

Nouveaux concepts sur la préhistoire des êtres vivants à la fin du XX^{ème} siècle

et au début du XXI^{ème} ..!

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Petit rappel : les avancées du XIXème siècle en biologie

Différence fondamentale et irréductible entre les êtres vivants et le monde « inanimé » : création du terme Biologie

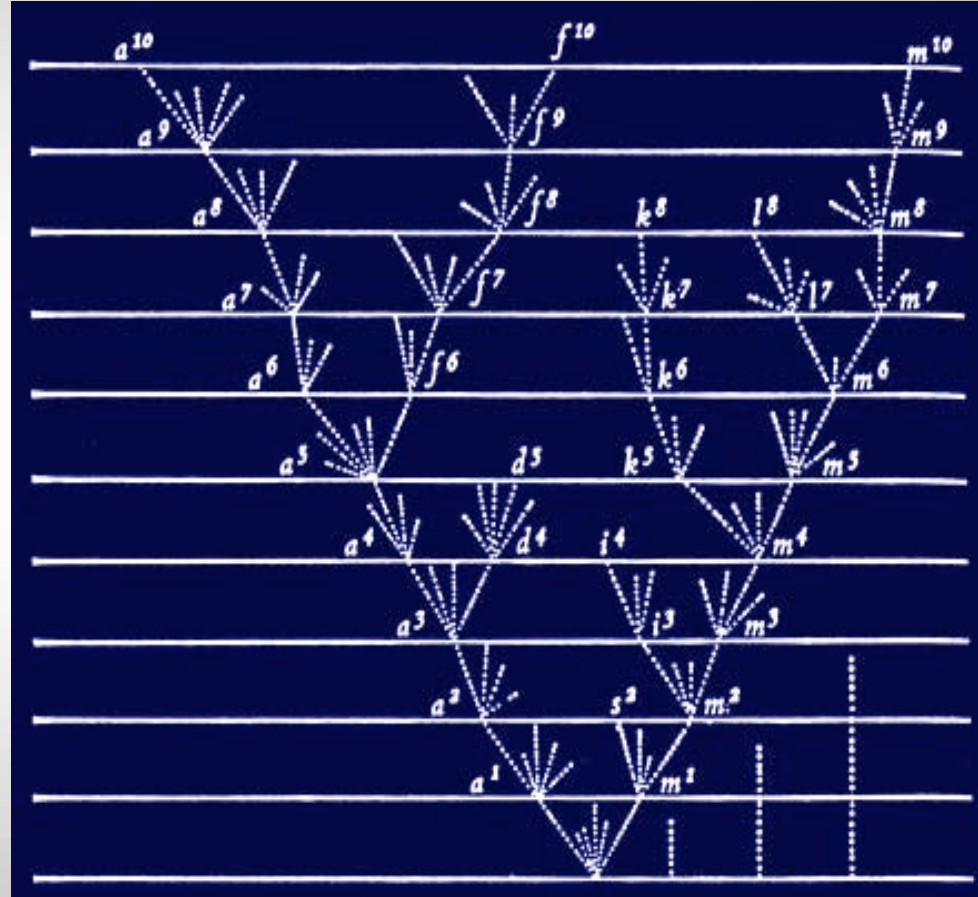
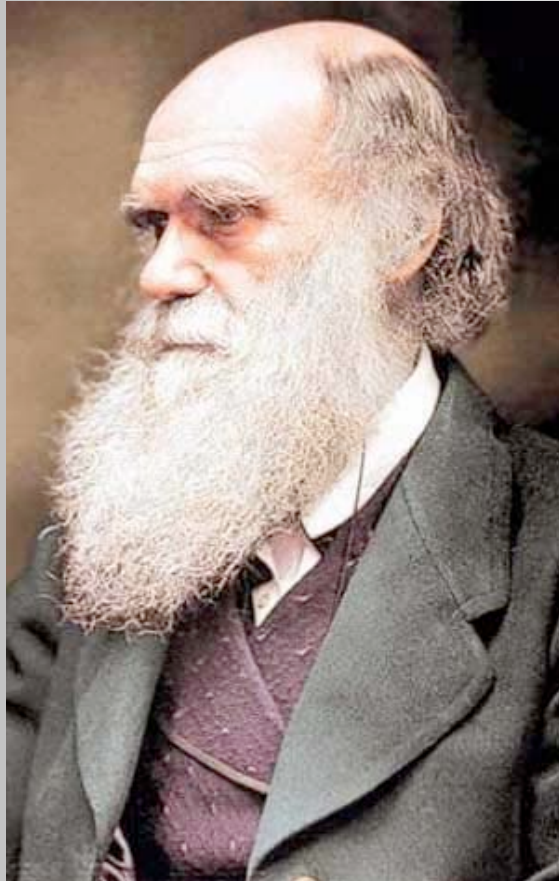
Théorie cellulaire

Notion d'évolution (histoire de la vie)



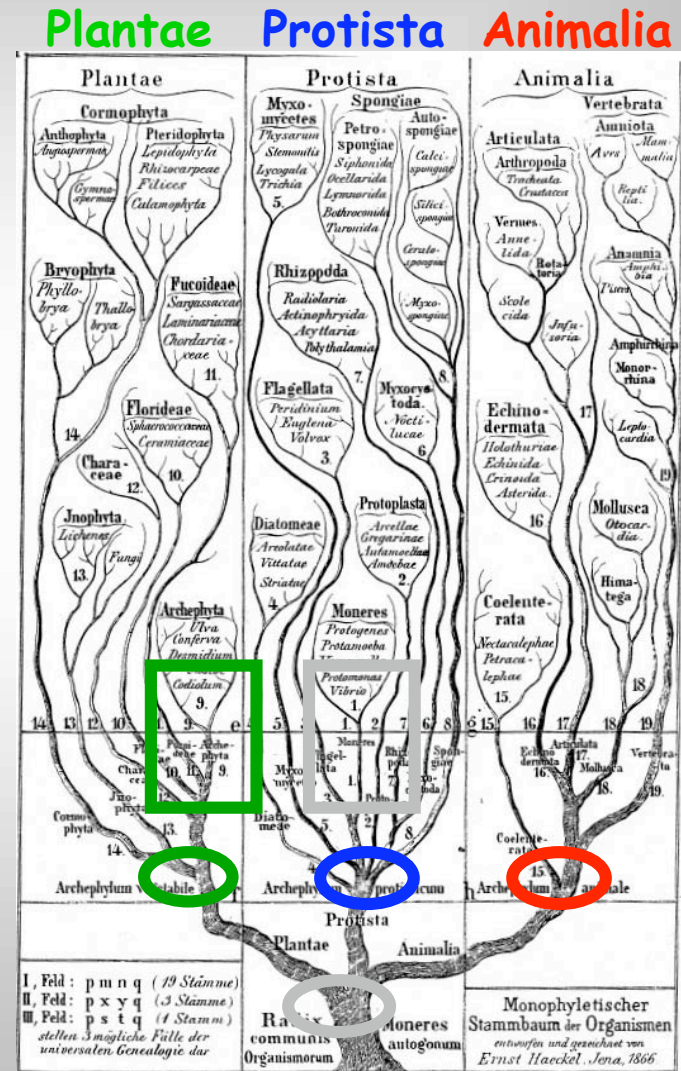
**Théorie de la sélection naturelle (Darwin) :
identification du mécanisme
de l'évolution**

Les êtres vivants ont une histoire...il reste à la déchiffrer



Le premier arbre universel du vivant (Haeckel, 1866)

- Séparation du monde vivant en 3 règnes **Plantae**, **Animalia** et **Protista**
- Objectif = clarifier la frontière Plantae/Animalia devenue trop floue à cause des micro-organismes
 - **Protista** = organismes unicellulaires, à l'exception des algues bleues-vertes
 - **Monera** = Protista dépourvus de noyau (futurs Procaryotes)
 - **Archephyta** = Algues bleues-vertes unicellulaires (Cyanobactéries)
- Cette classification ne rencontre pas un énorme succès et la dichotomie **Animalia/Plantae** se maintient

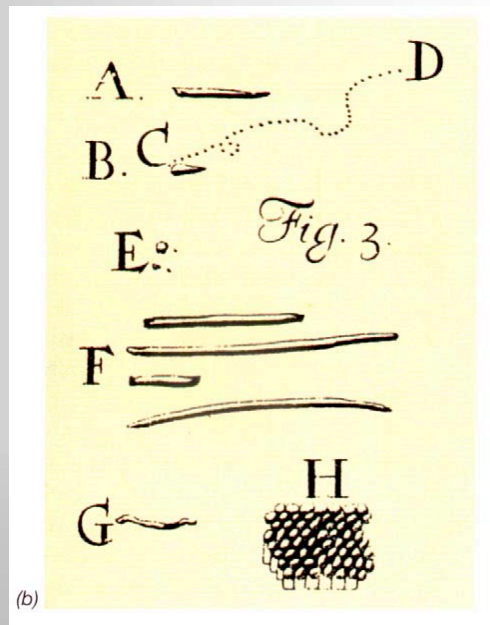
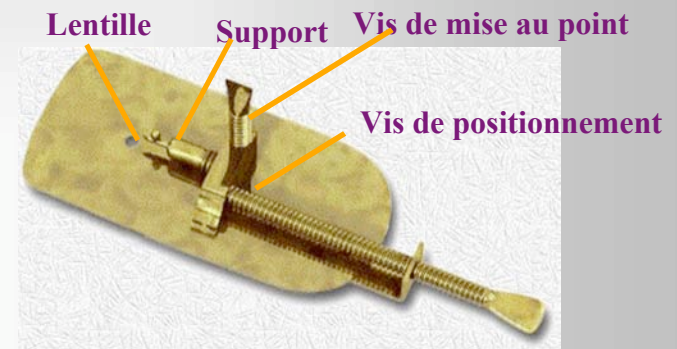


Les micro-organismes

Les micro-organismes ont été découverts au milieu du 17^{ème} siècle par Van Leeuwenhoek

Ces organismes sont

- Des intermédiaires probables entre le monde minéral et le monde vivant
- Classés au sein des Plantes ou au sein des animaux



La première moitié du XXème siècle
Les différentes approches pour reconstituer
l'histoire des êtres vivants

Phénétique

(qui se ressemble s'assemble)

Gradisme

(du simple au complexe)

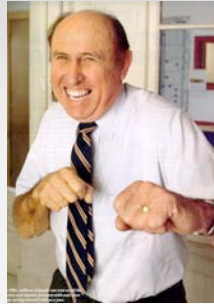
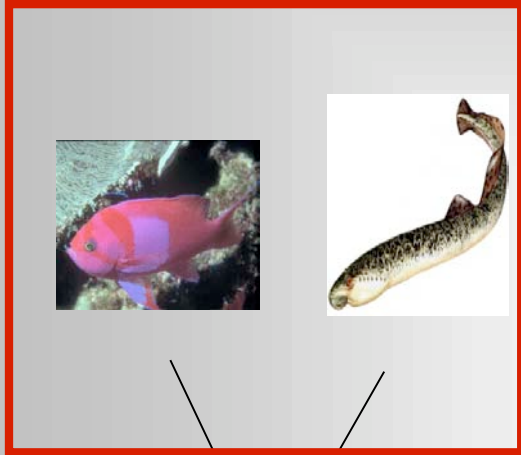
Phylogénétique évolutive

(analyse cladistique)

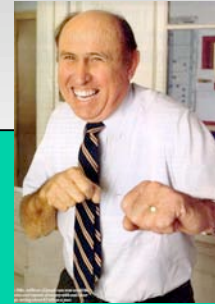
Willi Hennig (1950, 1966)



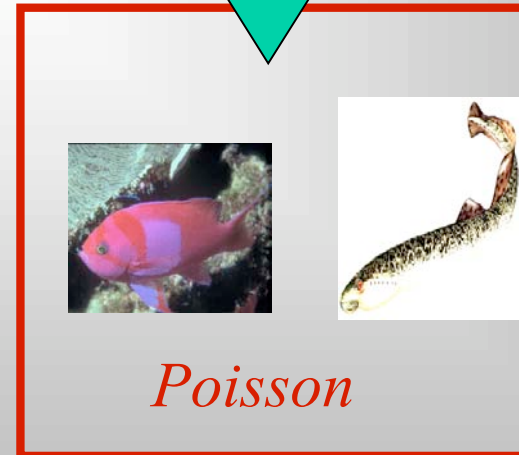
Phénétique



Gradisme



Mammifère



Poisson

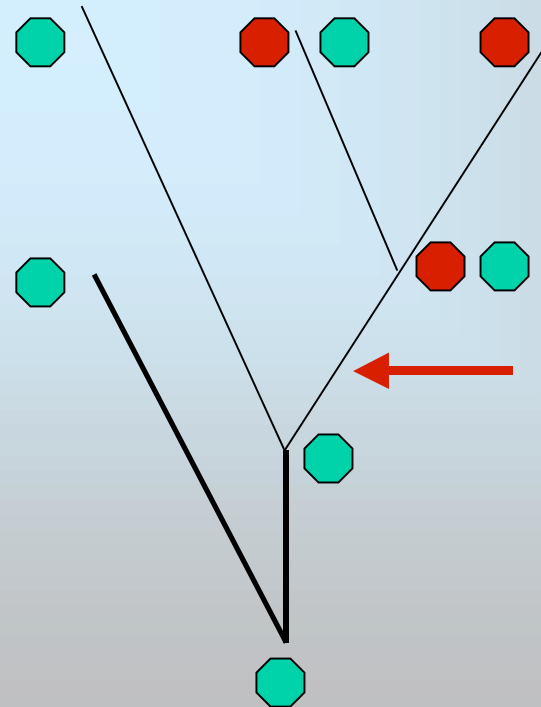
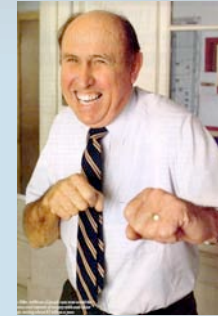
*Qui se ressemblent s'assemblent
Les poissons !*

Analyse Cladistique



Willi Hennig (1950, 1966)

Notion de synapomorphie *polarisation des caractères*



La première moitié du XXème siècle

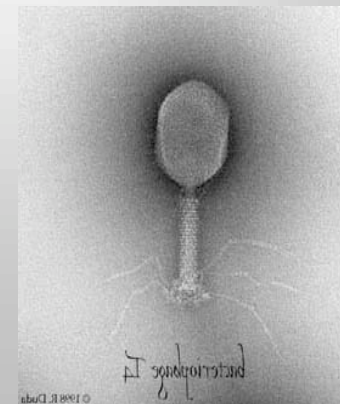
Unité chimique du monde vivant



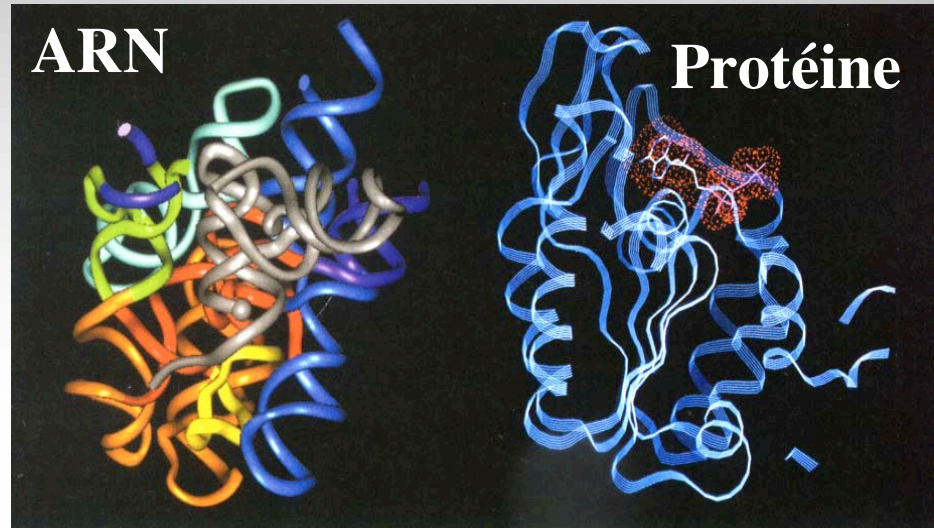
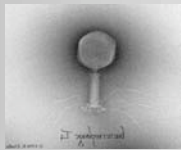
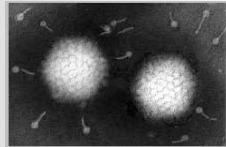
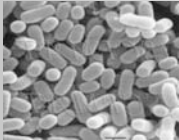
Identification du gène et des mécanismes de la « variation »
Théorie synthétique de l'évolution

Définition de deux types cellulaires : eucaryote et procaryote

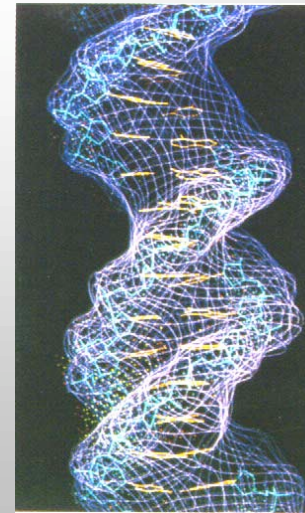
Découverte des virus
(une entorse à la théorie cellulaire ?)



**Tous les êtres vivants
actuels sont composés
des mêmes macromolécules**



**Ils ont une histoire commune
nous descendons tous
d'un même ancêtre**



ADN

La définition de la cellule Procaryote par Chatton (1937)

- Le microbiologiste français Édouard Chatton met en évidence des différences fondamentales entre les cellules bactériennes et des autres org...

=> Il propose de diviser le monde vivant selon ces 2 types cellulaires

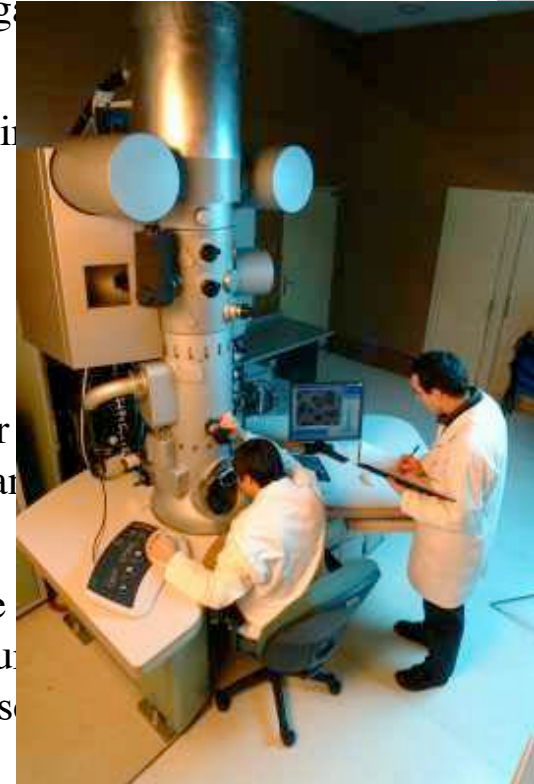
PROCARYOTES et **EUCARYOTES**

- **Procaryotes** = organismes à cellules sans noyau
- **Eucaryotes** = organismes à cellules avec noyau

- D'un point de vue évolutif, le terme **Procaryote** implique, parce que la cellule Procaryote, plus simple, s'est mise en place avant

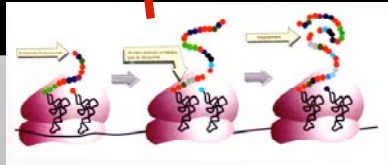
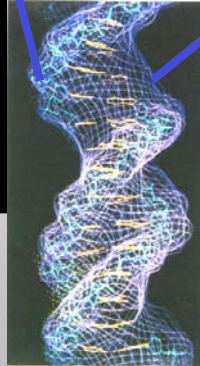
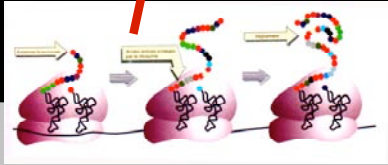
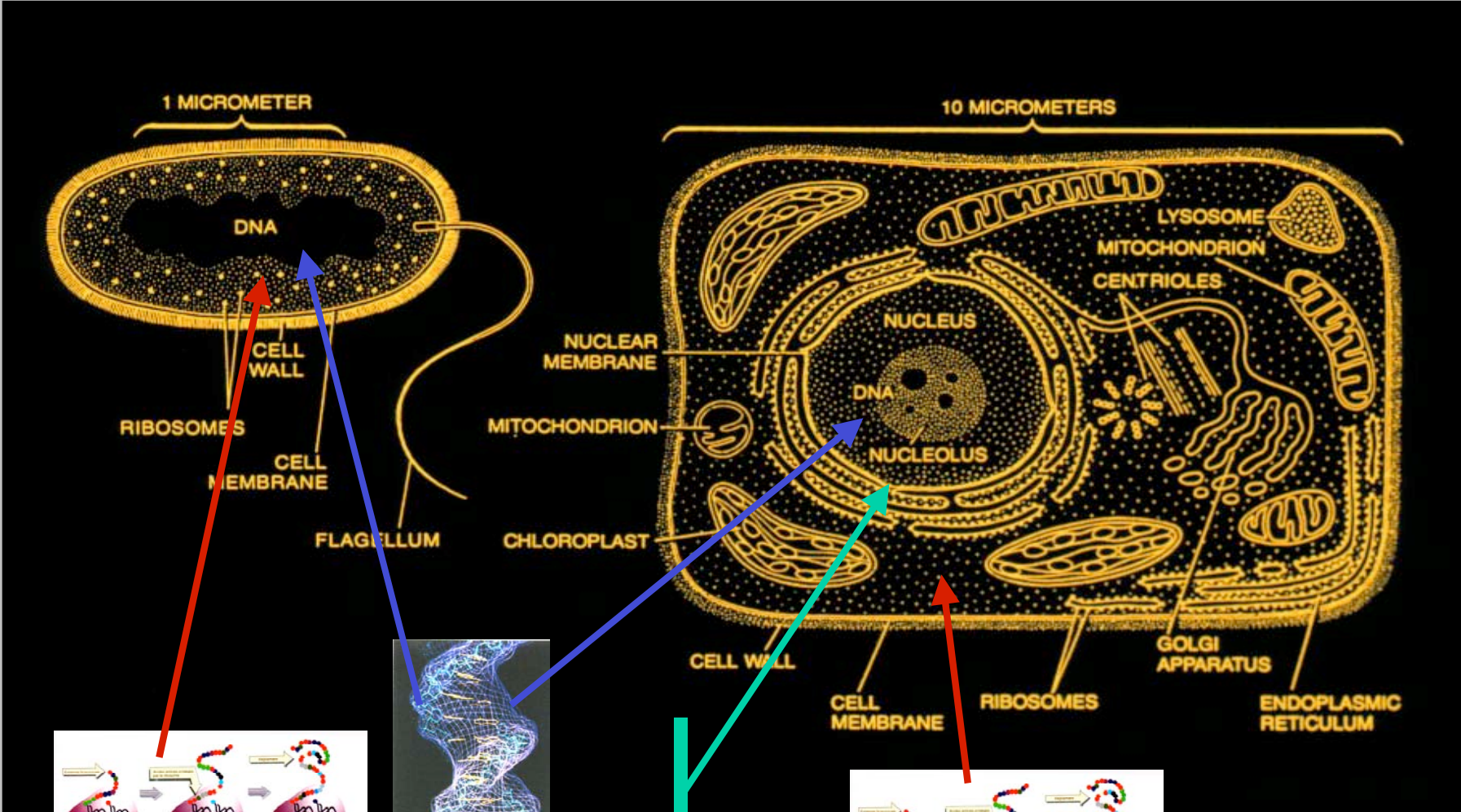
- Cette vision **gradiste** de la construction cellulaire au cours de l'évolution a influencé très profondément les esprits et définit comme un groupe naturel d'organismes **sur la base d'un caractère négatif** qu'est l'absence de

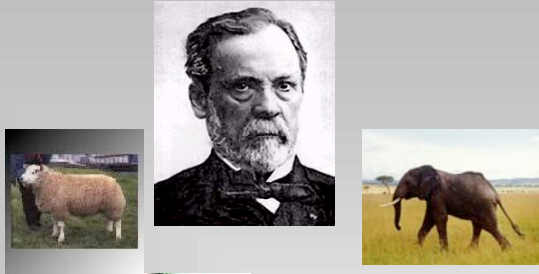
- Ces travaux ne reçoivent pas d'échos dans la communauté scientifique de l'époque et passent inaperçus jusqu'à dans les années 60



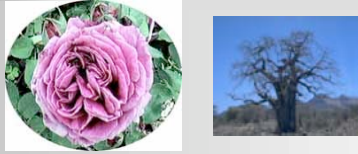
Procaryote

Eucaryote

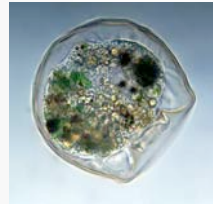




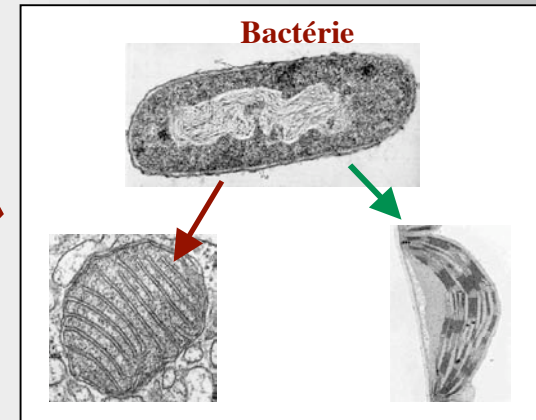
La vision traditionnelle du vivant



Eucaryotes supérieurs



« *Eucaryotes* » *inférieurs*

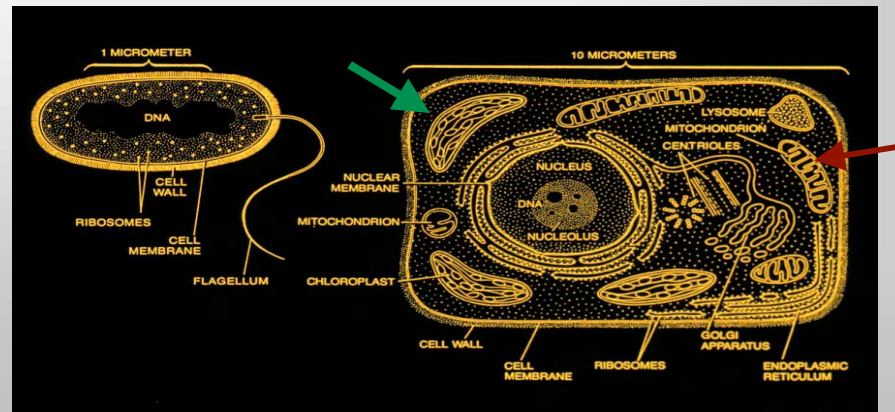
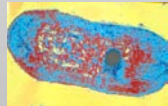
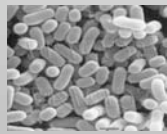
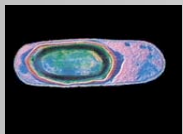


mitochondrie

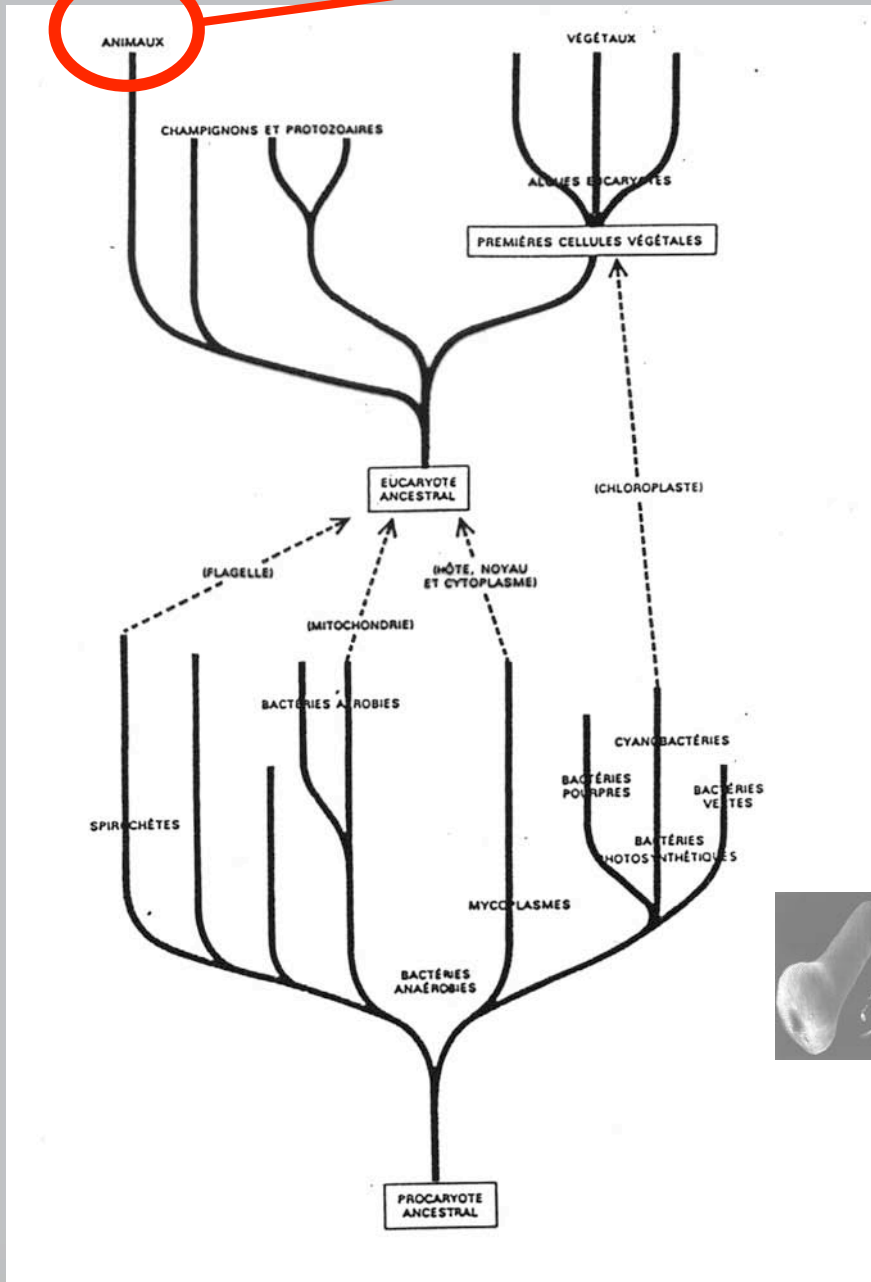
Chloroplaste



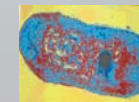
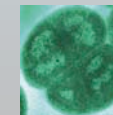
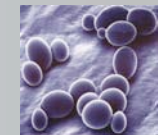
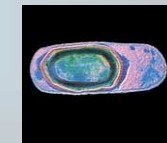
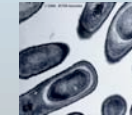
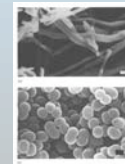
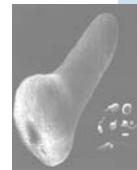
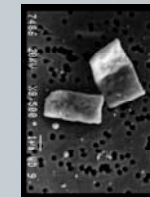
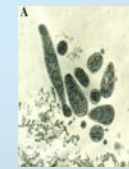
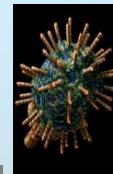
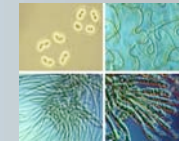
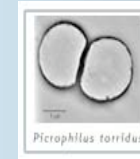
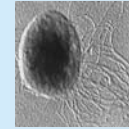
Procaryotes



Homo sapiens

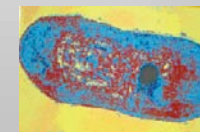
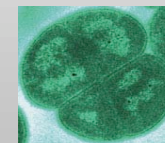
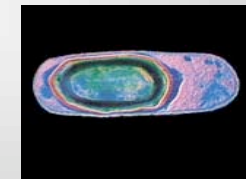
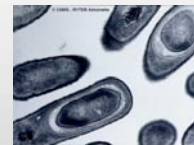
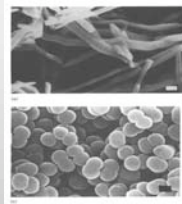
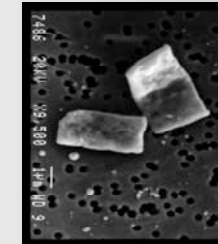
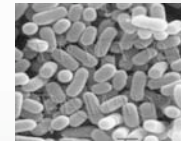
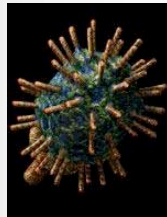
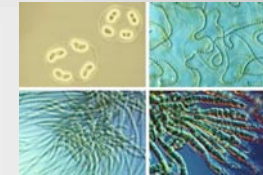
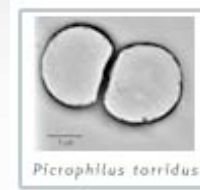


*L'arbre Universel
du vivant
Au début des années 70
La fusée à deux étages !*



?

Comment classer les microorganismes ?



Très peu de caractères homologues
Impossible de les polariser !

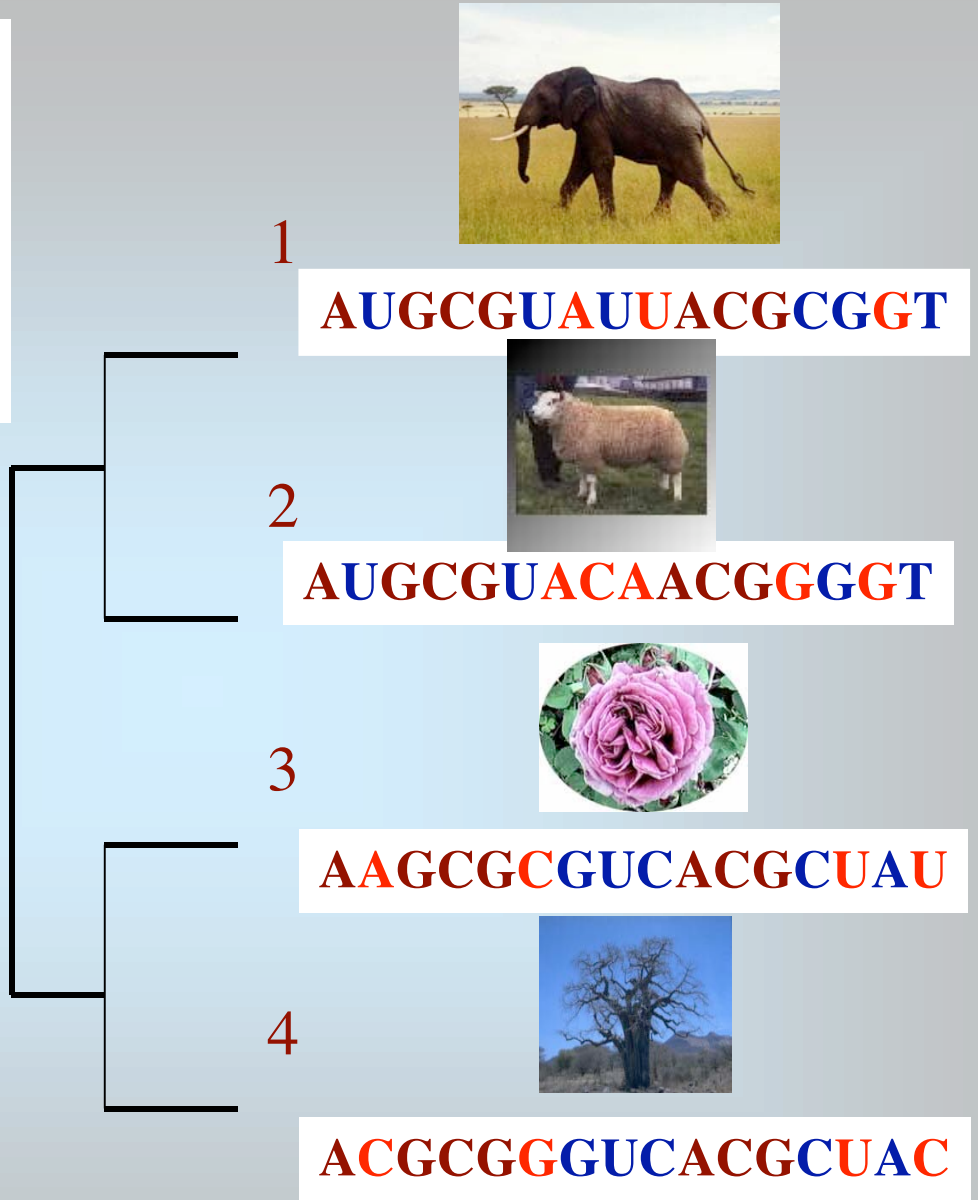
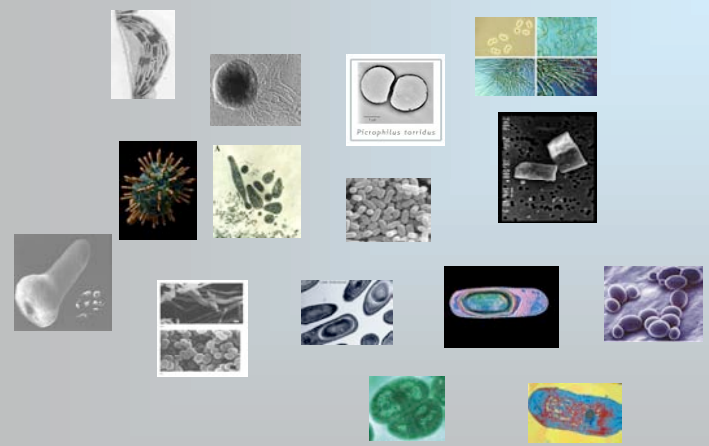
Les macromolécules, témoins de l'évolution

- **1955** : Sanger développe une méthode de séquençage des protéines et séquence l'insuline.
- **1965** : Zuckerkandl et Pauling publient leur article “ Molecules as Documents of Evolutionary History ” qui marque la transition vers l'ère des phylogénies moléculaires



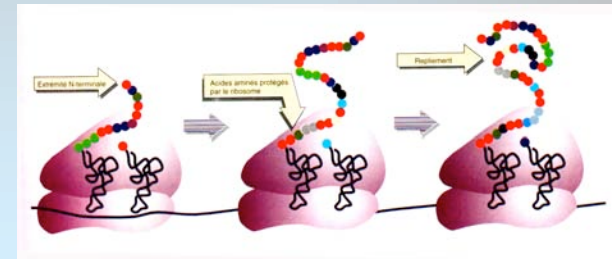
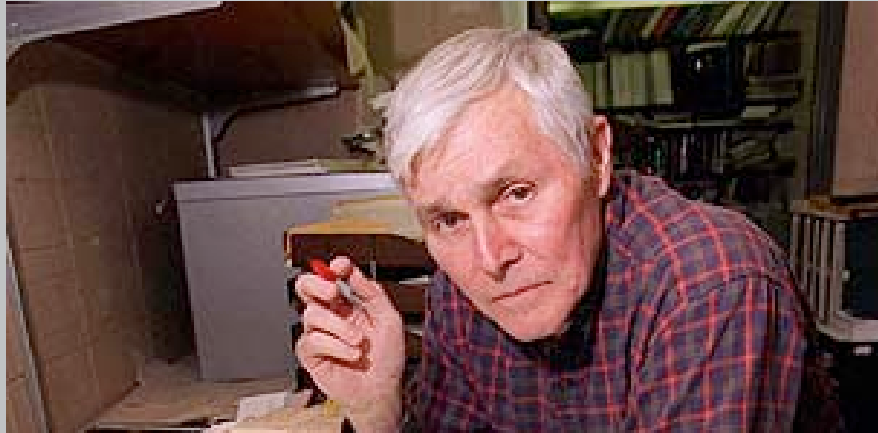
L'idée de comparer les
séquences des
macromolécules
pour retracer l'évolution
date de 1968
(Zuckerland et Pauling)

AUGCGUGUCACGCGAT



Il existe trois types de ribosome sur terre

**Carl Woese
1977**



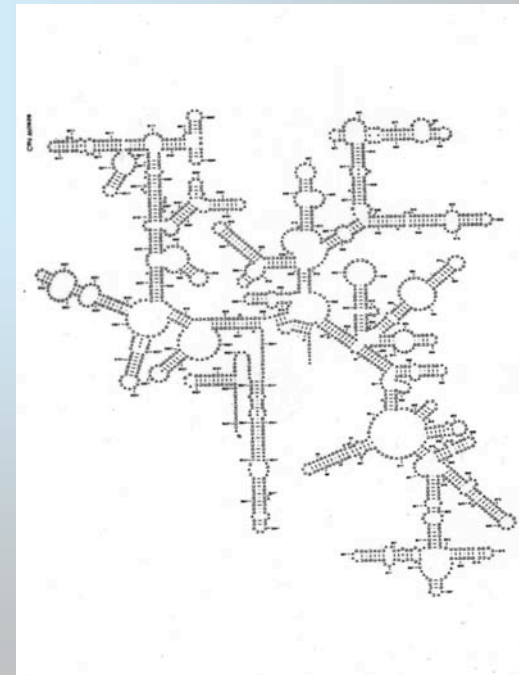
ubiquitaire

*même fonction
chez tous les organismes*

facile à isoler

*riche en information
(comparée au 5S)*

plus facile à étudier que le 23S



Production d'un catalogue d'oligonucléotides digérés par la RNase T1



La Rnase
T1
Coupe
En 3' d'un G

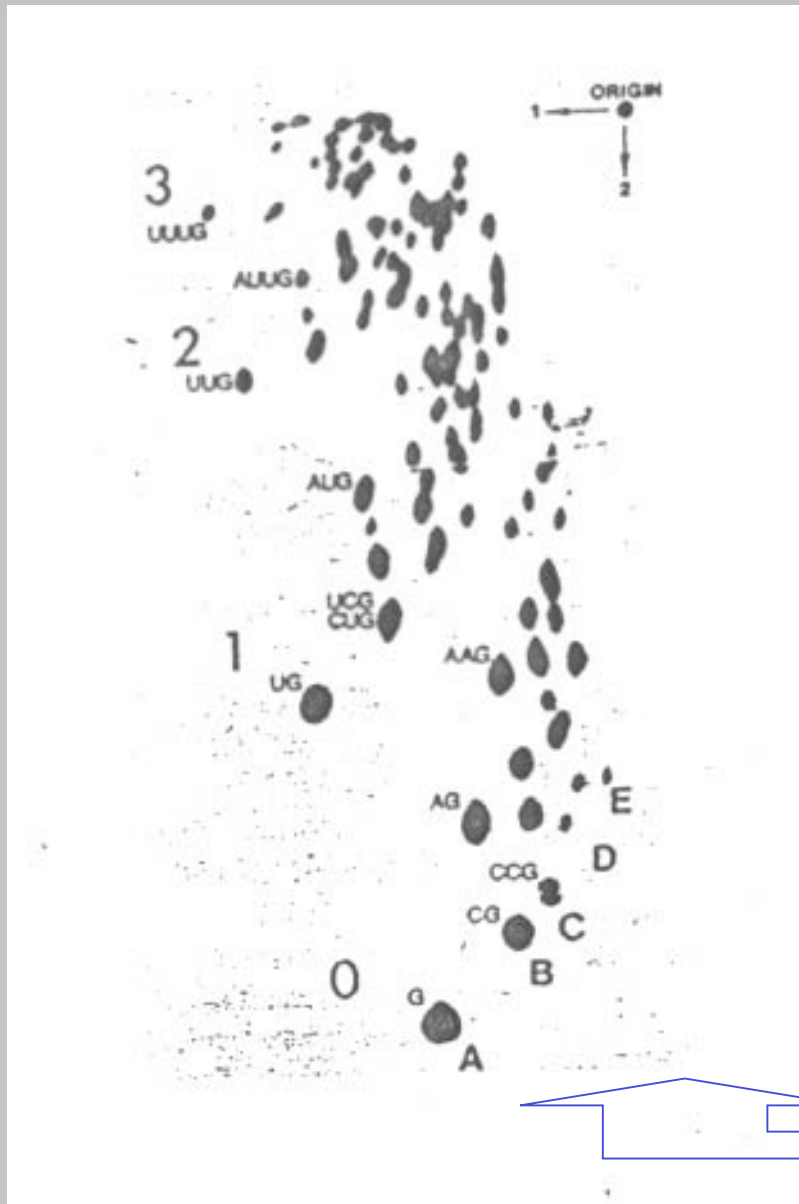
Oligo
 $N \geq 6$

6. CHAQUE NUCLÉOTIDE d'une molécule d'ARN est composé d'une base, d'un sucre, le ribose (S), et d'un groupement phosphate (P). Des enzymes appelées ribonucléases coupent la chaîne en des sites spécifiques. La ribonucléase T₁ la coupe par hydrolyse (insertion d'une molécule d'eau) à l'extrémité 3' du phosphate qui suit chaque nucléotide à guanine (G). Elle partage ainsi une longue molécule d'ARN en un certain nombre de courts fragments; chacun est composé d'un ou plusieurs nucléotides et se termine par la guanine (G).

7. L'EFFET DE LA RIBONUCLEASE T₁ sur un court segment de la molécule 16 S de *E. coli* apparaît ici : lorsque l'ARN 16 S est coupé de cette façon, sa séquence se scinde en fragments (des « mots ») dont la longueur varie d'un nucléotide (une « lettre ») à 20 nucléotides. La séquence des bases de chacun des mots est déterminée très précisément. Les mots de six lettres ou plus sont compilés dans un dictionnaire. La comparaison des dictionnaires des deux organismes se fait par le calcul en fonction du coefficient d'association S_{AB} . Ce coefficient est le rapport entre le double du nombre de lettres dans les mots (de six lettres au minimum) communs aux organismes A et B et le nombre total de lettres dans tous ces mots dans A et dans B.

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Marquage des cellules au P32



Isolement des ribosomes



Isolement des ARN ribosomiques



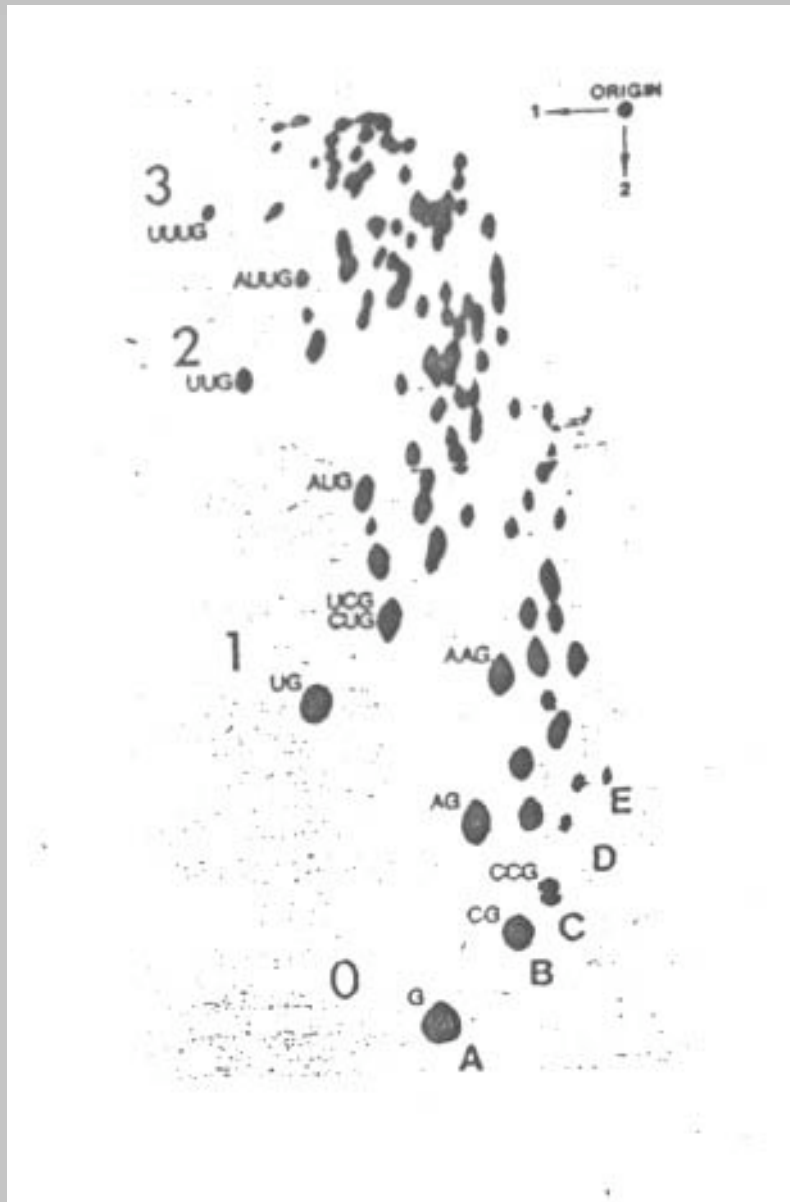
Isolement de l'ARN 16S



Digestion par la RNase T1



Autoradiographie



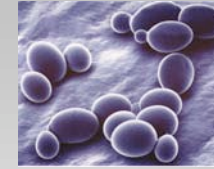
**Na = Nombre d 'oligo
dans le catalogue
De l'espèce a**

**Nb = Nombre d 'oligo
dans le catalogue
De l'espèce b**

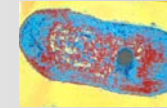
**Nab = Nombre d 'oligo
Commun aux catalogues
des espèces a et b**

$$\mathbf{S_{ab} = 2N_{ab}/N_a + N_b}$$

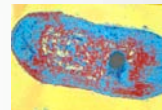
Homme-levure de bière 0.33



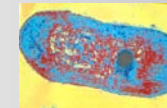
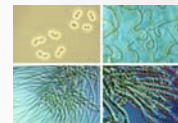
Homme-Colibacille 0.06



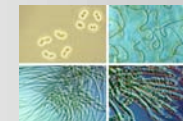
Levure de bière-Colibacille 0.05



Cyanobactérie-Colibacille 0.26



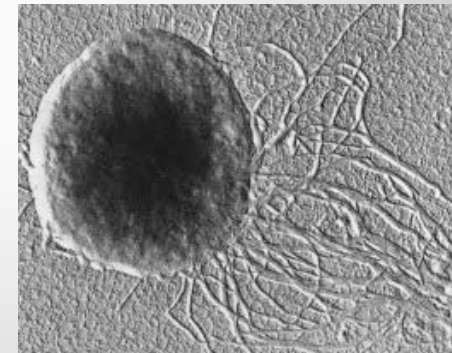
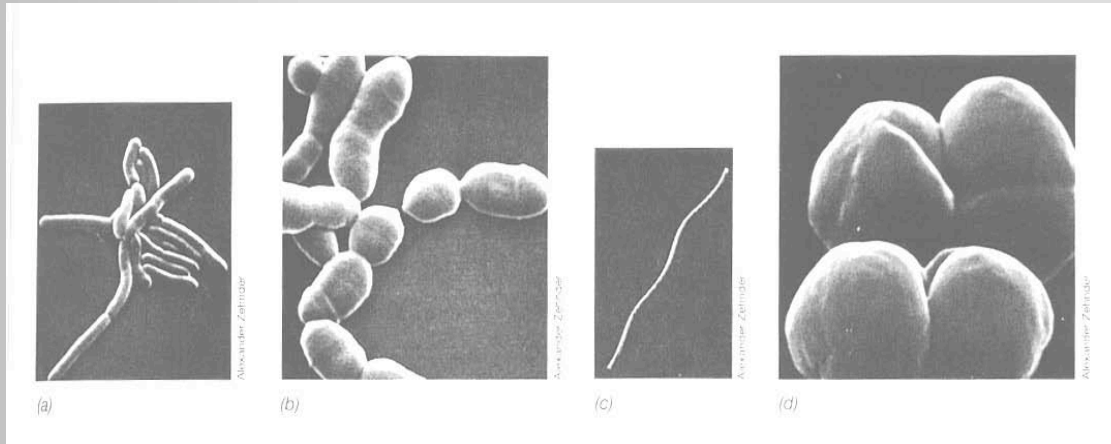
Cyanobactérie-Chloroplaste 0.31



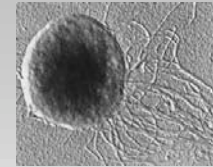
Plante-Chloroplaste 0.09



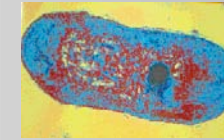
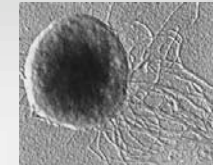
Comment classer les « bactéries » méthanogènes ?



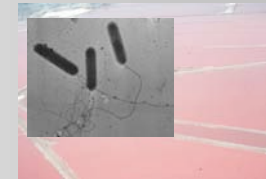
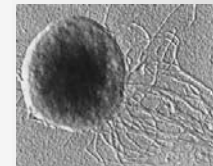
Méthanogène-Homme 0.05



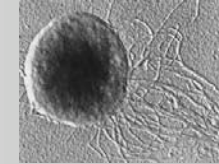
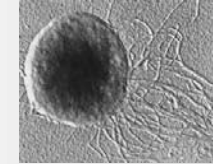
Méthanogène-Colibacille 0.06



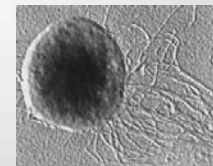
Méthanogène- Halobacterium 0.19



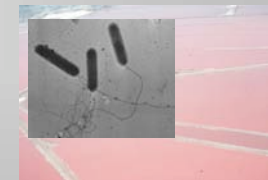
Méthanogène 1-Méthanogène 2 0.25



Méthanogène-Sulfolobus 0.13



Halobacterium-Sulfolobus 0.15



Phylogenetic structure of the prokaryotic domain: The primary kingdoms

(archaebacteria/eubacteria/urkaryote/16S ribosomal RNA/molecular phylogeny)

CARL R. WOESE AND GEORGE E. FOX*

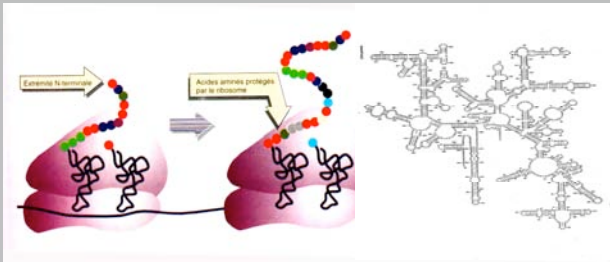
Department of Genetics and Development, University of Illinois, Urbana, Illinois 61801

Communicated by T. M. Sonneborn, August 18, 1977

ABSTRACT A phylogenetic analysis based upon ribosomal RNA sequence characterization reveals that living systems represent one of three aboriginal lines of descent: (i) the eubacteria, comprising all typical bacteria; (ii) the archaebacteria, containing methanogenic bacteria; and (iii) the urkaryotes, now represented in the cytoplasmic component of eukaryotic cells.

to construct phylogenetic classifications between domains; Prokaryotic kingdoms are not comparable to eukaryotic ones. This should be recognized by an appropriate terminology. The highest phylogenetic unit in the prokaryotic domain we think should be called an "urkingdom"—or perhaps "primary kingdom." This would recognize the qualitative distinction between prokaryotic and eukaryotic kingdoms and emphasize

« *the archaebacteria, containing methanogenic bacteria* »



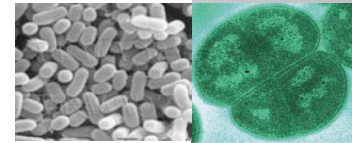
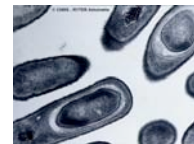
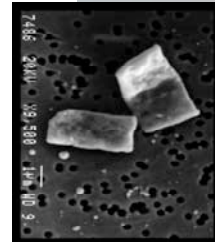
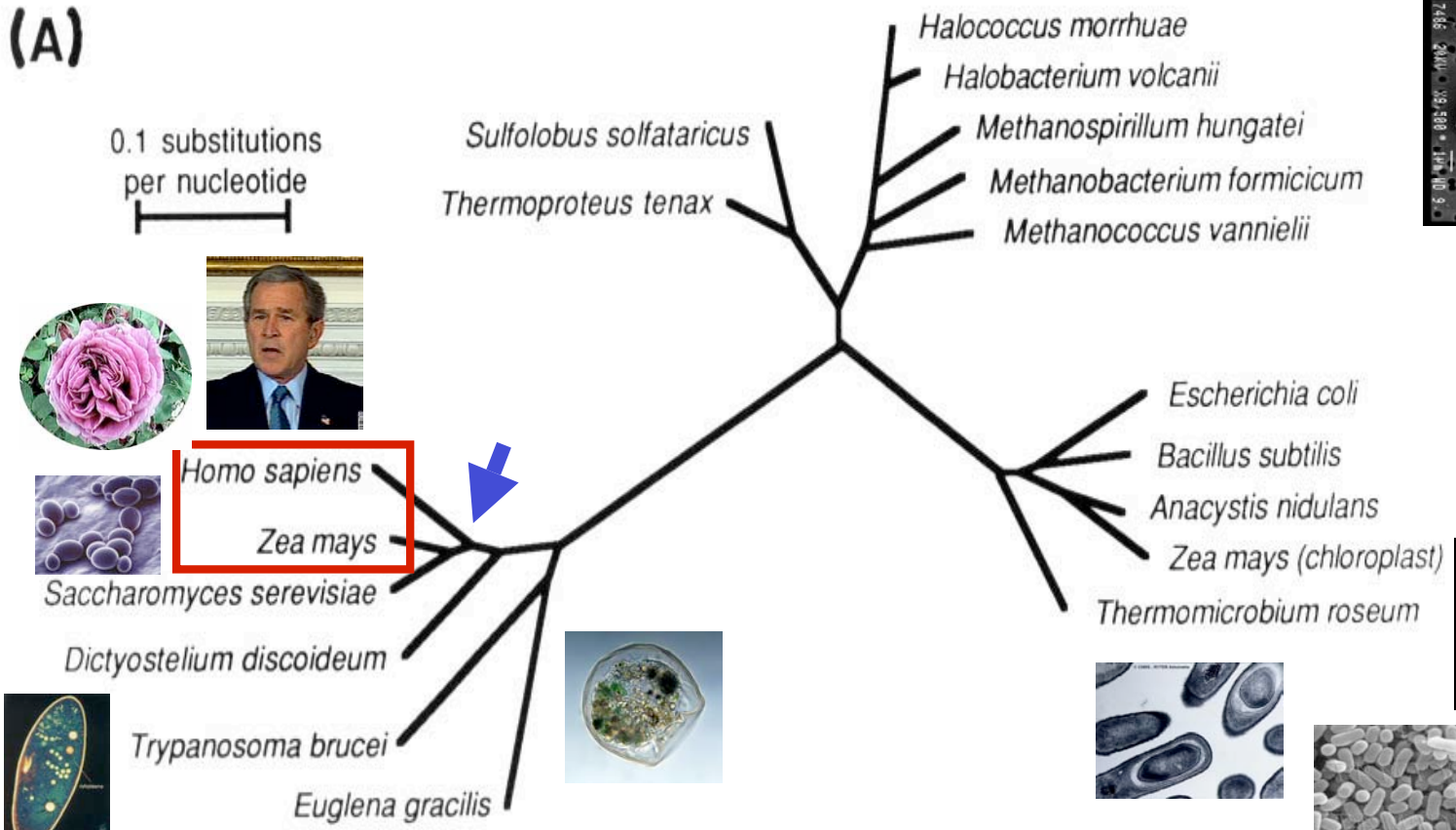
ARN16S



Archaea

(A)

0.1 substitutions per nucleotide

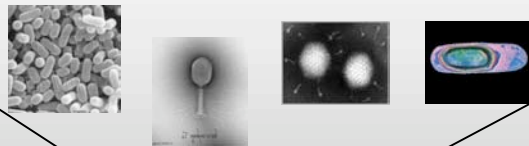


Eucaryotes

Bacteria

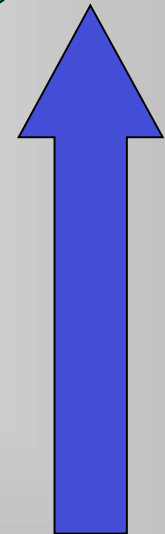


Macro-organismes



Micro-organismes

3-4 milliard d'années



Bacteries/Eucaryotes

Archaea

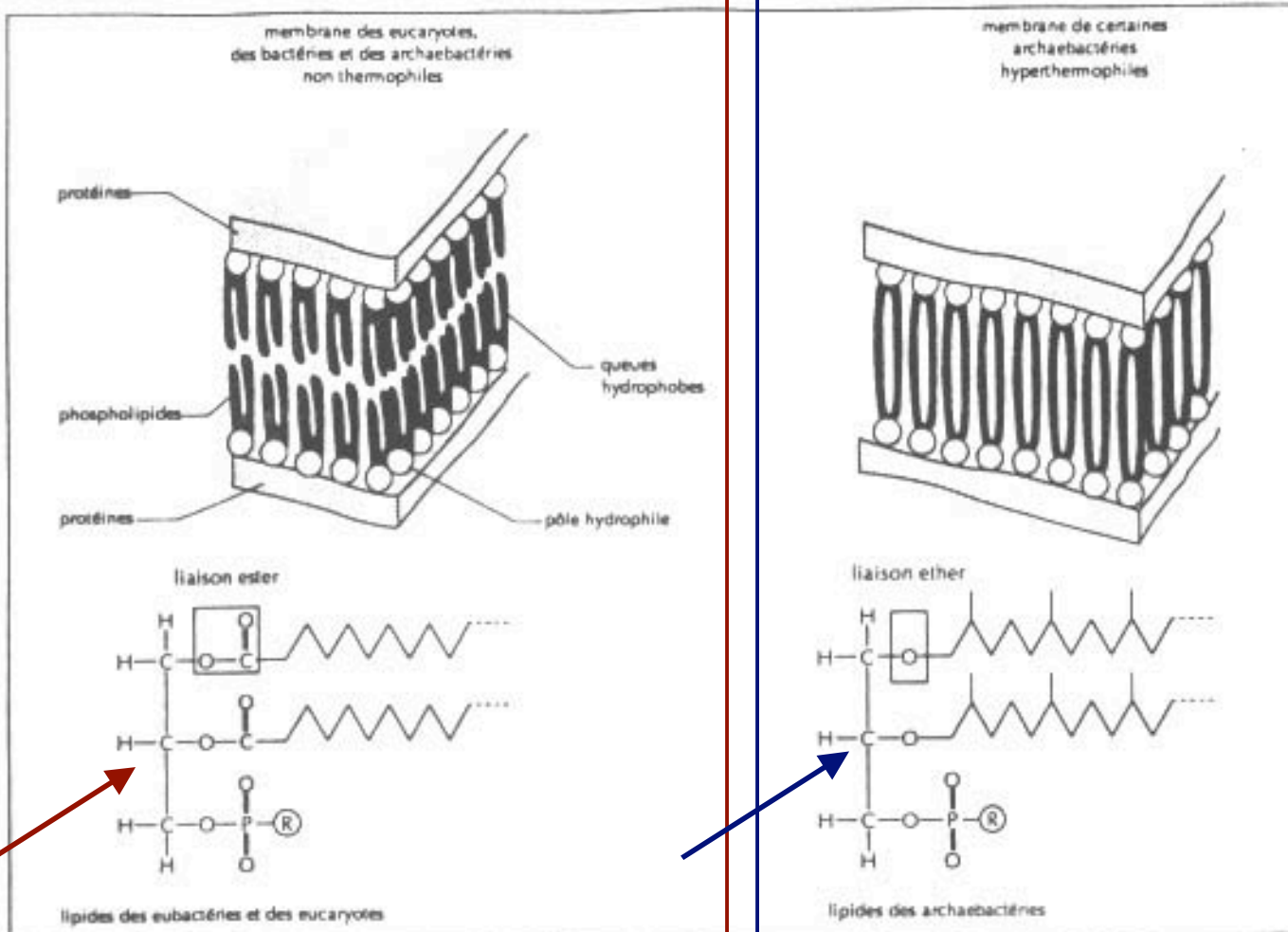
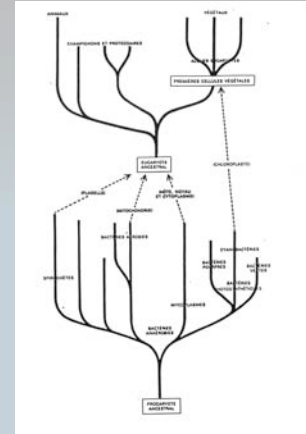
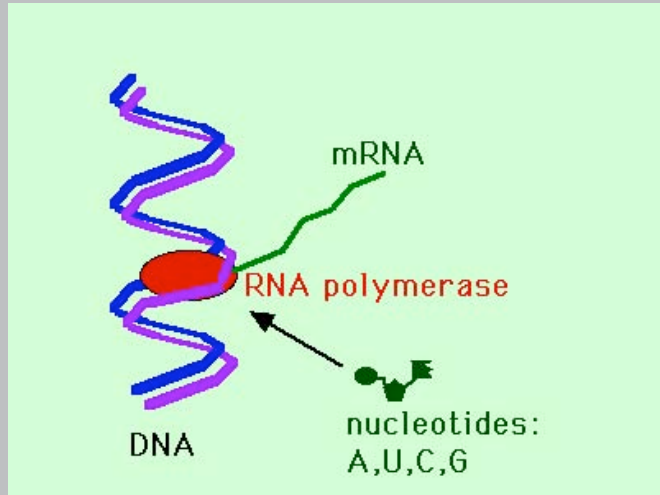


Figure 4 : Les lipides des archaebactéries comparés aux lipides des eubactéries et des eucaryotes.

D

L

Transcription

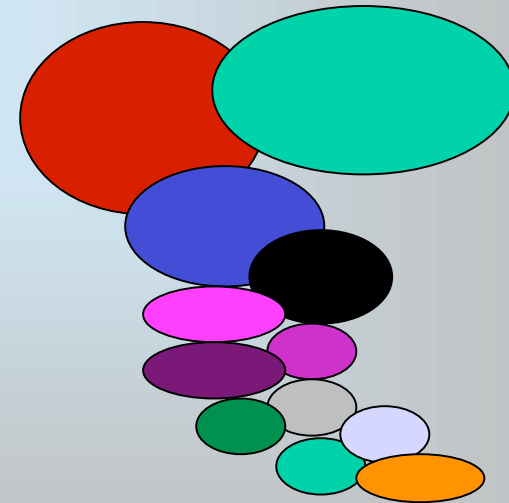
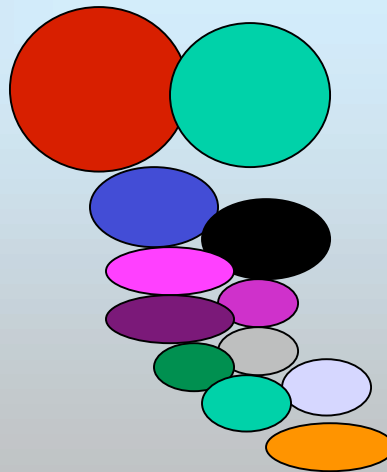
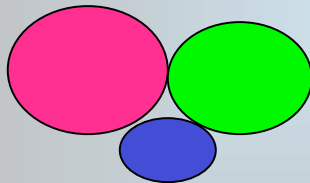
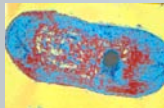
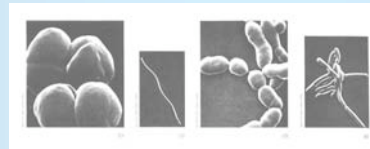


Eucarya

Archaea



Bacteria



1990 Article « Toward a natural system of organisms: Proposal for the domains Archaea, Bacteria, and Eucarya. *Woese CR, Kandler O, Wheelis ML*, *Proc Natl Acad Sci U S A*. 1990, 87:4576-9

4578 Evolution: Woese *et al.*

Proc. Natl. Acad. Sci. USA 87 (1990)

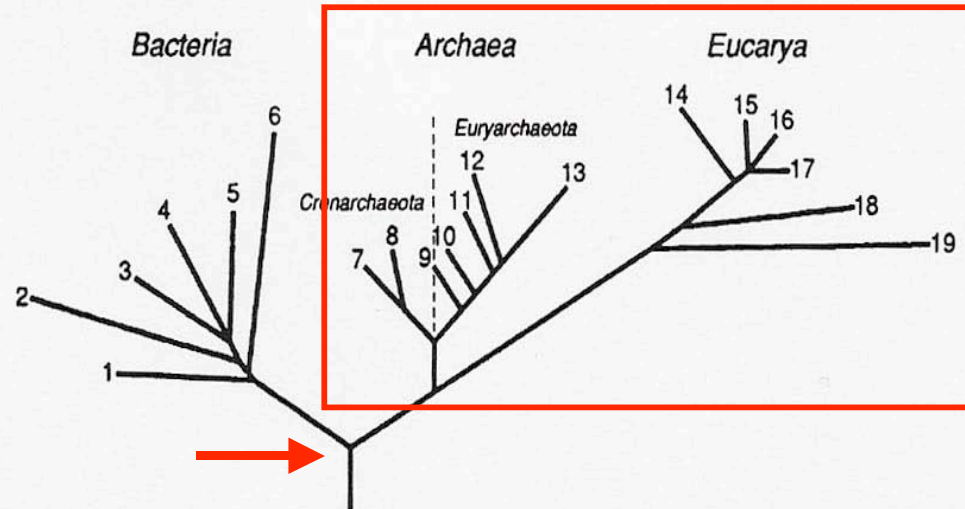
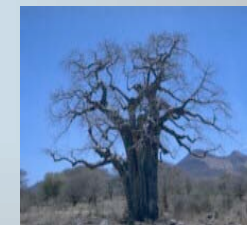
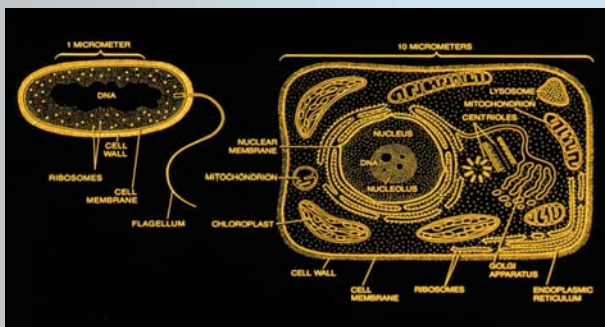
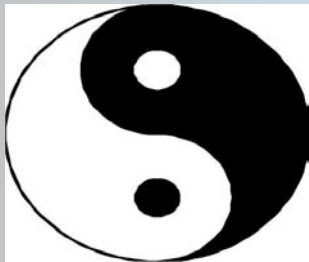


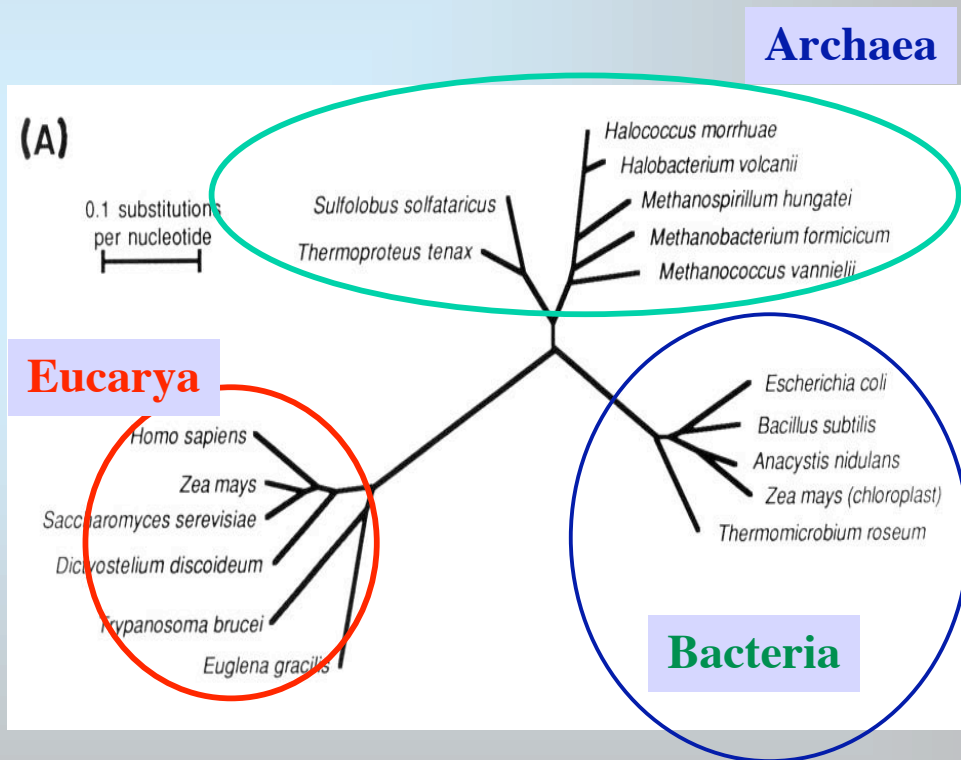
FIG. 1. Universal phylogenetic tree in rooted form, showing the three domains. Branching order and branch lengths are based upon rRNA sequence comparisons (and have been taken from figure 4 of ref. 2). The position of the root was determined by comparing (the few known) sequences of pairs of paralogous genes that diverged from each other before the three primary lineages emerged from their common ancestral condition (27). [This rooting strategy (28) in effect uses the one set of (aboriginally duplicated) genes as an outgroup for the other.] The numbers on the branch tips correspond to the following groups of organisms (2). Bacteria: 1, the Thermotogales; 2, the flavobacteria and relatives; 3, the cyanobacteria; 4, the purple bacteria; 5, the Gram-positive bacteria; and 6, the green nonsulfur bacteria. Archae: the kingdom Crenarchaeota: 7, the genus *Pyrodictium*; and 8, the genus *Thermoproteus*; and the kingdom Euryarchaeota: 9, the Thermococcales; 10, the Methanococcales; 11, the Methanobacteriales; 12, the Methanomicrobiales; and 13, the extreme halophiles. Eucarya: 14, the animals; 15, the ciliates; 16, the green plants; 17, the fungi; 18, the flagellates; and 19, the microsporidia.

En 2003, il reçoit le prix Craaford à Stockholm



**Le concept des trois domaines
et l'abandon de la dichotomie eucaryote/procaryote
ne sont pas encore accepté par tous les biologistes
*soit dans la théorie, soit dans la pratique***

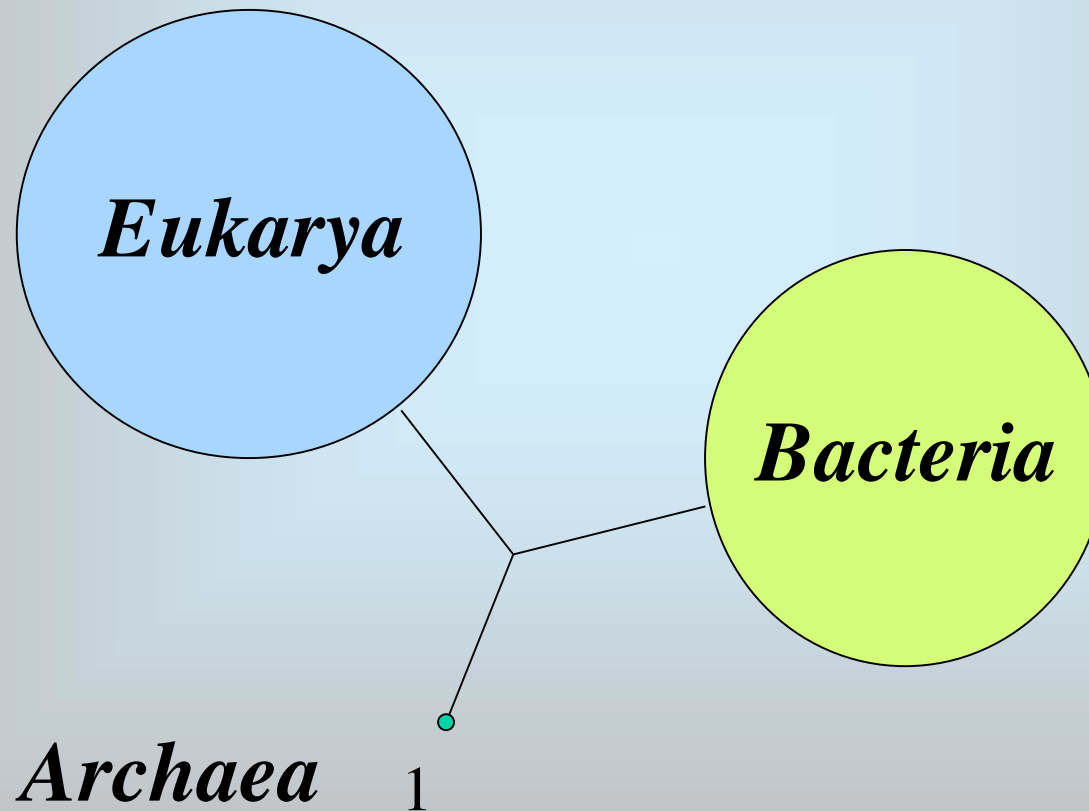






INSTITUT PASTEUR

L 'arbre universel du vivant à l'Institut Pasteur





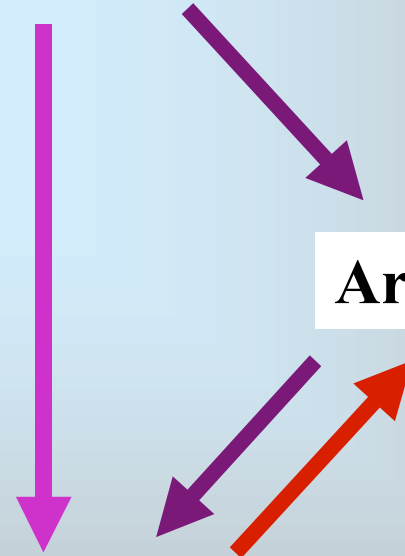
Ce qui est vrai pour le colibacille est vrai pour l'éléphant (Jacques Monod)



Bacteries

Archaea

Eucaryotes

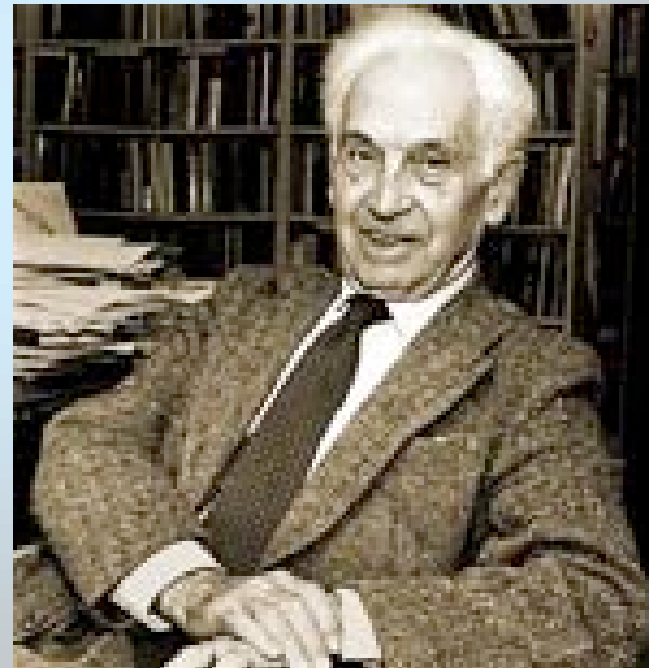


**Un petit nombre d'évolutionnistes Anglo-Saxon veulent
maintenir la dichotomie eucaryote/procaryote
(Lynn Margulis, Tom Cavalier-Smith, Ernst Mayr)
Gradisme**

1998: controverse avec Ernst Mayr (PNAS)



Carl R. Woese

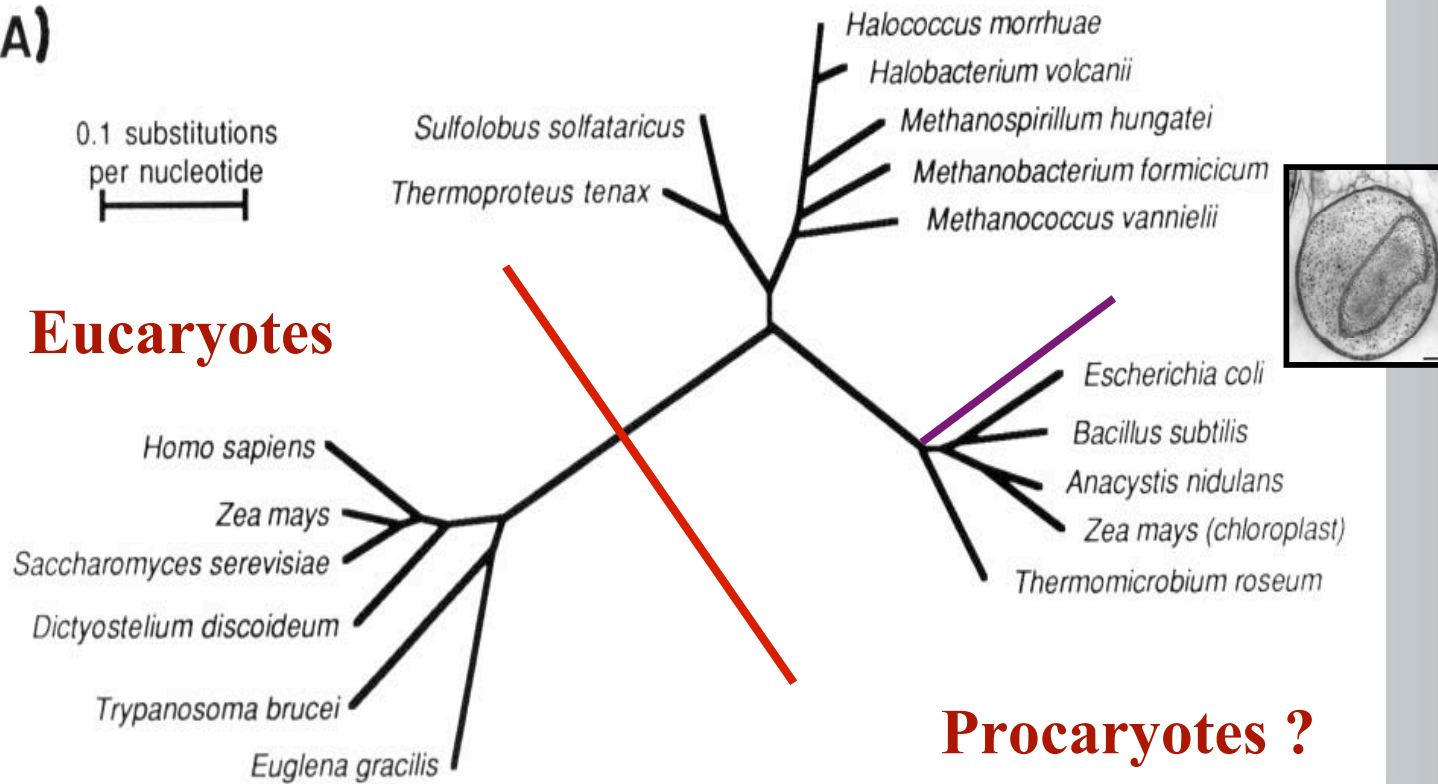


Ernst Mayr

Peut-on en finir une fois pour toute avec la distinction procaryote/eucaryote ?

(A)

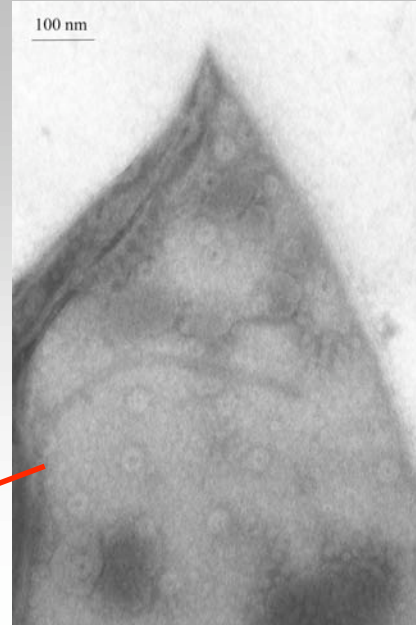
0.1 substitutions
per nucleotide



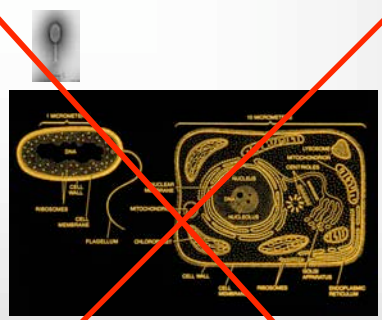
Eucaryotes

Procaryotes ?

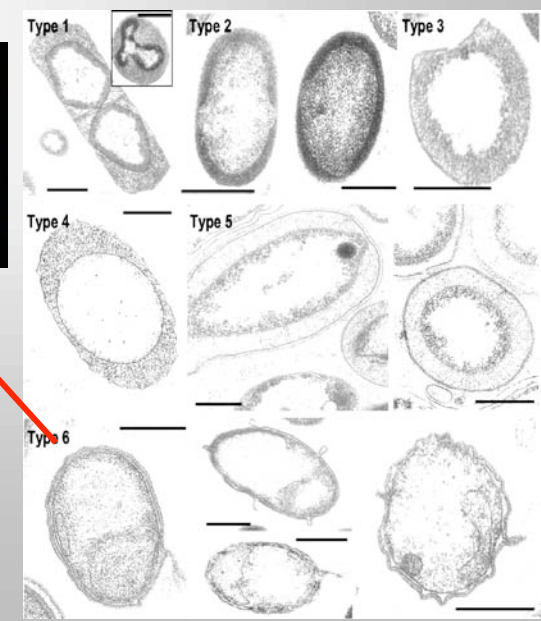
Gemmata obscuriglobus
Une bactérie eucaryote ?



John Fuerst
(Australie)



Cell compartmentalization
in symbionts from
***Aplysina aerophoba* sponge**



L'arbre de Woese : Cladisme ou Gradisme ?

4578 Evolution: Woese *et al.*

Proc. Natl. Acad. Sci. USA 87 (1990)

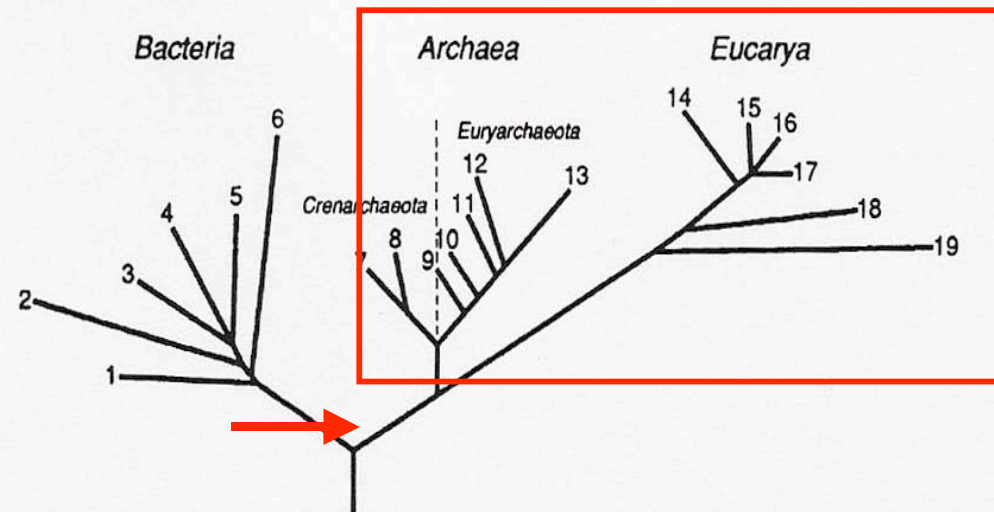
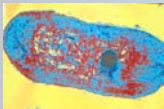


FIG. 1. Universal phylogenetic tree in rooted form, showing the three domains. Branching order and branch lengths are based upon rRNA sequence comparisons (and have been taken from figure 4 of ref. 2). The position of the root was determined by comparing (the few known) sequences of pairs of paralogous genes that diverged from each other before the three primary lineages emerged from their common ancestral condition (27). [This rooting strategy (28) in effect uses the one set of (aboriginally duplicated) genes as an outgroup for the other.] The numbers on the branch tips correspond to the following groups of organisms (2). Bacteria: 1, the Thermotogales; 2, the flavobacteria and relatives; 3, the cyanobacteria; 4, the purple bacteria; 5, the Gram-positive bacteria; and 6, the green nonsulfur bacteria. Archae: the kingdom Crenarchaeota: 7, the genus *Pyrodictium*; and 8, the genus *Thermoproteus*; and the kingdom Euryarchaeota: 9, the Thermococcales; 10, the Methanococcales; 11, the Methanobacteriales; 12, the Methanomicrobiales; and 13, the extreme halophiles. Eucarya: 14, the animals; 15, the ciliates; 16, the green plants; 17, the fungi; 18, the flagellates; and 19, the microsporidia.

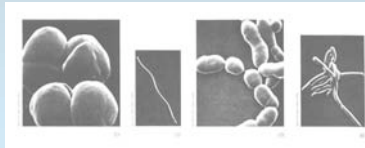
Le retour du gradisme

The Darwinian threshold (Woese, 2000)

Bactéries



Archées

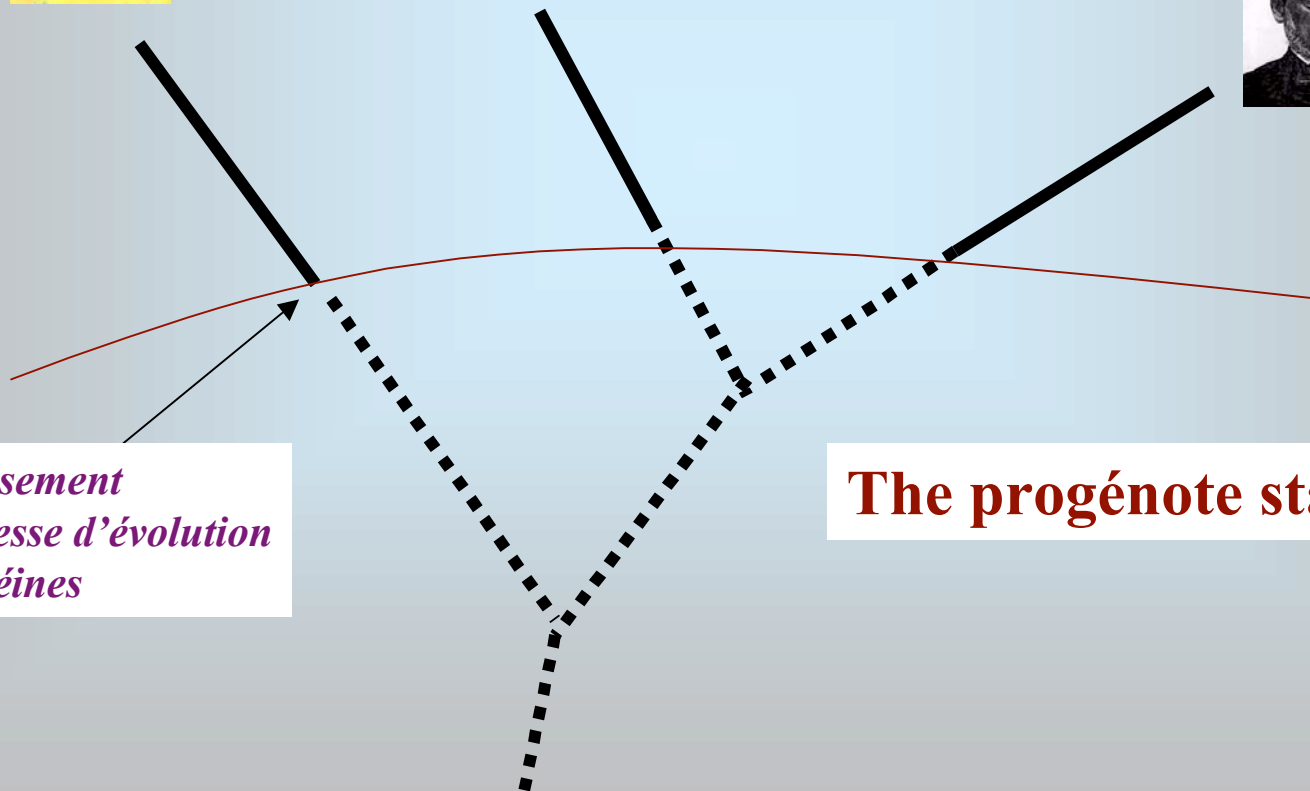


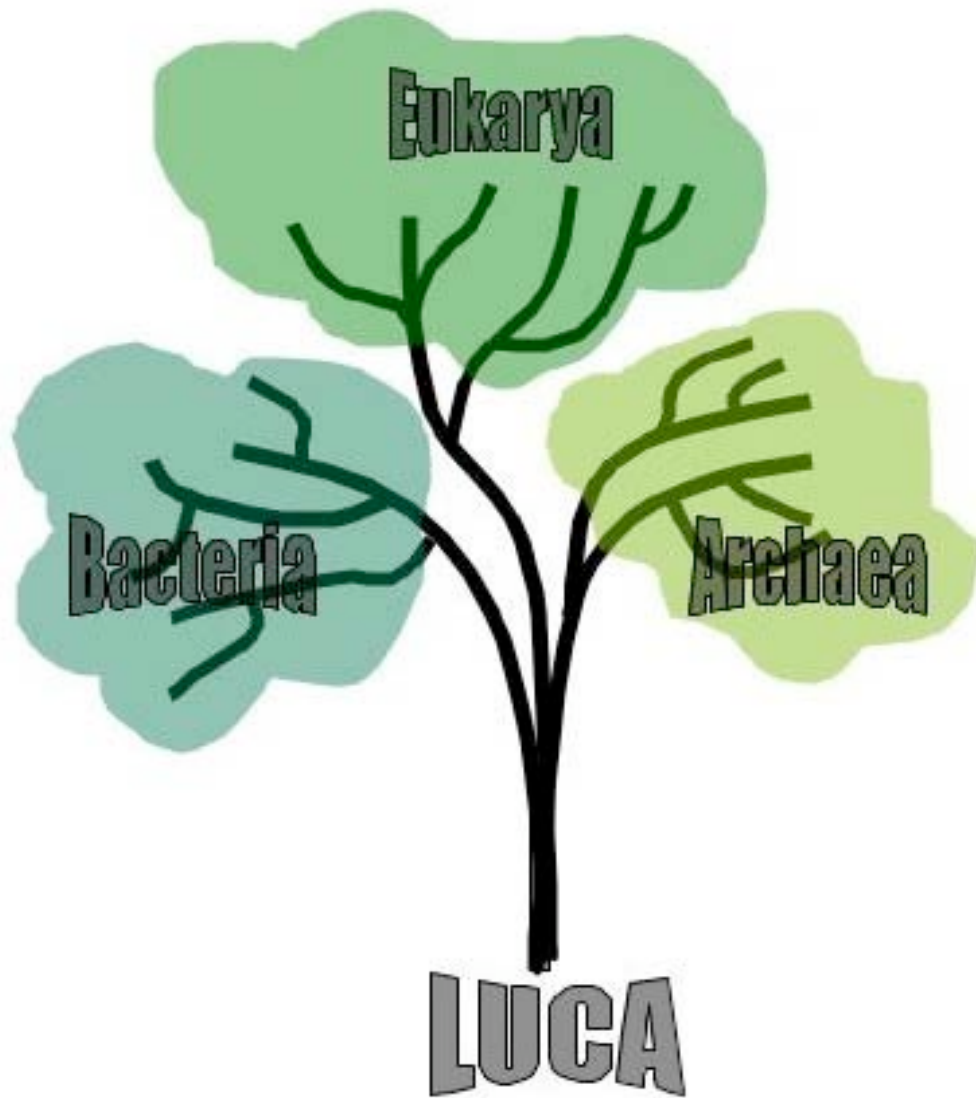
Eucarya



*Ralentissement
de la vitesse d'évolution
des protéines*

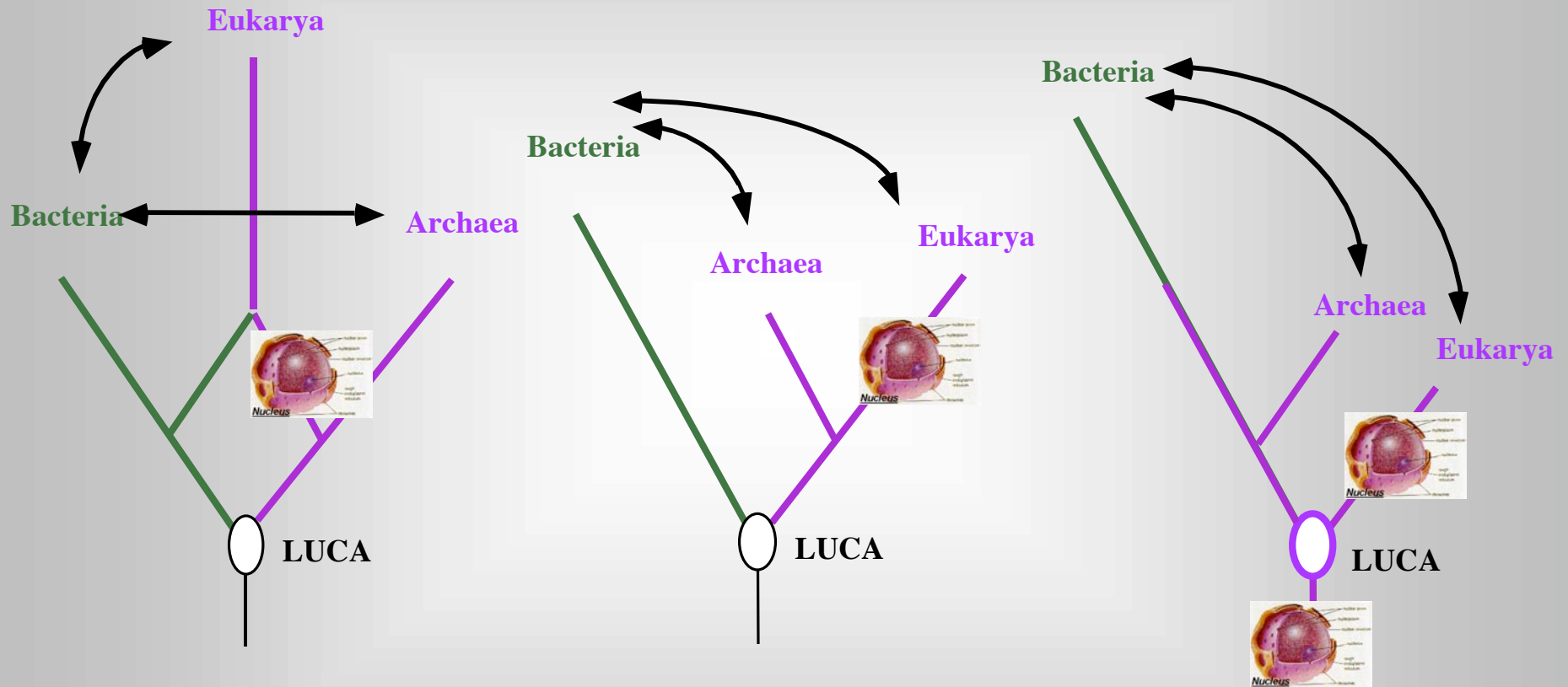
The progénote stage



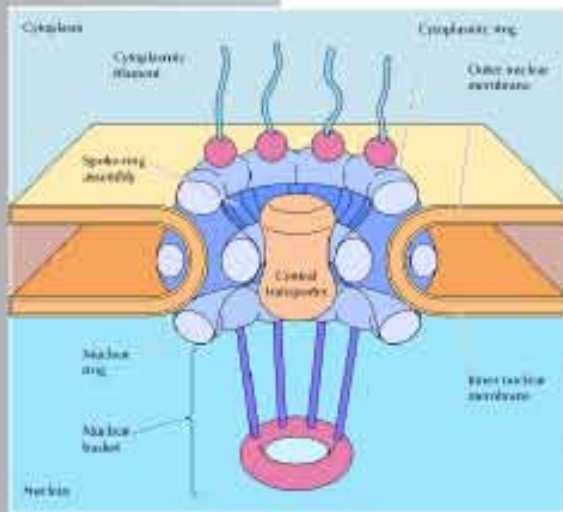
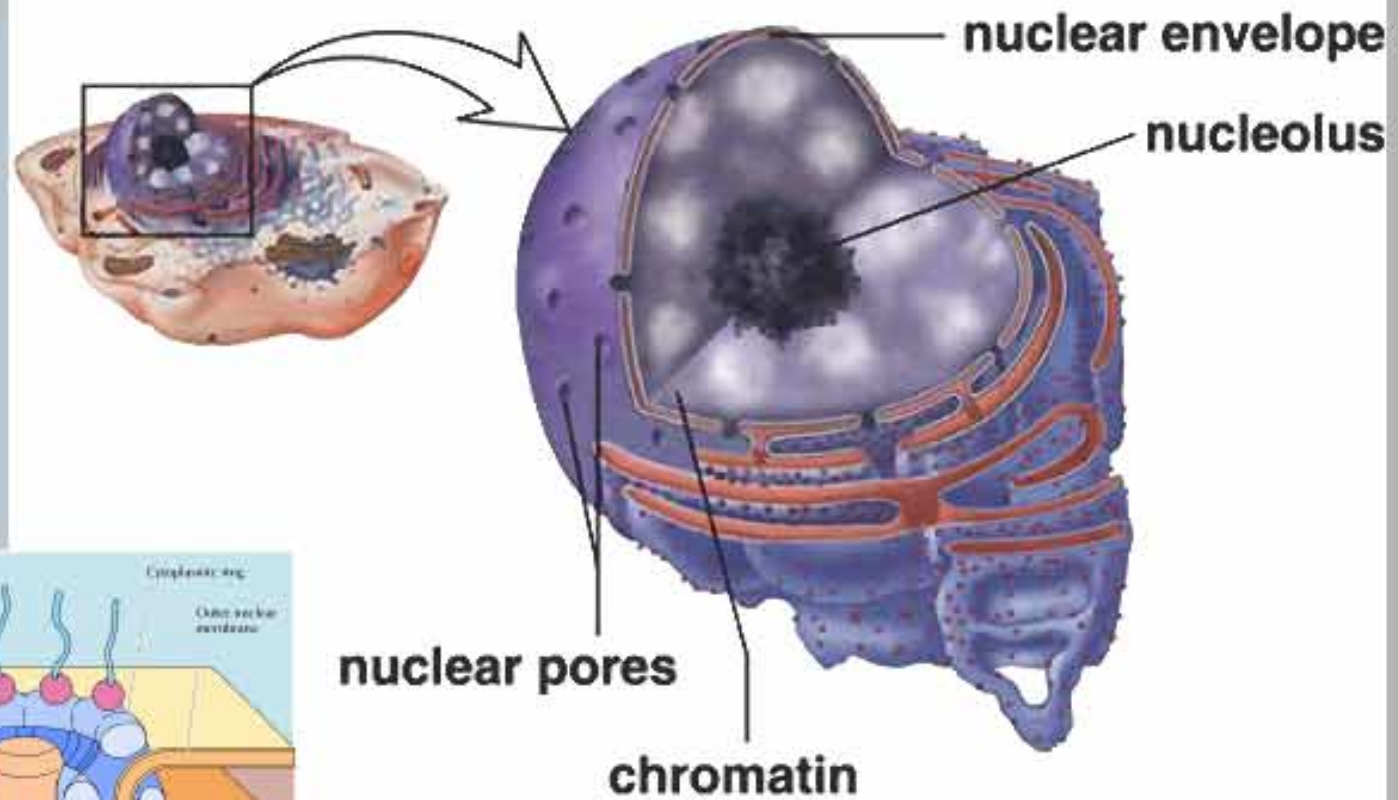


LUCA :
the
Last
Universal
Common
Ancestor

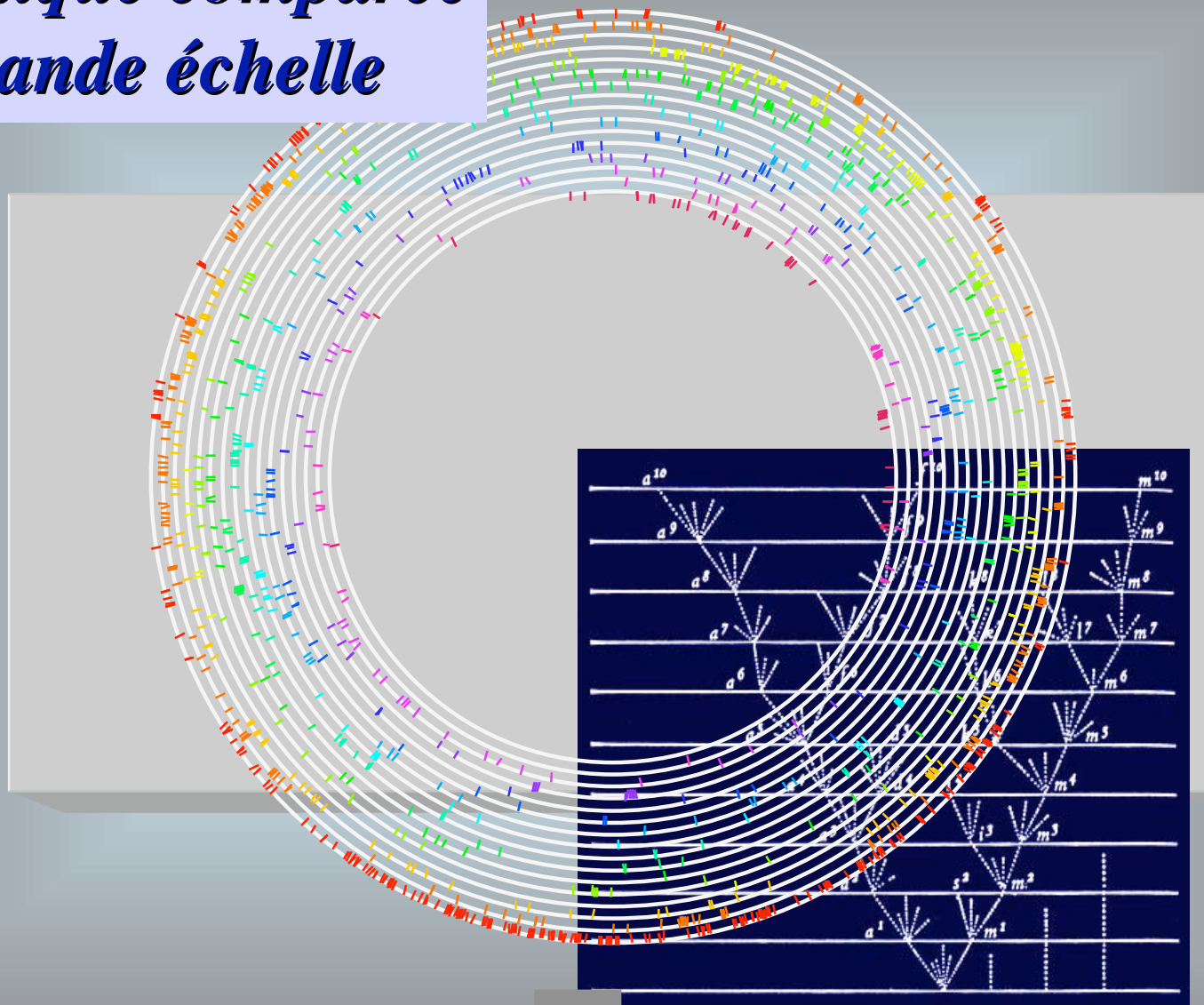
Three possible models for the Universal Tree of life



————— Informational proteins



Génomique comparée à grande échelle



La révolution génomique

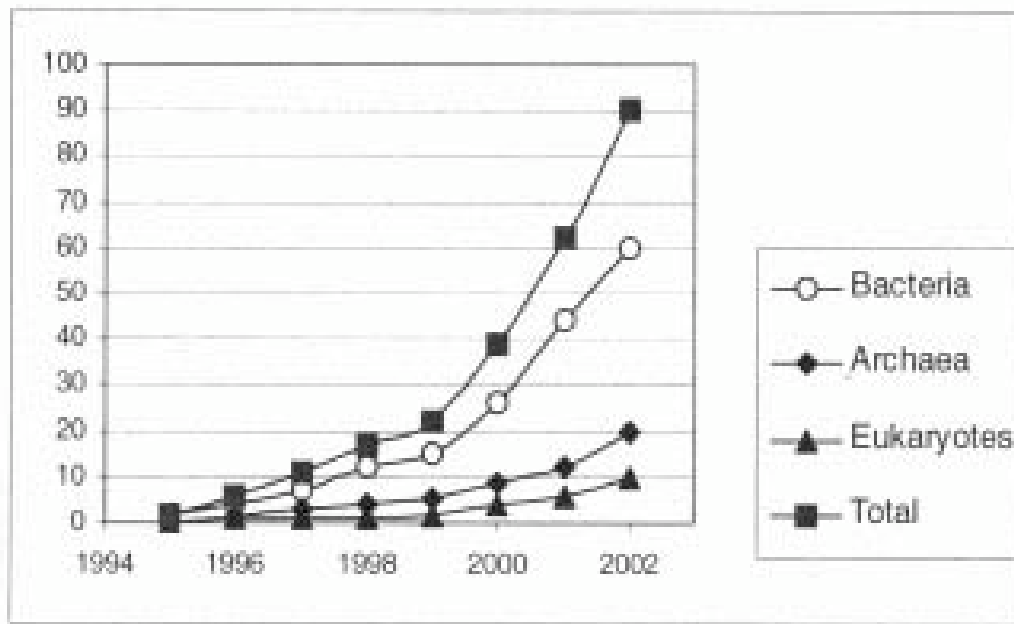


Figure 1.1. Growth of the number of completely sequenced genomes. The data are from Table 1.4. The 2002 figure is extrapolated from the 5-month results.



Les protéines universelles : sans doute héritées de LUCA

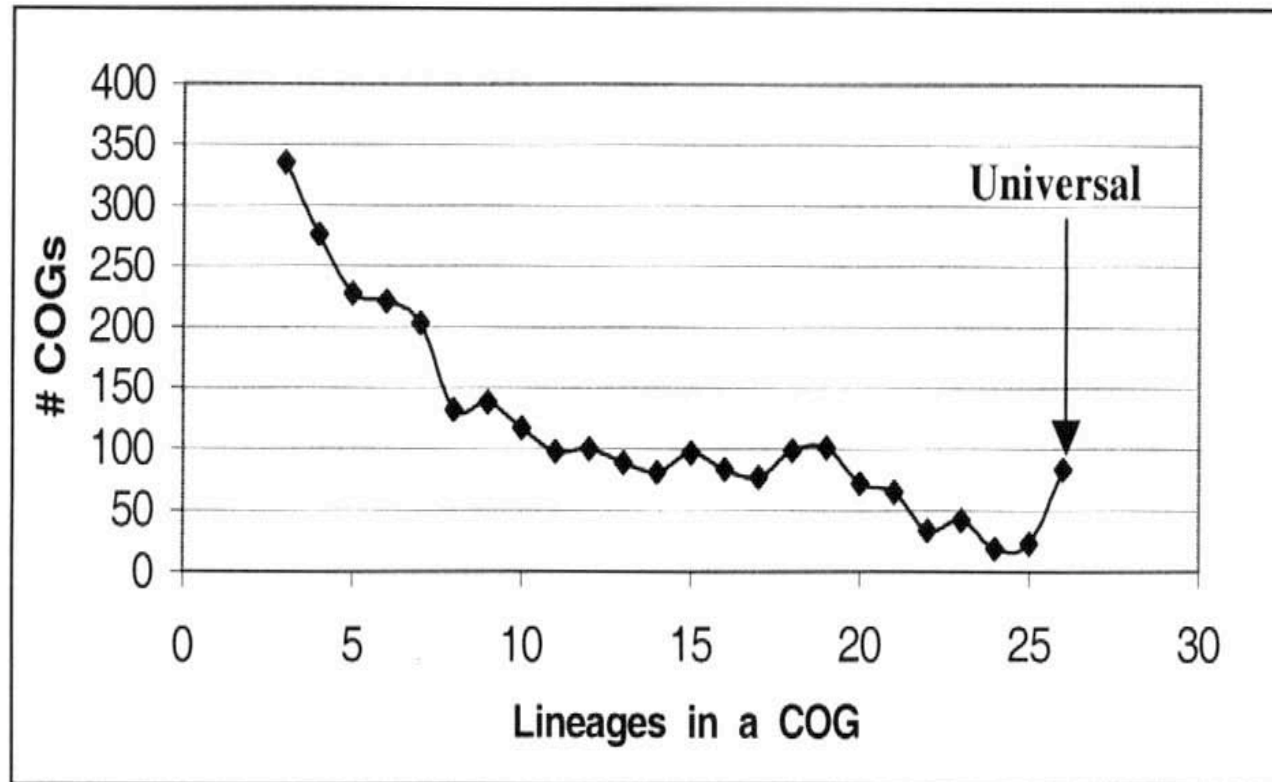


Figure 2.8. Distribution of different phylogenetic lineages in the COG database. The plot shows the number of protein families (COGs) in a release of the COG database (♦3.4), which included proteins from the given number of phylogenetic lineages out of the total of 26 lineages [827].



Eugene Koonin
(NCBI)

Les 60-100 protéines Universelles

30-40 protéines ribosomales
des amino-acyl tRNA synthétase **Synthèse des protéines**
Facteurs d'élongation

Facteurs impliqués dans le localisation des protéines
membranaires **LUCA avait une membrane**

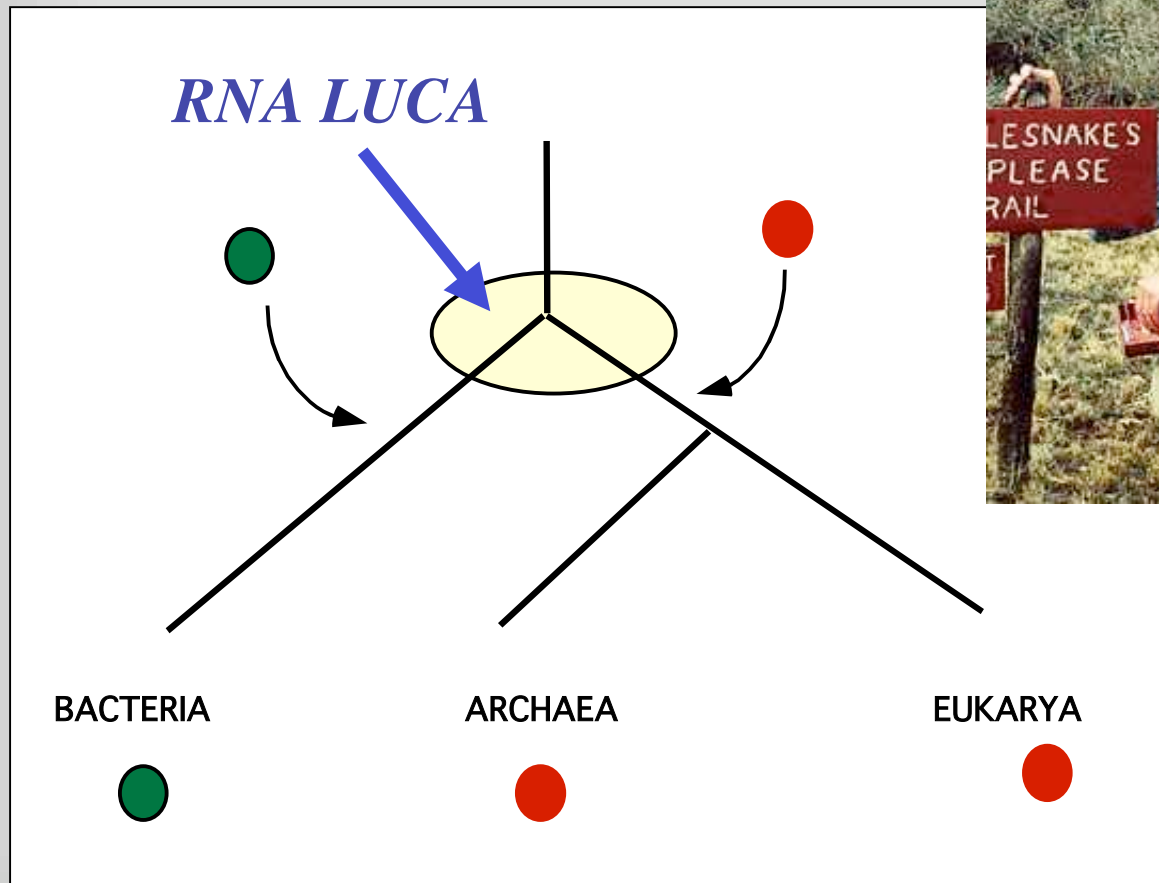
ATP synthétases

ARN polymérases
Quelques protéines 3R (recombinaison de l'ADN)

**On ne trouve pas dans la liste les protéines qui répliquent
l'ADN ??**

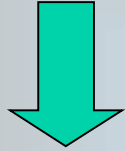
**Koonin's hypothesis : twice independent invention
of DNA and DNA replication mechanisms**

(Mushegian and Koonin, PNAS, 1996)

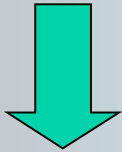


LUCA faisait-il encore parti du monde à ARN (Progénote)

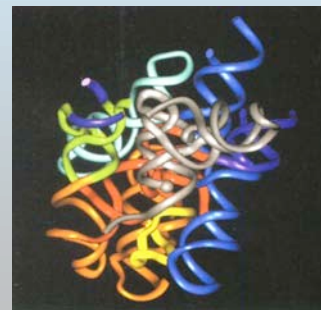
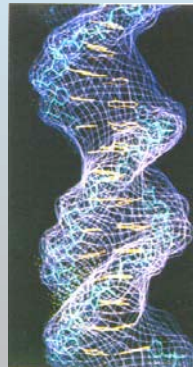
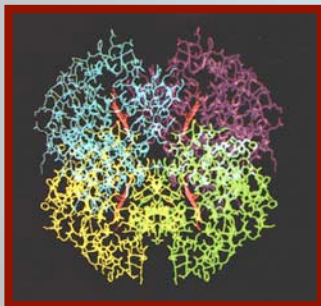
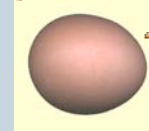
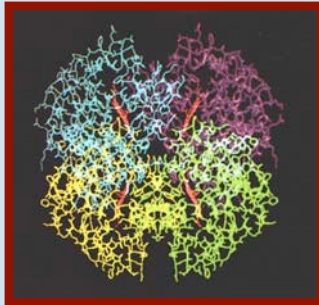
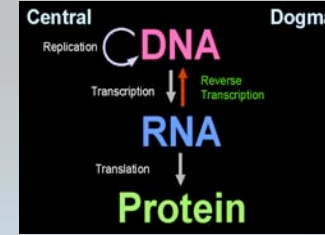
Monde à ARN



**Monde à ARN
+ protéines**

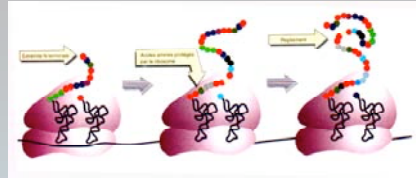


Monde à ADN



LUCA ?

Ou sont les virus dans l'arbre universel ?

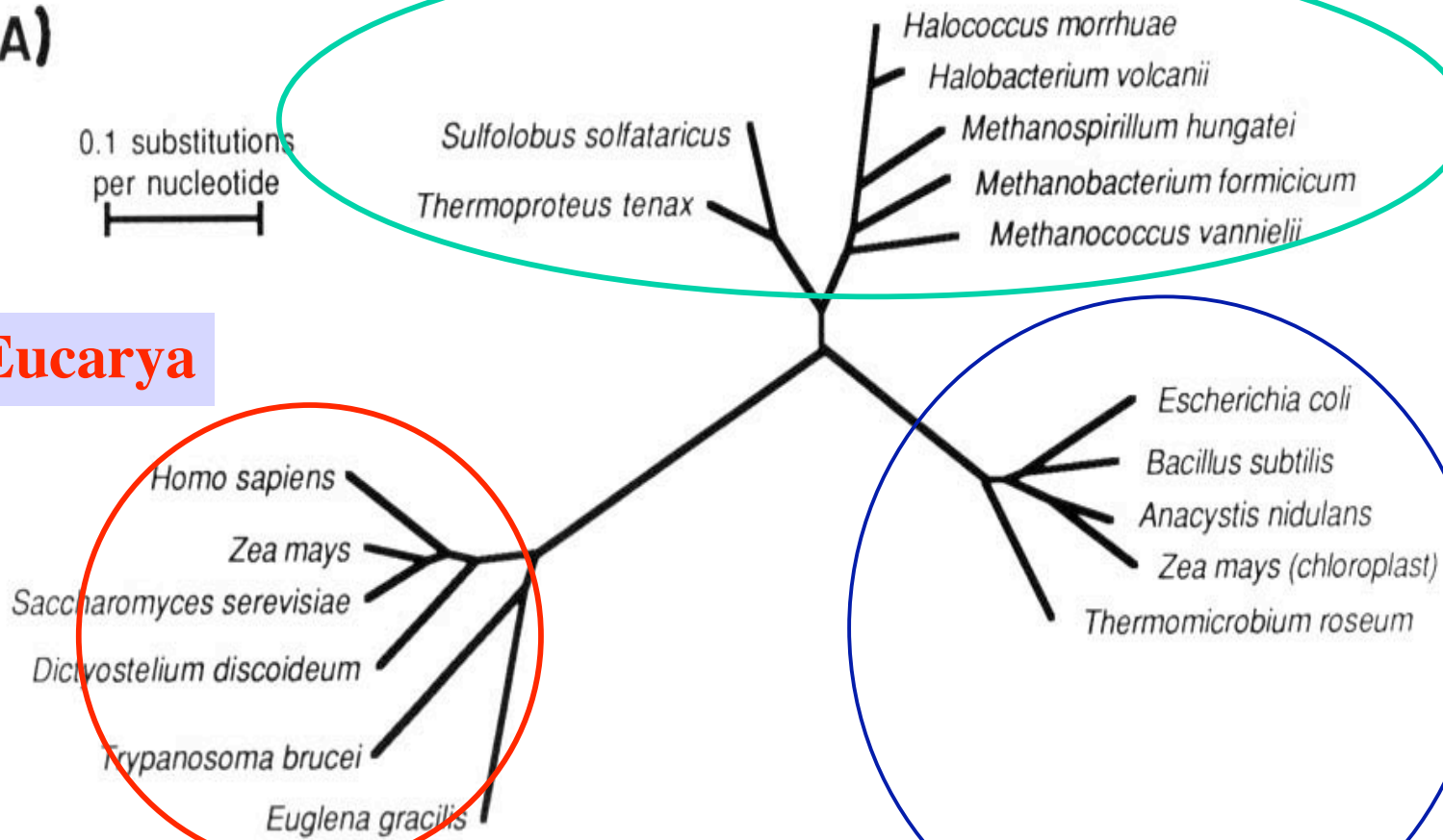


Archaea

(A)

0.1 substitutions per nucleotide

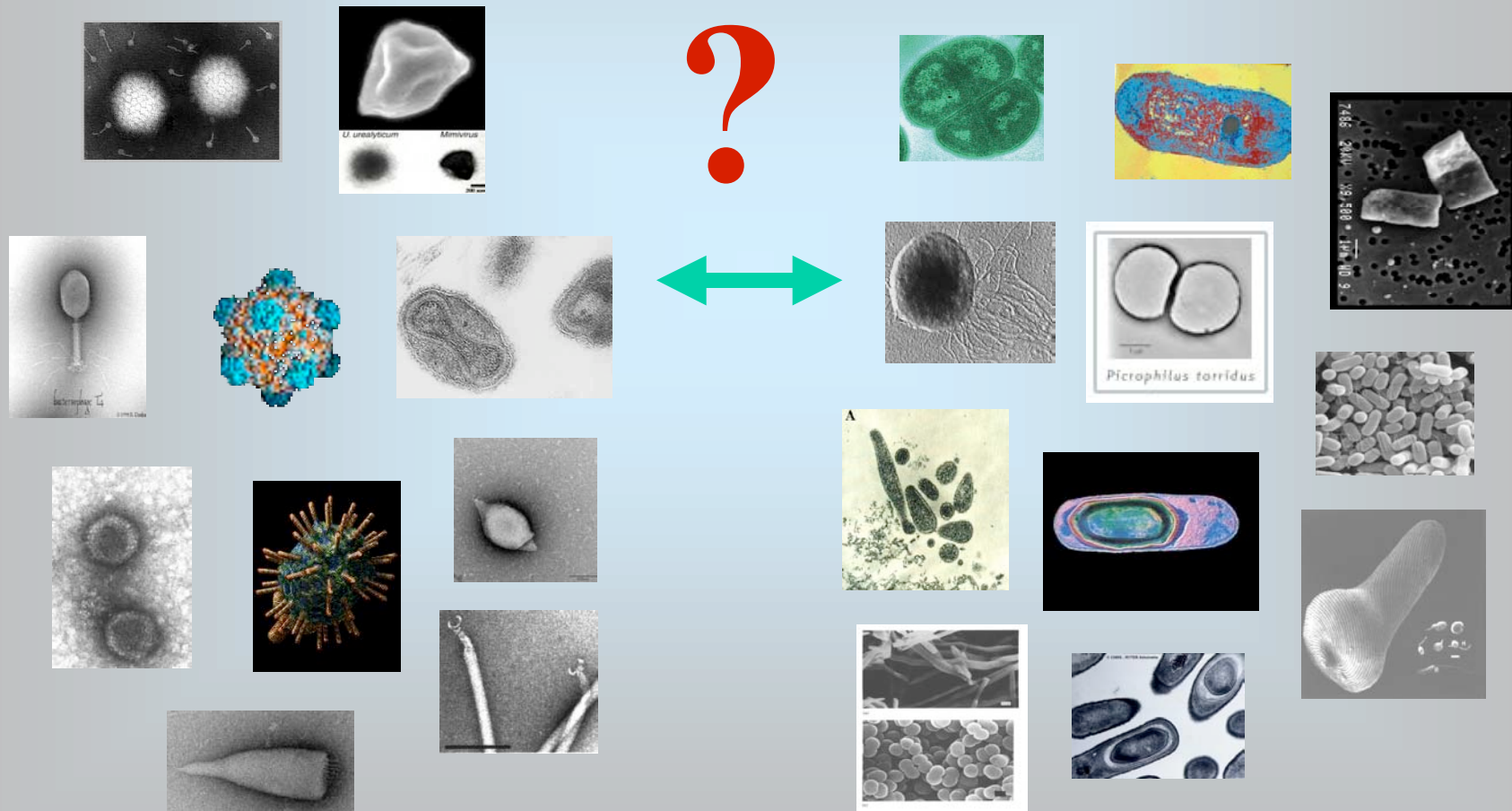
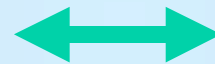
Eucarya



Quelles relations évolutives entre organismes cellulaires et virus ?

Virus

Cells



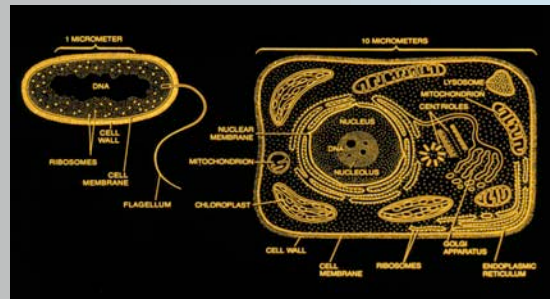
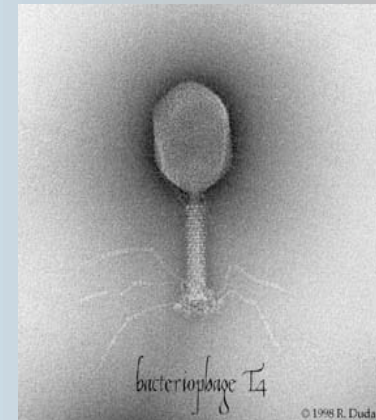
Hypothèse la plus populaires : les virus sont des gènes qui sont devenus indépendants ?



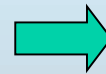
Gènes bactériens



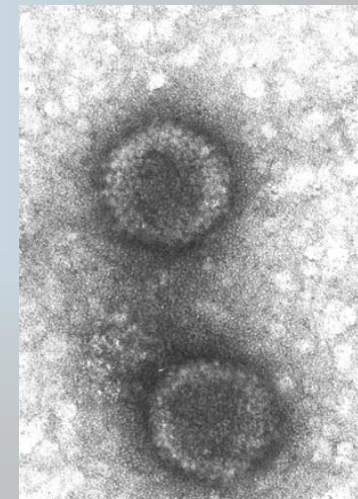
Génomes de bactériophages



Gènes eucaryotes



Génomes de virus « eucaryotes »



Elle est basée sur l'ancien concept procaryote/eucaryote

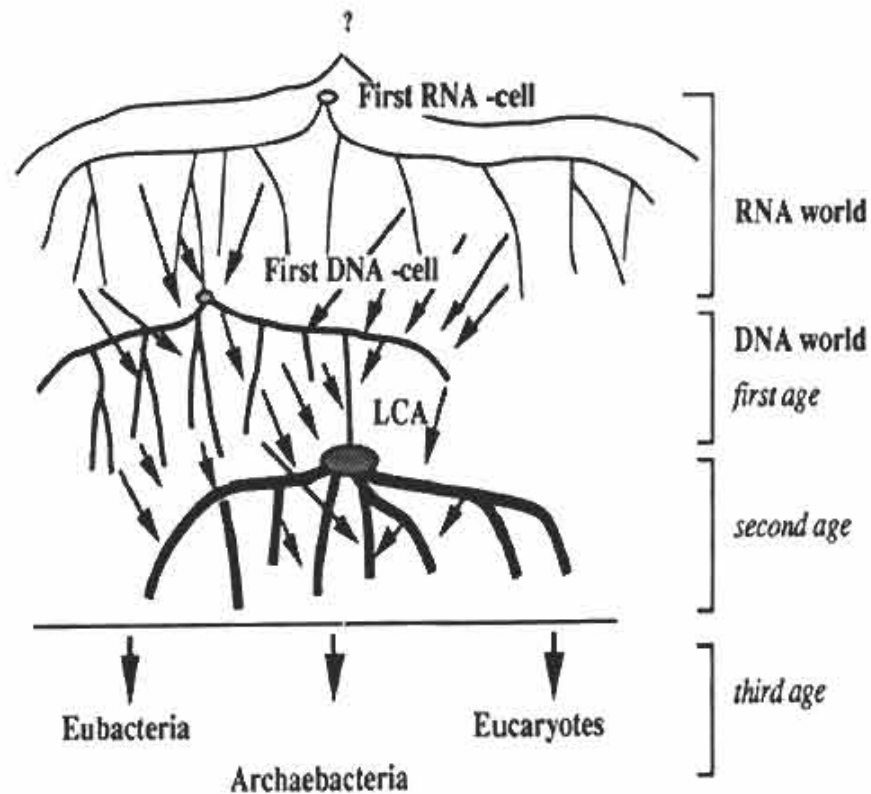
Third "Rencontres de Blois"
Château de Blois, France - October 14-19, 1991

"Frontiers of Life"

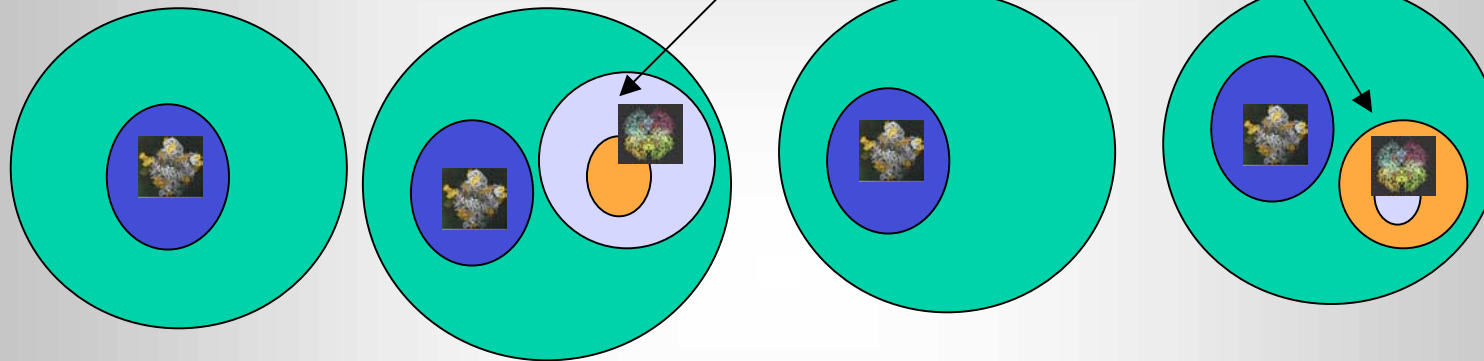
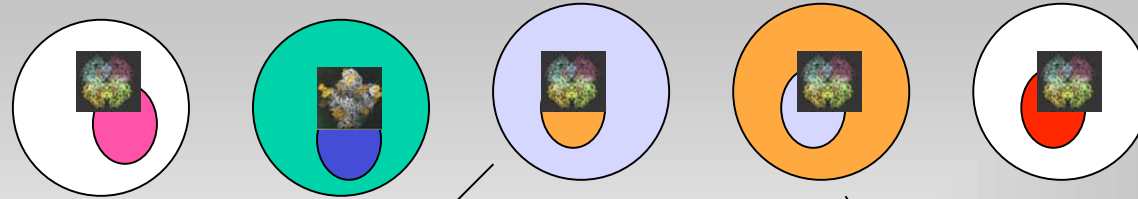
NEW HYPOTHESES ABOUT THE ORIGINS OF VIRUSES,
PROKARYOTES AND EUKARYOTES

Patrick FORTERRE

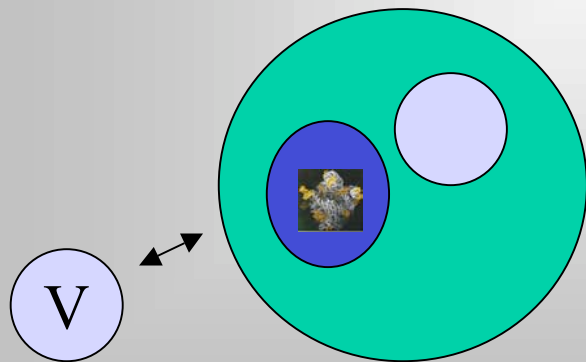
Institut de Génétique et Microbiologie, Bat. 409, Université Paris-Sud, 91405, Orsay Cedex,
France



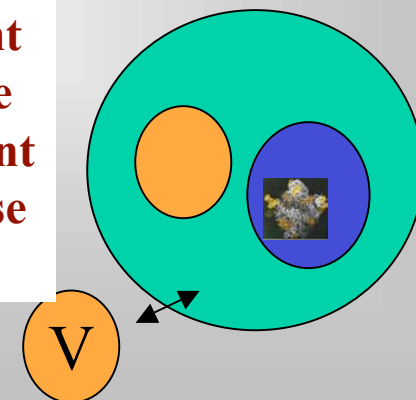
**Cellules à ARN
en compétition
avec différents systèmes
de synthèse protéiques**



**Le type « vert » avec l'ancêtre du ribosome
actuel a éliminé tous ses compétiteurs**

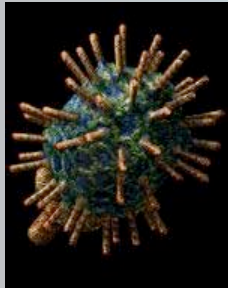


**Les anciens types qui ont
survécu en parasitant le
type « vert » abandonnent
leurs système de synthèse
protéiques**



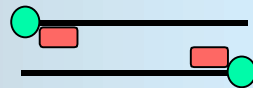
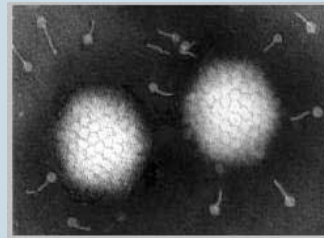
Ils se transforment en virus

Il existe des caractères homologues entre virus animaux et bactériophages: origine commune avant LUCA ?

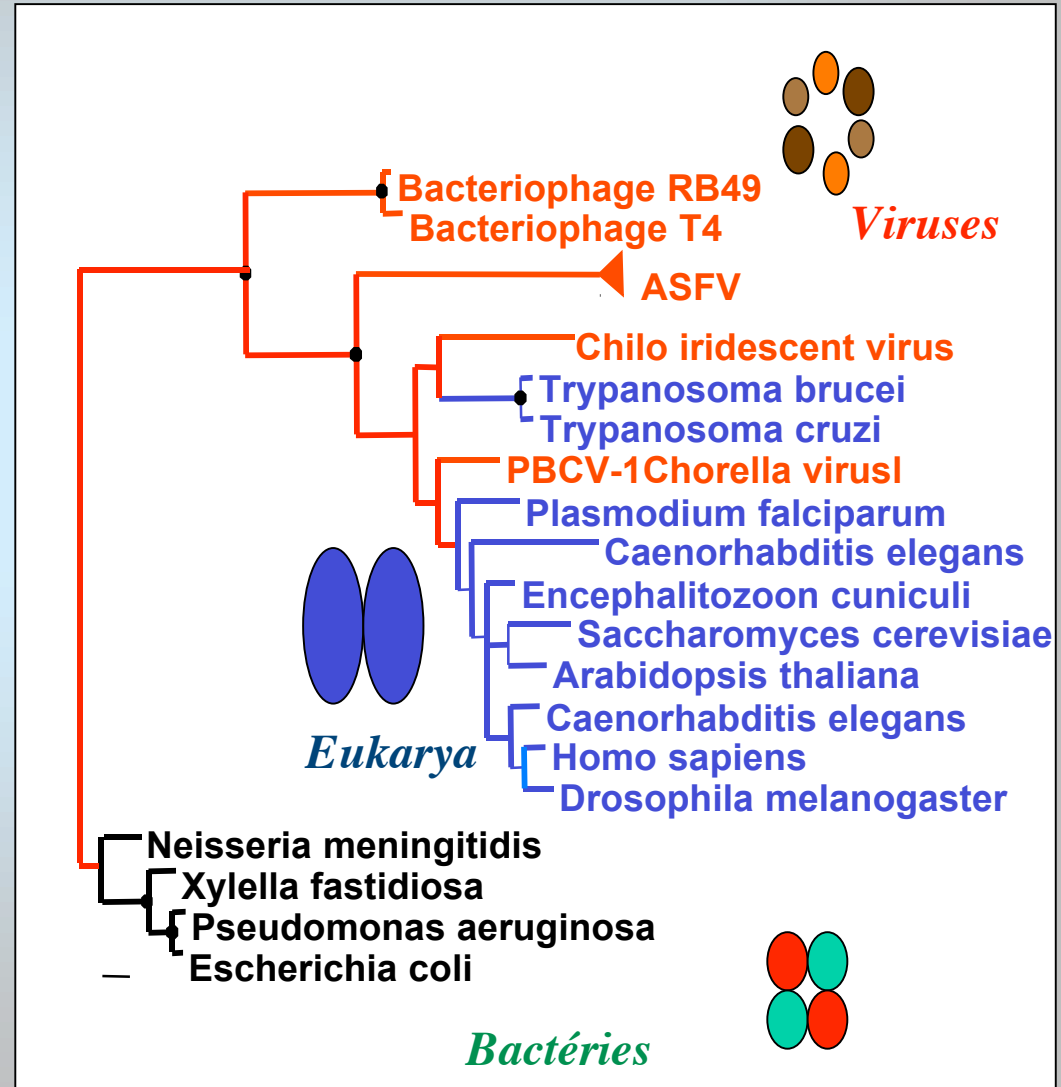


Génome du
bactériophage
Φ29

(*B. subtilis*)

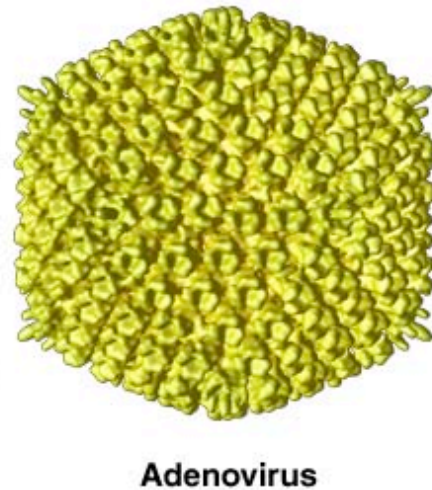
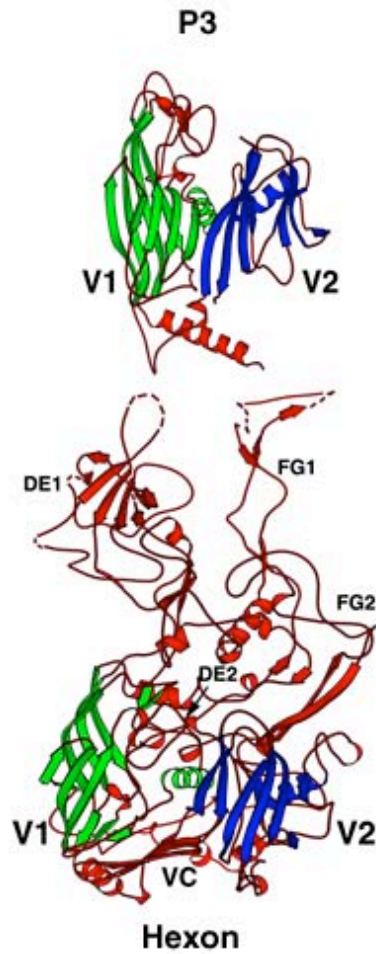
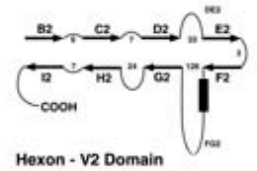
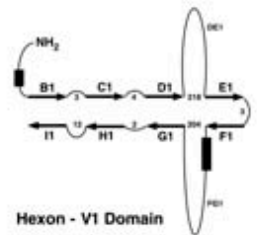
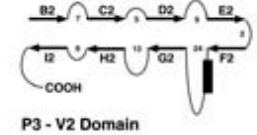
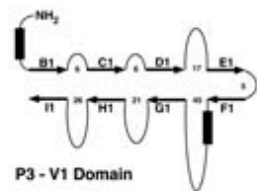


Génome des
Adenovirus
(*Homo sapiens*)

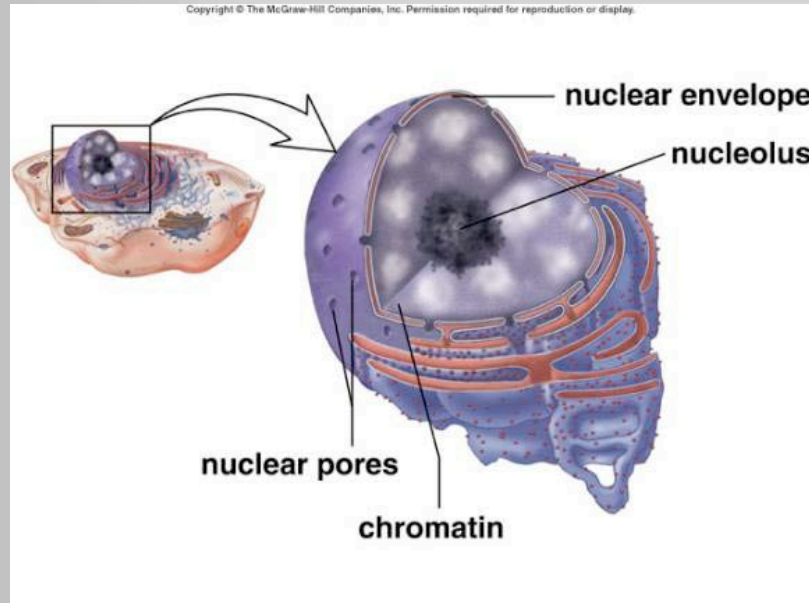




*Dennis Bamford
(Université d'Helsinki)*



Le retour des virus !

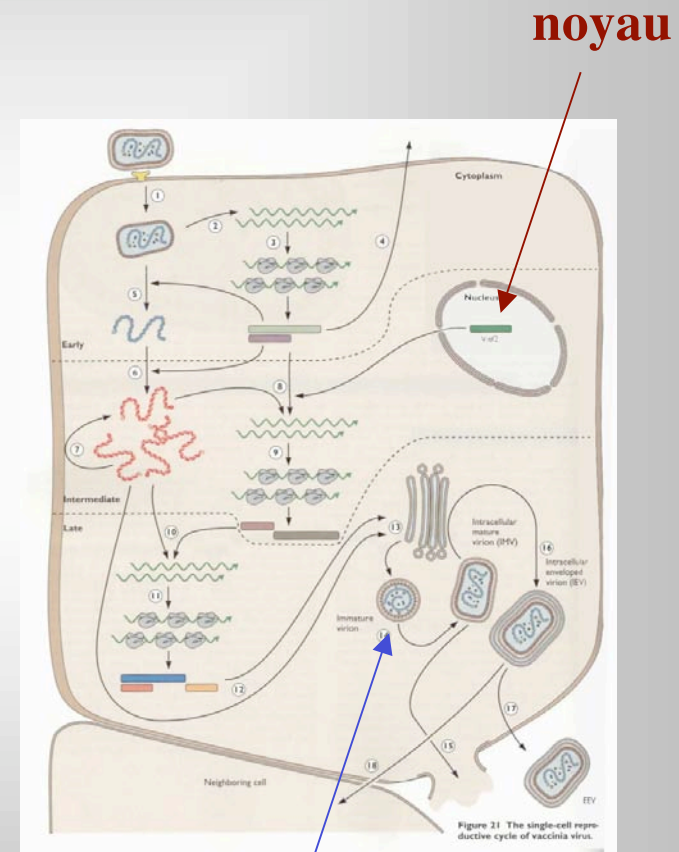


**Le noyau des cellules eucaryotes
dériverait d'un grand virus à ADN**

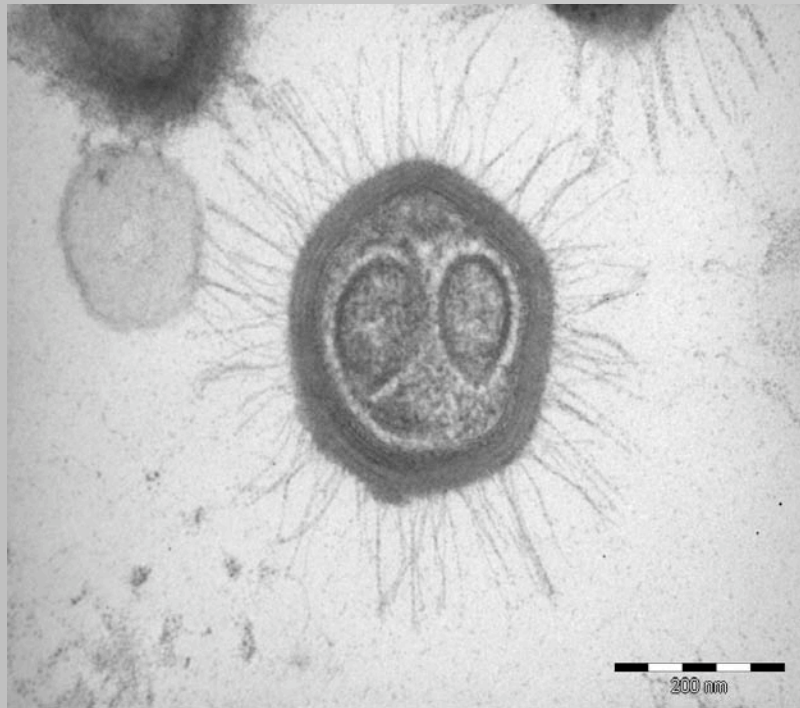
Takemura, J Mol Evol, 2001

Bell, LJ. Mol. Evol. 2001

Cycle du virus de la variole



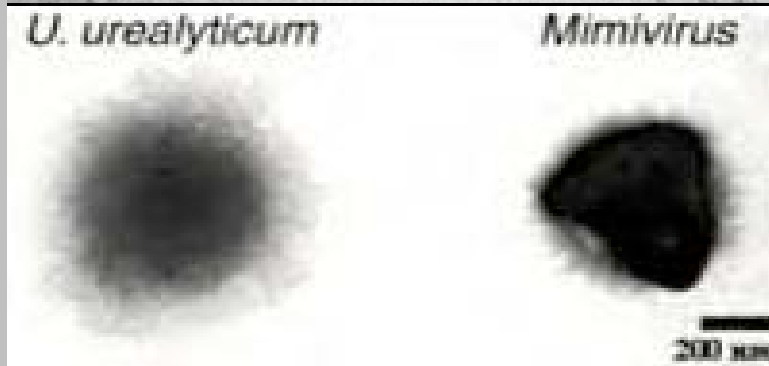
Mini-noyau (variole)



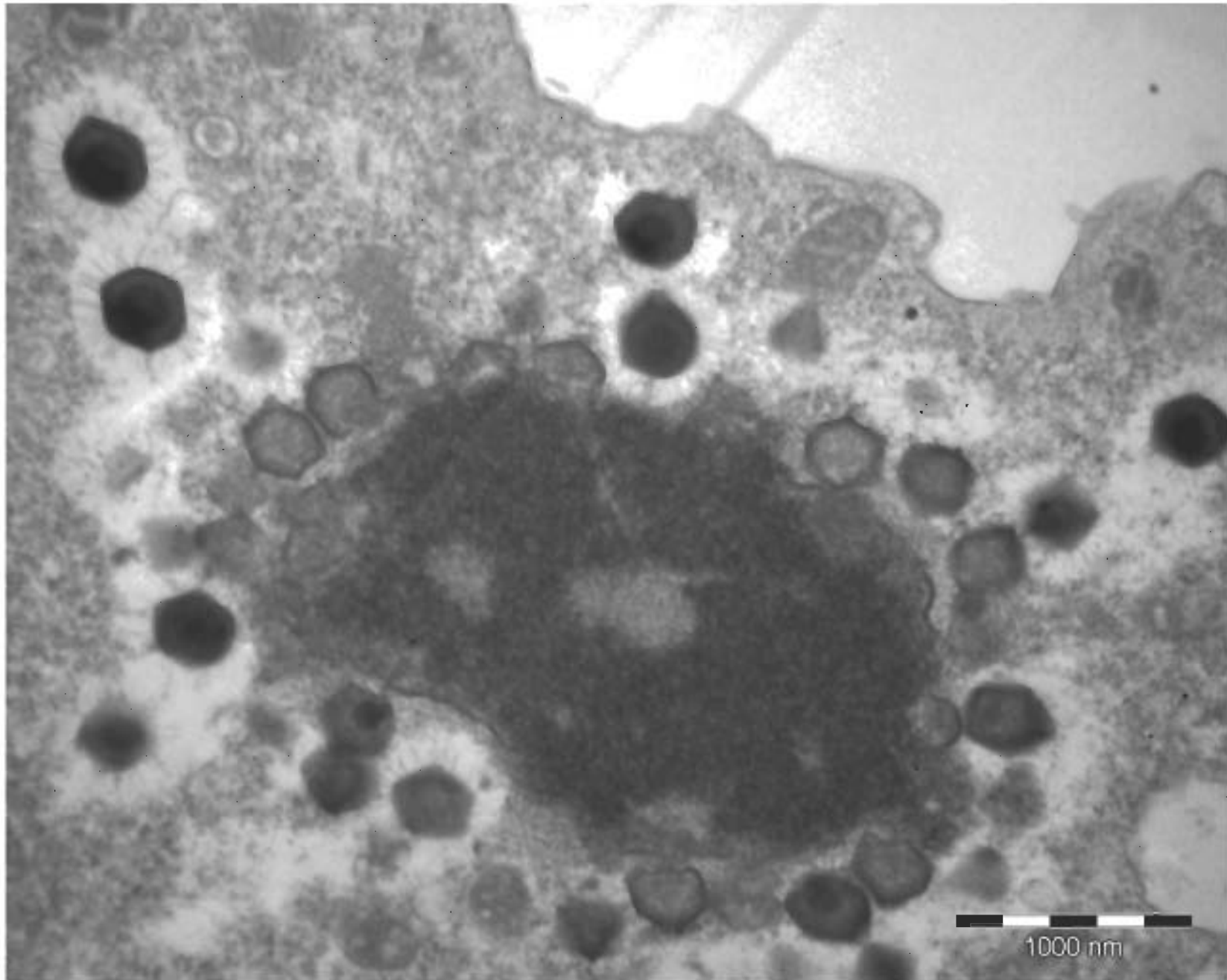
**The Mimivirus: un virus geant
(*mimic a microbe*) giantvirus.org**

*Didier Raoult.....
Jean-Michel Claverie
Science, Octobre 2004*

**un génome de 1200 000
paires de bases
(500 à 600 000
pour les plus petites bactéries)**



**Le génome du Mimivirus
code pour des protéines de
la traduction !**



Le mimivirus est-il le représentant d'un quatrième virus ? Est-il apparenté à l'ancêtre du noyau eucaryote ? Ou bien a-t-il volé ses protéines de traduction à des amibes contemporaines ?

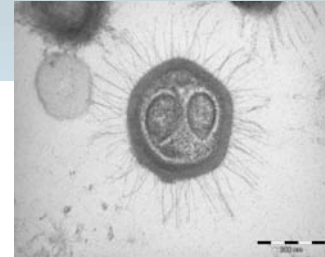
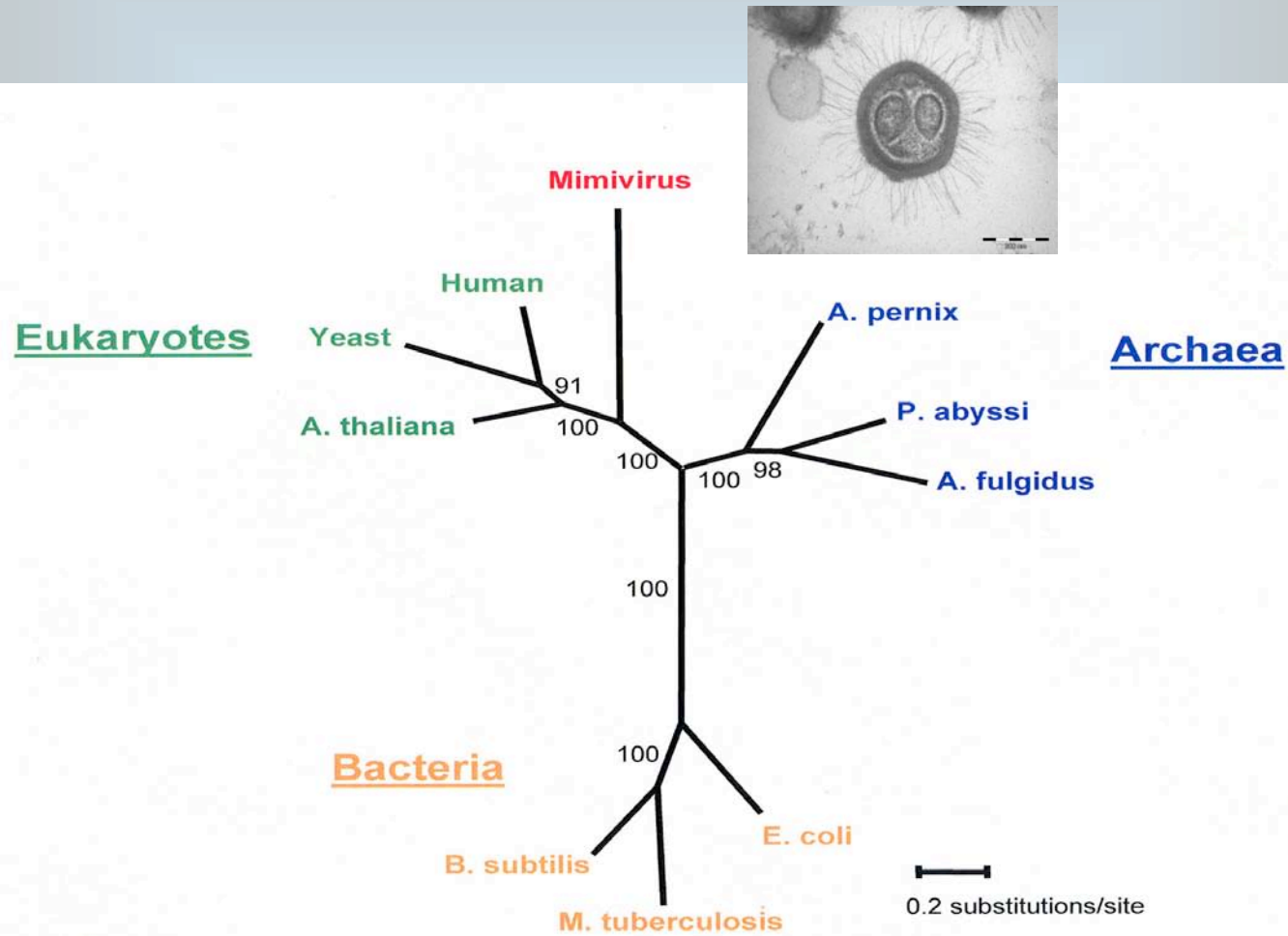
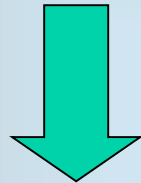


Fig. 3

Les virus ont-ils joué un rôle dans l'apparition de l'ADN ?

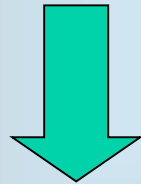
ARN (A, U, G, C)

ARN



ADN (A, U, G, C)

ADN-U

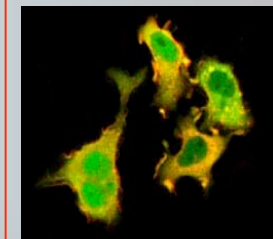
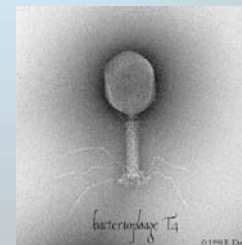
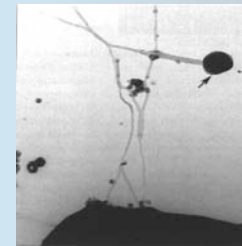
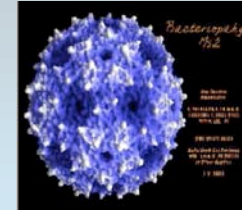


ADN (A, T, G, C)

ADN-T

Pourquoi l'ADN à-t-il remplacé l'ARN ?

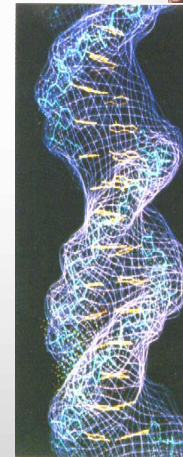
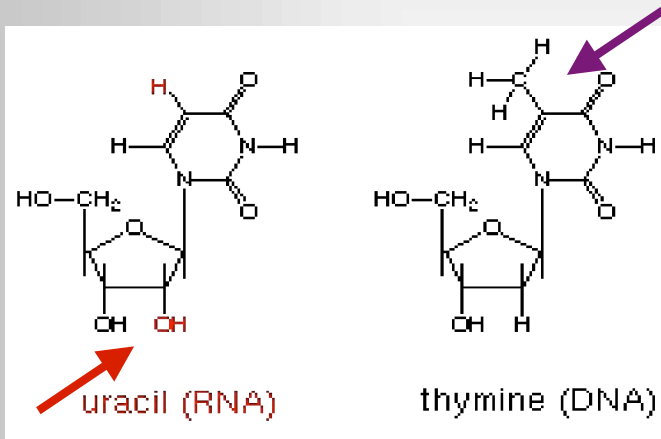
virus



La réponse traditionnelle

1°) L'ADN est plus stable que l'ARN

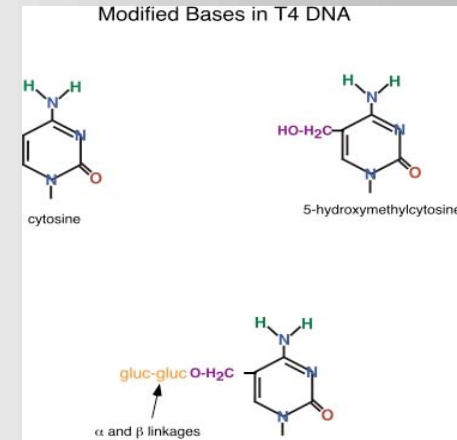
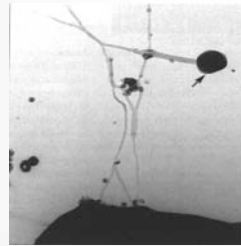
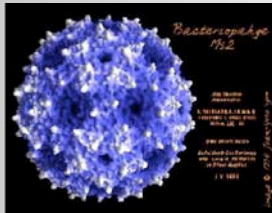
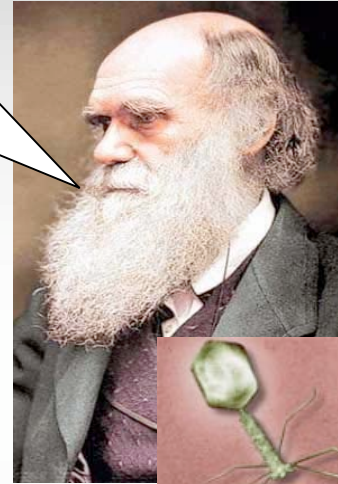
2°) il peut être corrigé pour la déamination des cytosines (C → U)



ce qui a permis l'augmentation
de la taille des génomes

Oui, mais seul Dieu pouvait le prévoir !

**Il faut comprendre quel a été l'avantage
sélectif acquis par le premier organisme
avec un génome à ADN**

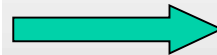


ADN-HMC

ARN



ADN-U



ADN-T

**Les virus à ARN ont pu inventer l'ADN-U (puis l'ADN-T)
tout comme le virus T4 a inventé l'ADN HMC**

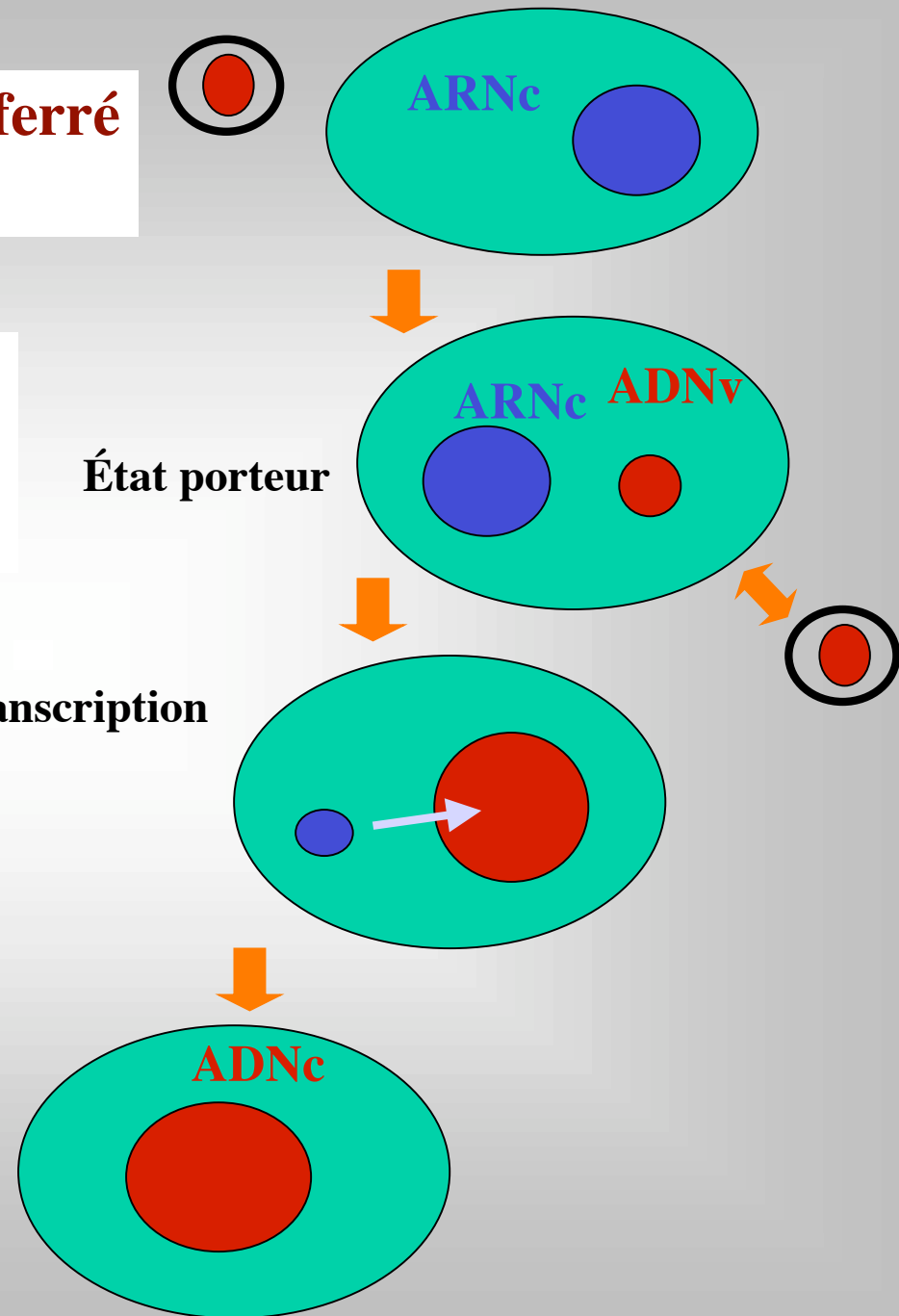
Forterre, Current opinion in Microbiol. 2002

**Comment l'ADN a-t-il été transféré
des virus aux cellules ?**

**Un virus à ADN a pu
prendre le contrôle d'une
cellules à ARN**

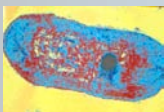


**Nos ancêtres
les virus ??**

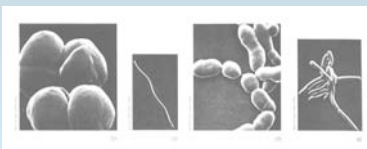


Monde à ADN

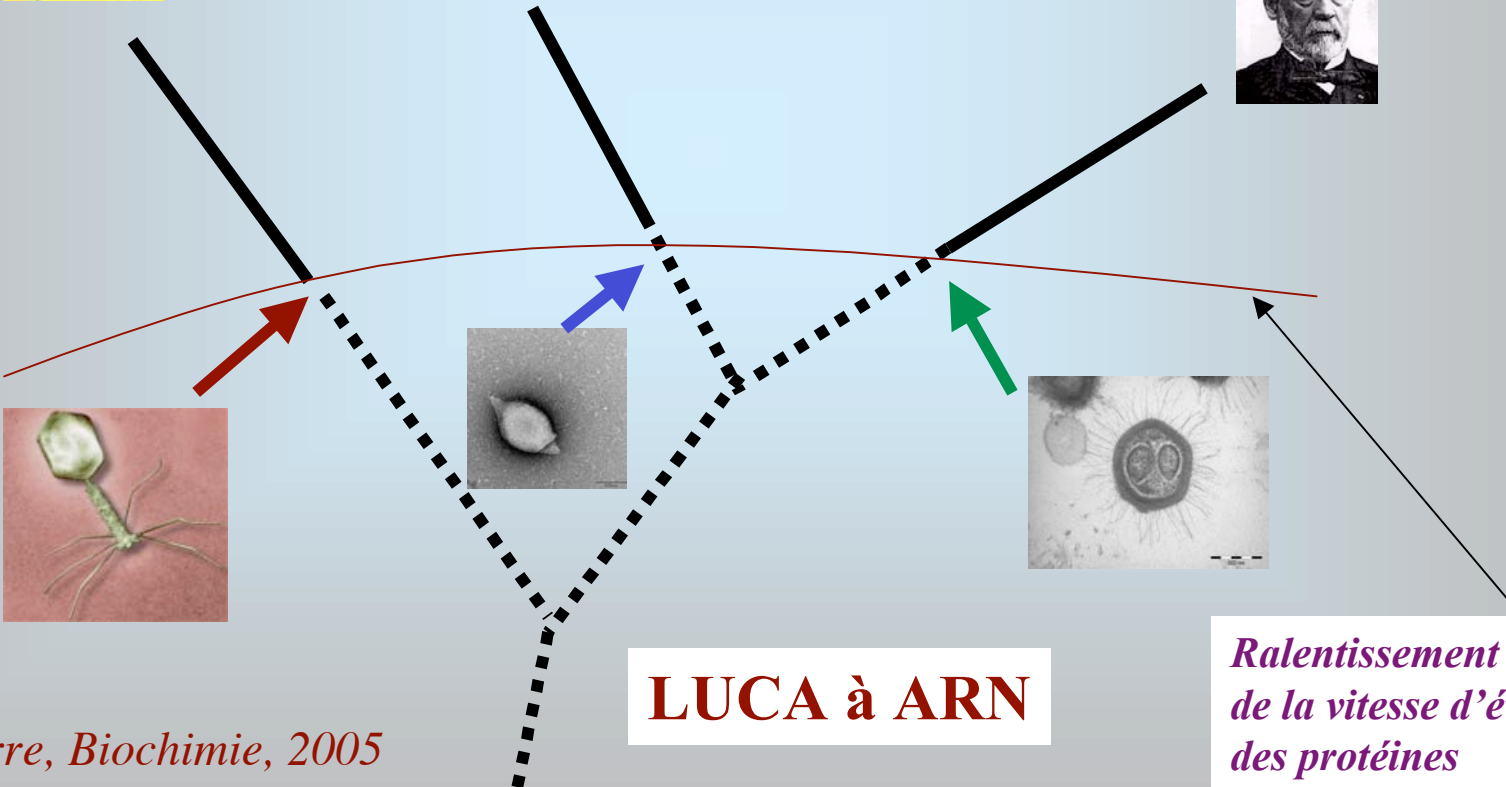
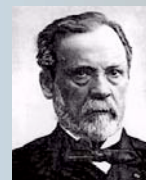
Bactéries



Archées



Eucarya



LUCA à ARN

Ralentissement de la vitesse d'évolution des protéines

Forterre, Biochimie, 2005

D'ou viendrons les nouvelles avancées du XXI^{ème} siècle ?

**nouvelles technologies
nouveaux concepts
poursuite de l'exploration**

