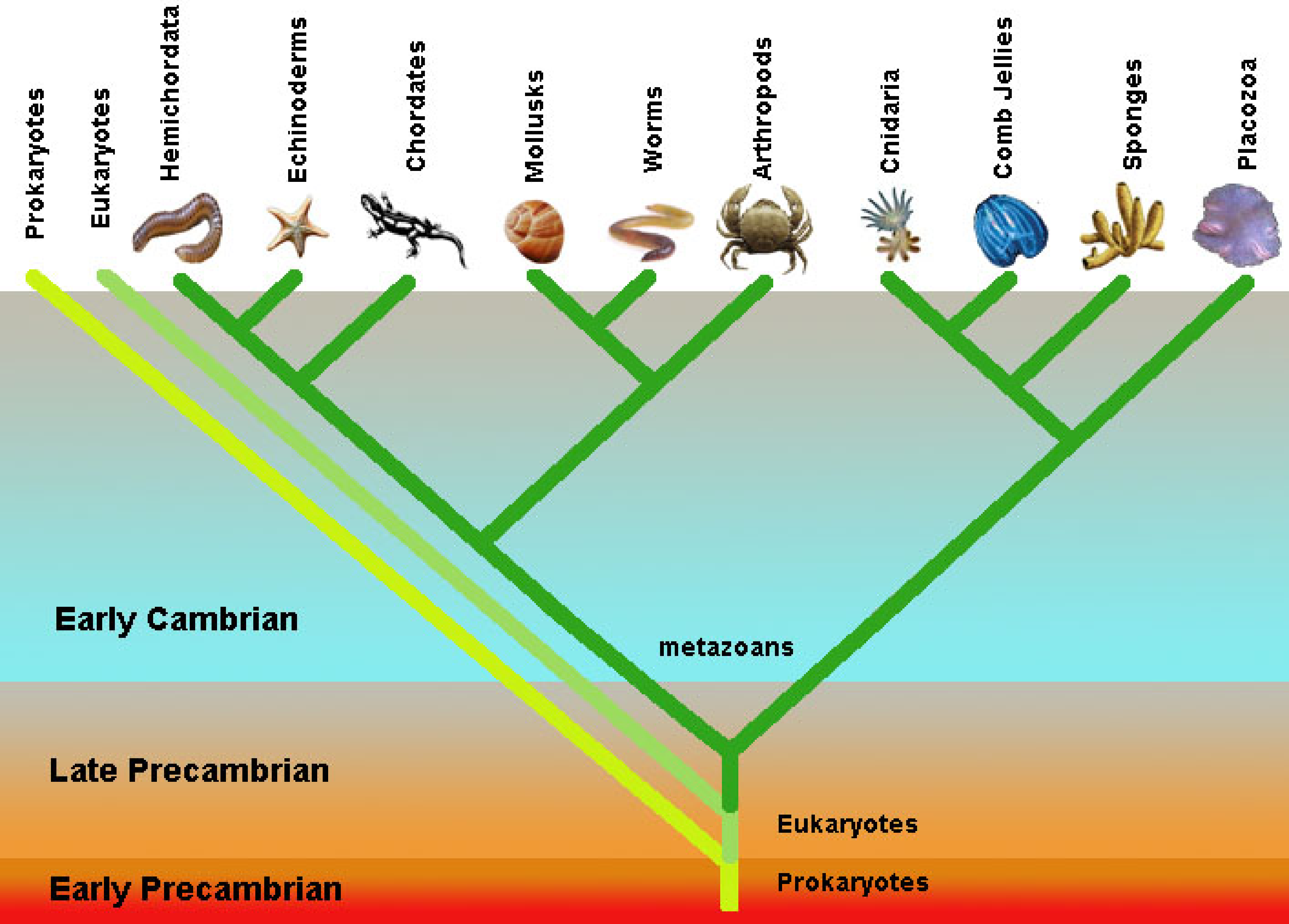


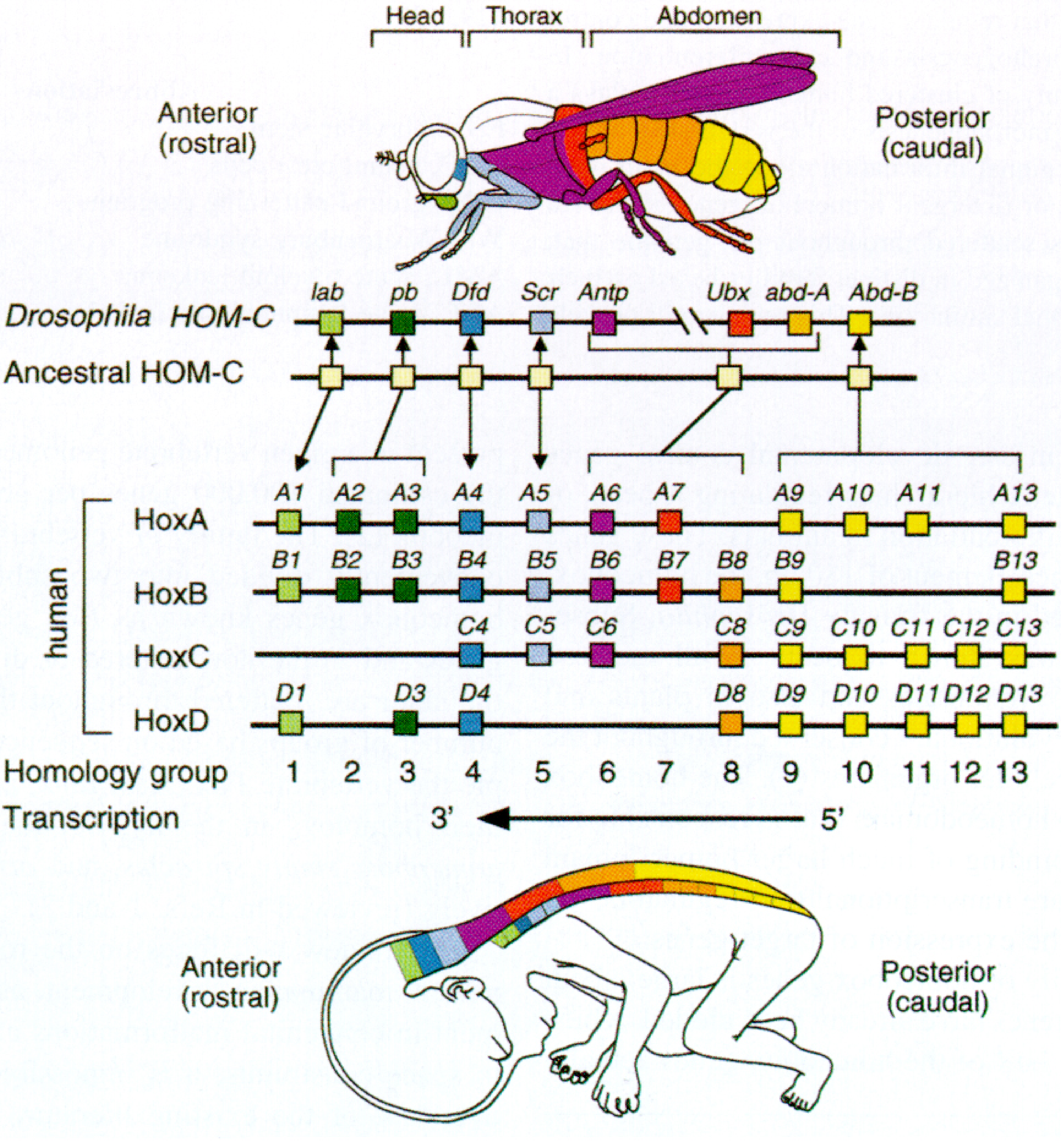
Depth (m)
0
500
1,000
1,500
2,000
2,500
2,750
3,000
3,200
3,300
CO2 (p.p.m.v.)
280
260
240
220
200
Temperature (°C)
2
0
−2
−4
−6
−8
CH4 (p.p.b.v.)
700
600
500
400
δ18Oatm (‰)
−0.5
0.0
0.5
1.0
Insolation J 65°N
100
50
0
−50
0
50,000
100,000
150,000
200,000
250,000
300,000
350,000
400,000
Age (yr BP)

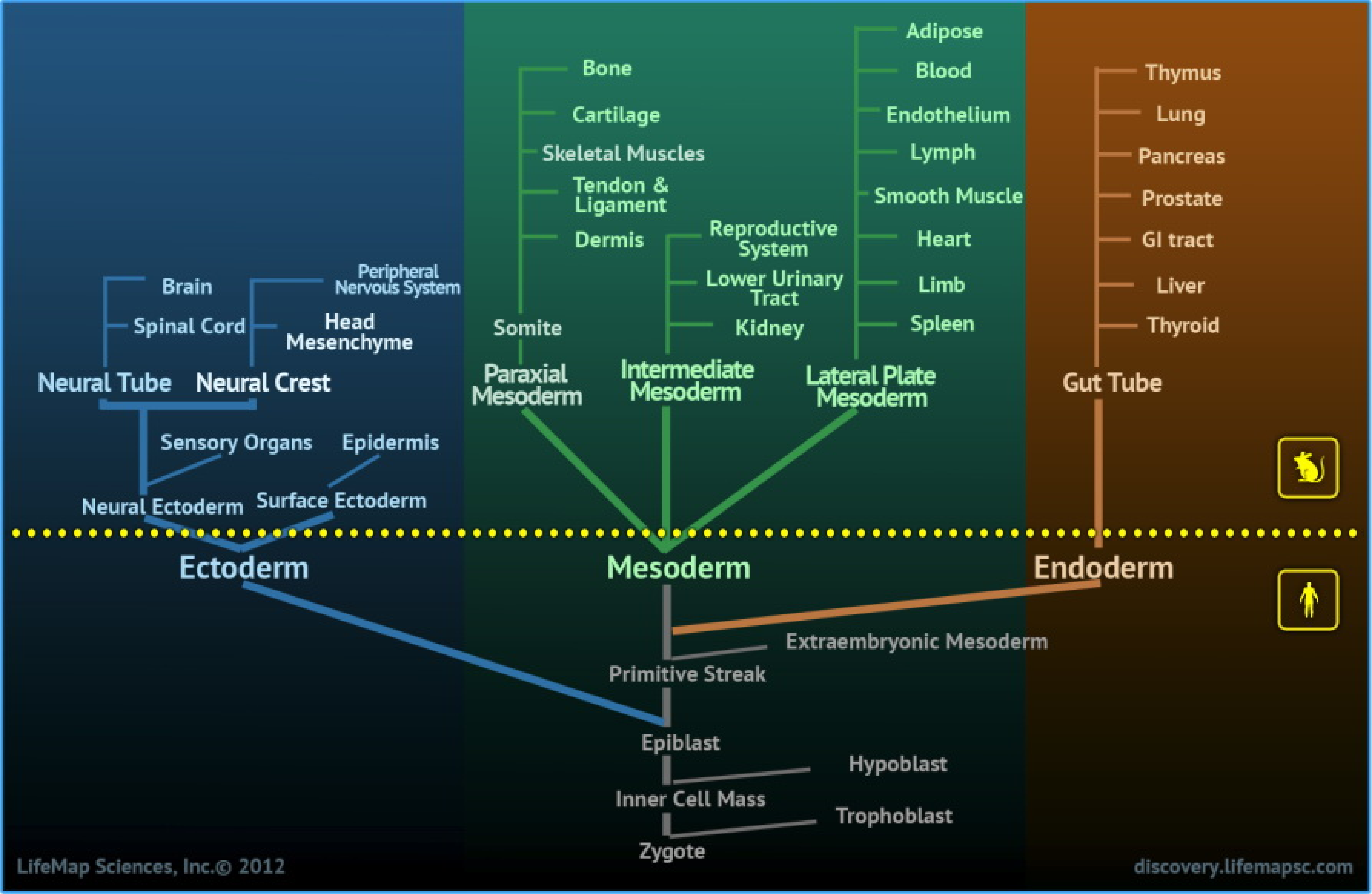
EON	ERA	PERIOD		EPOCH		Ma
Phanerozoic	Cenozoic	Quaternary		Holocene		0.01
				Pleistocene	Late	0.8
					Early	1.8
		Tertiary	Neogene	Pliocene	Late	3.6
					Early	5.3
				Miocene	Late	11.2
					Middle	16.4
					Early	23.7
				Oligocene	Late	28.5
					Early	33.7
			Paleogene	Eocene	Late	41.3
					Middle	49.0
					Early	54.8
				Paleocene	Late	61.0
					Early	65.0
	Mesozoic	Cretaceous		Late		99.0
				Early		144
		Jurassic		Late		159
				Middle		180
				Early		206
		Triassic		Late		227
				Middle		242
				Early		248
	Paleozoic	Permian		Late		256
				Early		290
		Pennsylvanian				323
		Mississippian				354
		Devonian		Late		370
				Middle		391
				Early		417
		Silurian		Late		423
				Early		443
		Ordovician		Late		458
				Middle		470
				Early		490
		Cambrian		D		500
				C		512
				B		520
				A		543
Precambrian	Proterozoic	Late				900
		Middle				1600
		Early				2500
	Archean	Late				3000
		Middle				3400
		Early				3800?

The "Cambrian Explosion"

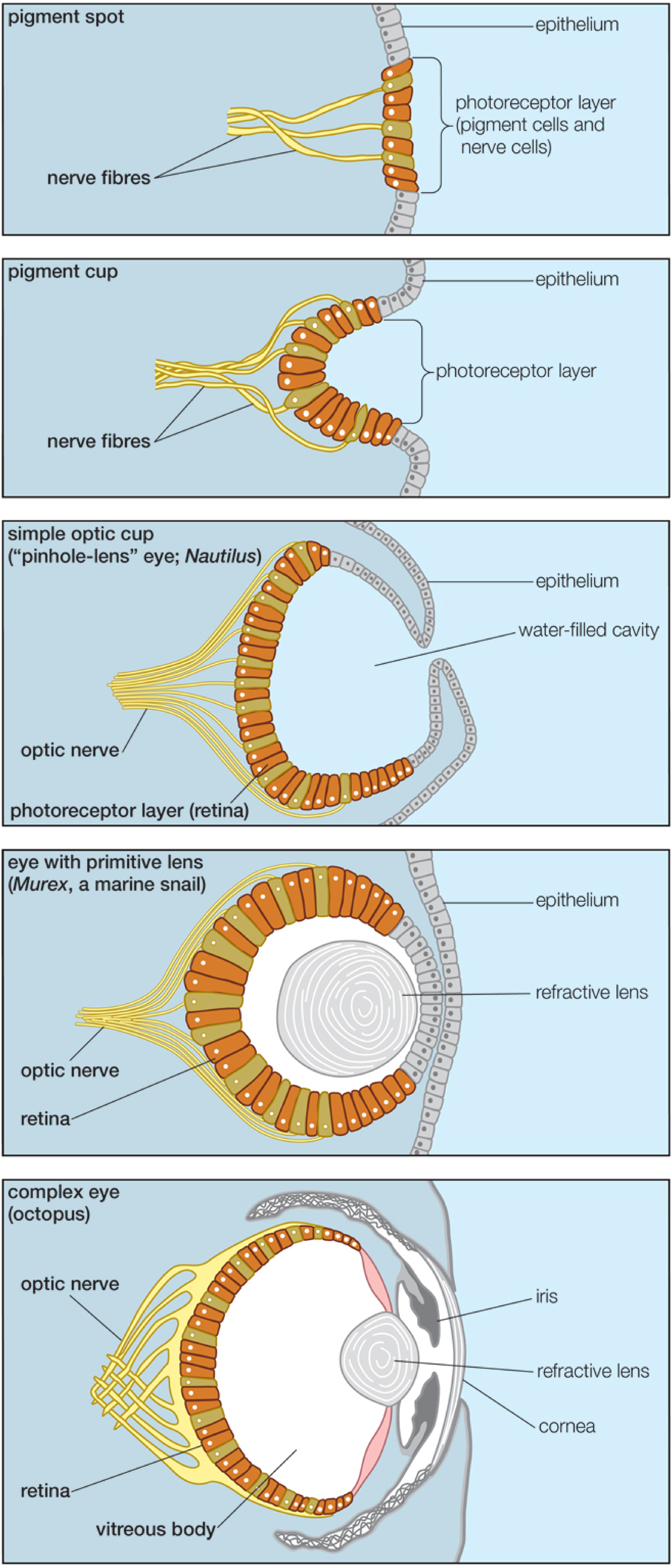
Evidence in the fossil record shows that all major phylla were established in the transition from Late Precambrian to Early Cambrian time




Head
Thorax
Abdomen
Anterior (rostral)
Posterior (caudal)
lab
pb
Dfd
Scr
Antp
Ubx
abd-A
Abd-B
Drosophila HOM-C
Ancestral HOM-C
A1 A2 A3 A4 A5 A6 A7 A9 A10 A11 A13
HoxA
B1 B2 B3 B4 B5 B6 B7 B8 B9 B13
HoxB
C4 C5 C6 C8 C9 C10 C11 C12 C13
HoxC
D1 D3 D4 D8 D9 D10 D11 D12 D13
HoxD
human
Homology group 1 2 3 4 5 6 7 8 9 10 11 12 13
Transcription 3' 5'
Anterior (rostral)
Posterior (caudal)


Adipose
Blood
Endothelium
Lymph
Smooth Muscle
Heart
Limb
Spleen
Bone
Cartilage
Skeletal Muscles
Tendon & Ligament
Dermis
Reproductive System
Lower Urinary Tract
Kidney
Somite
Thymus
Lung
Pancreas
Prostate
GI tract
Liver
Thyroid
Brain
Spinal Cord
Peripheral Nervous System
Head Mesenchyme
Neural Tube
Neural Crest
Paraxial Mesoderm
Intermediate Mesoderm
Lateral Plate Mesoderm
Gut Tube
Sensory Organs
Epidermis
Neural Ectoderm
Surface Ectoderm
Ectoderm
Mesoderm
Endoderm
Extraembryonic Mesoderm
Primitive Streak
Epiblast
Hypoblast
Inner Cell Mass
Trophoblast
Zygote
LifeMap Sciences, Inc.© 2012
discovery.lifemapsc.com

Stages of eye complexity in mollusks



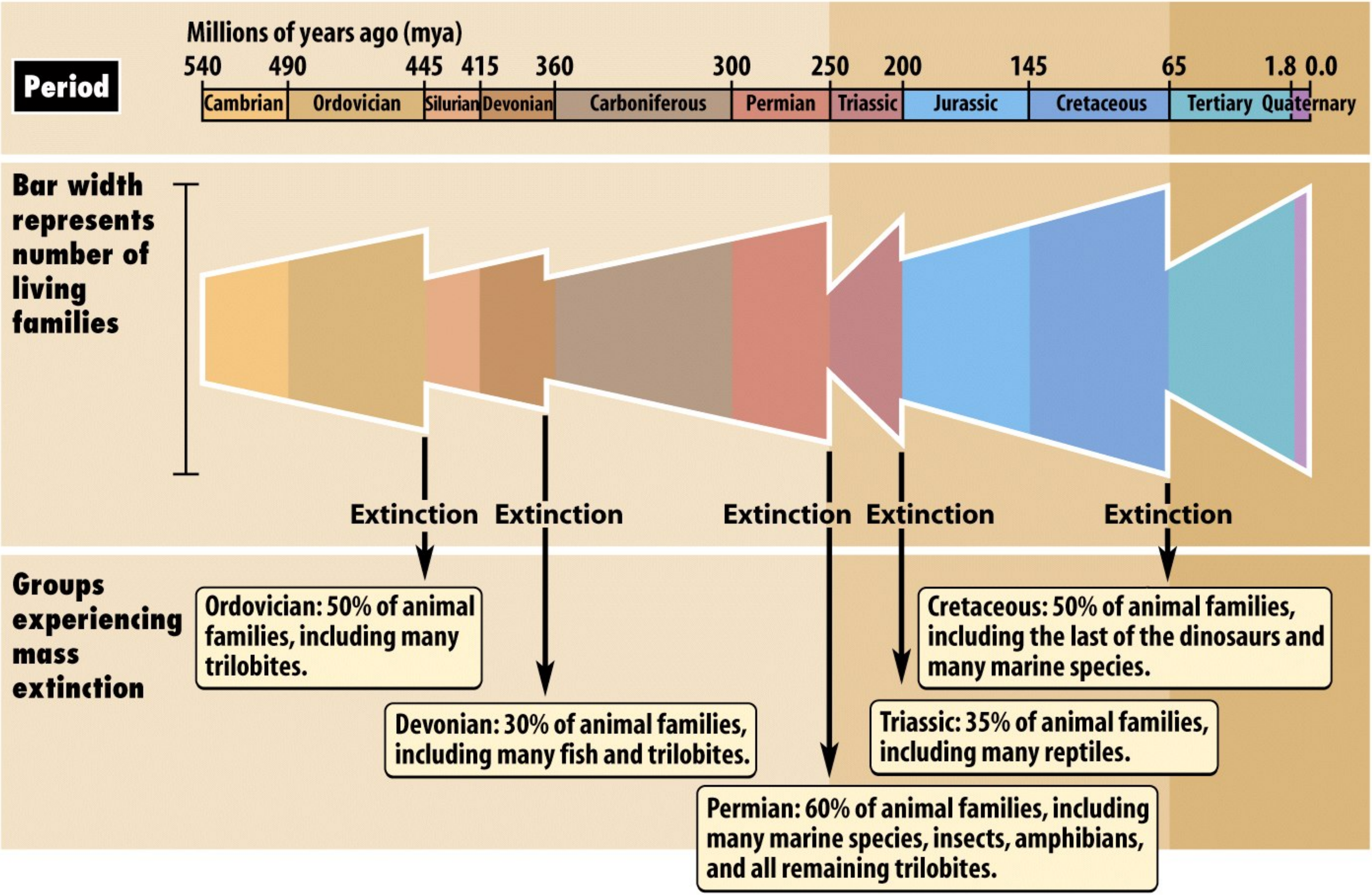
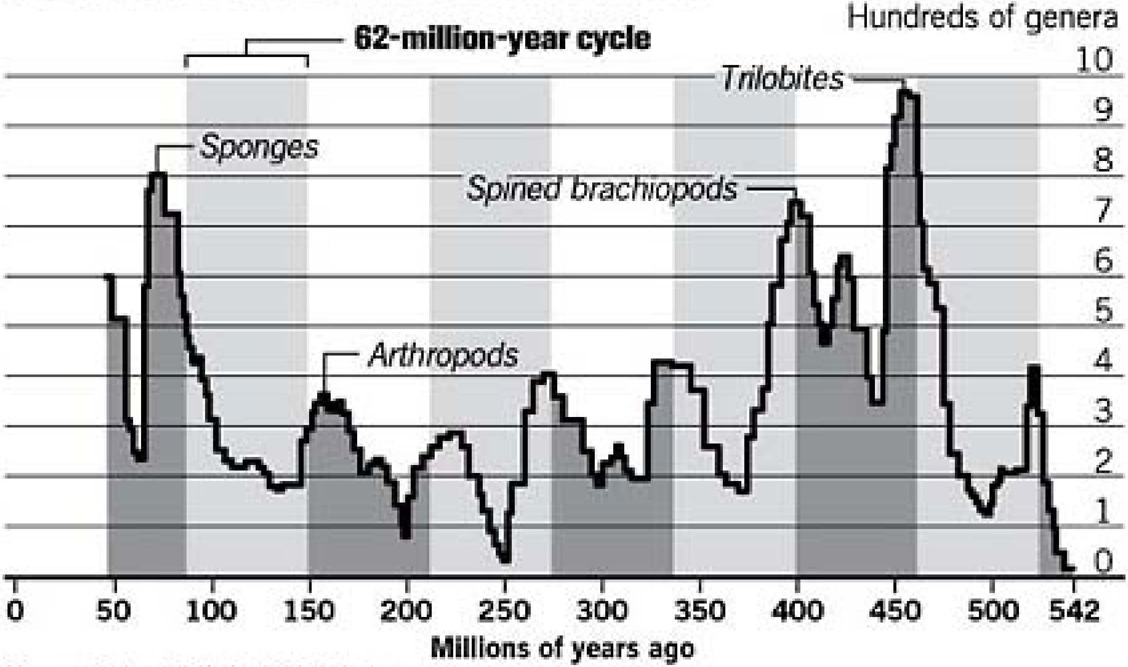


Figure 19-8 Discover Biology 3/e

Cycles of extinction and biodiversity

Berkeley scientists have discovered that marine life has flourished and become extinct in unexplained cycles every 62 million years. In the most recent example in the chart below, many types, or genera, of sponges grew most abundant and then vanished about 65 million years ago — the same period when a monster asteroid or comet crashed to Earth and drove the world's dinosaurs to extinction.

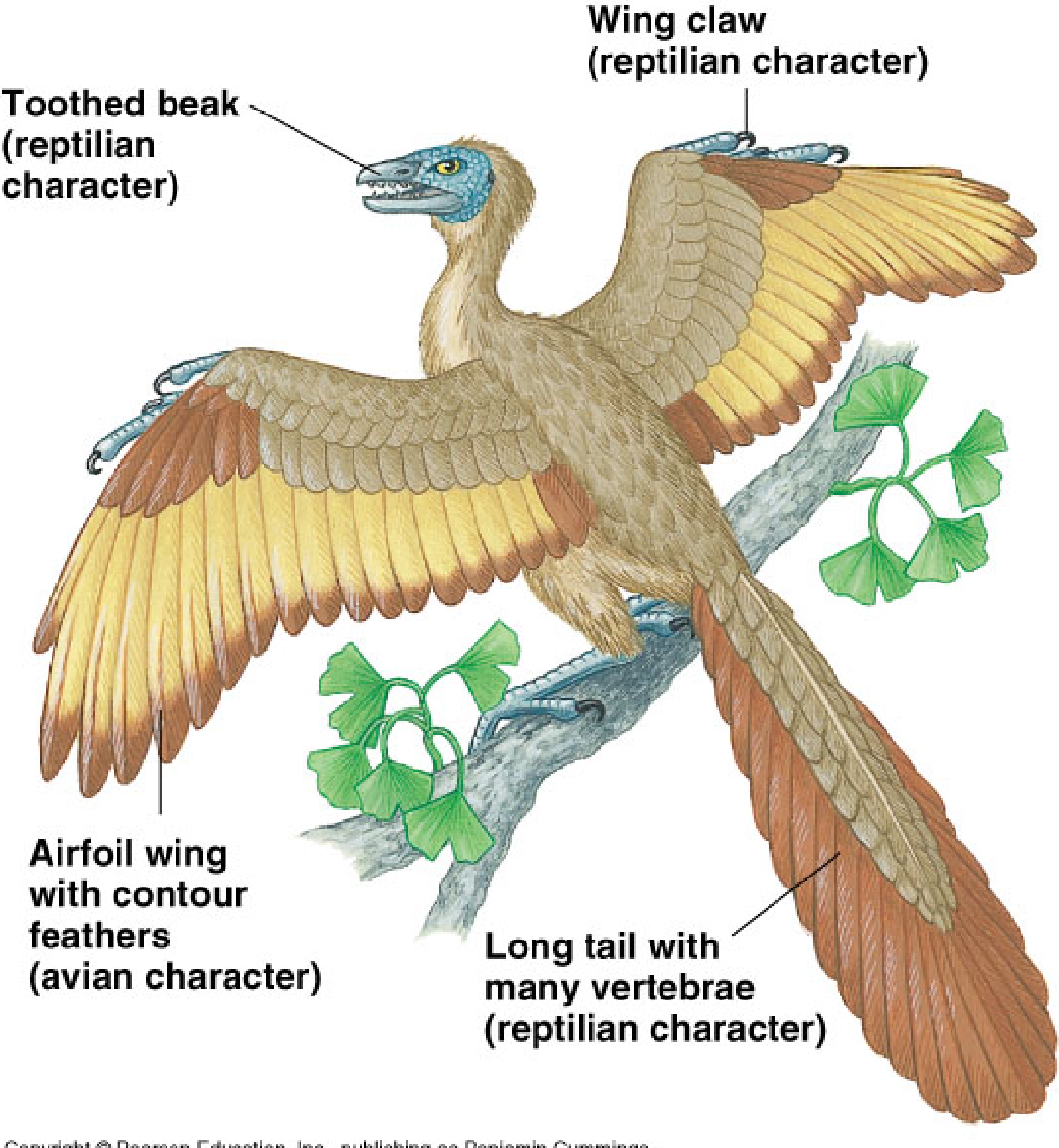


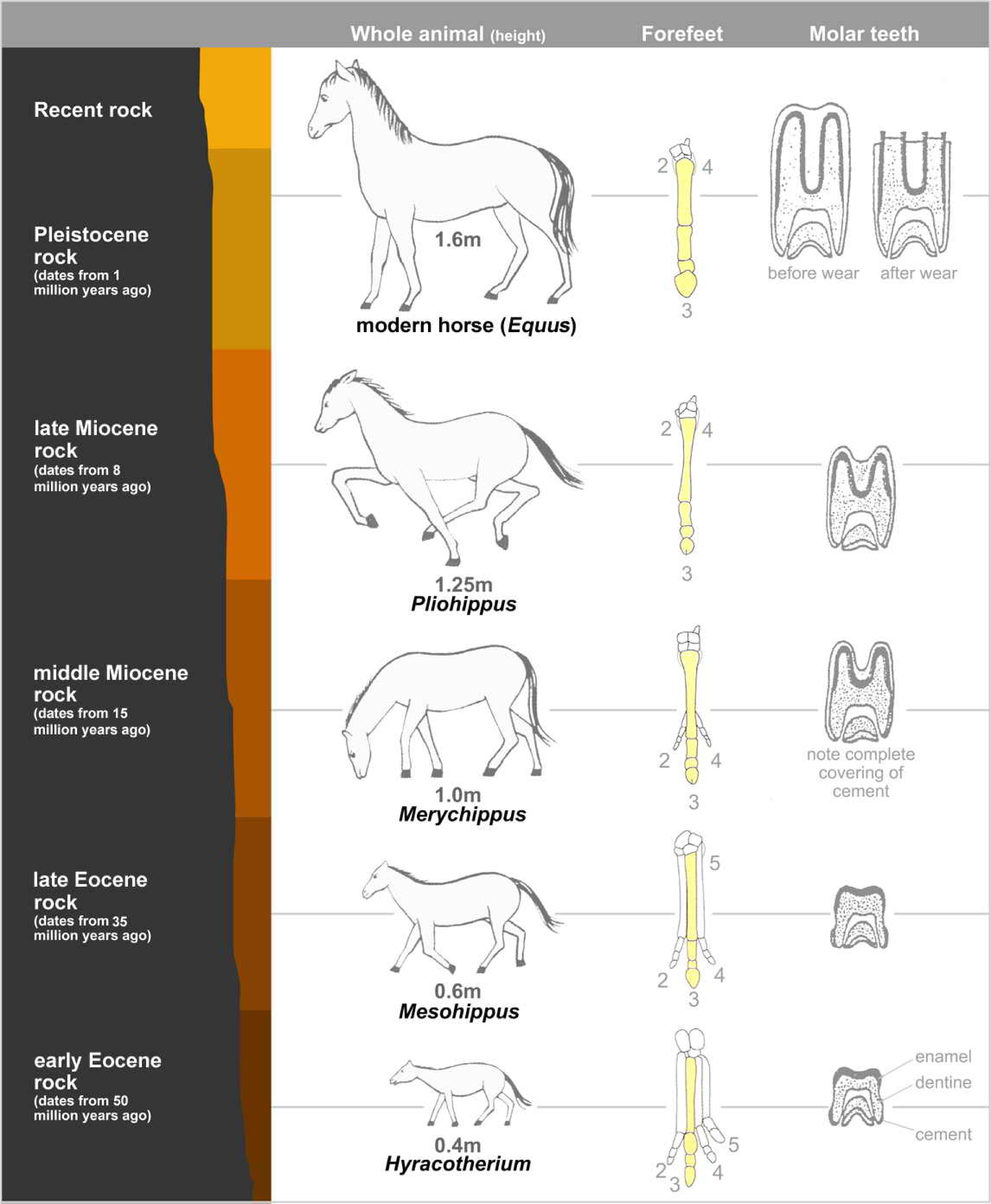
Source: Robert Rohde, UC Berkeley

The Chronicle


INCH
1
2
3
4
5
6
FaberCastell

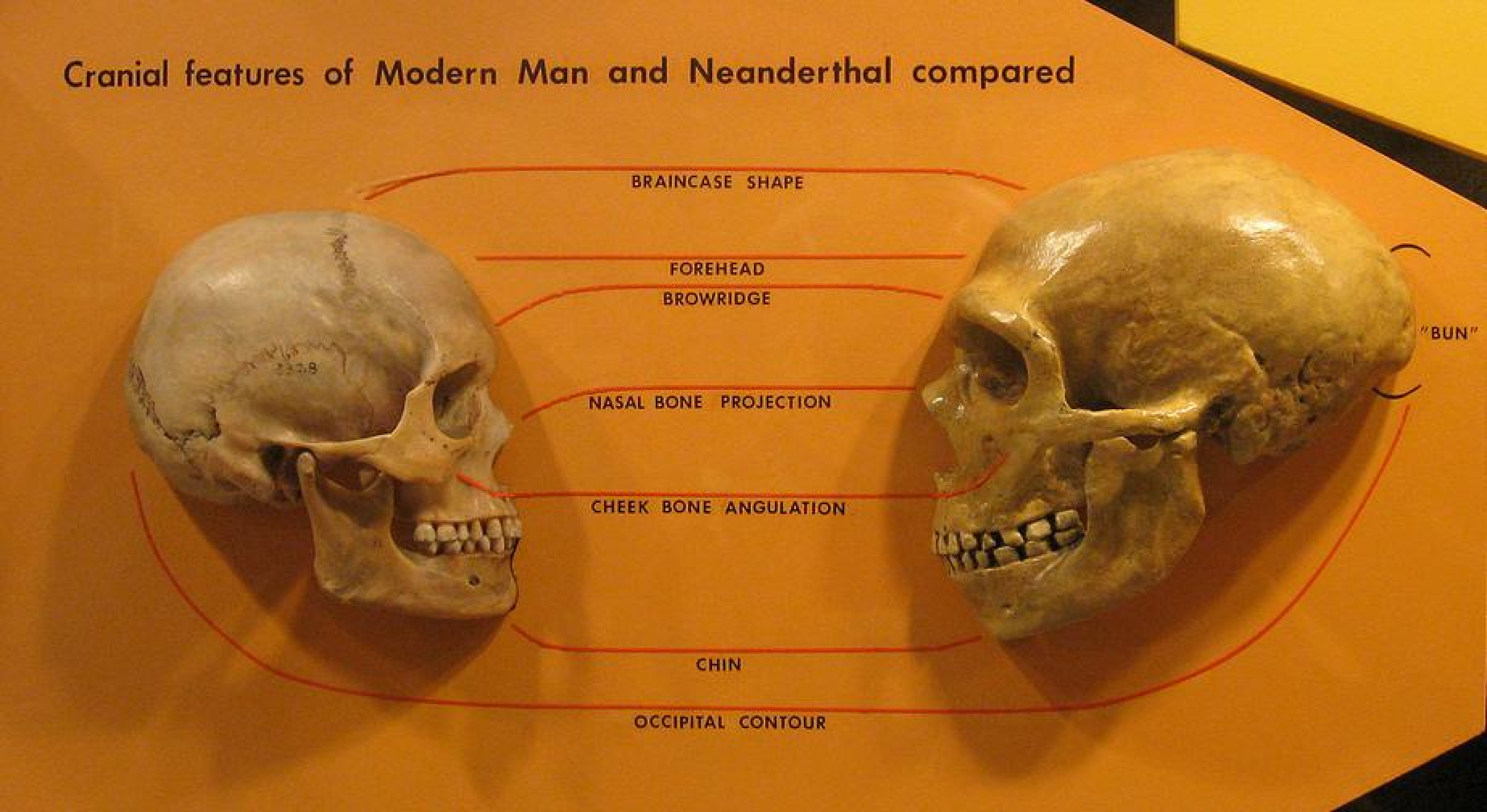

Des grands
singes à l'Homme


Wing claw
(reptilian character)
Toothed beak
(reptilian
character)
Airfoil wing
with contour
feathers
(avian character)
Long tail with
many vertebrae
(reptilian character)



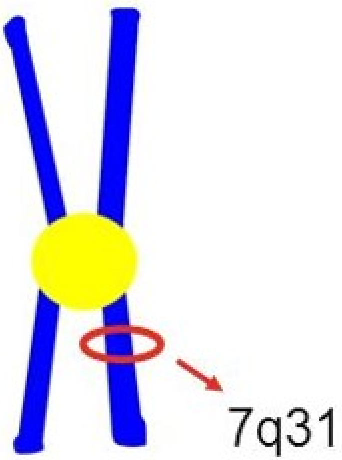
Whole animal (height)
Forefeet
Molar teeth
Recent rock
Pleistocene rock
(dates from 1 million years ago)
late Miocene rock
(dates from 8 million years ago)
middle Miocene rock
(dates from 15 million years ago)
late Eocene rock
(dates from 35 million years ago)
early Eocene rock
(dates from 50 million years ago)
1.6m
modern horse (Equus)
1.25m
Pliohippus
1.0m
Merychippus
0.6m
Mesohippus
0.4m
Hyracotherium
2
3
4
5
before wear
after wear
note complete covering of cement
enamel
dentine
cement

Taxonomic rank	Name	Common name	Mya
domain	**Eukaryota**	Cells with a nucleus	2,100
kingdom	Animalia	Animals	590
phylum	Chordata	Vertebrates and closely related invertebrates	530
subphylum	Vertebrata	Vertebrates	505
superclass	Tetrapoda	Tetrapods	395
superclass	Amniota	Amniotes, tetrapods that are fully terrestrially-adapted	340
class	**Mammalia**	Mammals	220
subclass	Theriiformes	Mammals that birth live young (i.e. non-egg-laying)	
infraclass	Eutheria	Placental mammals (i.e. non-marsupials)	125
superorder	Euarchontoglires	Supraprimates (primates, rodents, rabbits, tree shrews, and colugos)	100
mirorder	Primatomorpha	Primates and colugos	79.6
order	**Primates**	Primates	75
suborder	Haplorrhini	"Dry-nosed" (literally, "simple-nosed") primates (apes, monkeys, and tarsiers)	40
infraorder	**Simiiformes**	"Higher" primates (or Simians) (apes, old-world monkeys, and new-world monkeys)	
parvorder	Catarrhini	"Downward-nosed" primates (apes and old-world monkeys)	30
superfamily	**Hominoidea**	Apes	28
family	**Hominidae**	Great apes (Humans, chimpanzees, bonobos, gorillas, and orangutans)	15
subfamily	†Kenyapithecinae/Ponginae	Kenyapithecus and ramapithecus	14-12.5
subfamily	**Homininae**	Humans, chimpanzees, bonobos, and gorillas	8
tribe	**Hominini**	Homo and Australopithecina	5.8
subtribe	**Hominina**	Members of the genus Homo	3
genus	**Homo**	Humans, neanderthals, homo erectus, and their direct ancestors	2.5
species	*Homo sapiens* (archaic)	Humans	0.5
sub-species	*Homo sapiens sapiens*	Modern humans	0.2
sub-species	***Neurologically*** modern humans	Fully neurologically developed humans	0.2-0.07

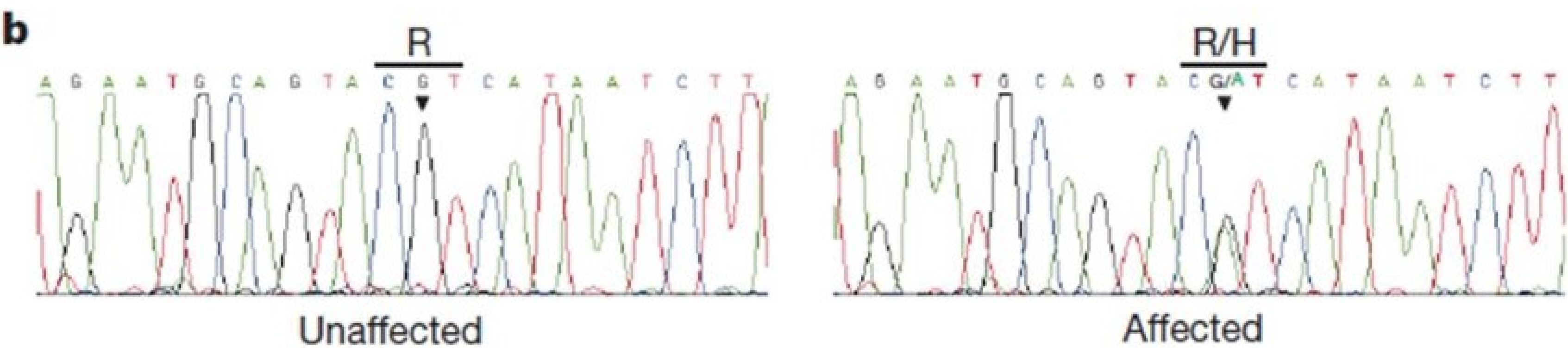

Cranial features of Modern Man and Neanderthal compared
BRAINCASE SHAPE
FOREHEAD
BROWRIDGE
"BUN"
NASAL BONE PROJECTION
CHEEK BONE ANGULATION
CHIN
OCCIPITAL CONTOUR

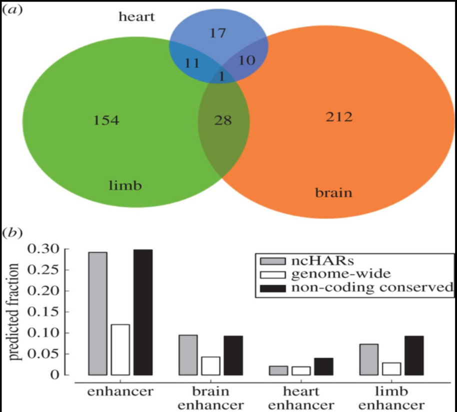
	Dates (years before present)	Milestone	Dating Methods
	4-7 million	Human & chimp ancestors diverge	Molecular genetic clock, Argon
	By 4 million	Bipedal walking becomes well developed	Argon
	2.6 million	Oldest stone toolmaking	Argon, Paleomagnetic
	1.8 million	*Homo erectus* expands out of Africa	Argon, Paleomagnetic
	800,000 – 200,000	Rapid brain expansion	Argon & Uranium-series Paleomagnetic
	250, 000 – 30,000	Neanderthals emerge, then become extinct; *Homo sapiens* emerges in Africa, then expands to other continents; symbolic culture begins to flourish	Thermoluminescence , Electron spin resonance, Carbon-14, Molecular genetic clock
	12,000 – 10,000	Origins of agriculture	Carbon-14 dating
	4,500	Origins of writing, state societies, civilization: Sumer & Egypt	Carbon-14 dating

Identification of the *FOXP2* Gene



By analyzing the KE family DNA sequences, scientists found that the speech problem was caused by a mutation in the *FOXP2* gene located on chromosome 7 region 7q31.





AQP7 (aquaporin 7) - copy number increase in humans key role in water transport across membranes play a role in thermoregulation (sweating) and energy mobilization enhanced capacity for **endurance running found in humans**

CKB (Creatine kinase brain) - expression of this gene is higher in the human brain than it is in other primates, provide more energy for use by the human brain from the phosphocreatine circuit. Availability of more energy to the brain play a role in the **increased human brain**

DRD4 (Dopamine receptor D4) - in human populations, there is variable number of tandem repeats (VNTR) within the coding region of the third exon of this gene, higher number of repeats are associated with increased **novelty seeking behavior**

FOXP2 (forkhead box P2) - transcription factor protein coding gene involved in regulation of gene expression differences occurred in human lineage, after human-chimpanzee common ancestor – **human language acquisition**

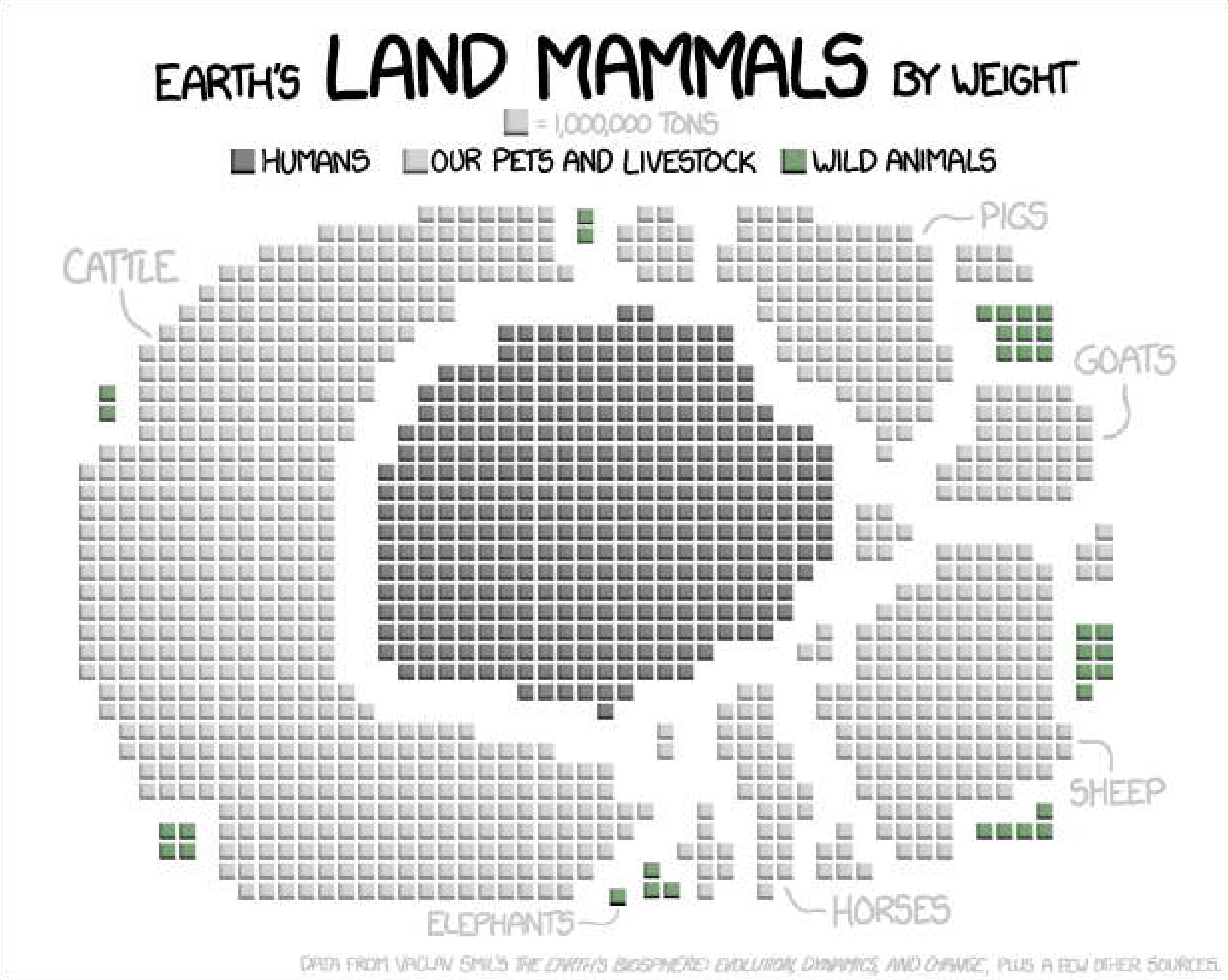
NBPF15 (Neuroblastoma breakpoint factor, member 15) - human lineage specific copy number increase. It is highly expressed in brain regions associated with **higher cognitive function**

MCR1 (Melanocortin 1 receptor) - Melanocortin, a pituitary peptide hormone, stimulate melanocytes; gene polymorphism is related to pigmentation in human – **skin colour**

MCPH-1 (Microcephalin 1) - undergone significantly higher rates of protein sequence evolution in primates than in rodents. Furthermore, the gene has undergone even more rapid evolution in humans including evidence of a selective sweep in human populations - **increases in brain size**

MYH16 (Myosin heavy chain 16) - gene is nonfunctional in human specialized muscle protein found only in muscles of the jaw if functional animals have powerful jaw muscles - **increased brain size and finer control of the jaw which facilitates speech**

SRGAP2 (SLIT-ROBO Rho GTPase activating protein 2) - directly regulates membrane deformation for proper neuronal migration and axon-dendrite morphogenesis. The human lineage underwent 3 partial duplication events - **resulted in human specific changes to the neocortex**


EARTH'S LAND MAMMALS BY WEIGHT
= 1,000,000 TONS
HUMANS
OUR PETS AND LIVESTOCK
WILD ANIMALS
CATTLE
PIGS
GOATS
SHEEP
HORSES
ELEPHANTS
DATA FROM VACLAN SMIL'S THE EARTH'S BIOSPHERE: EVOLUTION, DYNAMICS, AND CHANGE, PLUS A FEW OTHER SOURCES.

4.5 milijarde godina – formiranje Zemlje

4.0 milijarde godina – hlađenje površine i prestanak "bombardiranja" mogućnost pojave života, datiranje najstarijih stijena

3.85 milijarde godina – dokazi o postojanju života iz stijena s Grenlanda u kojima se nalazi ^{12}C nepobitan dokaz biogene fiksacije CO_2. Nijedan neživi proces ne može dovesti do toga

3.8 – 3.7 milijarde godina – Bakterije se odvajaju od Arhea + klorofil i fotosinteza evoluiraju u bakterijskoj liniji, Arhee nemaju klorofil, a samo neke Bakterije su fotosintetske

3.7 milijarde godina – BIFs dokaz kisika kao rezultata fotosinteze

3.5 milijarde godina – prvi stromatoliti

2.7 milijarde godina – prvi dokati o postojanju eukariota STERANES

2.1 milijarde godina – eukariotski mikrofosili (Science 257, 232-235 1992)

2.0 milijarde godina - porast koncentracije kisika u atmosferi

1.5 milijarde godina – razina kisika u atmosferi dosegnula današnju, pojava kloroplasta i mitohondrija

1.2 milijarde godina – divergencija eukariotskih koljena,

670 milijuna godina - razdvajanje kralježnjaka i bezkralježnjaka, postojanje Hox genskih klastera

530 milijuna godina – Kambrijska eksplozija

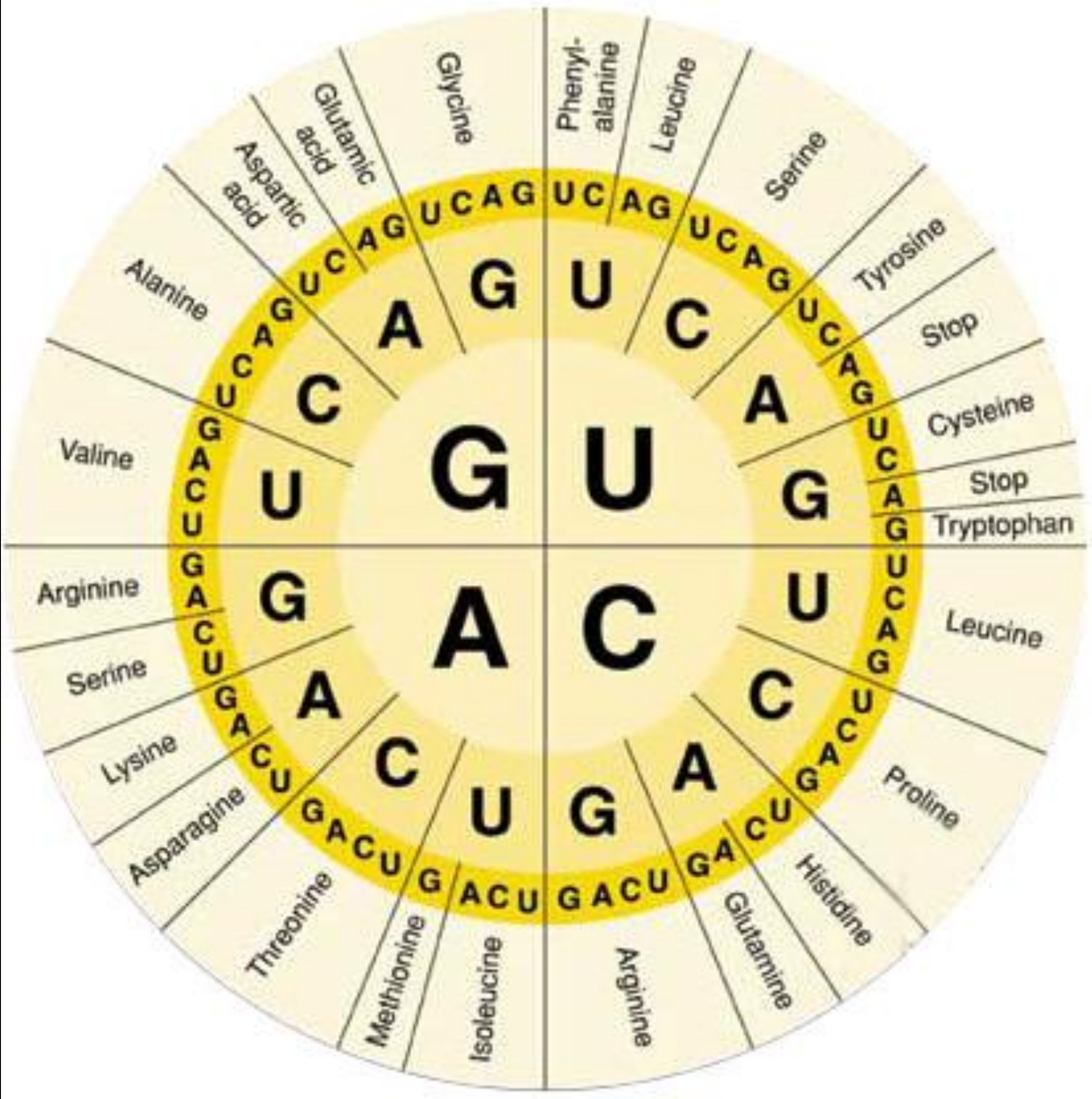
420 milijuna godina – divergencija kralježnjaka, biljke i gljive naseljavaju kopno

380 milijuna godina – kralježnajci naseljavaju kopno

360 milijun godina – golosjemenjače se razdvajaju od kritosjemenjača

310 milijuna godina – ptice i ostali kralježnjaci se razdvajaju

Genetički kod



Mutacije

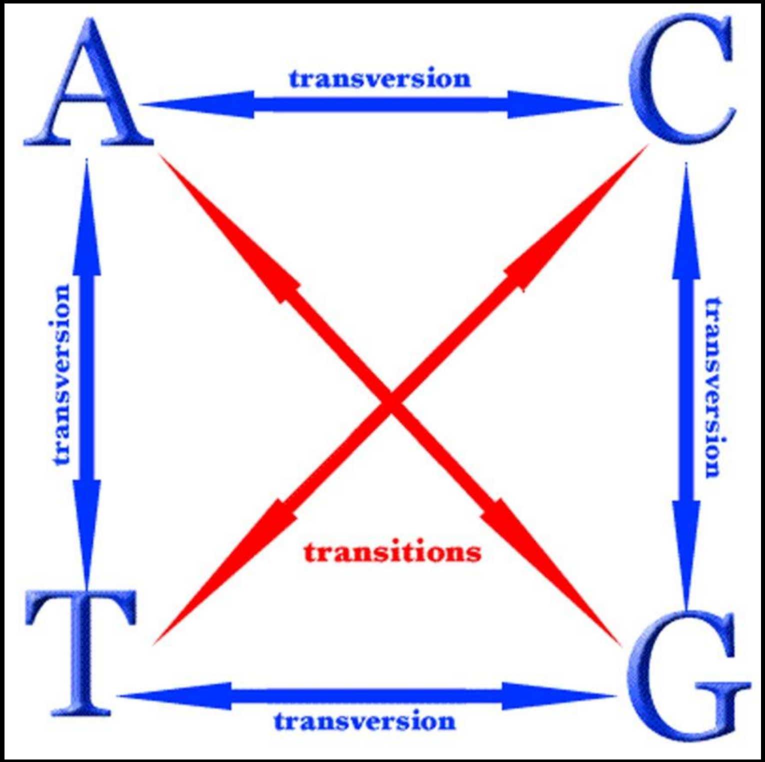
Greške pri replikaciji ili popravku DNA

1. Supstitucije – tranzicije A u G ili C u T (4) i transverzije A u C ili A u T (8)

a) Synonymous - tihe

b) Nonsynonymous

i) Missense – druga ak ii) Nonsense – STOP kodon



64

61x9=549

70% - treći synonymous
100% - drugi nonsynonymous
96% - prvi nonsynonymous

393 missense

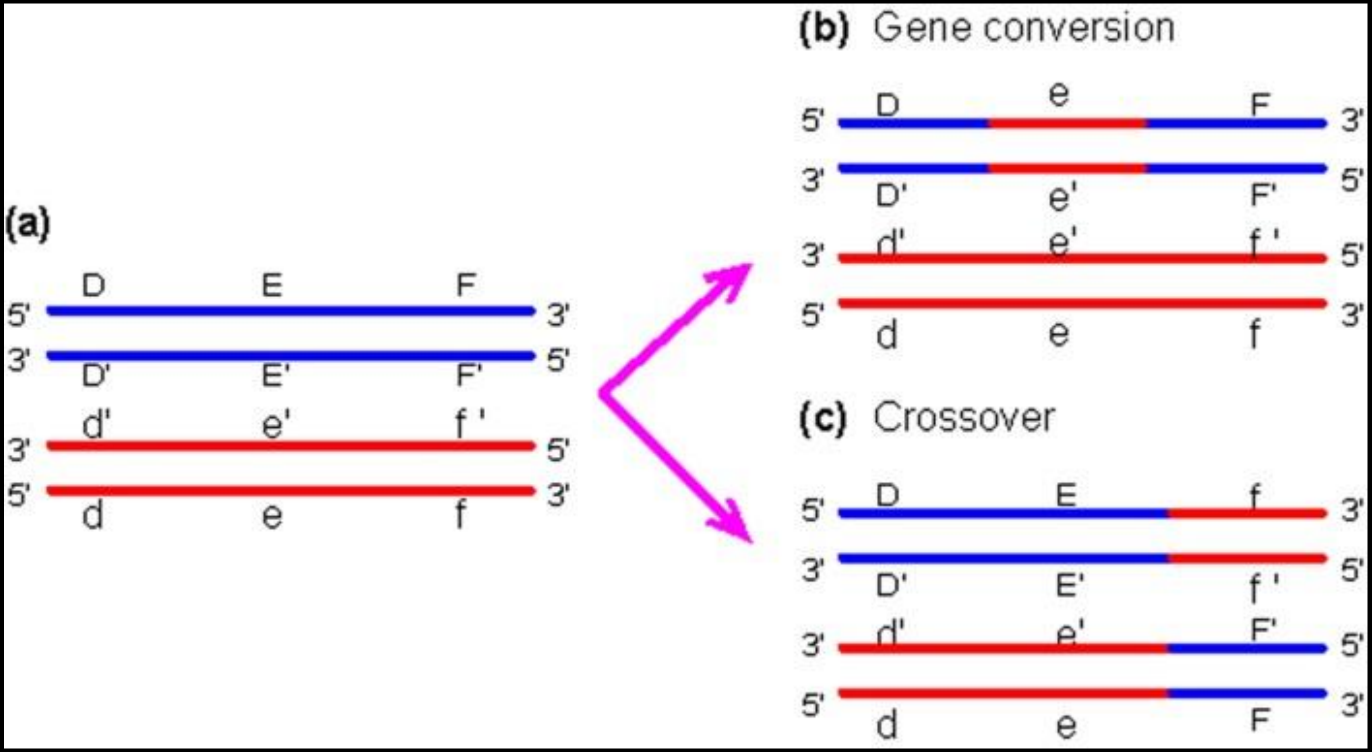
23 nonsnse

131 samesense

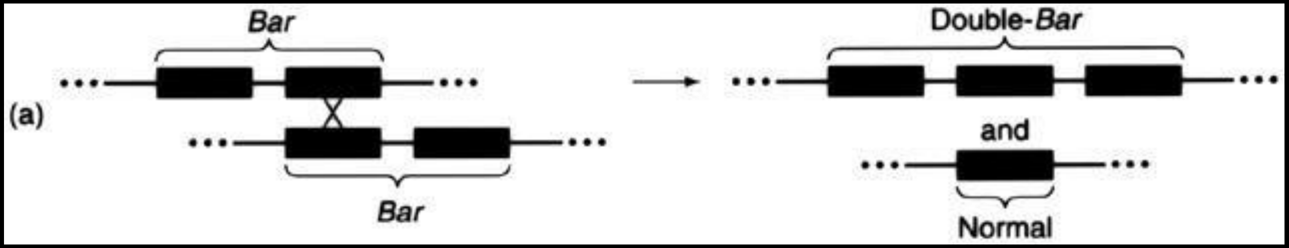
Mutacije

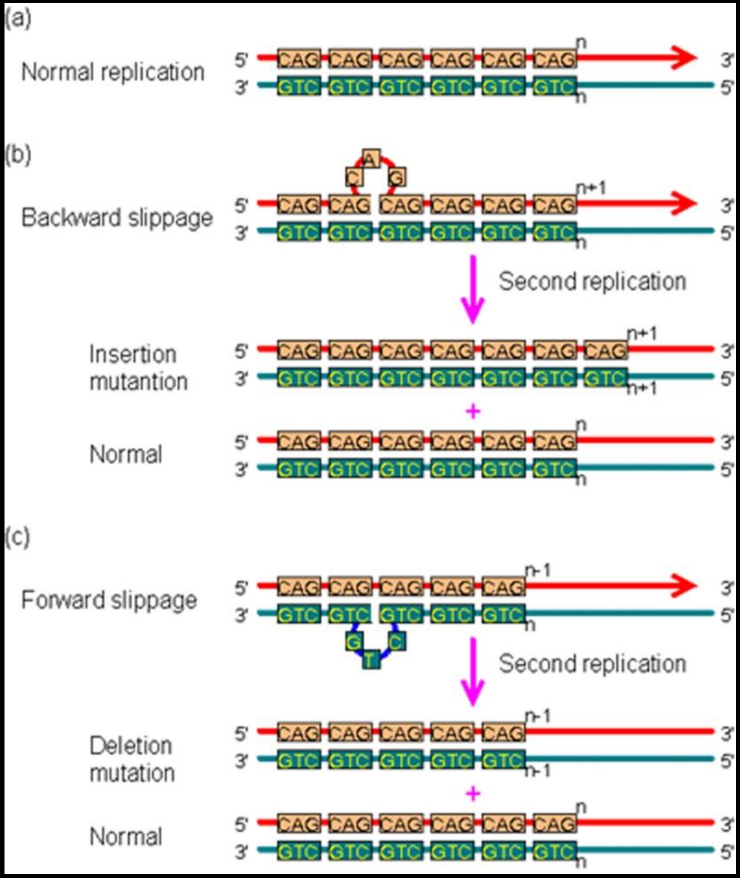
2. Rekombinacije – homologne rekombinacije

a) Crossing-over – recipročna
b) Gene conversion – nerecipročna



Mutacije



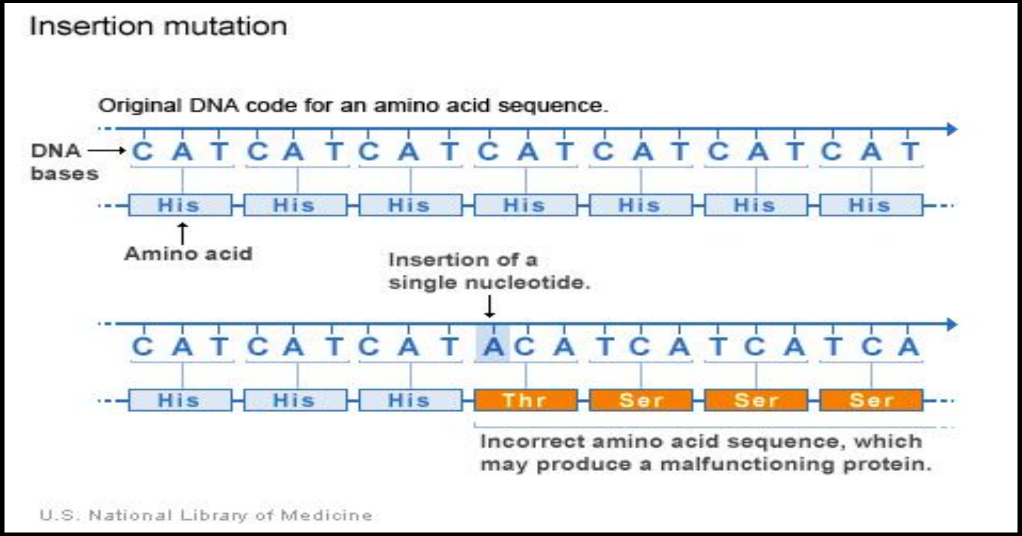


3. Delecije

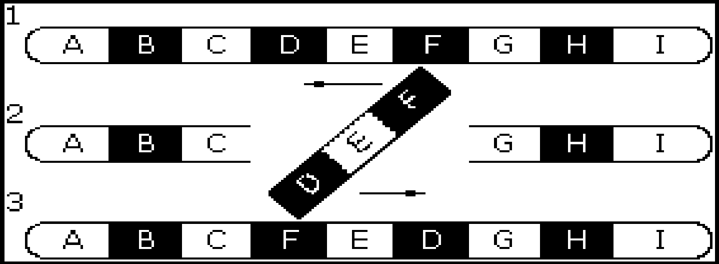
a) Unequal crossing-over
b) Replication slippage
c) Transpozicija

Frameshift mutacija

4. Insercije – INDELS ili gaps



5. Inverzije – rotacija DNA fragmenta za 180°



Hotspots – 5‘-CG-3‘ ili CpG (euk) 5‘-TT-3 ‘ (prok) + palindromi

Lokus – kromosomska ili genomska pozicija gena

Aleli – alternativne forme gena na nekom lokusu

Evolucija = promjena genetičkog ustrojstva POPULACIJA

Molekularna evolucija

Ishodišna područja

Populacijska genetika

Molekularna biologija

Interesna područja

Prebiotska evolucija

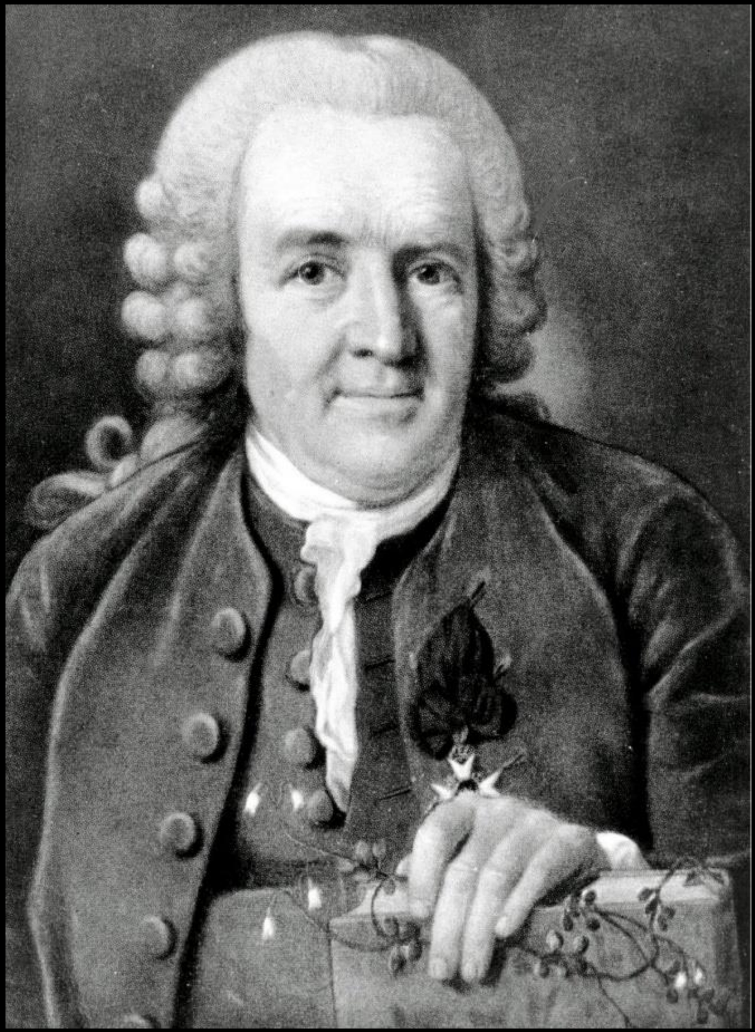
Evolucija makromolekula

Molekularna filogenetika

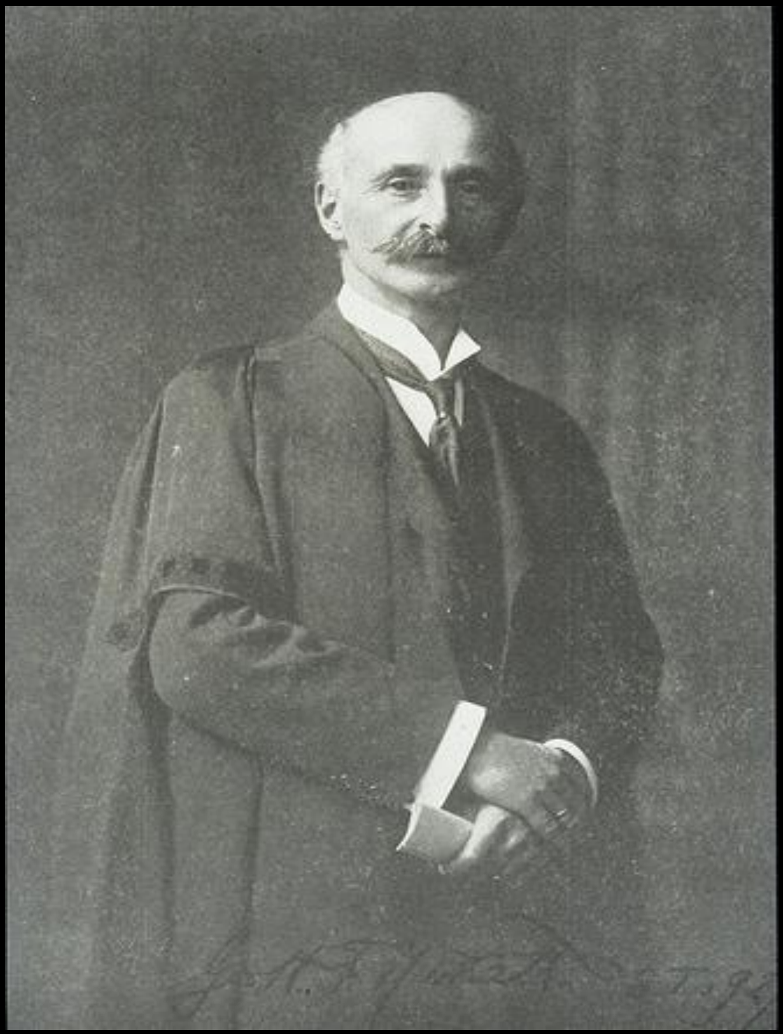
Najznačajniji znanstvenici i njihova otkrića

Zuckerkandl & Pauling – Molekulski sat
Motoo Kimura — Neutralna mutacijska teorija
Masatoshi Nei — Adaptivna evolucija
Walter M. Fitch — Filogenetska rekonstrukcija
Walter Gilbert — RNA svijet
Susumu Ohno — Genska duplikacija
John H. Gillespie — Matematika adaptacije
Wilson & Sarich — Evolucija hominida

Frederick Sanger – Sekvenciranje proteina i DNA
Oliver Smithies – Elektroforeza
Karry Mullis – PCR
Edwin Southern – Hibridizacija
Joe Felsenstein – Filogenetske metode
Perutz & Kendrew – Proteinska kristalografija
Arber, Smith & Nathans – Restrikcijske endonuleaze
Cohen, Berg & Boyer – Rekombinantna DNA tehnologija



Carl Linnaeus (1758) Systema naturæ per regna tria naturæ, secundum classes, ordines, genera, species, cum characteribus, differentiis, synonymis, locis



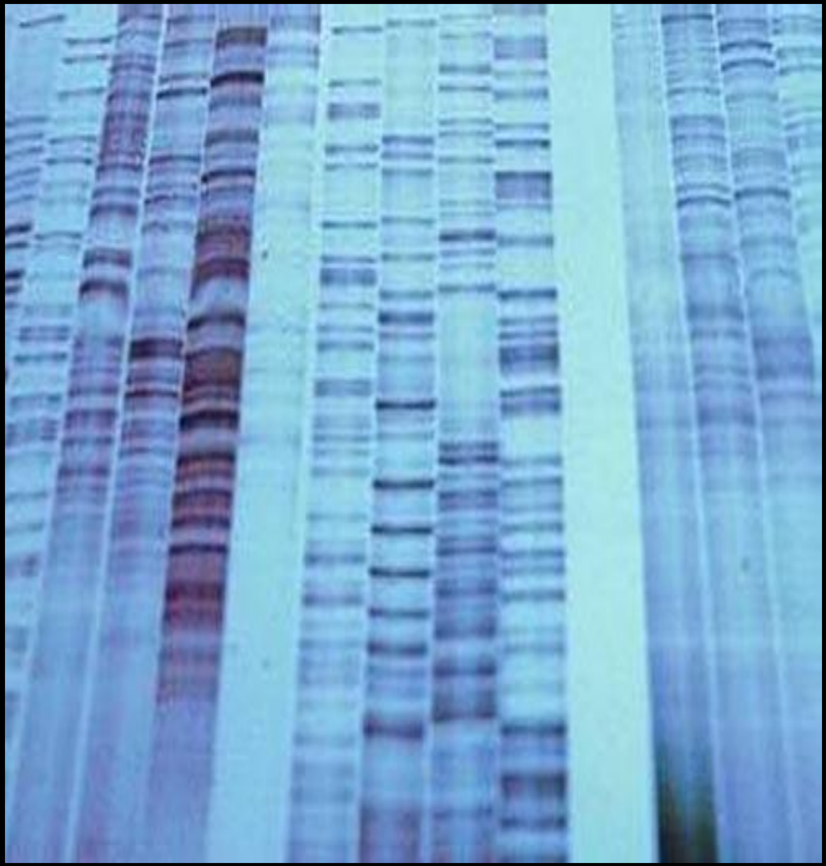
Nuttall, G.H.F. (1901) The new biological test for blood in relation to zoological classification. *Proc. Roy. Soc.* **69**: 150-153.

Molekularna evolucija

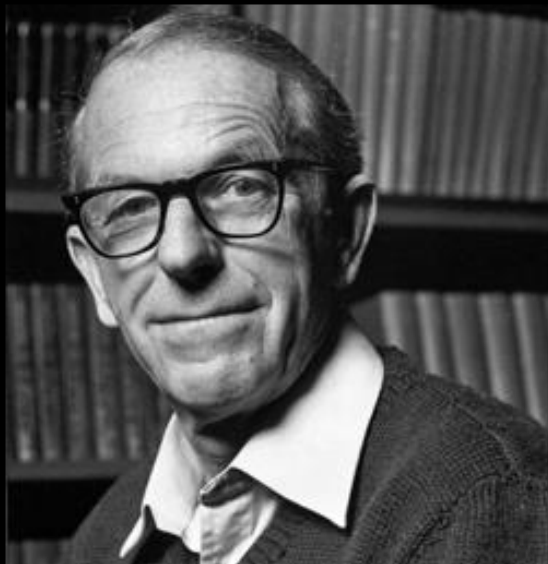
Dvije ere:

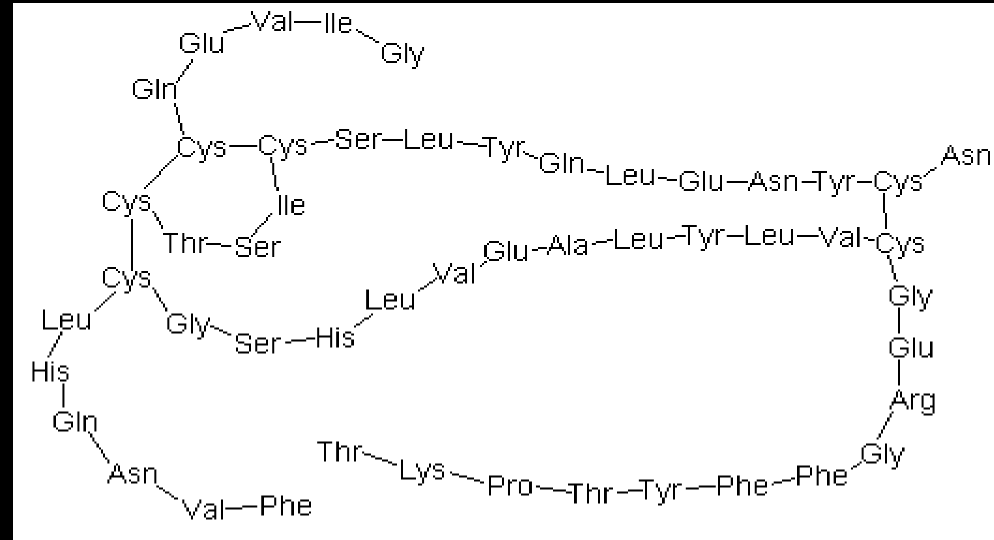
1. Pred DNA – početak 1950-te: sekvenciranje (1952) i elektroforeza (1955)

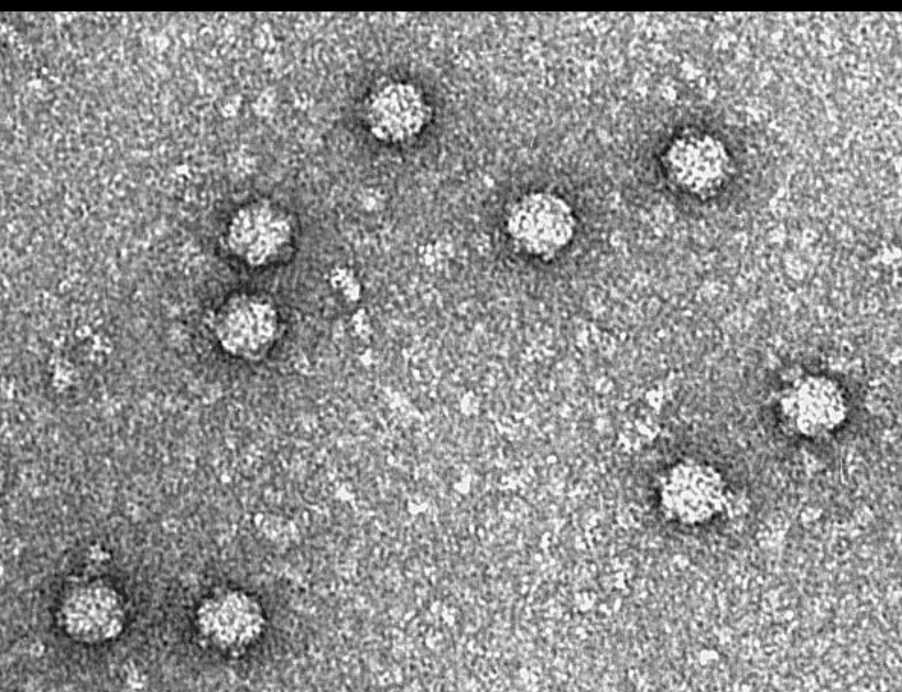
2. DNA – početak 1980-te: PCR (1983)

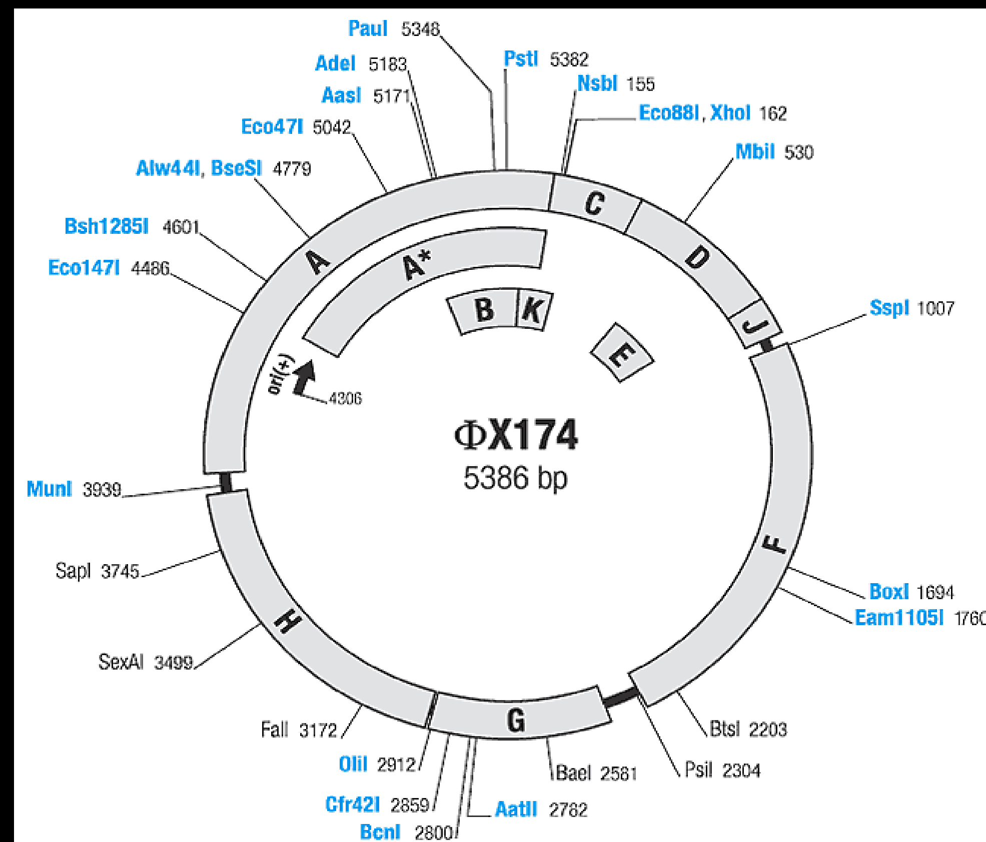


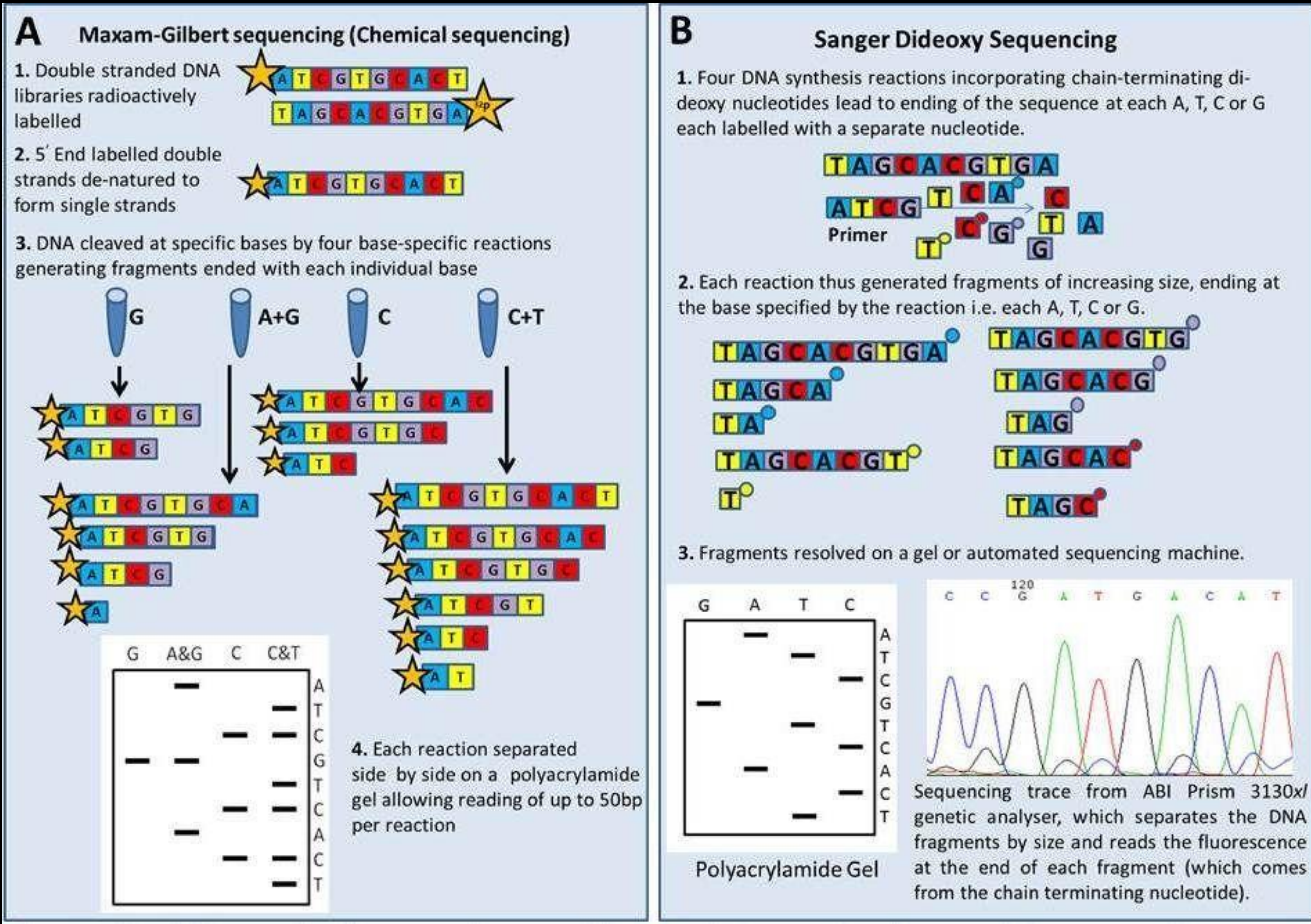
Frederick Sanger (1918 - 2013)

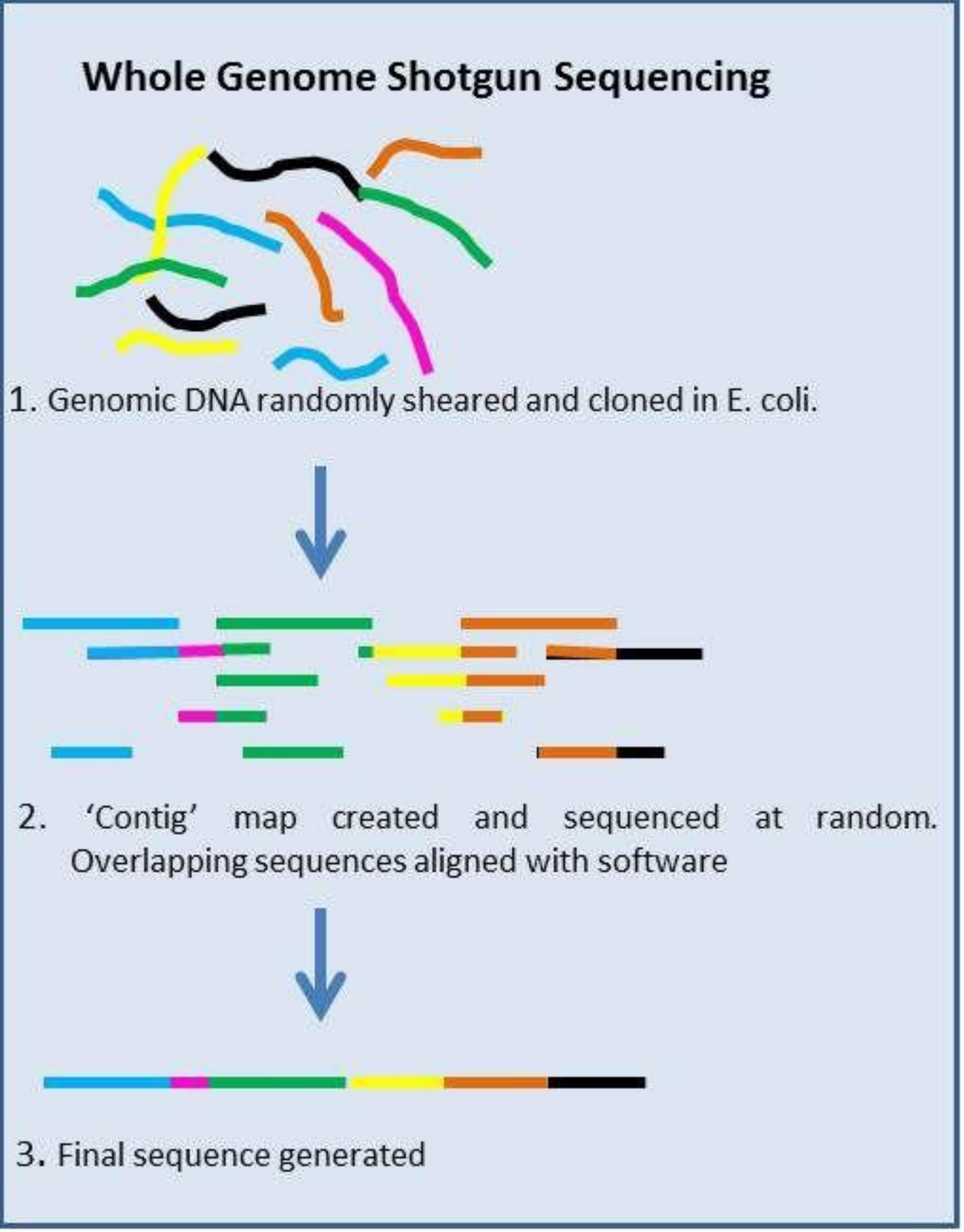


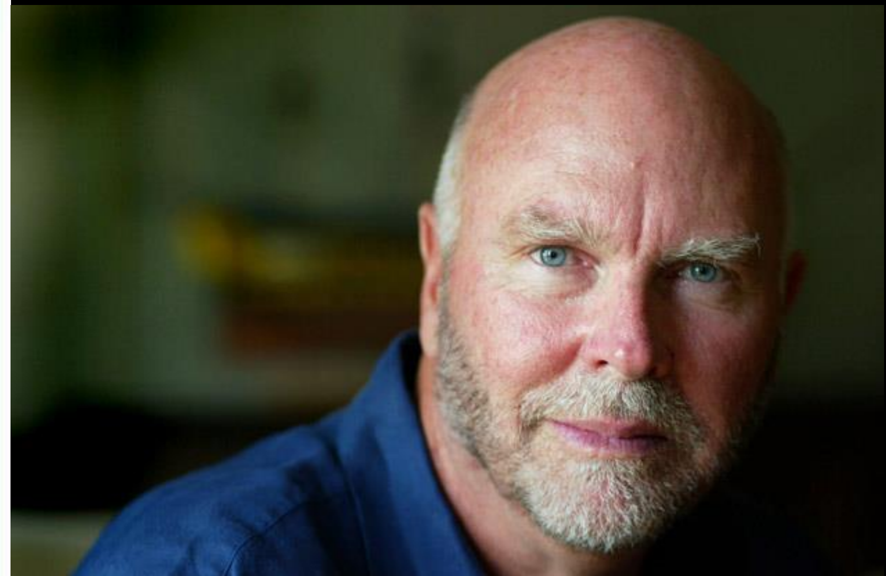






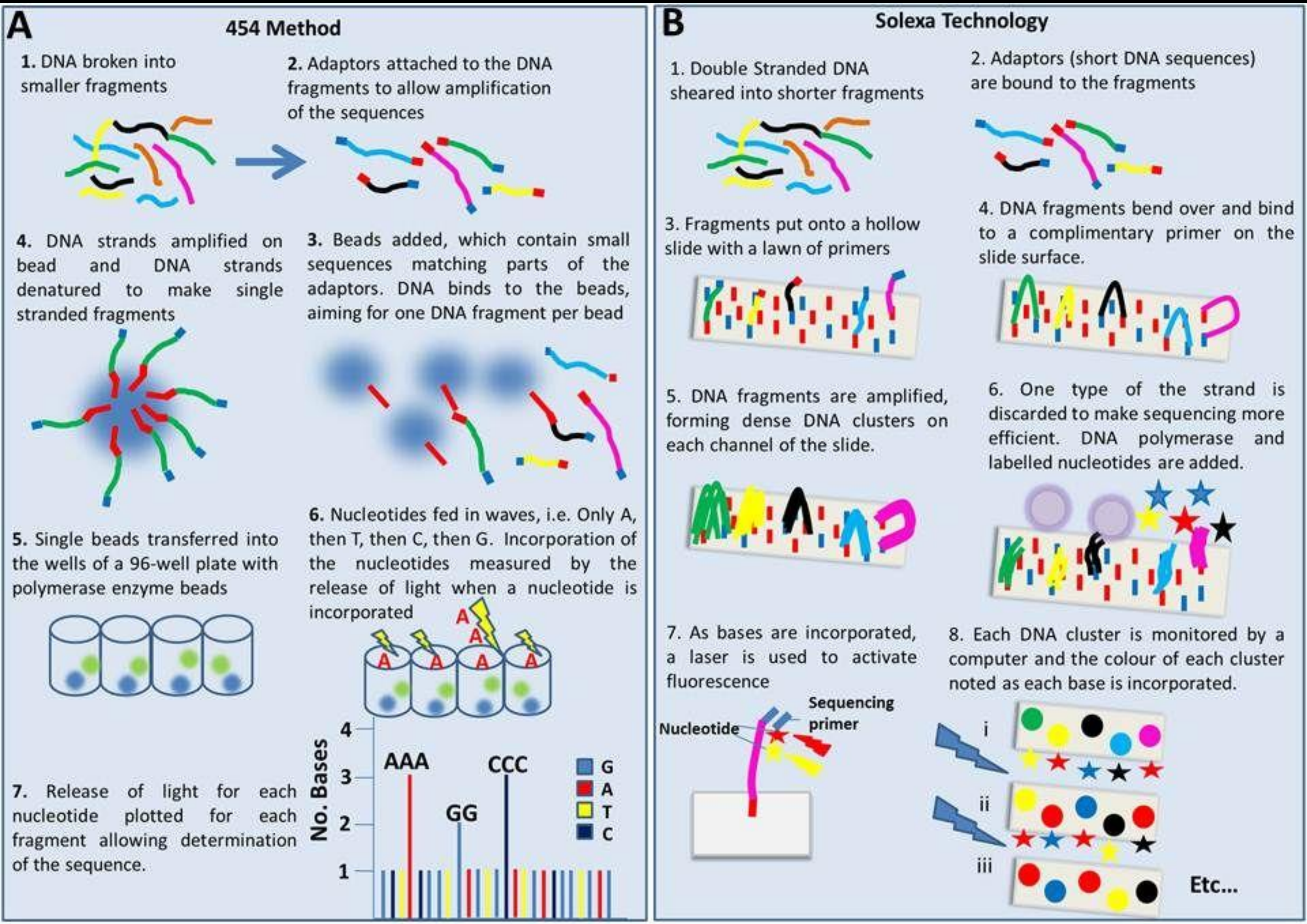

A
Maxam-Gilbert sequencing (Chemical sequencing)
1. Double stranded DNA libraries radioactively labelled
2. 5′ End labelled double strands de-natured to form single strands
3. DNA cleaved at specific bases by four base-specific reactions generating fragments ended with each individual base
G
A+G
C
C+T
G
A&G
C
C&T
4. Each reaction separated side by side on a polyacrylamide gel allowing reading of up to 50bp per reaction
B
Sanger Dideoxy Sequencing
1. Four DNA synthesis reactions incorporating chain-terminating di-deoxy nucleotides lead to ending of the sequence at each A, T, C or G each labelled with a separate nucleotide.
TAGCACGTGA
ATCG
Primer
2. Each reaction thus generated fragments of increasing size, ending at the base specified by the reaction i.e. each A, T, C or G.
3. Fragments resolved on a gel or automated sequencing machine.
G
A
T
C
Polyacrylamide Gel
120
Sequencing trace from ABI Prism 3130xl genetic analyser, which separates the DNA fragments by size and reads the fluorescence at the end of each fragment (which comes from the chain terminating nucleotide).



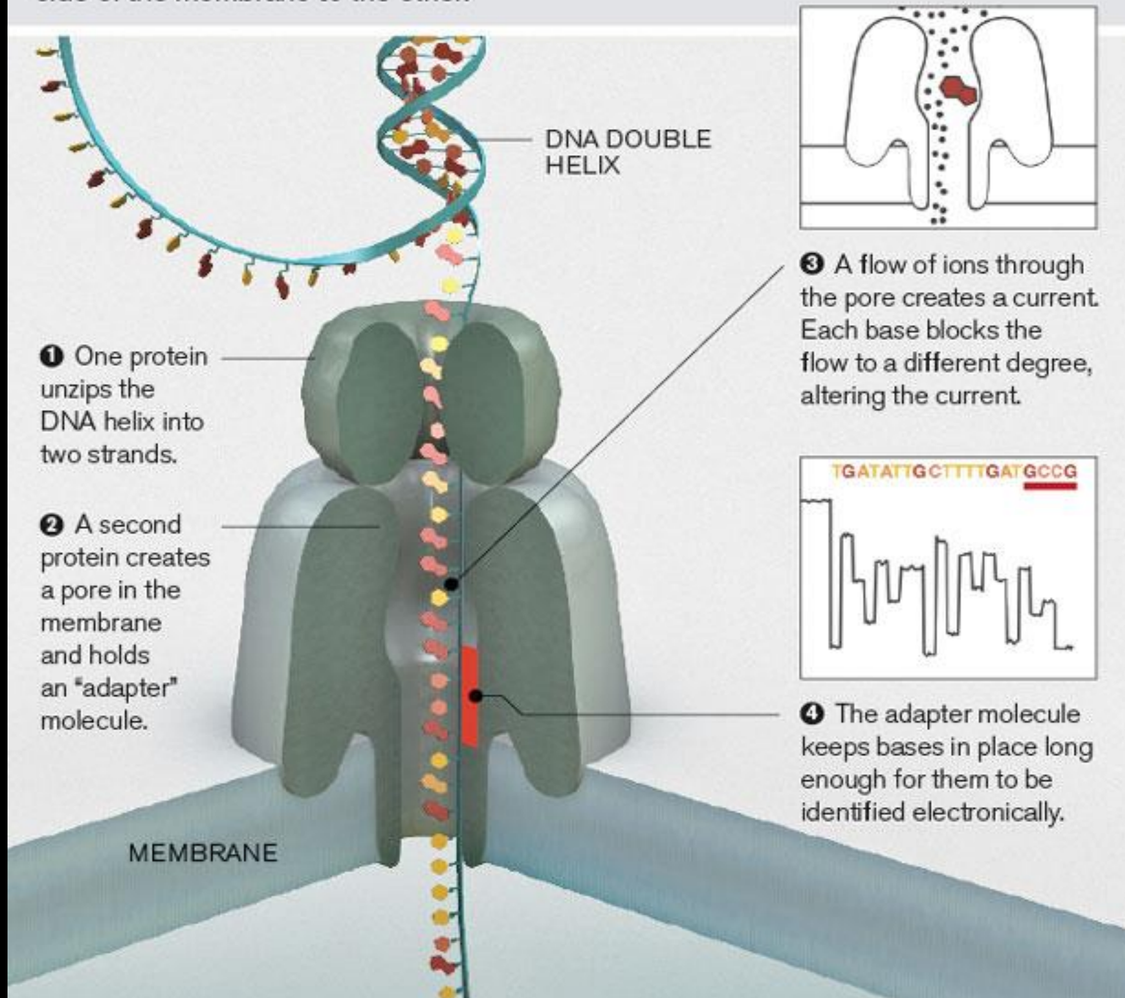


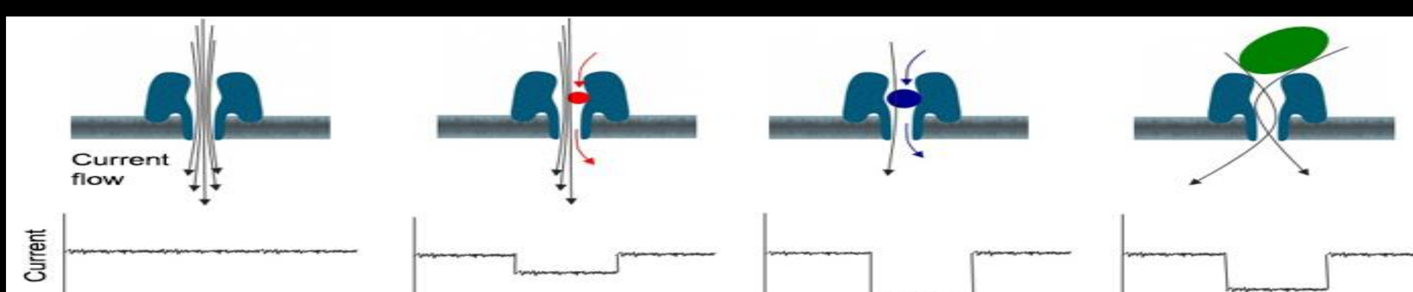
Craig Venter (1946 -)

GenapSys A Paradigm Shift in DNA Sequencing
LaserGen, Inc.
Nabsys
illumina
QIAGEN
454 SEQUENCING
genia
STRATOS genomics inc.
gnubio
Oxford NANOPORE Technologies
Noblegen BIOSCIENCES
life technologies
Semiconductor Sequencing for Life
ion torrent
Complete genomics


A
454 Method
1. DNA broken into smaller fragments
2. Adaptors attached to the DNA fragments to allow amplification of the sequences
3. Beads added, which contain small sequences matching parts of the adaptors. DNA binds to the beads, aiming for one DNA fragment per bead
4. DNA strands amplified on bead and DNA strands denatured to make single stranded fragments
5. Single beads transferred into the wells of a 96-well plate with polymerase enzyme beads
6. Nucleotides fed in waves, i.e. Only A, then T, then C, then G. Incorporation of the nucleotides measured by the release of light when a nucleotide is incorporated
7. Release of light for each nucleotide plotted for each fragment allowing determination of the sequence.
No. Bases
AAA
GG
CCC
G
A
T
C
B
Solexa Technology
1. Double Stranded DNA sheared into shorter fragments
2. Adaptors (short DNA sequences) are bound to the fragments
3. Fragments put onto a hollow slide with a lawn of primers
4. DNA fragments bend over and bind to a complimentary primer on the slide surface.
5. DNA fragments are amplified, forming dense DNA clusters on each channel of the slide.
6. One type of the strand is discarded to make sequencing more efficient. DNA polymerase and labelled nucleotides are added.
7. As bases are incorporated, a laser is used to activate fluorescence
Nucleotide
Sequencing primer
8. Each DNA cluster is monitored by a computer and the colour of each cluster noted as each base is incorporated.
i
ii
iii
Etc...

DNA can be sequenced by threading it through a microscopic pore in a membrane. Bases are identified by the way they affect ions flowing through the pore from one side of the membrane to the other.

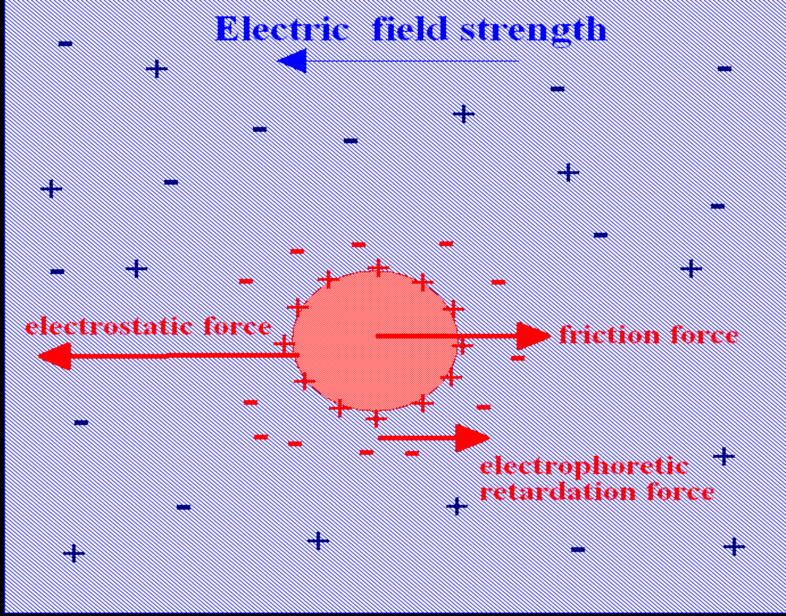




Applied Biosystems -
3730xl DNA Analyzer

Oxford Nanopore
Technologies -
The MinION™

F. F. Reuss 1807



1930s – prva SUKROZNA gel-elektroforeza

1955 – primjena ŠKROBNE elektroforeze – loša razlučivost

1959 – početak AKRILAMIDNE elektroforeze (Raymond and Weintraub) – moguća kontrola veličine pora

1964 – DISK GEL elektroforeza (Ornstein and Davis)

1969 – primjena DENANTURIRAJUĆIH agensa posebno SDS-a - za separaciju proteinskih podjedinica (Beber and Osborn)

1970 – Laemmli razdvojio 28 komponenti faga T4 SDS elektroforezom

1975 - 2-DIMENZIONALNI gelovi (O'Farrell) i IZOELEKTRIČNO FOKUSIRANJE

1977 – gelovi za SEKVENCIRANJE

Krajem **1970**tih – AGAROZNI GELOVI

1983 – elektroforeza u IZMJENIČNOM POLJU (puls field) – omogućeno odvajanje velikih molekula

1983 – KAPILARNA elektroforeza

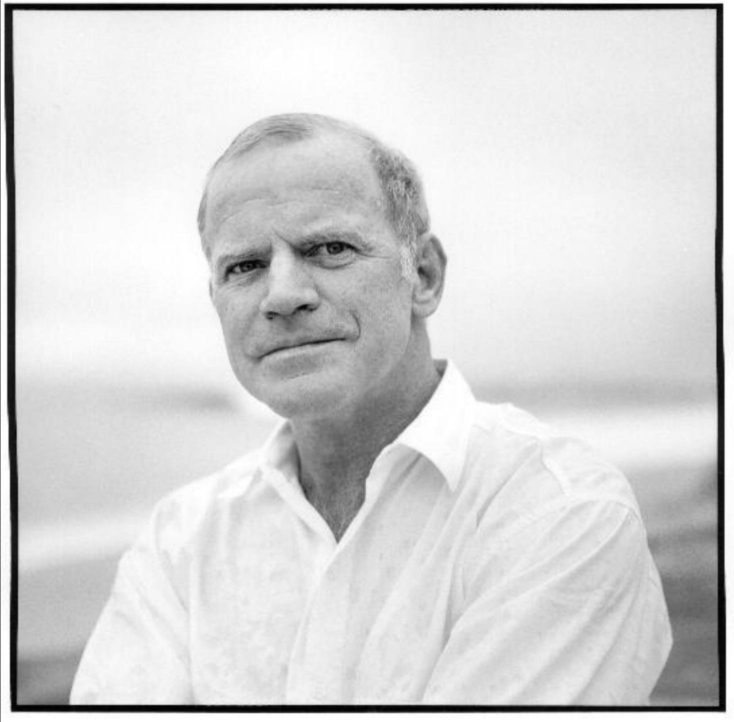
1989 - Applied Biosystems izbacio na tržište Real-time PCR

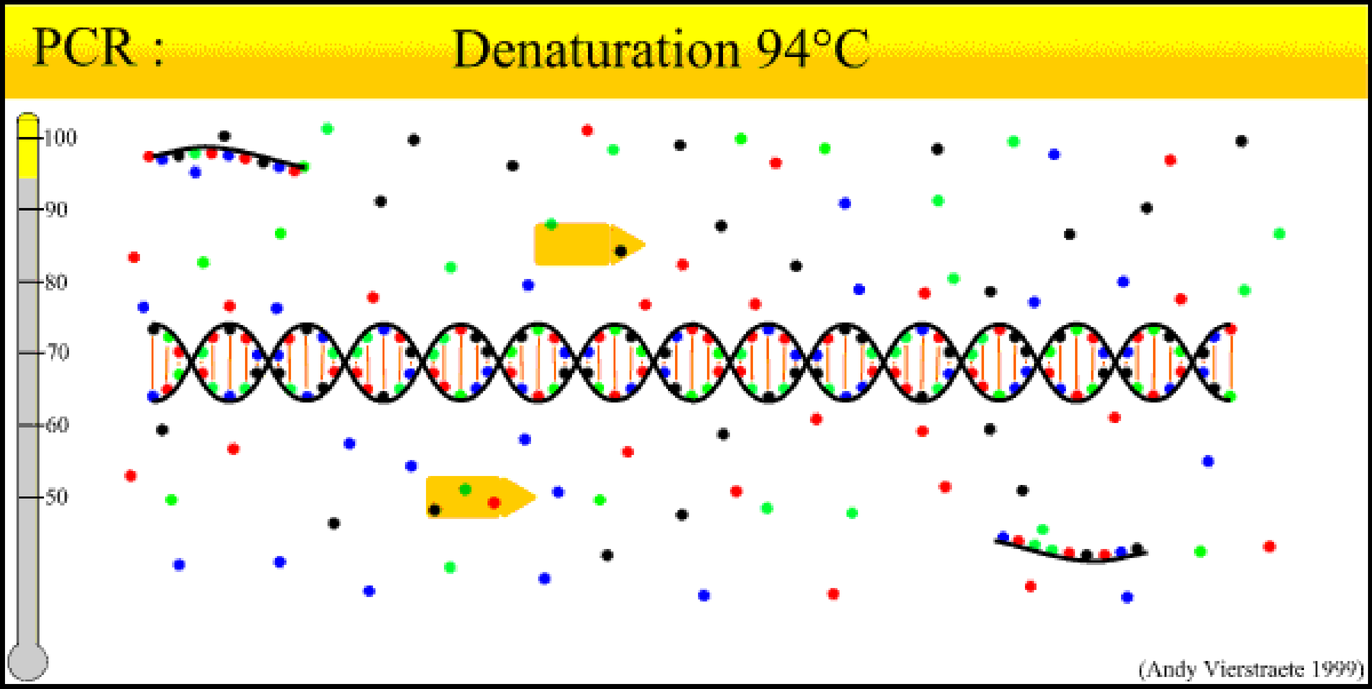
Oliver Smithies (1925 - 2017)

PCR

Karry Mullis (1944 - 2019)

It always gives me a boost when some poor bastard that's been in there for 10 years is set free."





Allele-specific - koristi SNPs
Assembly *(PCA)* – umjetna sinteza dugih DNA sekvenci
Asymmetric – sa suviškom jedne početnice
Helicase-dependent amplification – stalna temperatura
Hot-start – reducirana nespecifična amplifikacija
Intersequence-specific *(ISSR)* – amplificira regije između ponavljanja
Inverse - rezultira sekvencama s obje strane poznate
Ligation-mediated – kratke DNA poveznice
Methylation-specific *(MSP)* – za otkrivanje metilacija na CpG otocima u genomu
Miniprimer PCR – S-Tbr polimeraza & smalligos
Multiplex Ligation-dependent Probe Amplification *(MPLA)* – amplifikacija višestrukih ciljeva jednim parom početnica
Multiplex-PCR – više setova početnica u jednoj reakcijskoj smjesi
Nested PCR – povećana specifičnost amplifikacije upotrebom dva para početnica
Overlap-extension PCR: *(OE-PCR)* – tehnika GI
Quantitative Real Time PCR *(Q-PCR ili QRT-PCR ili RTQ PCR)* – za mjerenje količine PCR produkata, najprecizniji PCR, nije RT
RT-PCR *(**R**everse **T**ranscription PCR)* – za amplifikaciju RNA, RNA u cDNA
Solid Phase PCR – početnice vezane za solidno stanje
TAIL-PCR – za izolaciju nepoznatih sekvenci iza poznatih
Touchdown PCR – reduciranje nespecifičnih amplifikacija
PAN-AC – izotermalni PCR in vivo
Universal Fast Walking – dvostrani PCR

Restrikcijske endonukleaze

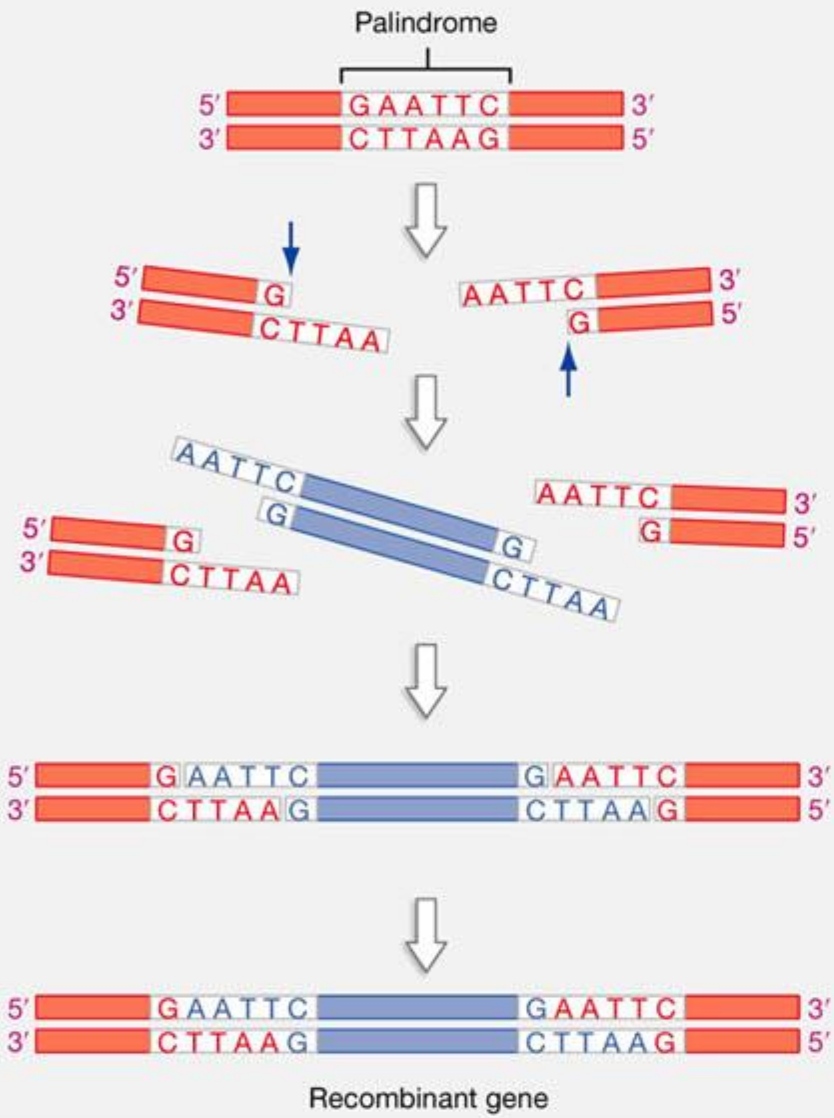
Werner Arber (1929 -), Daniel Nathans (1928-1999) Hamilton Smith (1931 -)

Dio restrikcijsko modifikacijskog sustava bakterija za obranu od viralne infekcije

Rekombinantna DNA tehnologija

3000 otkrivenih - 600 komercijalno dostupnih – 3 tipa

RECOMBINANT DNA TECHNOLOGY



1. The restriciton enzyme *Eco*R1 recognizes this palindrome.

2. The restriction enzyme cuts the palindrome at the locations indicated.

3. Add a different DNA fragment cut by this same enzyme, *Eco*R1.

4. The fragment attaches by complementary base pairing.

5. DNA ligase catalyzes formation of phosphodiester bonds to close between fragments.

Molekulski sat

1965 – Molecular clock theory

Emile Zuckerkandl (1922 -2013) & Linus C. Pauling (1901-1994)

Za neku makromolekulu evolucije je otprilike konstantna u svim evolucijskim linijama

Pobudila veliki interes za proučavanje evolucije putem molekula

1. paralela s radioizotopima
2. filogenija lakša
3. stupanj razlike govori o mehanizmima molekulske evolucije

Velika razlika u "kucanju" molekulskog sata znači veliku promjenu u supstitucijskoj učestalosti **odnosno** uzimajući u obzir NMT značajnu promjenu evolucijskih faktora

Tako da velika promjena u učestalosti ukazuje na

1. adaptivna evolucija
2. gubitak funkcije
3. relaksacija funkcionalnih pritisaka
4. velika redukcija u efektivnoj veličini populacije

Velik utjecaj i puno kontroverzi

Generacijsko vrijeme – apsolutno vrijeme

Lokalni satovi – dokazani na glodavcima

Usporavanje sata u hominoidnoj liniji – pred milijun godina

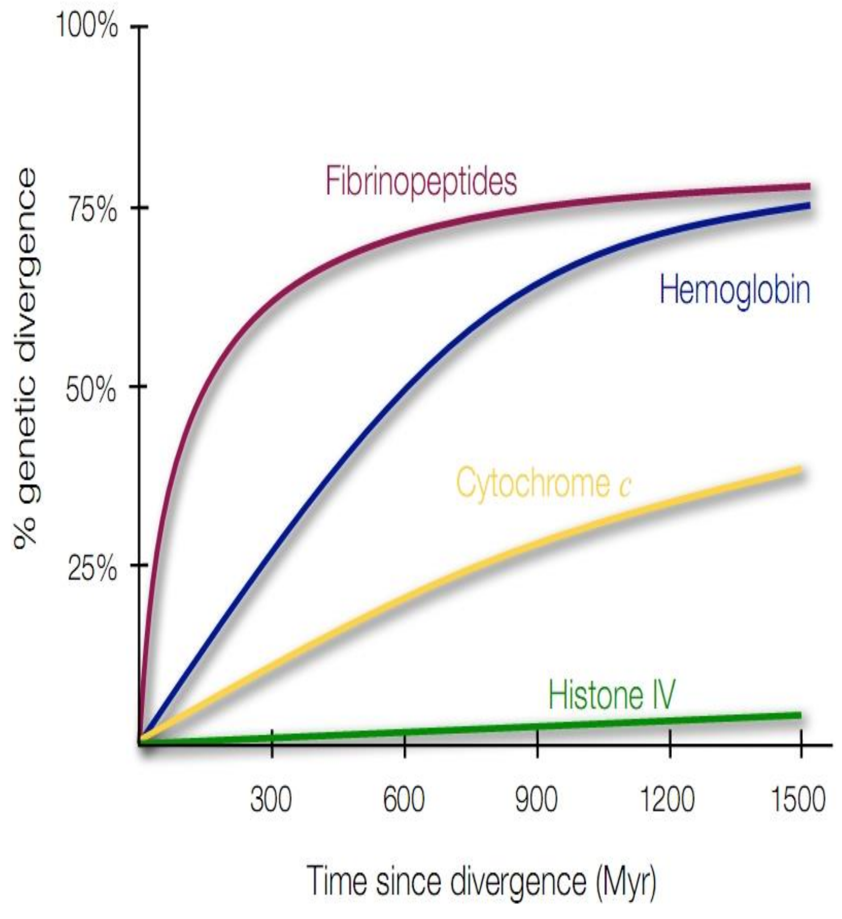
Mutacijska učestalost u muškoj liniji – veća nego u ženskoj

Savršeni proteini iz prve generacije – histoni i ubiquitin

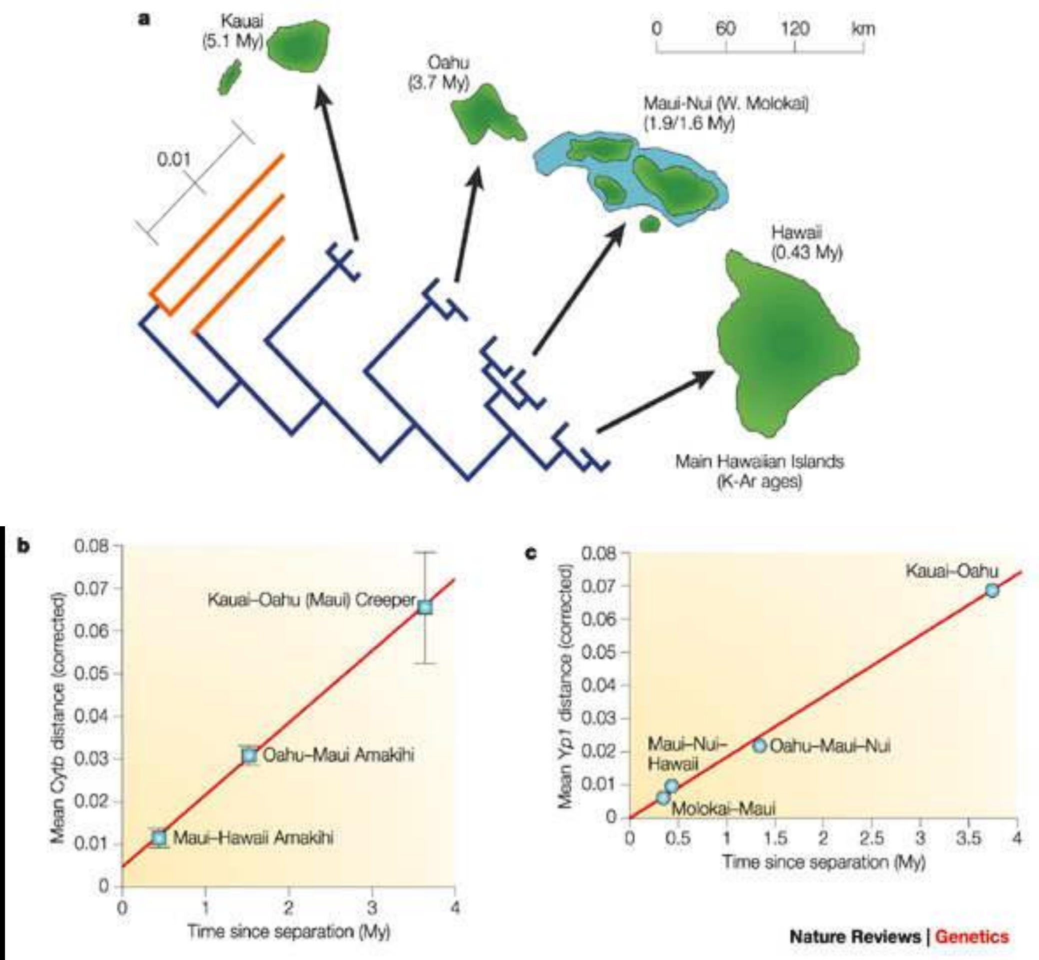
Uzroci varijabilnosti učestalosti među linijama

1. Efikasnost popravka DNA – veća sporiji sat
2. Hipoteza efekta generacijskog vremena – kraće vrijeme brži sat
3. Hipoteza metaboličke aktivnosti – veća aktivnost brži sat

mtDNA pokazala diobu u 2 skupine homeotermne i poikilotermne



Geologija = paleontologija = molekularna BIOLOGIJA



Različiti proteini različita brzina „kucanja” sata

Neutralna teorija molekulske evolucije

1968 - Neutral theory of molecular evolution

Motoo Kimura (1924 -1994)

Većina promjena na molekulskoj razini je posljedica nasumičnog drifta neutralnih ili gotovo neutralnih mutacija

Jack L. King and Thomas H. Jukes (1969) "Non-Darwinian Evolution"

Neodarvinisti vs Neutralisti

Neodarvinisti	Neutralisti
Mutacije i selekcija glavni pokretač evolucije	Mutacije i nasumični drift glavni pokretač evolucije
Mutacije su + ili -	Mutacije su većinom 0
Primijećeni polimorfizam u populacijama je fiksno stanje u molekulskoj evoluciji	Primijećeni polimorfizam u populacijama je prijelazna faza u molekulskoj evoluciji
Polimorfizam se održava jer povećava fitnes	Polimorfizam i supstitucija su dvije strane iste medalje molekularne evolucije

Bitni rezultati debate za evoluciju

1. Drift jako bitan faktor u evoluciji posebno na molekulskoj razini
2. Evolucija na molekulsko razini i polimorfizam populacije su rezultati istog fenomena

Gotovo neutralna mutacijska hipoteza

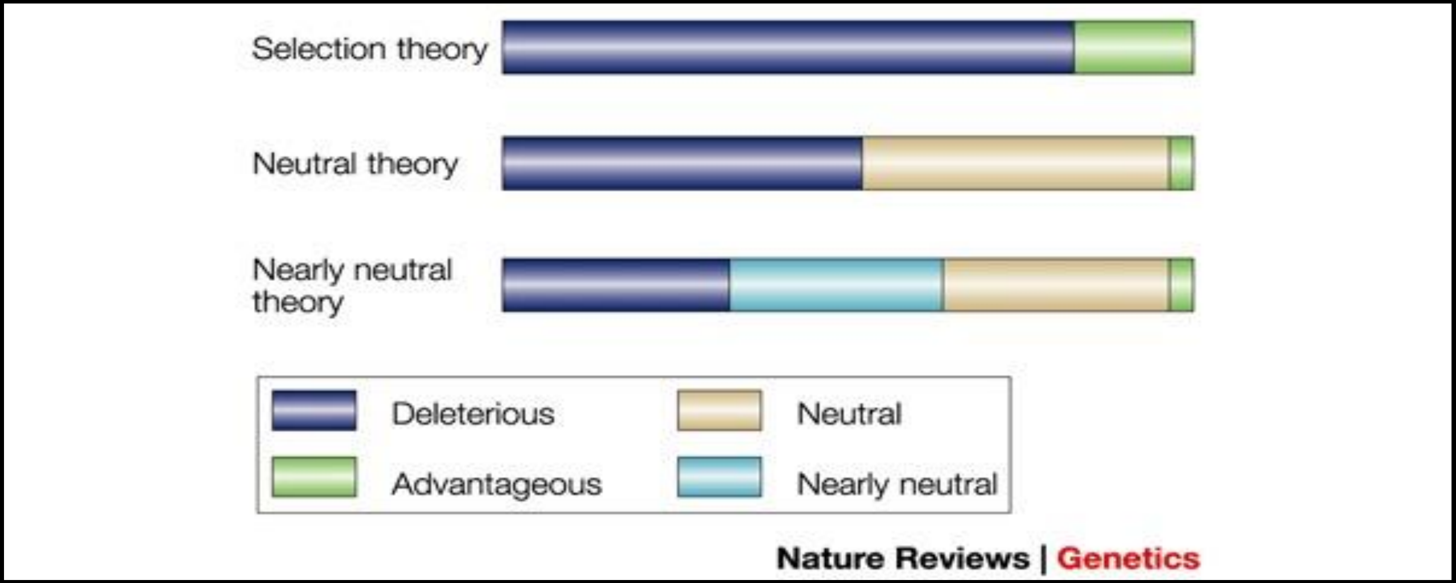
1973 - Nearly neutral mutation hypothesis ili Nearly neutral theory of molecular evolution

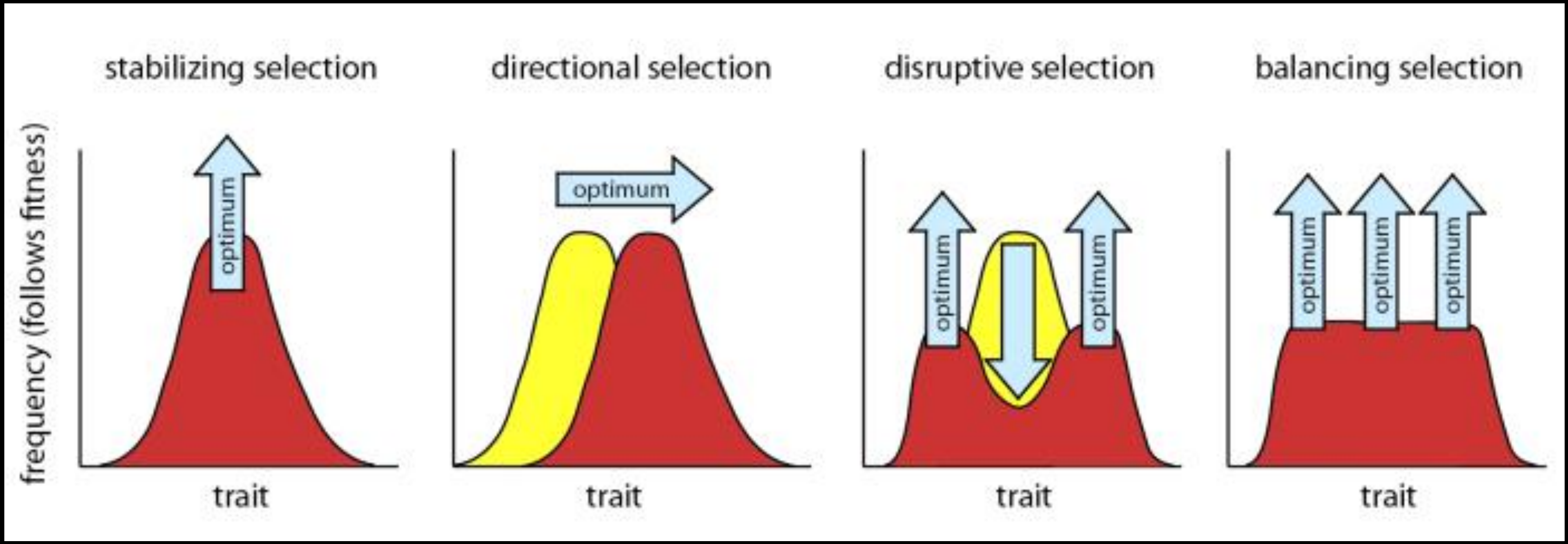
Mutacije koje nisu striktno neutralne ni jako selektivne (slightly deleterious)

Tomoko Ohta (1933 -)

Testirala svoju teoriju preko MC; omjer sinonimnih i nesinonimnih učestalosti kod primata, papkara i glodavaca.

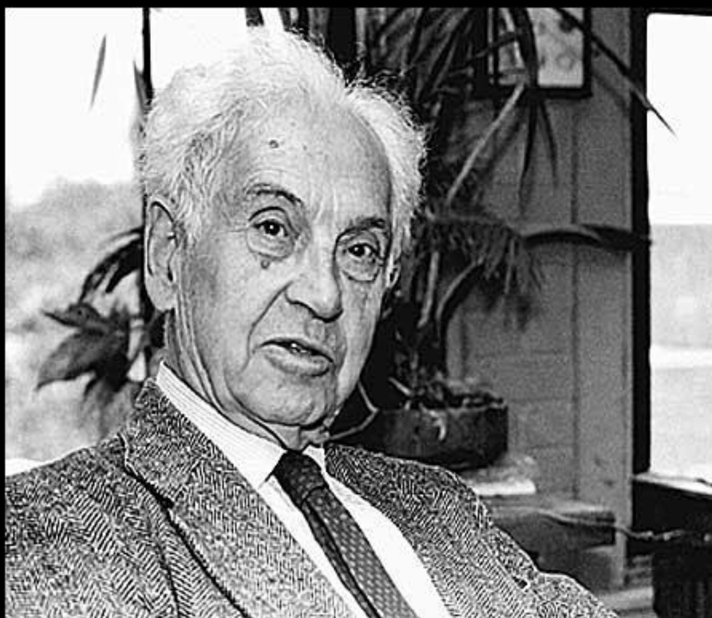
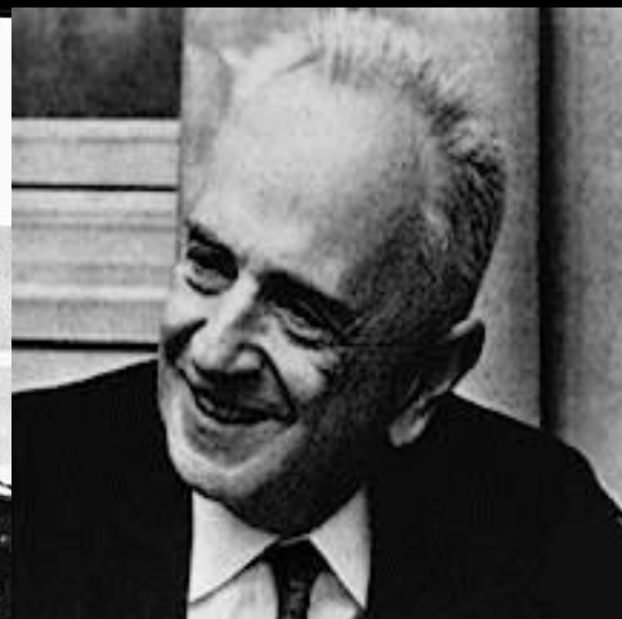
Pod NNMT očekuje se veći udio sinonimnih učestalosti prema nesinonimnim kod godavaca nego kod primata ili papkara


Selection theory
Neutral theory
Nearly neutral theory
Deleterious
Neutral
Advantageous
Nearly neutral
Nature Reviews | Genetics


stabilizing selection
directional selection
disruptive selection
balancing selection
frequency (follows fitness)
optimum
trait

Molecular wars

Ernst Mayr (1904-2005) Theodosius Dobzhansky (1900 -1975) George Simpson (1902-1984)


Tvorci moderne evolucijske sinteze

Kako pomiriti molekularnu i klasičnu (organismal) biologiju; pojava molekularno - morfološkog paradoksa.

Biokemičari i molekularni biolozi (Pauling & Zuckerkandl)

Molecular wars

Ultimativni i proksimativni oblici uzroka u biologiji –
oboje potrebno da bi se u potpunosti objasnio fenomen **Mayr 1961**

Kako je nešto poprimilo određenu funkciju – evolucijska biologija

Kako nešto funkcionira – molekularna biologija

Kartezijanski i Darvinistički pristupi istraživanju u biologiji
Dobzhansky 1964

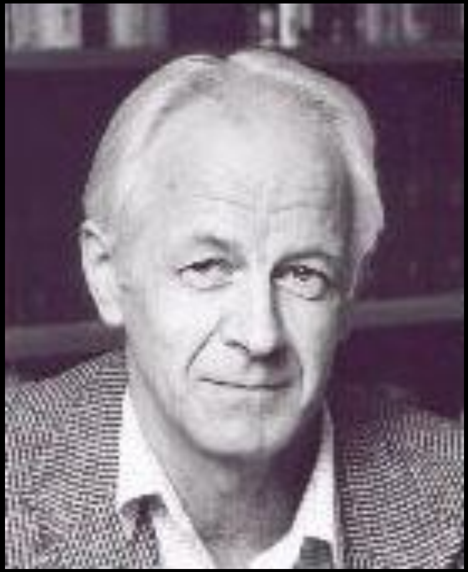
Kartezijanski ili redukcionistički – opisati biološki fenomen u okviru kemije i fizike – molekularna biologija

Darvinistički ili kompozitni – shvatiti adaptivnu korisnost struktura i procesa na organizam i vrste kao i ekološku funkciju u zajednici u kojoj se te vrste pojavljuju – evolucijska biologija

Dakle klasična biologija niti se može zaključiti iz niti reducirati na molekularnu biologiju

Molecular wars

Allan Wilson (1934-1991) & Vincent Sarich (1934 - 2012)



Homo se odvaja od Apes pred 4 – 5 milijuna godina; koristeći principe molekulskog sata i molekularne biologije u evoluciji i antropologiji. Kasniji fosilni nalazi (Lucy et al.) potvrdili njihov osporavani rad

Sarich VM, Wilson AC. Immunological time scale for hominid evolution.
***Science* 158, 1967, p. 1200-1203**

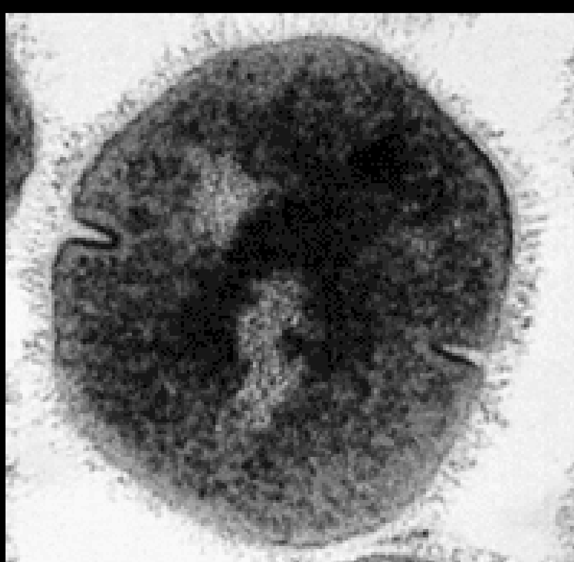
A. C. Wilson, R. L. Cann, S. M. Carr, M. George Jr., U. B. Gyllensten, K. Helm- Bychowski, R. G. Higuchi, S. R. Palumbi, E. M. Prager, R. D. Sage, and M. Stoneking (1985) "Mitochondrial DNA and two perspectives on evolutionary genetics". *Biological Journal of the Linnean Society* 26:375-400

Teorija mitohondrijske Eve (mt-MRCA) + razrješenje paradoksa i molekulskog rata

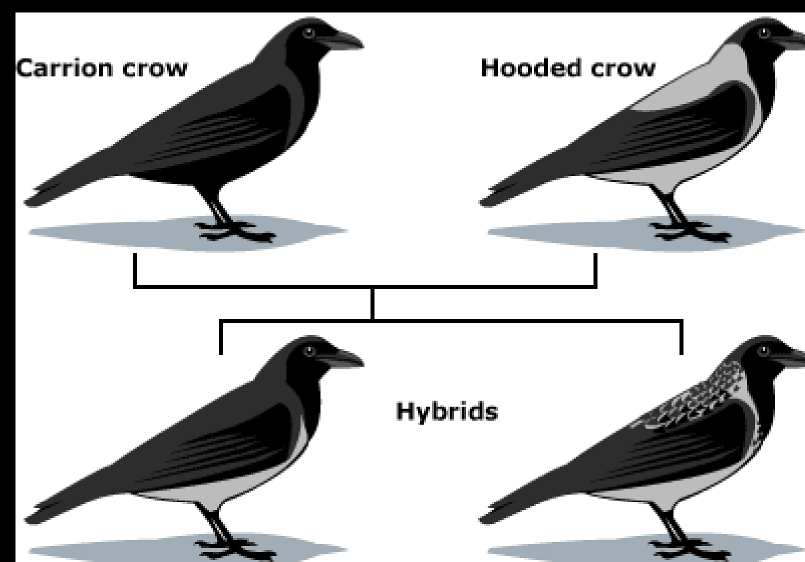
	WINGS	BEGINS W/ LETTER B	ANYTHING ELSE
BAT	☑	☑	☐
BIRD	☑	☑	☐
BUTTERFLY	☑	☑	☐

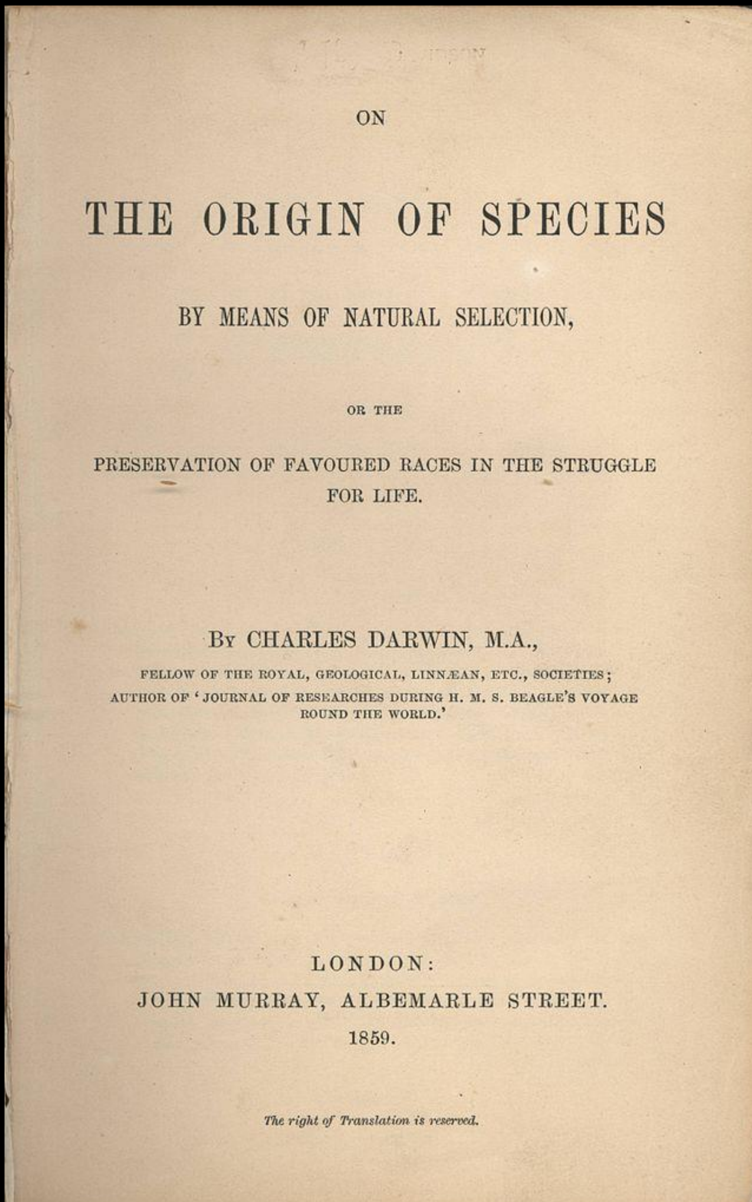
Theridion grallator

Streptococcus pyogenes



Corvus corone *Corvus cornix*




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.

The right of Translation is reserved.

Često se kaže da ne postoji drugi problem u biologiji koji je toliko otporan na riješenje kao što je problem vrste - Ernst Mayr

"... Bio sam iznenađen koliko je nejasna i proizvoljna razlika između vrsta i varijeteta "
Darwin (1859)

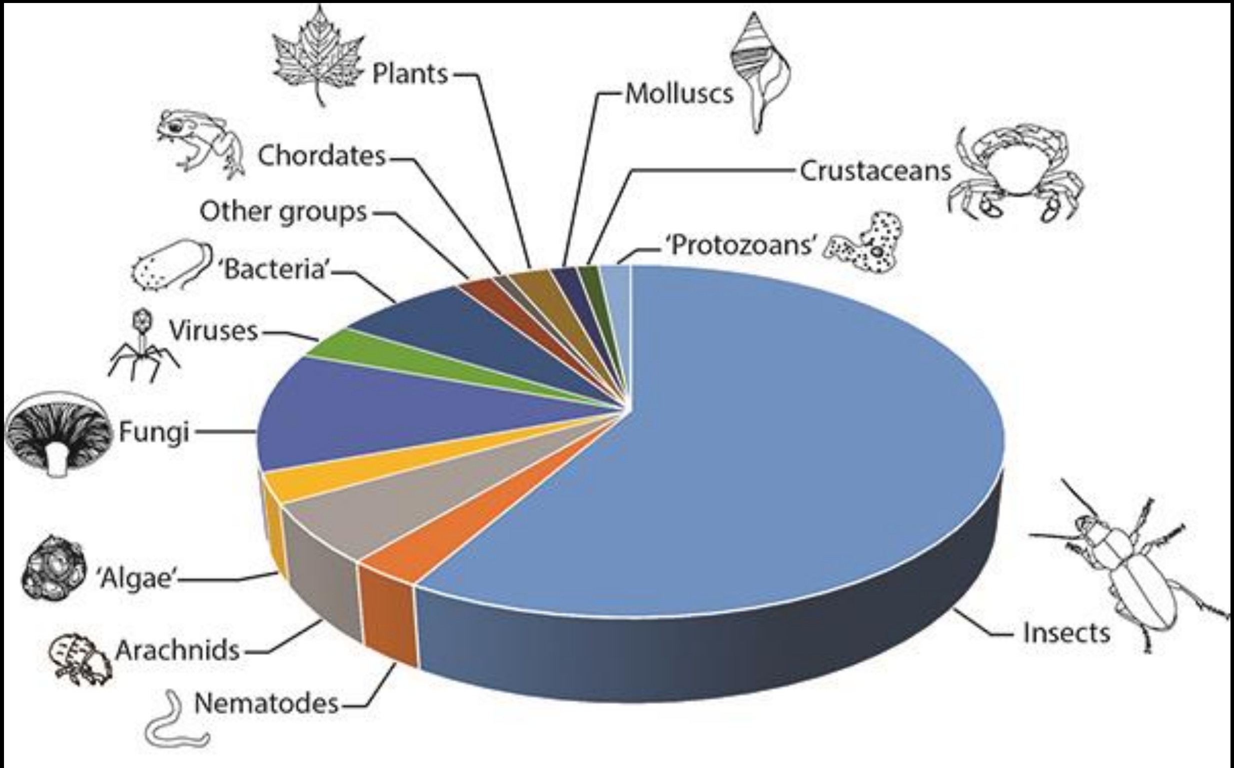
„Koncept vrste je ustupak našim jezičnim navikama i neurološkim mehanizmima"
Haldane (1956)

“ Problem vrste nije primarno empirijski već je prožet i filozofskim pitanjima koja traže, no ne mogu se odgovoriti, empirijskim dokazima."
Pigliucci (2003)

ŠTO JE ŽIVOT? ŠTO JE VRSTA?

Specijacija

Mikroevolucija —Specijacija→ Makroevolucija



Kriteriji

1. Odvojenost

2. Kohezija

3. Monofilija

4. Raznolikost - a) dijagnostički nivo b) fenetički kluster c) genetički klaster

Koncept vrste

Table 15.1 The biological species concept and some recently proposed alternatives (Futuyma 1997)

BIOLOGICAL SPECIES CONCEPT A species is a group of individuals fully fertile inter se, but barred from interbreeding with other similar groups by its physiological properties (producing either incompatibility of parents, or sterility of the hybrids, or both). (Dobzhansky 1935)

Species are groups of actually or potentially interbreeding natural populations that are reproductively isolated from other such groups. (Mayr 1942)

EVOLUTIONARY SPECIES CONCEPT A species is a single lineage (an ancestral-descendant sequence) of populations or organisms that maintains its identity from other such lineages and which has its own evolutionary tendencies and historical fate. (Wiley 1978)

PHYLOGENETIC SPECIES CONCEPTS A phylogenetic species is an irreducible (basal) cluster of organisms that is diagnosably distinct from other such clusters, and within which there is a parental pattern of ancestry and descent. (Cracraft 1989)

A species is the smallest monophyletic group of common ancestry. (de Queiroz and Donoghue 1990)

RECOGNITION SPECIES CONCEPT A species is the most inclusive population of individual biparental organisms that share a common fertilization system. (Paterson 1985)

COHESION SPECIES CONCEPT A species is the most inclusive population of individuals having the potential for phenotypic cohesion through intrinsic cohesion mechanisms. (Templeton 1989)

ECOLOGICAL SPECIES CONCEPT A species is a lineage (or a closely related set of lineages) that occupies an adaptive zone minimally different from that of any other lineage in its range and which evolves separately from all lineages outside its range. (Van Valen 1976)

INTERNODAL SPECIES CONCEPT Individual organisms are conspecific by virtue of their common membership in a part of the genealogical network between two permanent splitting events or between a permanent split and an extinction event. (Kornet 1993)

Source: Coyne (1994).

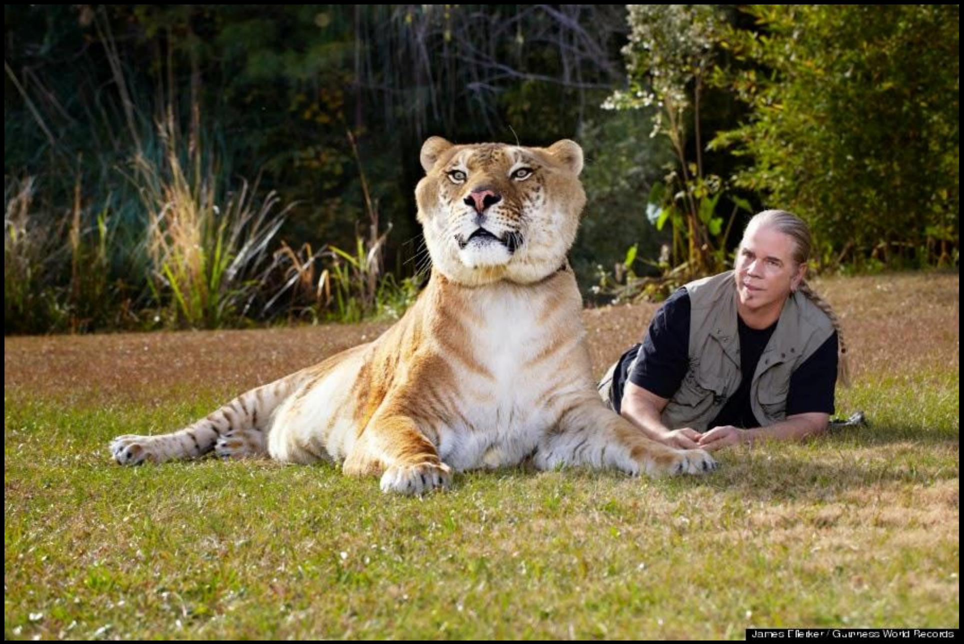
BSC – Biološki koncept vrste (Mayr 1942)

Ključni kriterij – uspješna reprodukcija

Problem – Nespolno razmnožavanje i hibridi

Bakterije i virusi
Core & Auxiliary genome

Liger – Tigon – Coywolf



Father	Mother	Lion Hybrid
Lion	Tiger (tigress)	Liger
Tiger	Lion (lioness)	Tigon (tion, tigron, tiglon)
Lion	Tigon	Li-tigon
Lion	Liger	Li-liger (liliger)
Lion	Leopard	Liard (Lipard)
Leopard	Lion (lioness)	Leopon (Lepon)
Lion	Jagulep	Lijagulep (Lijagleop)
Tiger	Liger	Ti-liger (tig-liger)
Jaguar	Lion (lioness)	Jaglion (jaguon)

X

=

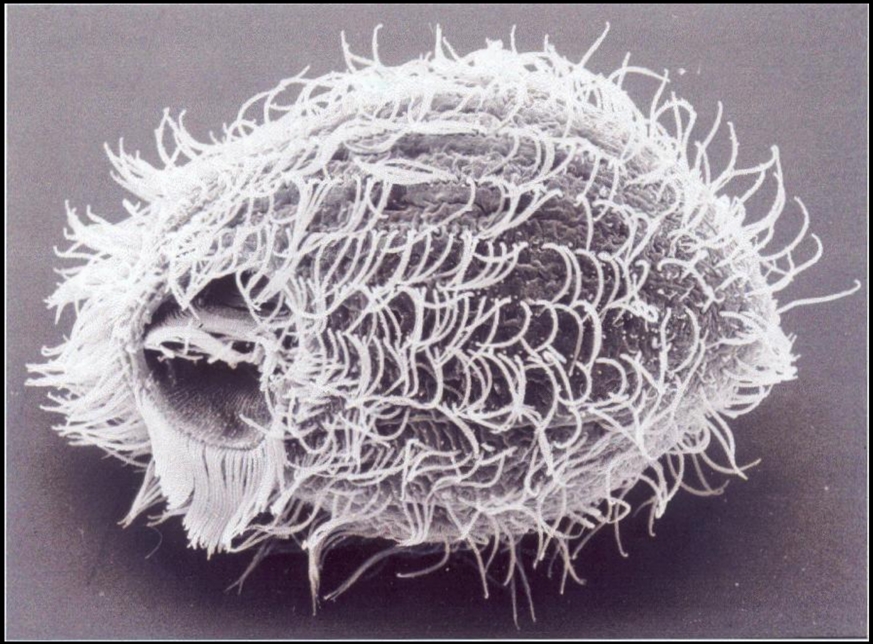
PSC – Filogenetički koncept vrste (Cracraft 1983)

Ključni kriterij – monofilija

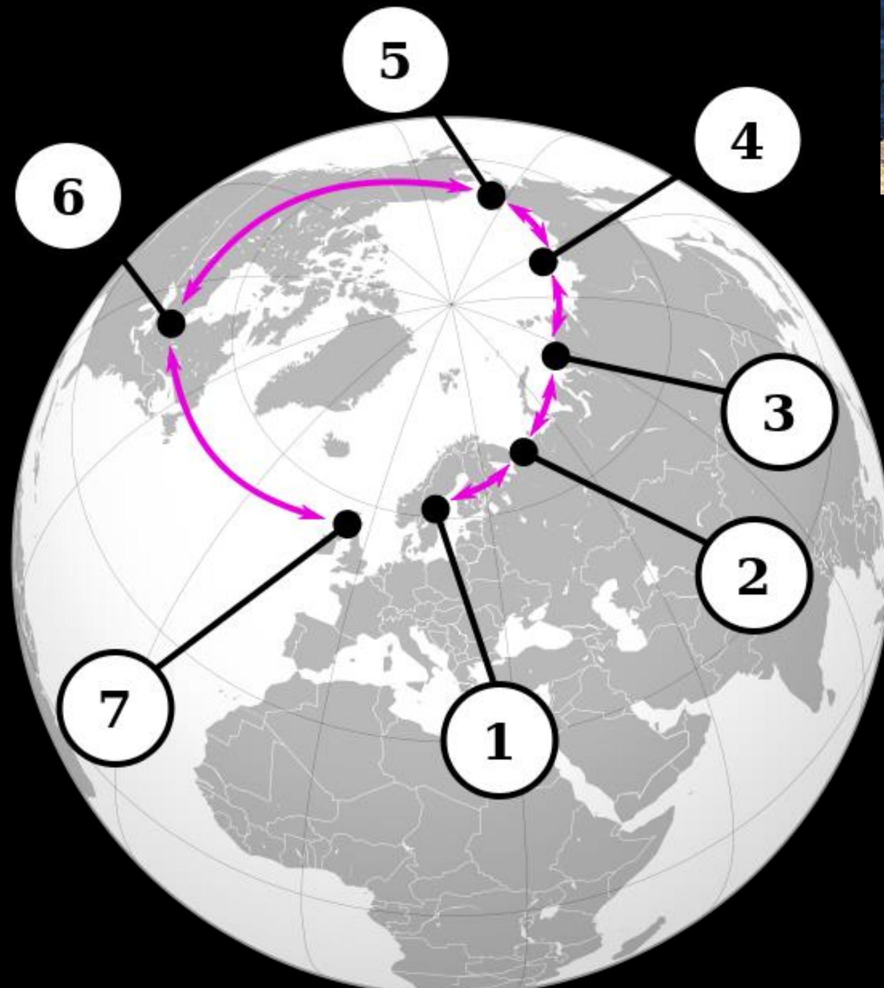
Prednost – izbjegava problem reproduktivne izolacije

Problem – koliko osobina treba imati skupina da bi bila vrsta

Sestrinske vrste – Kriptične vrste (Sibling species)
Tetrahymena pyriformis kompleks (15 – 100)

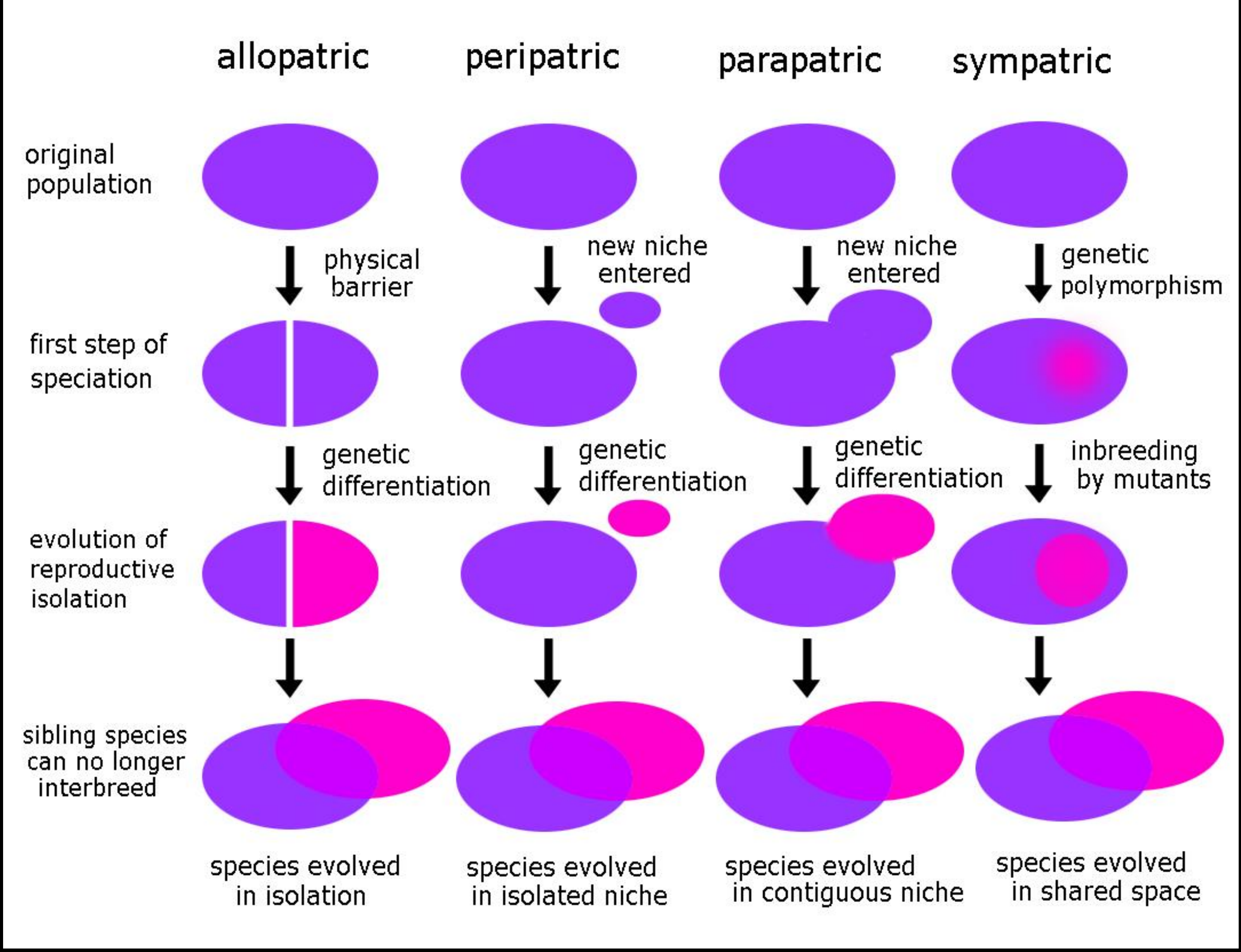


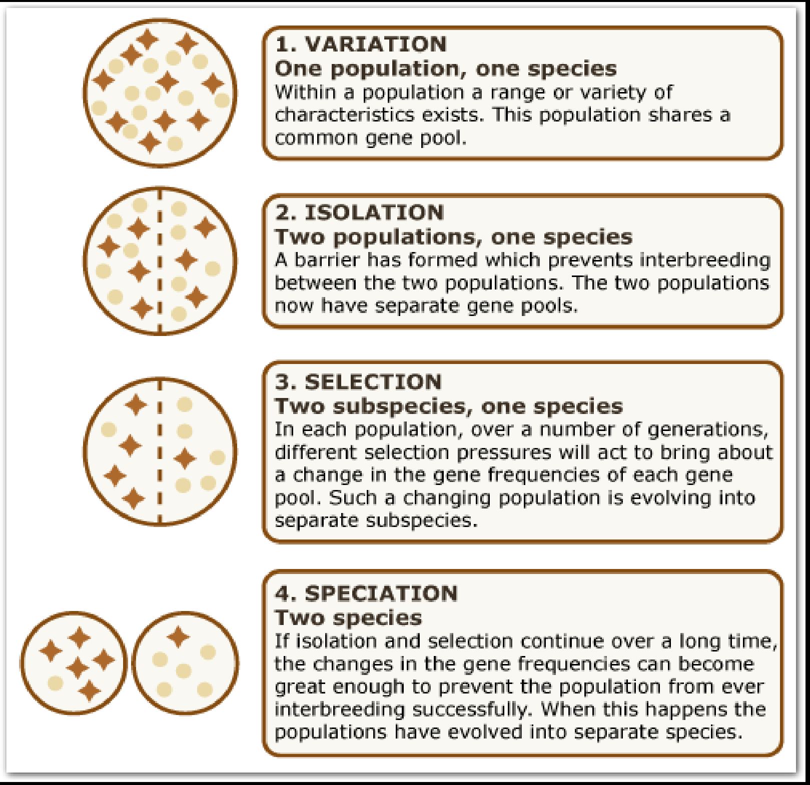
Prstenaste vrste (Ring species)



Specijacija centralni proces evolucije
Elementarni makroevolucijski proces rezultat mikroevolucije – selekcija i drift

Specijacija





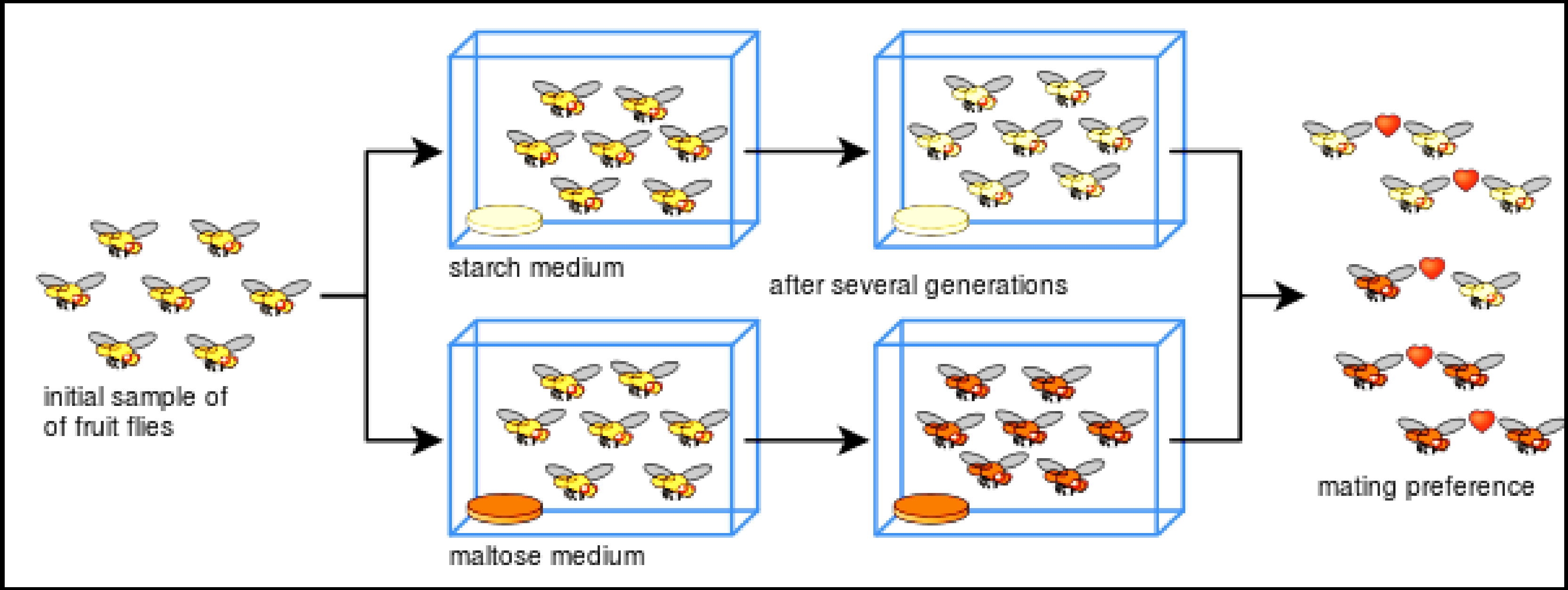
→ Alopatrija

Fizička izolacija + selekcija = Reproduktivna izolacija

Simpatrija

Disruptivna selekcija

Preferencijalno križanje



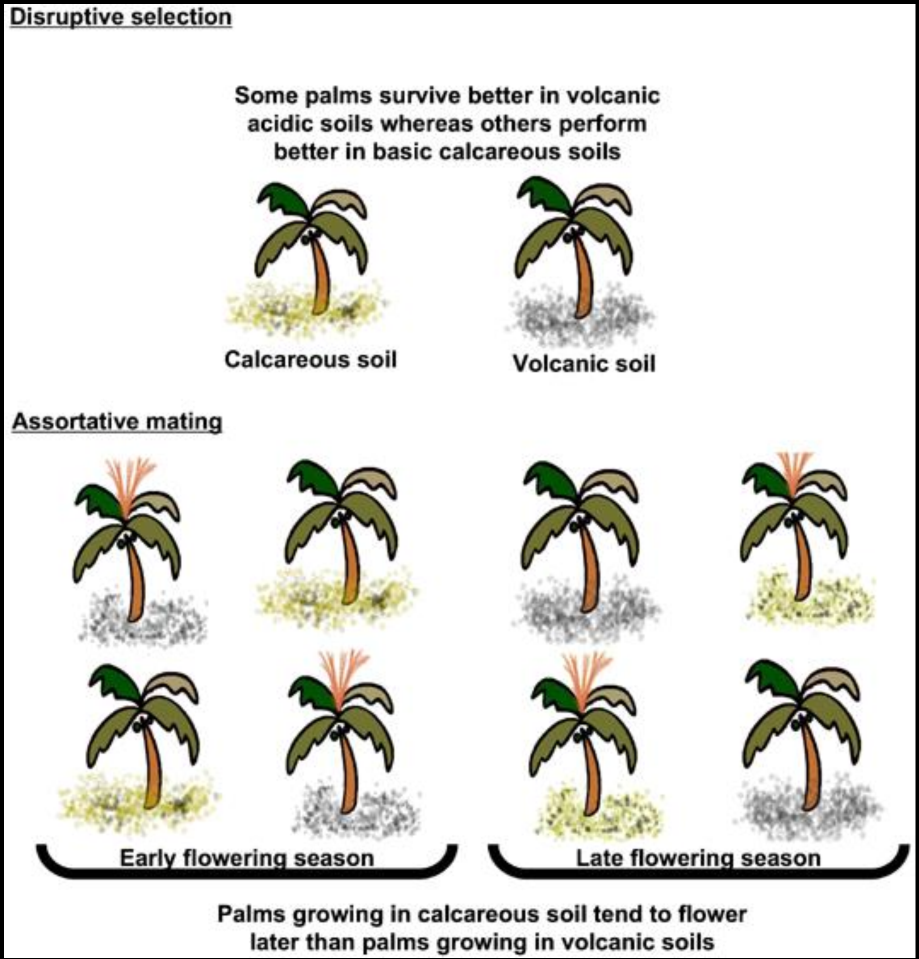
Simpatrijska specijacija

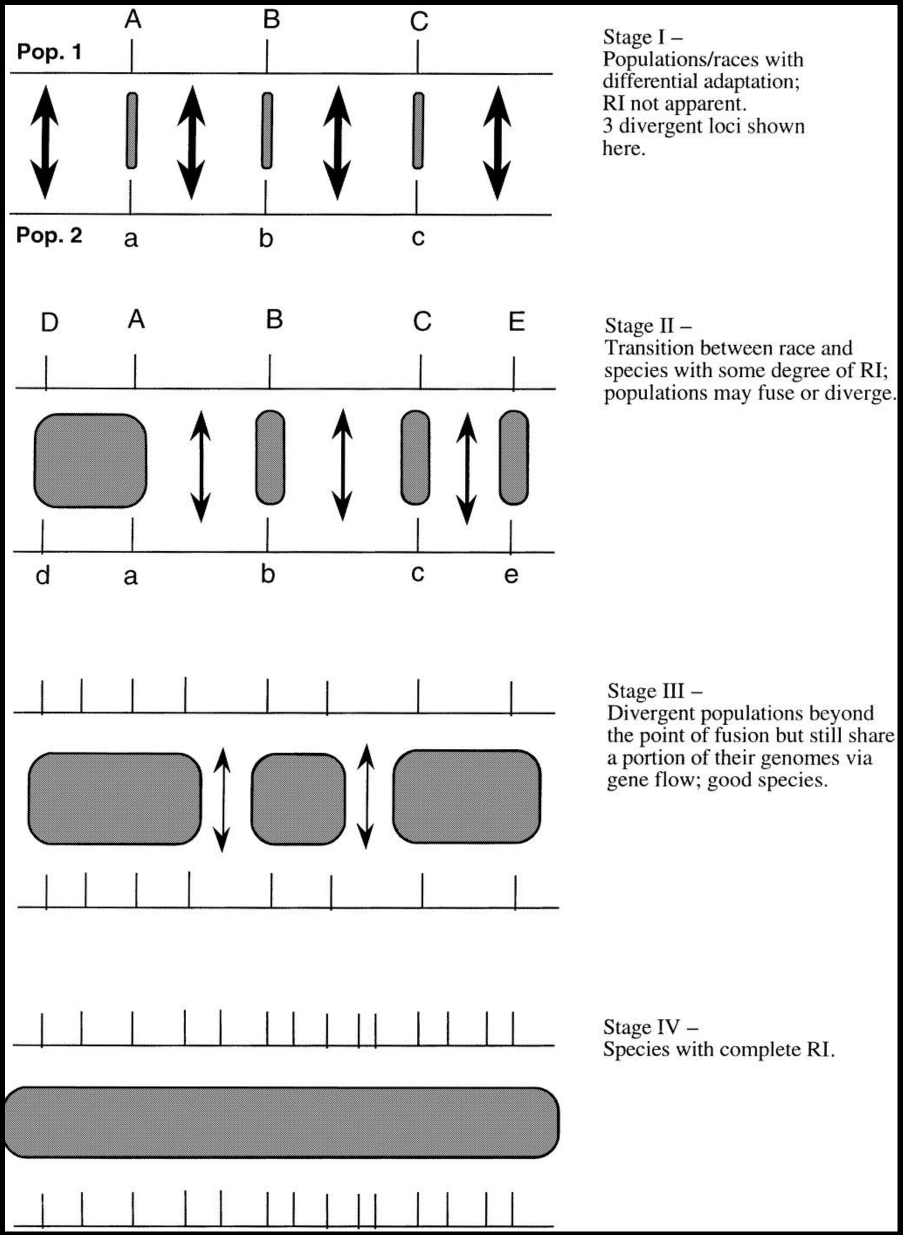
1. Kompetitivna specijacija
   - Drugi plijen
   - Parenje ovisno o veličini

2. Promjena domadara
   - Kod parazita
   - Fitofagni insekti

3. Razlika u vremenu cvata
   - Adaptacija na uvjete

4. Promjena u genetičkom sustavu
   - Ploidije





Wu 2001 – Journal of Evolutionary biology

Specijacija na razini gena

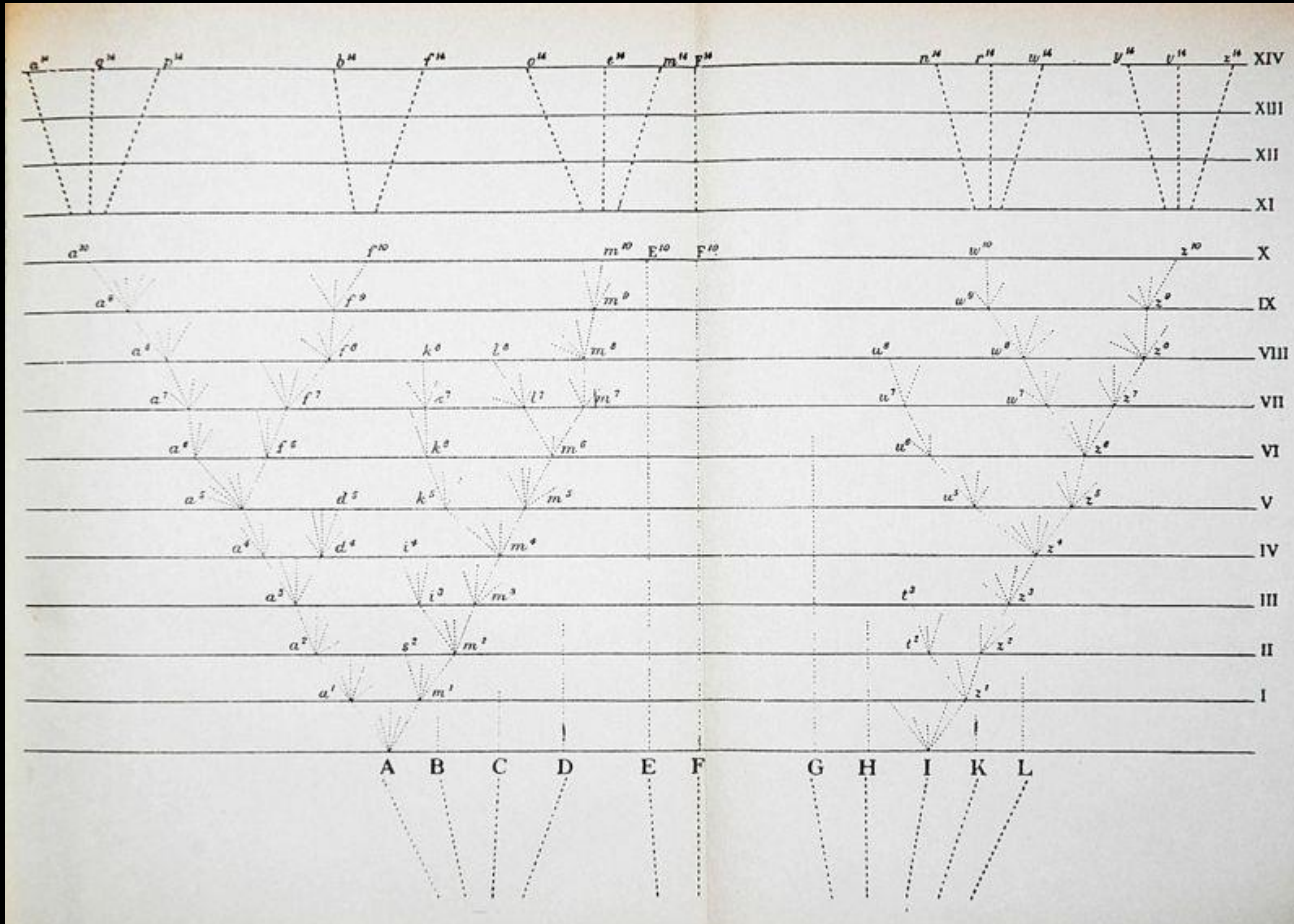
1. 3 lokusa RI nije vidljiva
2. Tranzicija
3. Divergentne populacije
4. Vrste vidljiva RI

Mehanizmi reproduktivne izolacije

TABLE 26.1 **Mechanisms of Reproductive Isolation**

	Process	Example
Prezygotic Isolation		
Temporal	Populations are isolated because they breed at different times.	Bishop pines and Monterey pines release their pollen at different times of the year.
Habitat	Populations are isolated because they breed in different habitats.	Parasites that begin to exploit new host species are isolated from their original population.
Behavioral	Populations do not interbreed because their courtship displays differ.	To attract male fireflies, female fireflies give a species-specific sequence of flashes.
Gametic barrier	Matings fail because eggs and sperm are incompatible.	In sea urchins, a protein called bindin allows sperm to penetrate eggs. Differences in the amino acid sequence of bindin cause matings to fail between closely related populations.
Mechanical	Matings fail because male and female reproductive structures are incompatible.	In alpine skypilots (a flowering plant), the length of the floral tube varies. Bees can pollinate in populations with short tubes, but only hummingbirds can pollinate in populations with long tubes.
Postzygotic Isolation		
Hybrid viability	Hybrid offspring do not develop normally and die as embryos.	When ring-necked doves mate with rock doves, less than 6 percent of eggs hatch.
Hybrid sterility	Hybrid offspring mature but are sterile as adults.	Eastern meadowlarks and western meadowlarks are almost identical morphologically, but hybrid offspring are largely infertile.

Bakterije – raznolikost sekvence = genetička izolacija – izostanak rekombinacije



The time will come I believe, though I shall not live to see it, when we shall have fairly true genealogical (phylogenetic) trees of each great kingdom of nature.

Darwin's letter to Thomas Huxley 1857

Filogenetika

- rekonstruirati točne genealoške veze među organizmima

- procijeniti vrijeme divergencije između organizma od trenutka kada su dijelili zajedničkog pretka

Filogenetička stabla

- de facto graf
- prikaz odnosa među organizmima ili genima
- usporedivo s pedigreom koji nam pokazuje koji geni ili organizmi su najsrodniji
- svako filogenetičko stablo sastoji se od karakterističnih dijelova i posjeduje jedinstvenu topologiju

Filogenetička stabla

čvorovi i ogranci

taksonomske jedinice

odnosi među taksonomskim jedinicama

vanjski ili krajnji čvorovi (OTUs)

i

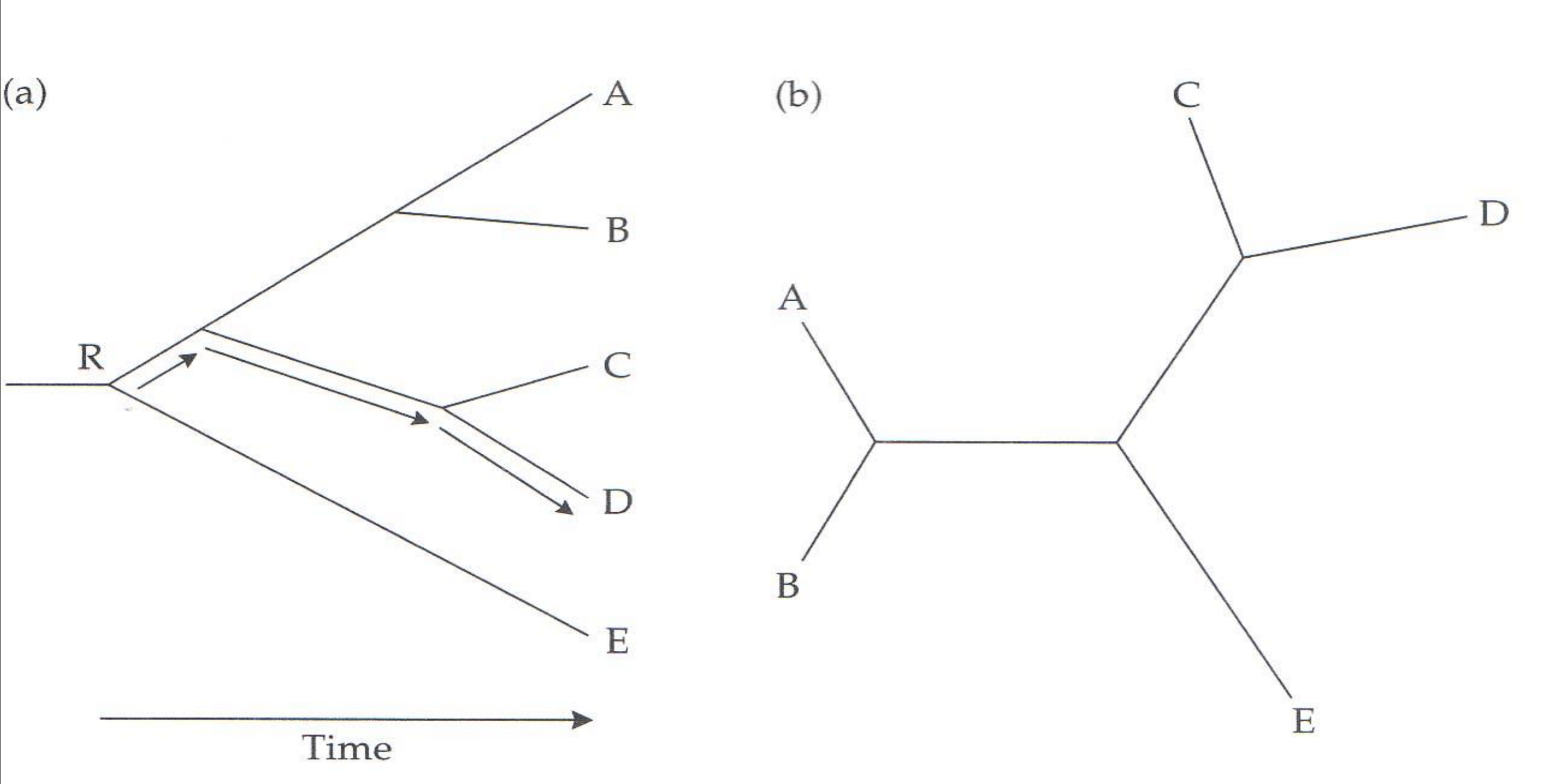
unutarnji čvorovi (HTUs)

vanjski ili periferni ogranci – završavaju opisanim grupama

i

unutarnji ogranci – povezuju hipotetske pretke

Filogenetička stabla



ukorijenjeno i neukorijenjeno

Filogenetička stabla

Najlakši način za procjenu vremena divergencije je pretpostaviti da sekvence nakupljaju promjene linearno u vremenu odnosno da postoji molekulski sat.
(Pauling i Zuckerkandl 1965)

Apsolutno točan molekulski sat ne postoji;

postoji samo određena razlika u učestalosti evolucijskih događaja

- metaboličku aktivnost
- generacijsko vrijeme
- učinak uskog grla boce
- selektivni pritisak

Da bi se molekulski sat mogao primijeniti kod izrade filogenetskog stabla, vremenski okvir mora biti poznat što znači da stablo mora biti ukorijenjeno

↓

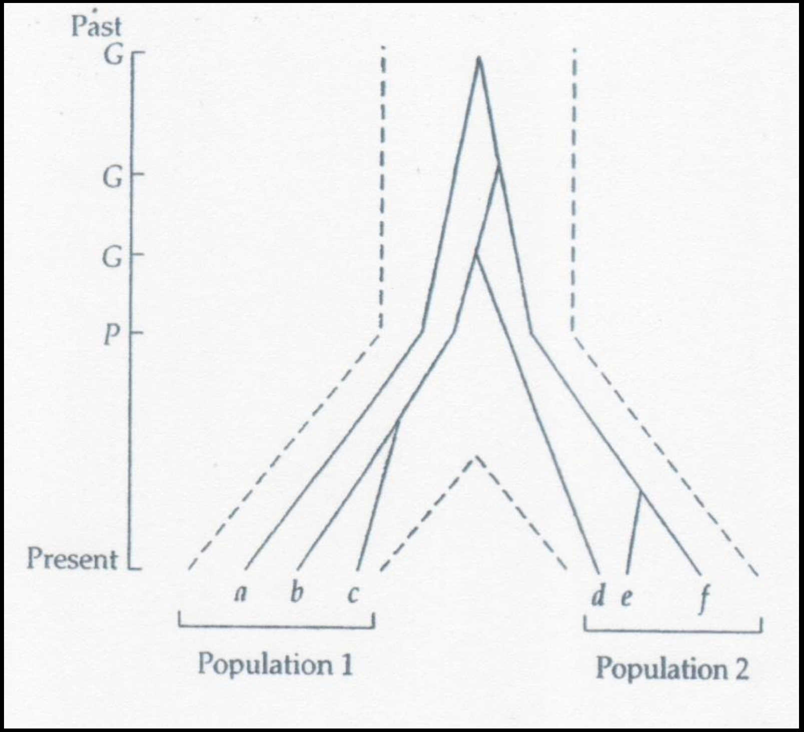
VANJSKA GRUPA (*outgroup*)

Filogenetička stabla

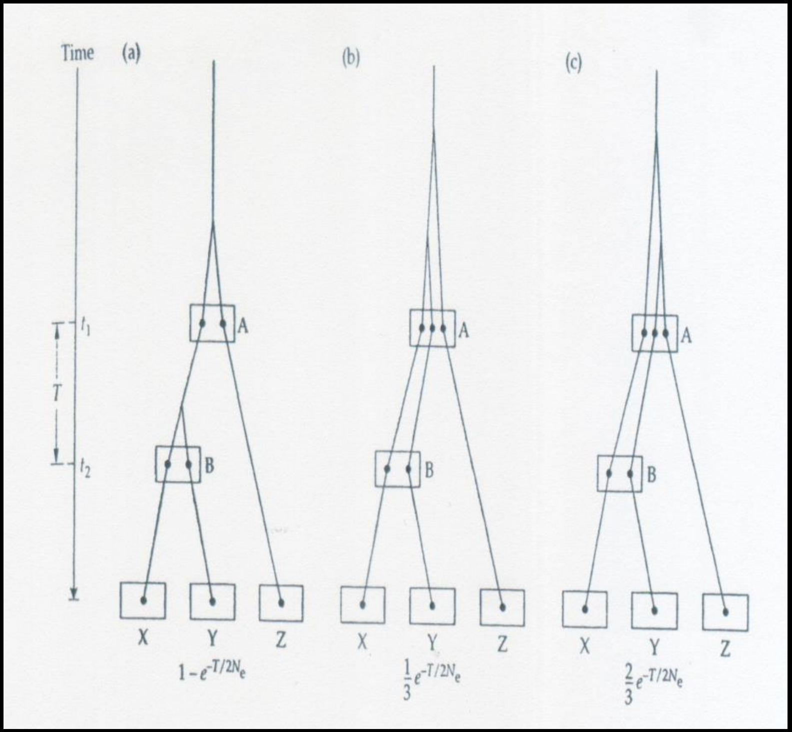
Vrsta i gena

Razlika:

divergencija dvaju gena iz dvije vrste može biti evolucijski starija od divergencije samih vrsta



topologija genskog stabla može se razlikovati od topologije stabla vrsta

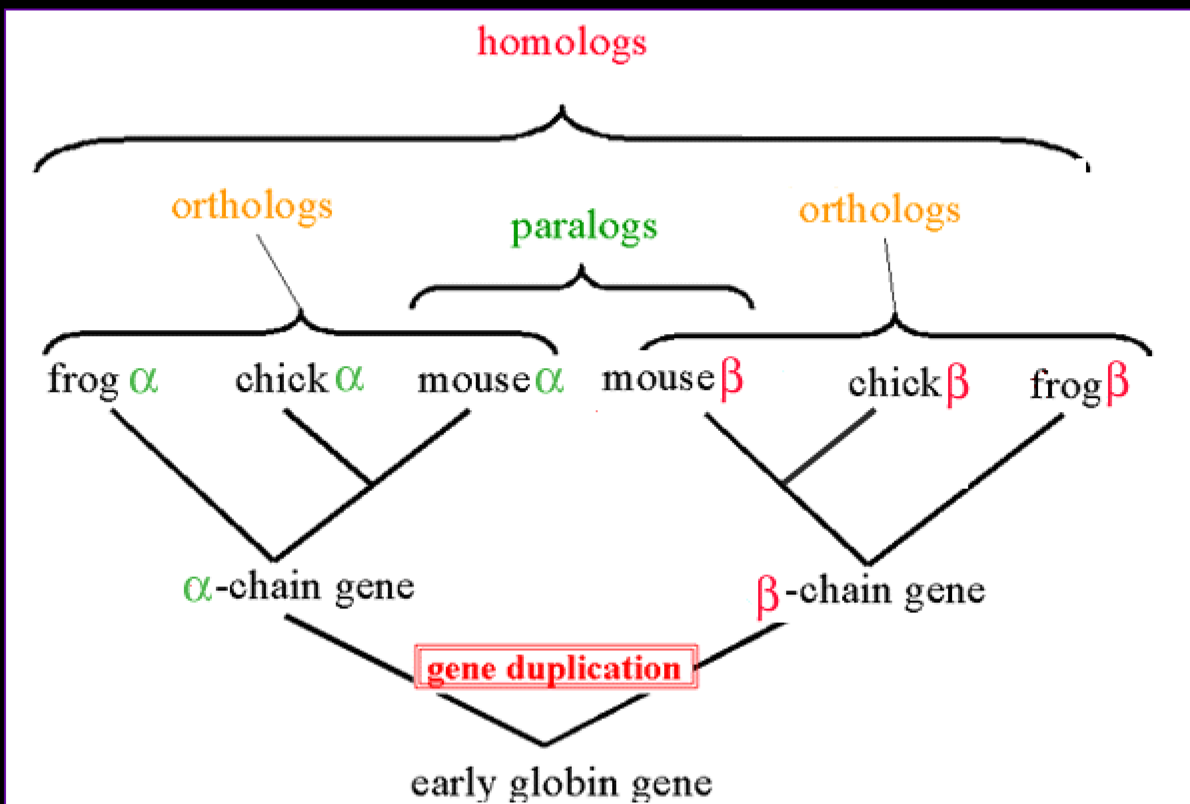


Koristiti DNA sekvence različitih lokusa koji su evoluirali neovisno jedan od drugoga

Ortologni i paralogni → duplikacijskih događaja

↓

specijacijskih događaja → **Filogenija vrsta**



Paralogni geni
duplikacija

Ortologni geni
specijacija

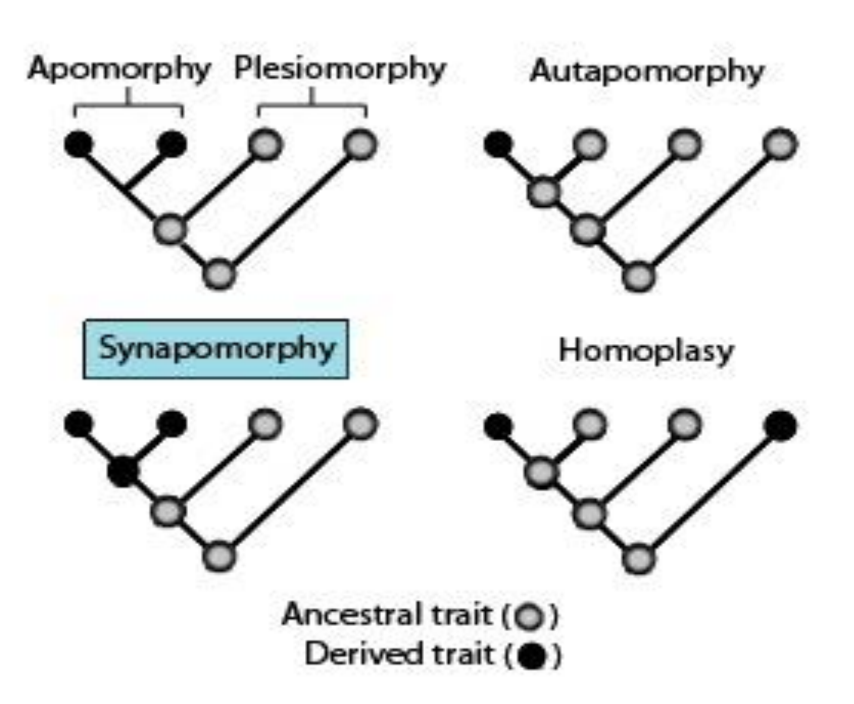
Ksenologni geni
horizontalni transfer

Ohnologni geni
duplikacijom genoma

Vrste stanja karaktera na filogenetičkom stablu

- **Sinapomorfija**
  izvedeno karakterno stanje koje dijele dva ili više taksona rezultat nasljeđivanja od **neposrednog** zajedničkog pretka, **ne dijele se** s nijednom drugom vrstom
  haltere kod Diptera

- **Simpleziomorfija**
  ancestralno karakterno stanje koje dijele dva ili više taksona potomaka rezultat nasljeđivanja od **dalekog** zajedničkog pretka **dijele se** s drugim vrstama koje su imale zajedničkog pretka
  pet prstiju kod štakora i majmuna ali i kod gmazova

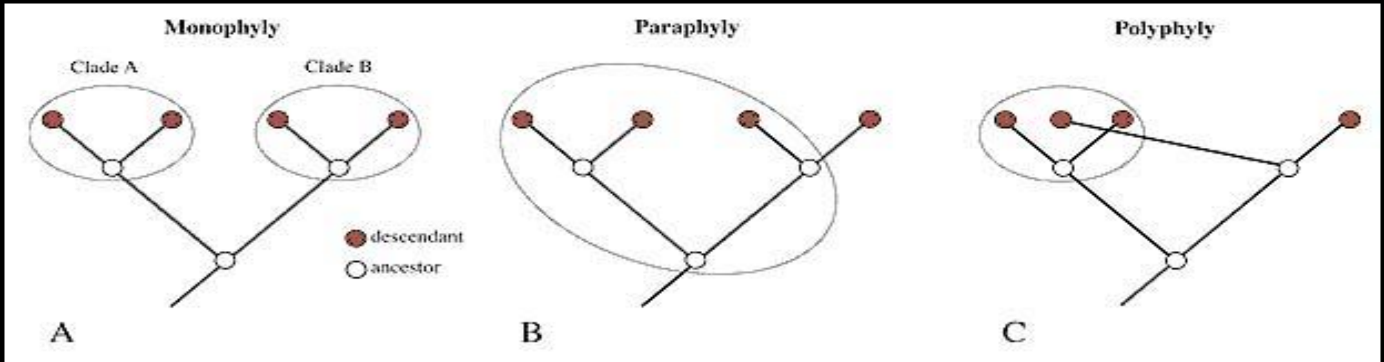


- **Homoplazija**
  sličnosti koje mogu zavarati o eventualnoj srodnosti rezultat konvergencije, paralelizma i reverzne evolucije **nisu rezultat** nasljeđivanja od zajedničkog pretka
  krila kod kukaca i ptica

Odnosi između podataka na filogenetičkom stablu

- **Monofiletička grupa**
  kladij (*clade*)
  jedan od zadataka klasifikacije organizama; svi članovi porijeklom od jednog zajedničkog pretka koji nije predak niti jednoj drugoj grupi organizama izvan opisane
  psi
- **Parafiletička grupa**
  članovi koji nisu porijeklom od najmlađeg zajedničkog pretka, uključuje neke ali ne sve potomke
  gmazovi
- **Polifiletička grupa**
  vrste nisu porijeklom od istog zajedničkog pretka već od više njih koji su ujedno i preci vrstama koje su klasificirane u drugim grupama
  ptice i šišmiši

Sinapomorfija je dakle povezana s monofilijom, simpleziomorfija s parafilijom, a homoplazija s polifilijom.



Koliko ima filogenetičkih stabala?

- Broj bifurkatnih neukorijenjenih stabala (Nx) za **n** taksonomskih jedinica gdje je **n** (broj taksonomskih jedinica) veći ili jednak od 3 iznosi:

  $$Nx = (2n - 5)! / (2n\text{-}3\ (n - 3)!)$$

- Broj bifurkatnih ukorijenjenih stabala (Ny) za **n** taksonomskih jedinica gdje je **n** (broj taksonomskih jedinica) veći ili jednak od 2 iznosi:

  $$Ny = (2n - 3)! / (2n\text{-}2\ (n - 2)!)$$

n=2	Nx=1	Ny=1
n=3	Nx=3	Ny=1
n=4	Nx=15	Ny=3
n=5	Nx=105	Ny=15
n=6	Nx=954	Ny=105
n=7	Nx=10 395	Ny=954
n=8	Nx=135 135	Ny=10 395
n=9	Nx=2 027 025	Ny=135 135
n=10	Nx=34 459 425	Ny=2 027 025

Metode za rekonstrukciju filogenetičkih stabala

	Metode koje koriste strategiju iscrpnog pretraživanja (**Exhaustice Search**)	Metode koje koriste strategiju postupnog klasteriranja (**Stepwise Clustering**)
Metode bazirane na stanju karaktera (**Character State**)	Najveća štedljivost (***Maximum Parsimony***) MP Najveća vjerojatnost (***Maximim Likelihood***) ML	
Metode bazirane na matrici udaljenosti (**Distance Matrix**)	**Fitch-Margoliash** FM	**U**nweighted **P**air **G**roup **M**eth od with **A**rithmetic Mean (**UPGMA**) Susjedno sparivanje (***Neighbor Joining***) NJ

Filogenetički biljezi

mnoštva različitih karaktera

nedvosmislena
stanja karaktera

pogodni za statističke obrade

Filogenetički biljezi

biljeg kojeg koristimo za analizu mora pokazivati varijabilnost

multialelni geni, mikrosateliti i mitohondrijska DNA kod životinja ili kloroplasna DNA kod biljaka

visoko konzervirani molekularni biljezi ili dijelovi gena korisni su za proučavanje filogenetičkih odnosa na višim sistematskim razinama.

hipervarijabilni molekularni biljezi ili dijelovi gena su korisni za razrješavanje filogenetičkih odnosa na nižim sistematskim razinama

konflikt između molekularnih i morfoloških dokaza u filogeniji

pravo pitanje u filogeniji je da li nam određeni biljeg daje odgovore za rješavanje problema koji imamo

da li postoji jasan genetički otklon (*bias*) kod upotrijebljenih biljega i da li su podaci sakupljeni na takav način da je moguće napraviti filogenetičku usporedbu te u konačnici postaviti određenu hipotezu na osnovi njihove analize

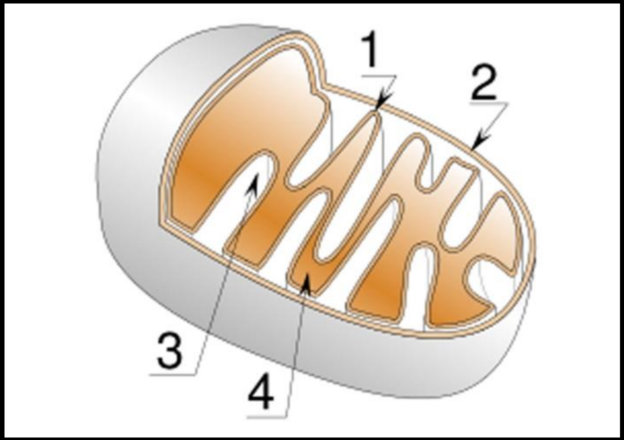
Filogenetički biljezi

	Carstvo	Koljeno	Razred	Red	Porodica	Rod	Vrsta	Populacija
Biljezi u jezgrinoj DNA								
16 & 18S rRNA	—	—	—	—	- -			
23 & 28S rRNA			—	—	—	- -		
5.8S rRNA	—	—	—	- -				
IGS							—	—
ITS						—	—	—
Biljezi u mtDNA								
12S rRNA		—	—	—	- -			
16S rRNA					—	—	- -	
ND1				- -	—	—	—	- -
ND2				- -	—	—	—	- -
COI				- -	—	—	—	- -
COII				- -	—	—	—	- -
Cytb				- -	—	—	—	- -
D-Loop							—	—

Filogenetički biljezi

Mitohondriji

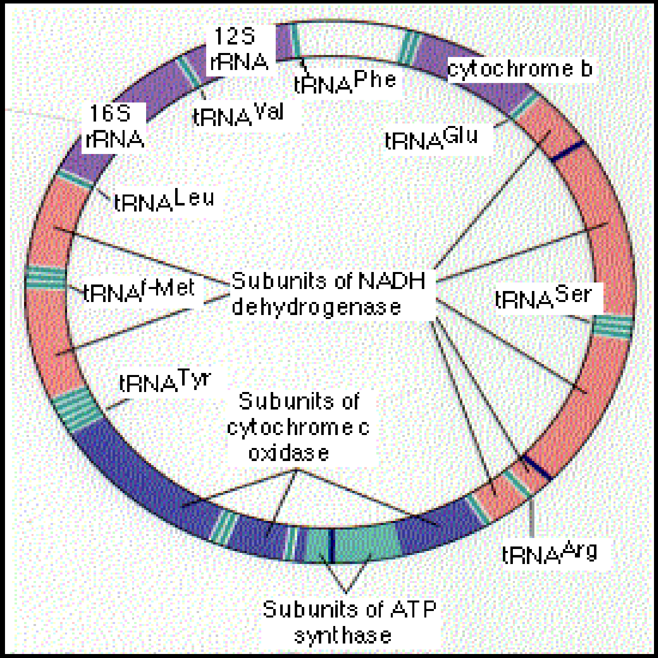
- elipsoidni, poluautonomni organeli, duljine oko 2 µm i širine 0.5 µm, veliki poput bakterija, koji žive u endosimbiontskom odnosu sa stanicom u kojoj se nalaze
- građeni od dva membranska sustava, unutarnjeg (1) i vanjskog (2)
- unutarnja membrana tvori svojom nabranošću karakterističan sustav pregrada koje nazivamo *cristae* (3)
- međumembranski prostor i *matrix* (4) koji je omeđen unutarnjom membranom
- oksidativna fosforilacija se događa na unutarnjoj mitohondrijskoj membrani dok se ciklus limunske kiseline i oksidacija masnih kiselina odvijaju u matrix-u mitohondrija



Filogenetički biljezi

Mitohondrijska DNA (mtDNA)

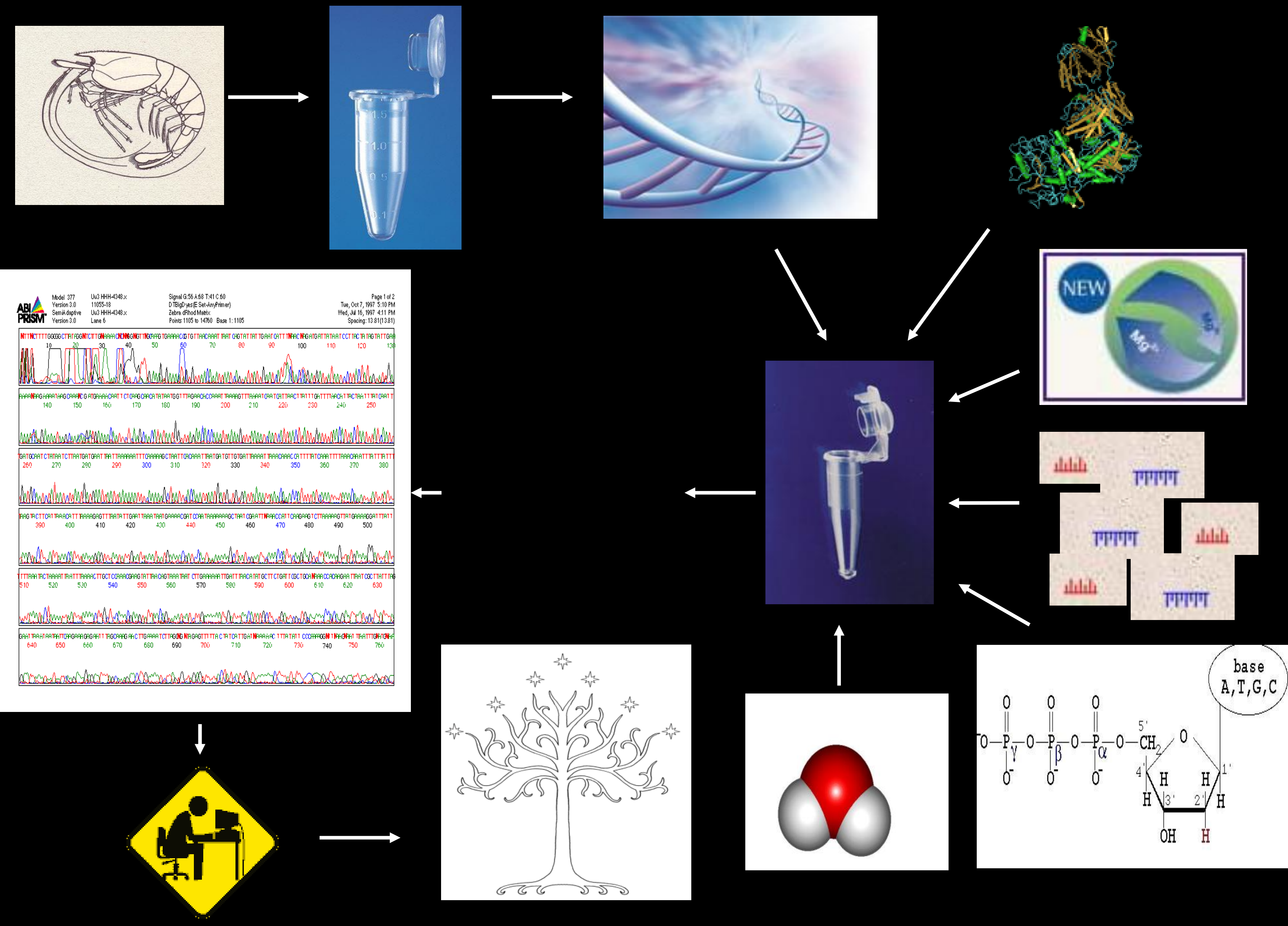
- građom, veličinom i organizacijom sliči prokariotskoj, bakterijskoj DNA, gotovo sve eukariotske stanice, osim Archaezoa skupine Protista
- kod životinja najčešće je kružna dvolančana molekula, osim kod nekih žarnjaka gdje je u obliku jedne ili dvije linearne molekule, veličine od 14 do 42 tisuće parova baza (pb)
- kodiraju 13 proteinskih molekula, 22 molekule tRNA i 2 molekule rRNA (16 S rRNA i 12S rRNA), postoji i nekodirajuće područje tzv. kontrolna regija koja se kod sisavaca naziva D-Loop, to je A+T bogata regija i varijabilne je duljine



Filogenetički biljezi

- lakoće izolacije
- veliki broja kopija
- nepostojanje genske rekombinacije
- nasljeđivanje po majčinoj liniji i time manja efektivne veličina populacije
- relativno velike brzine evolucije obzirom na jezgrinu DNA

Rezultiraju bifurkatnim genskim stablima i omogućavaju laku i brzu analizu populacija kod kojih nema izmjene gena (*gene flow*) kao i njihovo geografsko pozicioniranje


ABI PRISM
NEW
base
A,T,G,C

Programi i metode

Filogenetička analiza:
PAUP* 4.0b10 (Swoford 2001), PHYLIP 3.65 (Felsenstein 1993), MEGA 5 (Kumar, Tamura i Nei 2004) TREE-PUZZLE 5.2 (Schmidt, Strimmer, Vingron i von Haeseler 2002), TREECON 1.3b (Van de Peer 1994), ModelTest 3.7 (Posada i Crandall 1998), MT gui 1.0 (Nuin 2005) Mr. Bayes 3.1.1 (Huelselbeck i Ronquist 2003), BioEdit 7.0.5.2 (Hall 1999), ClustalX 1.83 (Thompson i sur. 1997,1999), TreeView 1.6.6 (Page 2001), GeneDoc 2.1.000 (Nicholas i Nicholas 1997.), SplitsTree 4.0 (Huson i Briant 2005)

Pretraživanja baza podataka:
BLAST (Altschul i sur. 1990)

Unos sekvenci u bazu podataka:
Sequin 12.0

Metode filogenetičke analize:
UPGMA, FITCH, KITCH, NJ, BIONJ, ME, ME+MC, QP, MP, ML, BA.

Molekularno filogenetička analiza

<u>unos sekvenci u bazu</u>

GenBank baza sekvenci pri *NCBI*-ju gdje nakon provjere dobivaju svoje pristupne brojeve (*Accesion Numbers*)

<u>globalno sravnjivanje</u>

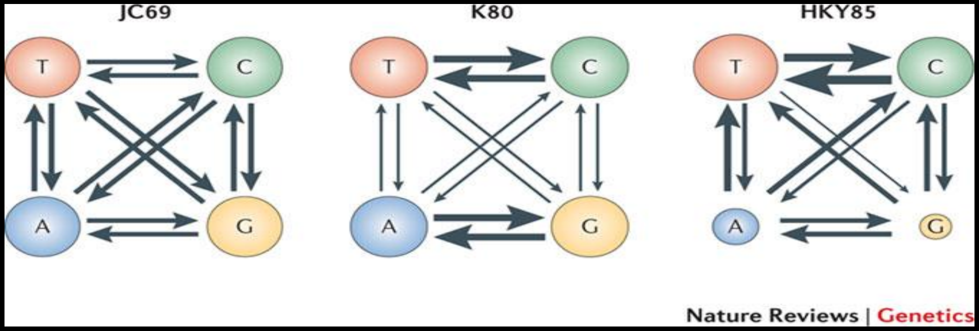
Višestruko sravnjivanje (*multiple alignment*) sekvenci je temelj i osnova svakog molekularno filogenetskog istraživanja

<u>lokalno sravnjivanje</u>

Fleksibilnija od tehnike globalnog sravnjivanja prednost da može pronaći regije koje se pojavljuju u različitom redoslijedu ili orijentaciji u različitim sekvencama

<u>odabir evolucijskog modela</u>

Filogenetska rekonstrukcija bazira se na statističkoj obradi podataka te ju je nemoguće provesti bez određenih modela vjerojatnosti



Metode filogenetičke analize

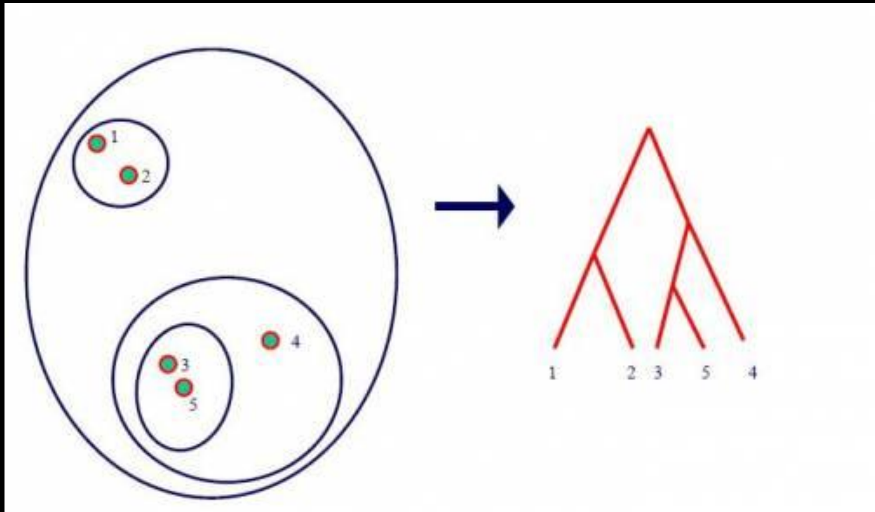
UPGMA

(Unweight Pair Group Method with Arithmetric Mean - Sokal i Michener 1958)

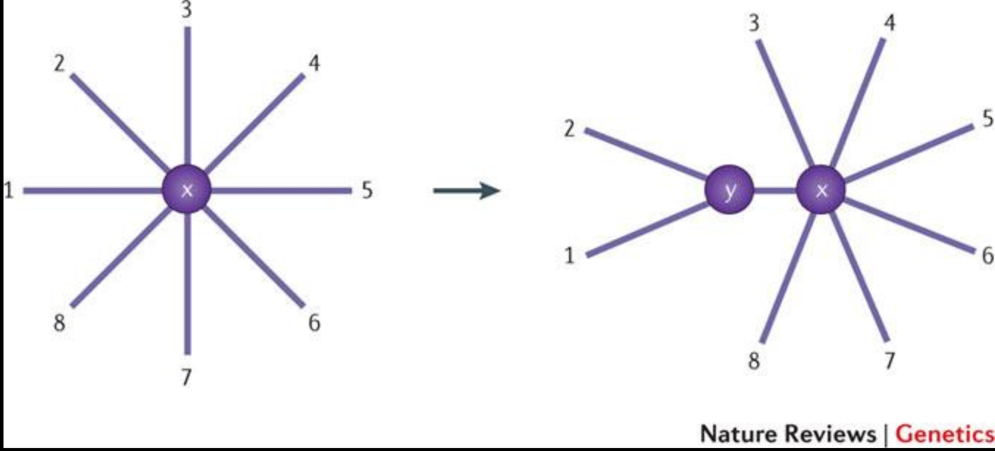
- najstarija i najjednostavnija metoda originalno razvijena za konstrukciju taksonomskih fenograma; stabala koja su odražavala fenotipske sličnosti među taksonomskim jedinicama.

- klasteriranje se vrši potragom za najmanjom međusobnom razlikom između dvaju članova u matrici udaljenosti; novo formirani klaster tada zamjenjuje taksone koje je predstavljao u matrici.

- pretpostavlja da je evolucijska učestalost u svim granama ista što znači da nijedna grupa ne nakuplja mutacije brže od ostalih; gotovo uvijek ta pretpostavka nije točna stoga UPGMA daje pogrešna stabla kada su evolucijske učestalosti različite unutar različitih ogranaka.



Metode filogenetičke analize



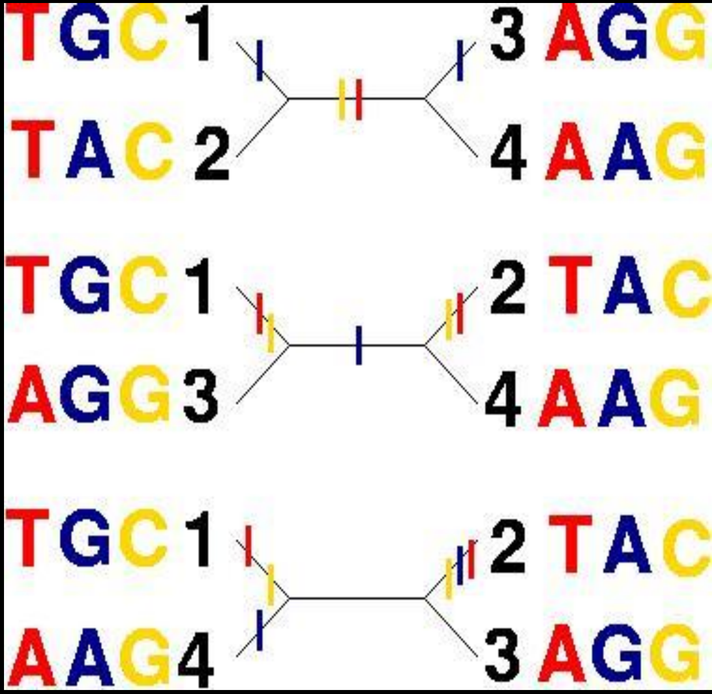
Susjedno sparivanje
(Neighbor Joining - Saitou i Nei 1987)

- rekonstruira filogenetička stabla postupnim pronalaženjem "susjednih parova", koji su u stvari parovi taksonomskih jedinica povezani jednim unutarnjim čvorom; metoda se svodi se na princip minimalne evolucije

- ova metoda ne nastoji grupirati najsrodnije taksonomske jedinice, nego radije minimalizira duljinu svih unutarnjih grananja čime i duljinu cijelog stabla; možemo je smatrati metodom koja primjenjuje princip štedljivosti u metodologiji matrice udaljenosti

- počinje od pretpostavke o grmolikom stablu koje nema unutarnjih grananja, u prvom koraku ovaj algoritam uvodi prvi unutarnji ogranak i računa duljinu rezultirajućeg stabla; algoritam zatim postupno radi parove svih mogućih taksonomskih jedinica međusobno i konačno spaja taksonomske jedinice koje će dati najkraće stablo

Metode filogenetičke analize

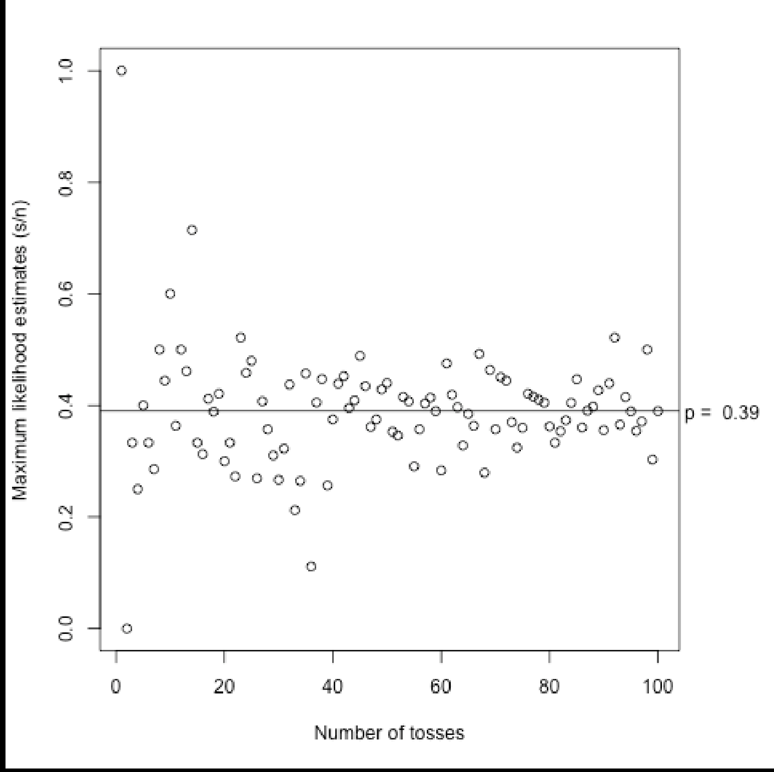


Najveća štedljivosti

(Maximu Parsimony - Fitch 1977)

- bazira se na filozofskom principu poznatom kao *Ockham's razor*, nastoji pronaći filogenetičko stablo takve topologije da je za njeno objašnjenje potreban najmanji mogući broj promjena karaktera (npr. mutacija)
- algoritam najveće štedljivosti počinje proračune na osnovi predodređenog stabla određene topologije, to stablo se zatim nastoji rekonstruirati upotrebom najmanjeg mogućeg broja promjena karaktera potrebnih da bi se objasnili svi čvorovi stabla na svakoj poziciji sekvence. Zatim se provjerava sljedeća topologija na isti način. Nakon što su sve smislene topologije provjerene odabire se ono stablo za koje je bio potreban najmanji broj promjena
- metoda najveće štedljivosti ne radi nikakve eksplicitne pretpostavke kao prethodne metode osim one o kriteriju štedljivosti, a to znači da je ono stablo koje zahtjeva manji broj supstitucija bolje od onog stabla koje zahtjeva veći broj. To ujedno znači da takvo stablo smanjuje broj homoplazijskih događaja poput paralelizama, konvergencije i povratnih supstitucija

Metode filogenetičke analize



Najveća vjerojatnost
(Maximum Likelihood - Felsenstein 1973)

- metoda najveće vjerojatnosti proračunava vjerojatnost očekivanja svake moguće nukleotidne ili aminokiselinske pozicije u ancestralnom (unutarnjem) čvoru i rekonstruira vjerojatnost strukture stabla iz tih vjerojatnosti. Vjerojatnost svih smislenih topologija stabala traži se na ovaj način i najvjerojatnije stablo se izabire kao istinito.
- metoda najveće vjerojatnosti je najdosljednija od svih metoda, ako su pretpostavke koje se koriste za konstrukciju funkcije vjerojatnosti nerealne metoda najveće vjerojatnosti može postati nedosljedna; događa se ukoliko supstitucijski model za sekvence koju proučavamo nije realističan ili kada se za učestalost evolucijskih događaja uzima da je konstantna, bilo među mjestima ili među linijama, a ona to nije
- radi eksplicitne pretpostavke o evolucijskoj učestalosti i uzorku nukleotidne supstitucije; programi za izbor učestalosti evolucijskih događaja i uzorka supstitucije omogućavaju obrađivanje raznih situacija; računalno jako zahtjevna.

Metode filogenetičke analize

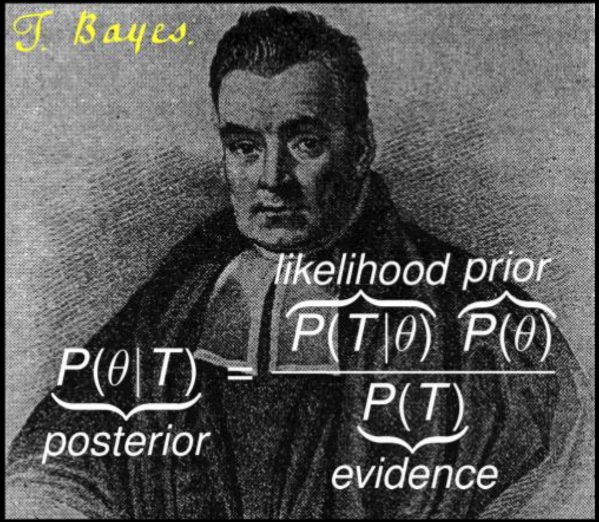
- temelji se na spoznaji o tzv. naknadnim vjerojatnostima (*posterior probabilities*), vjerojatnostima koje su procijenjene na osnovi nekog modela; taj model se naziva prethodno očekivanje (*prior expectations*) i konstruira se nakon određenih spoznaja o podacima

- za razliku od prethodnih poznatih i uvriježenih metoda filogenetičke analize; metoda Bayesian analize je relativno nova u filogenetičkoj analizi; metoda izbora kod većine najnovijih filogenetičkih istraživanja

- dvije najveće kvalitete Bayesian analize, pred ostalim tipovima analize:

(i) sposobnosti algoritma da traži grupe najboljih stabala, a ne jedno najbolje stablo

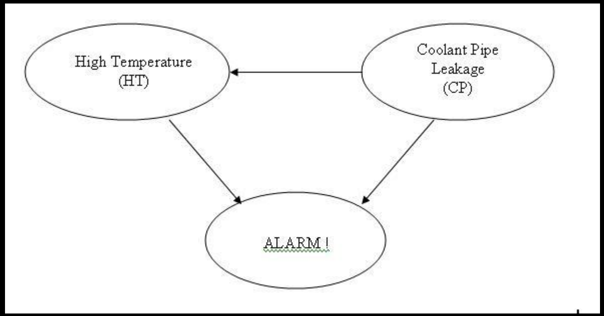
(ii) mogućnosti izmjene informacija tijekom analize među više neovisnih potraga za najboljom grupom stabala



$$\underbrace{P(\theta|T)}_{posterior} = \frac{\overbrace{P(T|\theta)}^{likelihood}\ \overbrace{P(\theta)}^{prior}}{\underbrace{P(T)}_{evidence}}$$

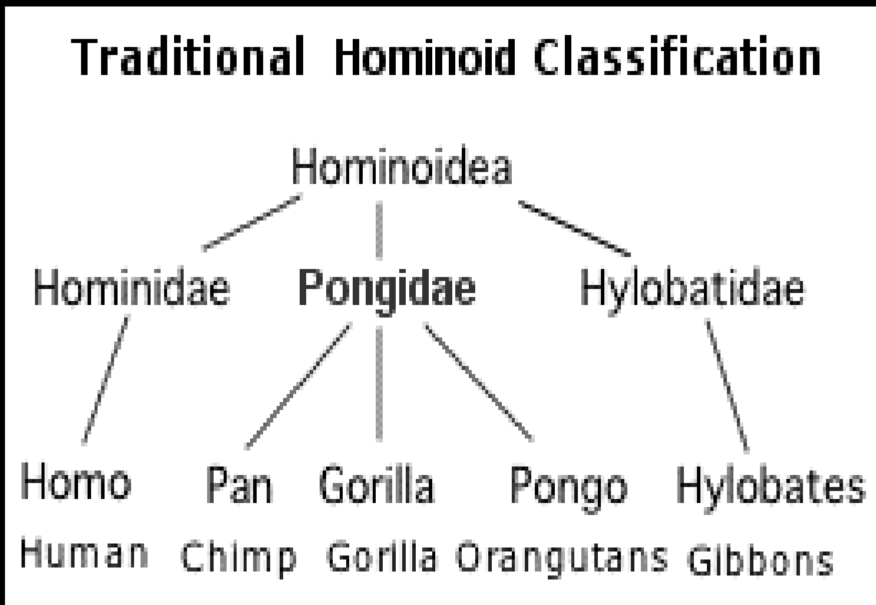
Bayesian analiza

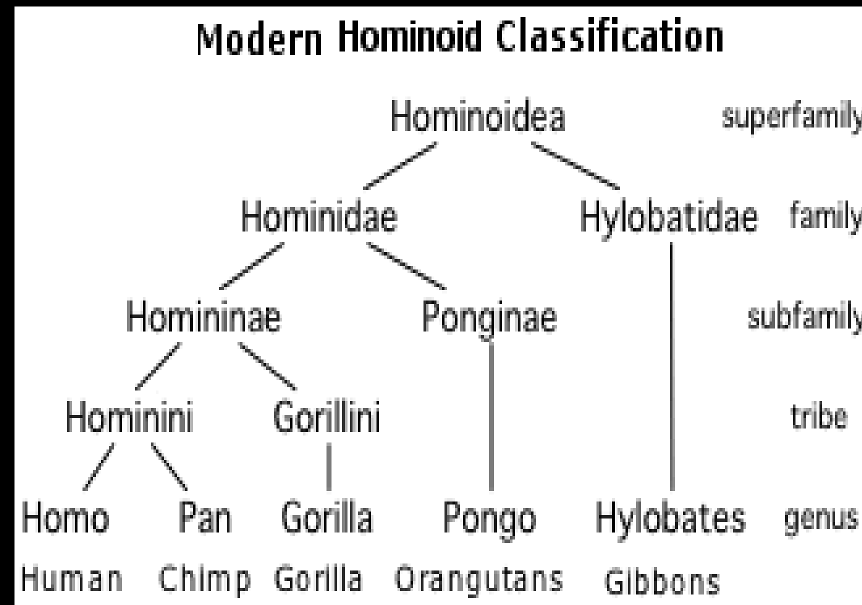
(Rannala i Yang 1996)



Primjeri

Najbliži srodnici ljudi - čimpanze, gorile, orangutani, giboni?





Porijeklo modernog čovjeka

Iz Afrike (*Out of Africa*) ili Multiregionalna teorija

Fosilna DNA (*Ancient DNA*) – Higuchi i Pääbo

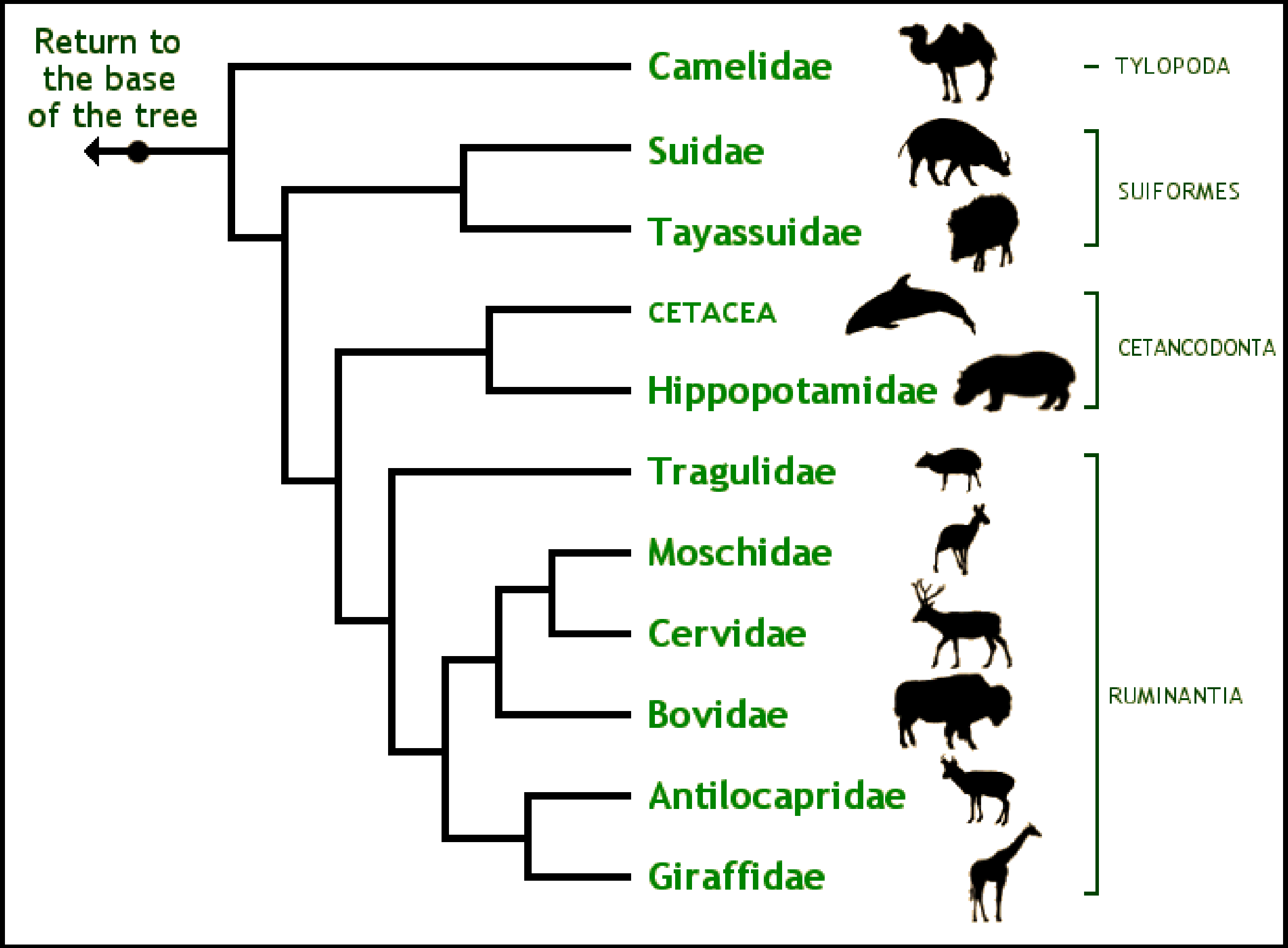
Srodnici kitova, dupina i pliskavica

Cetartiodactyla = Cetacea + Artiodactyla

Podredovi Suiformes (Svinje i Nilski konji),

Tylopoda (Deve i Ljame) i

Ruminantia (Krave, Žirafe, Koze, Jeleni i Sobovi)



Animalia – *COI*

Plantae – *rbcL & matK*

Fungi – *ITS*

Protista – *18s rDNA*

Prokaryota – *16S rDNA & rpoB*

Paul Hebert (2003)
University of Guelph
Ontario, Canada

"DNA barcoding"

IDENTIFICIRANJE VRSTA