ENDOSIMBIOSI

dalla biologia una lezione sulla risoluzione dei conflitti

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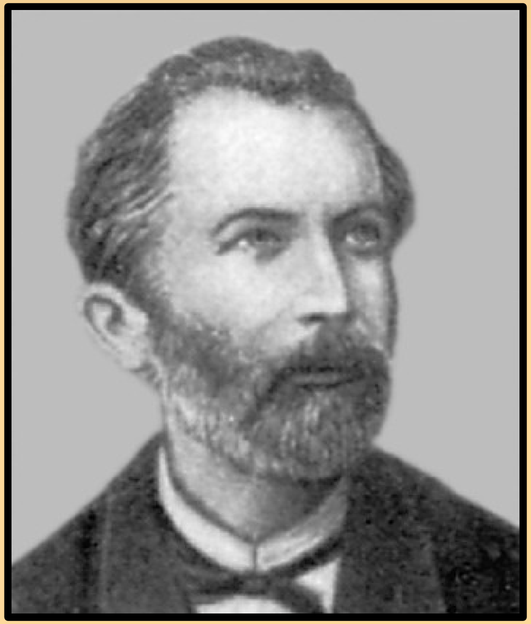
Definire la simbiosi

Simbiosi:
dal greco: συν = insieme; βιος = vita



Anton de Bary

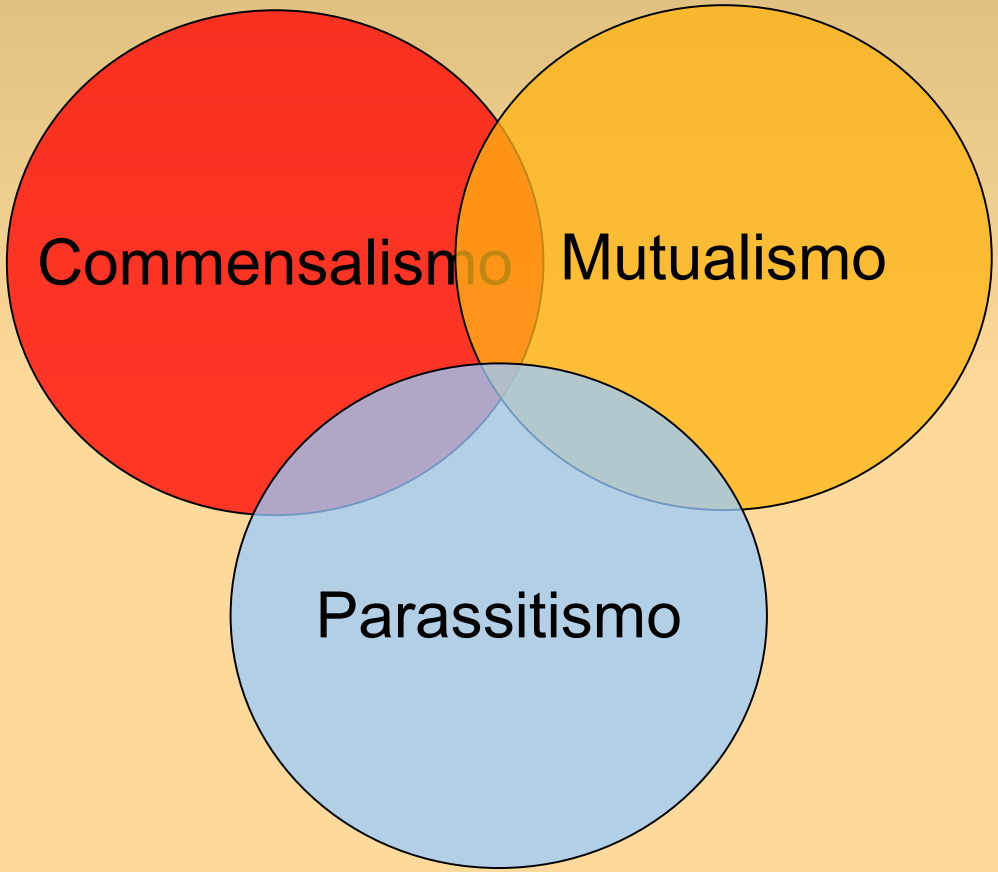
Simbiosi

Commensalismo

Mutualismo

Parassitismo

Simbiosi

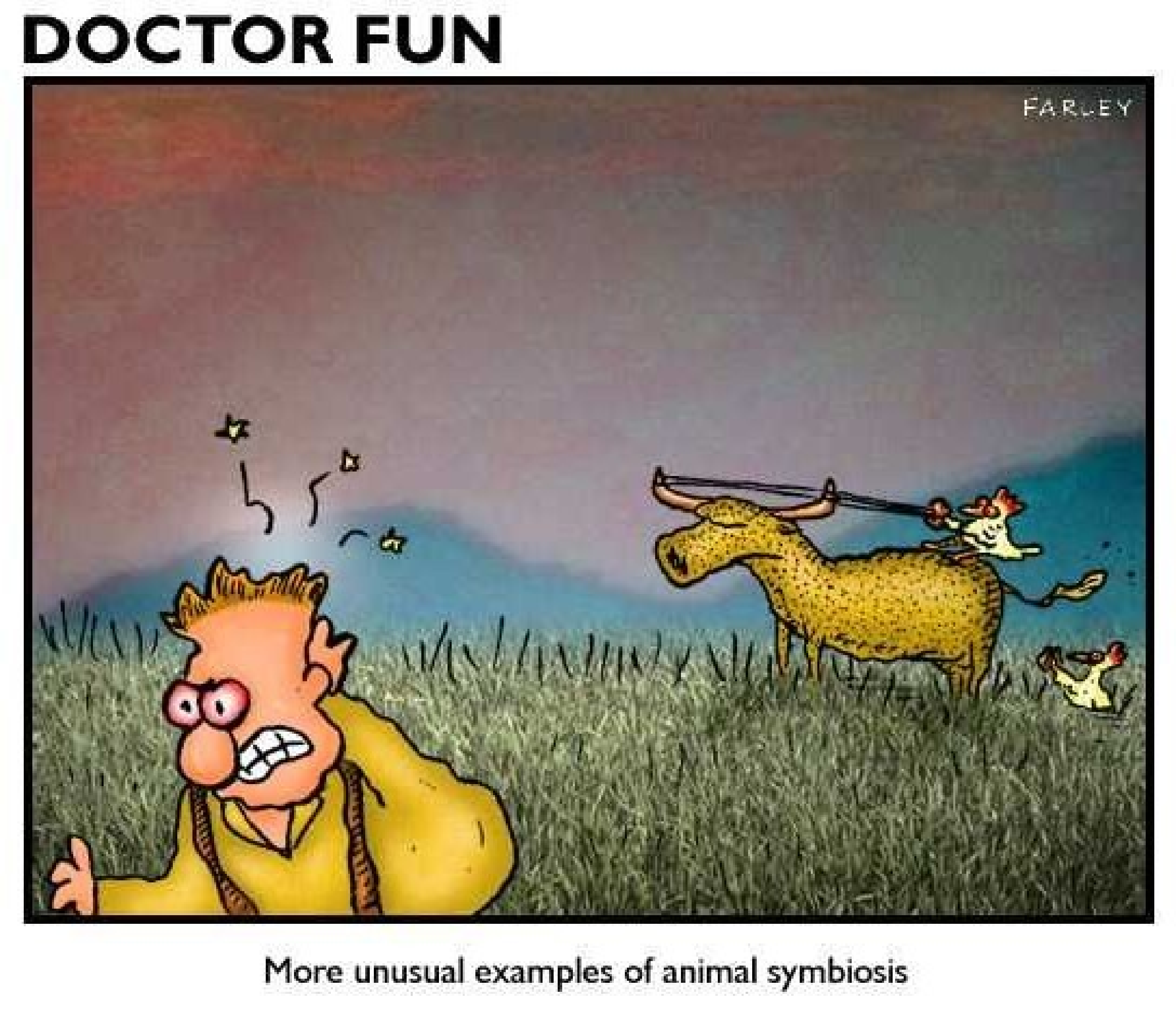


Commensalismo

Mutualismo

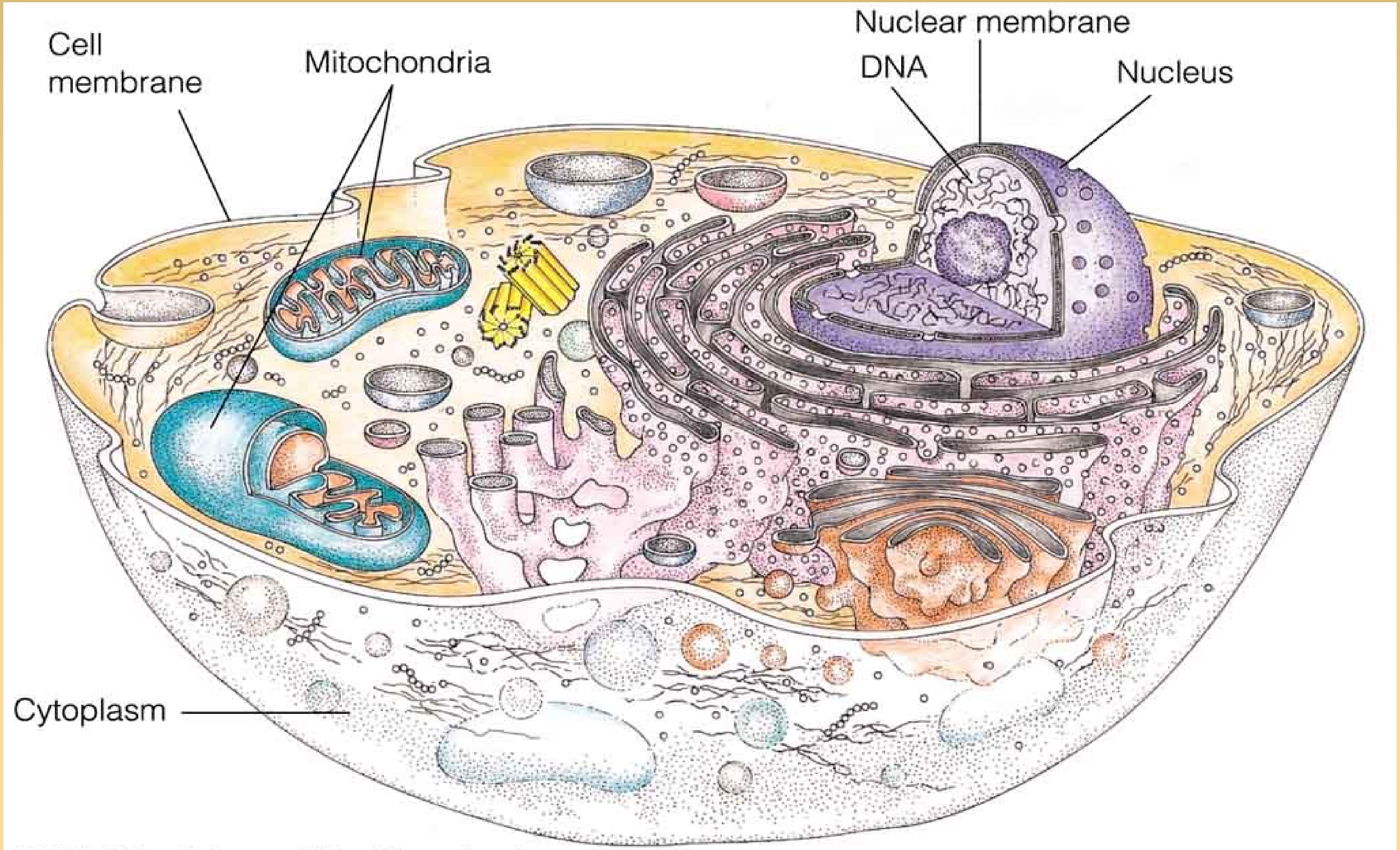
Parassitismo

Simbiosi


DOCTOR FUN
FARLEY

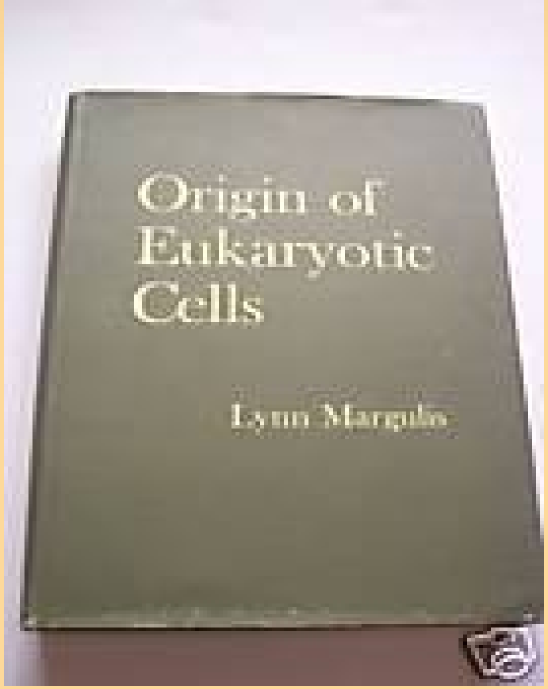
More unusual examples of animal symbiosis

L'endosimbiosi / simbiosi intracellulare


Cell membrane
Mitochondria
Nuclear membrane
DNA
Nucleus
Cytoplasm

La teoria seriale dell'endosimbiosi

Lynn Margulis

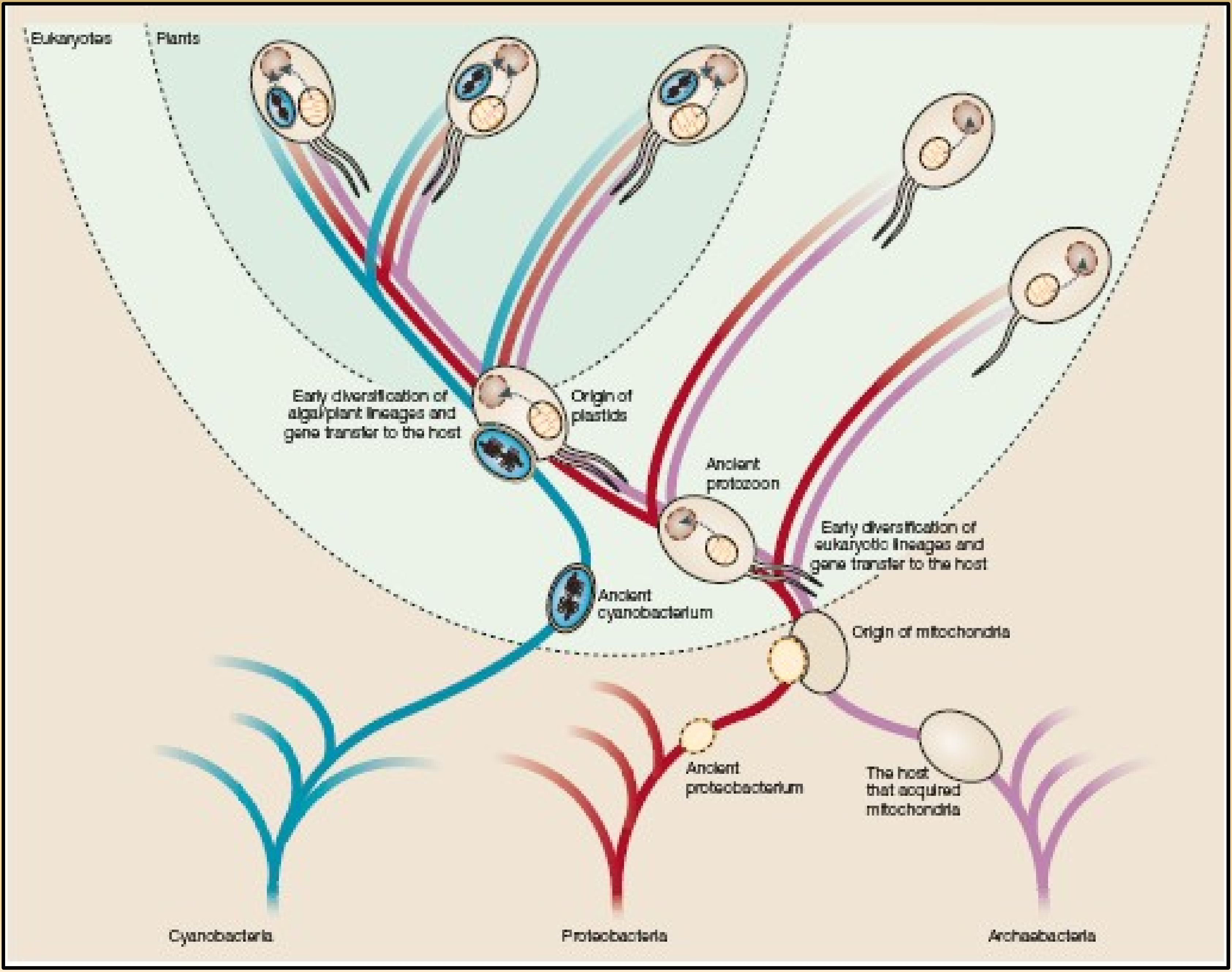

Origin of Eukaryotic Cells
Lynn Margulis

La teoria seriale dell'endosimbiosi

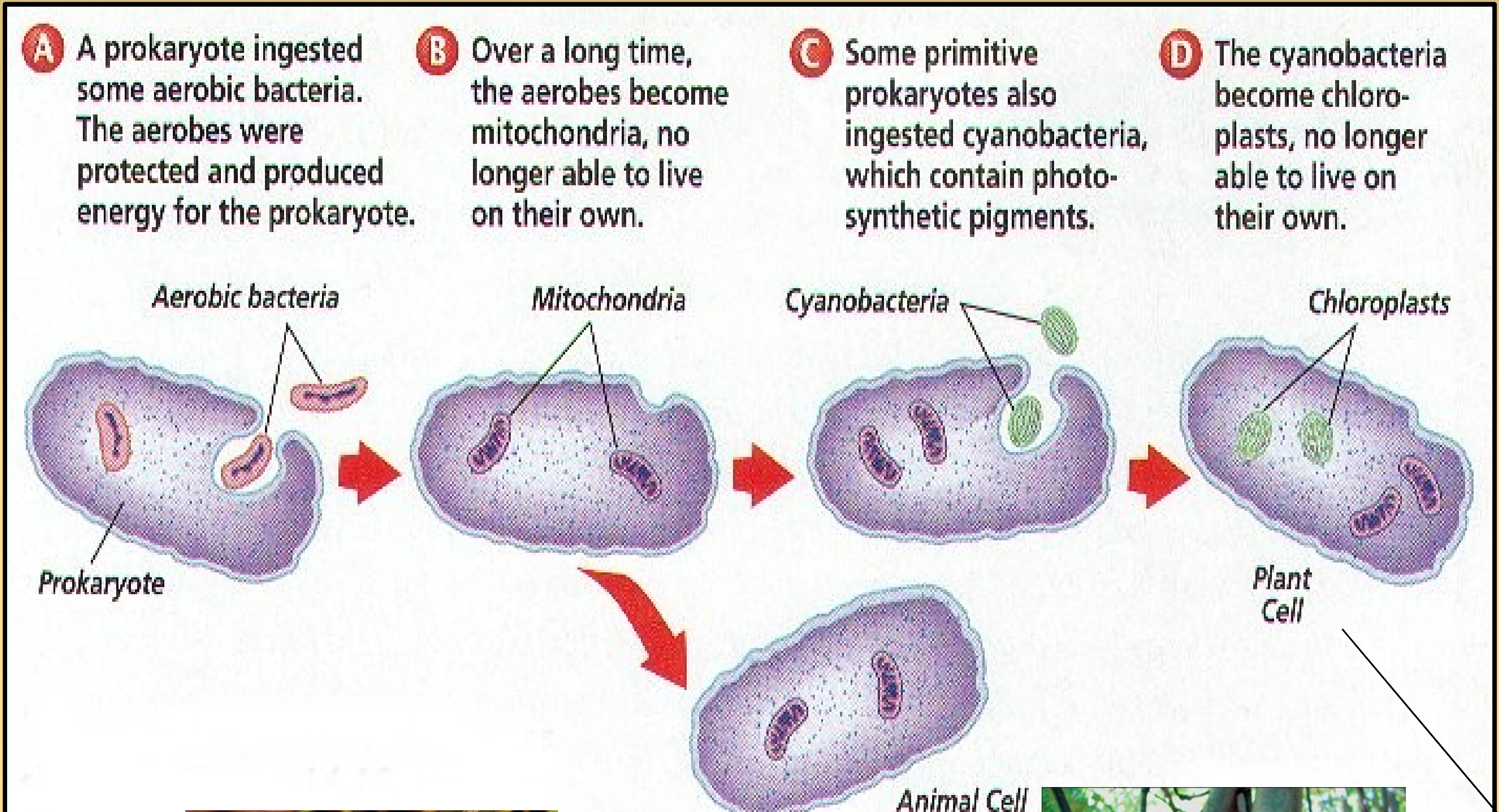
Lynn Margulis

“life did not take over the globe by combat, but by networking”

La teoria seriale dell'endosimbiosi


Eukaryotes
Plants
Early diversification of algal/plant lineages and gene transfer to the host
Origin of plastids
Ancient protozoon
Early diversification of eukaryotic lineages and gene transfer to the host
Ancient cyanobacterium
Origin of mitochondria
Ancient proteobacterium
The host that acquired mitochondria
Cyanobacteria
Proteobacteria
Archaebacteria

La teoria seriale dell'endosimbiosi



A A prokaryote ingested some aerobic bacteria. The aerobes were protected and produced energy for the prokaryote.

B Over a long time, the aerobes become mitochondria, no longer able to live on their own.

C Some primitive prokaryotes also ingested cyanobacteria, which contain photosynthetic pigments.

D The cyanobacteria become chloroplasts, no longer able to live on their own.

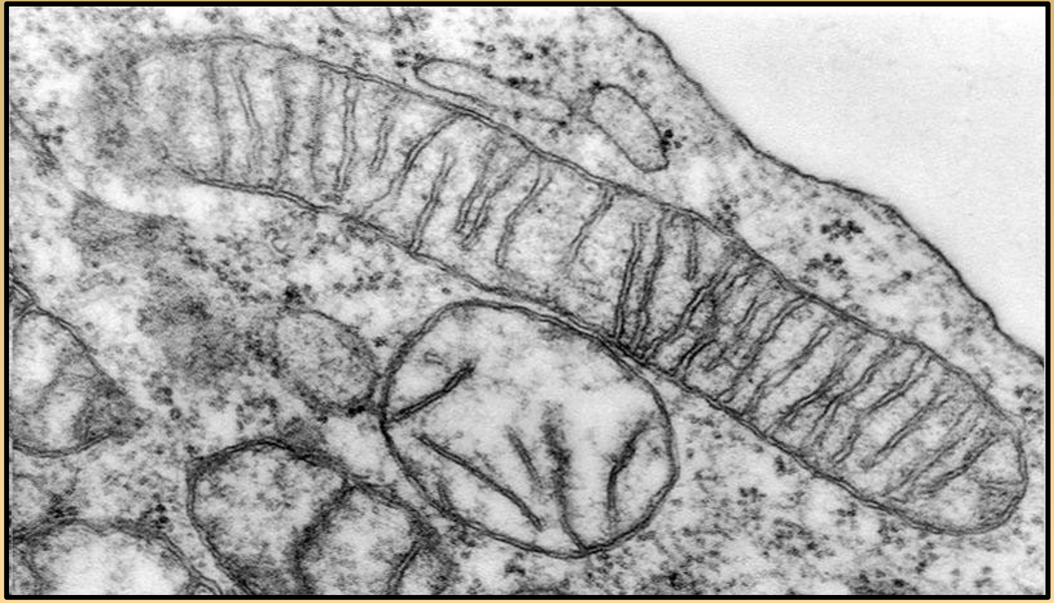
Aerobic bacteria
Prokaryote
Mitochondria
Cyanobacteria
Chloroplasts
Plant Cell
Animal Cell

piante

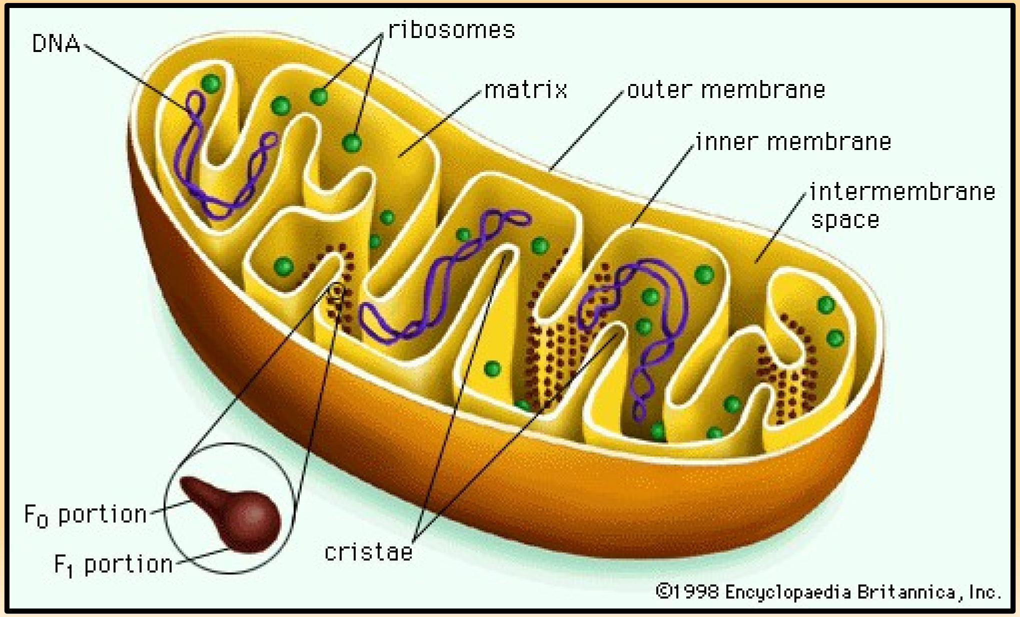
animali

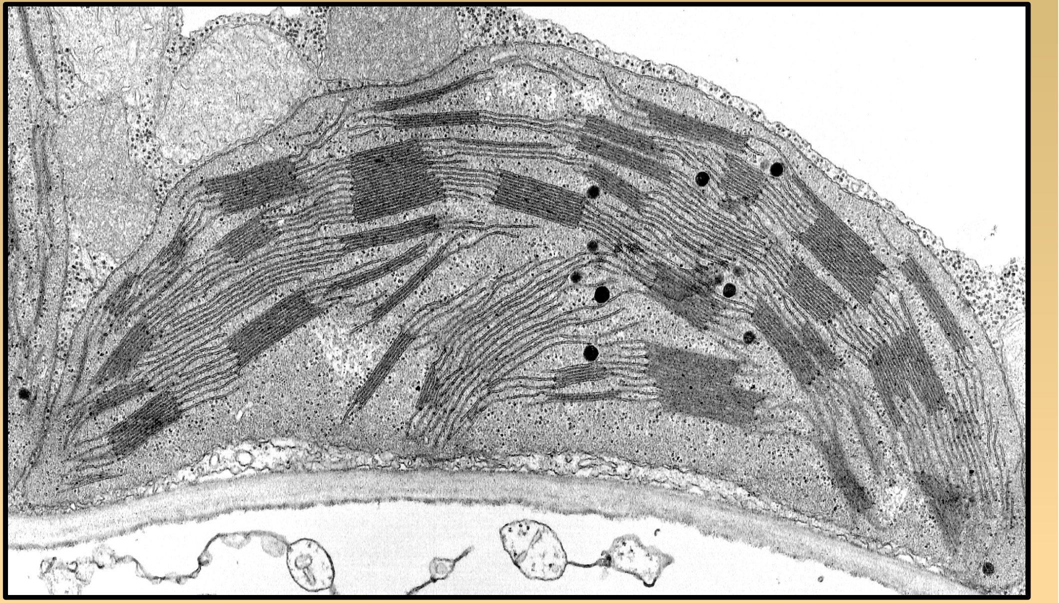
funghi

La teoria seriale dell'endosimbiosi

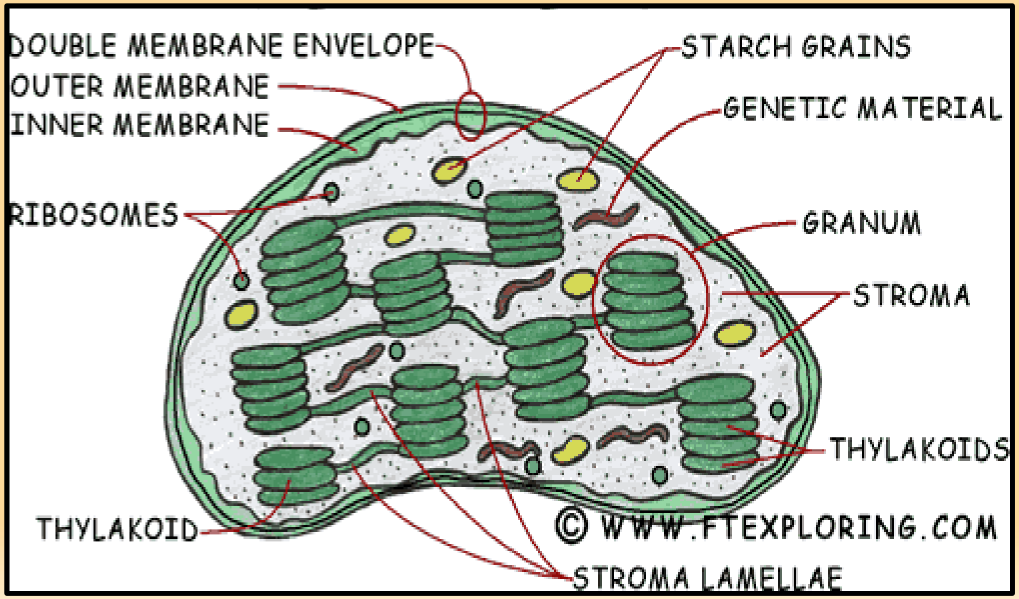


mitocondrio

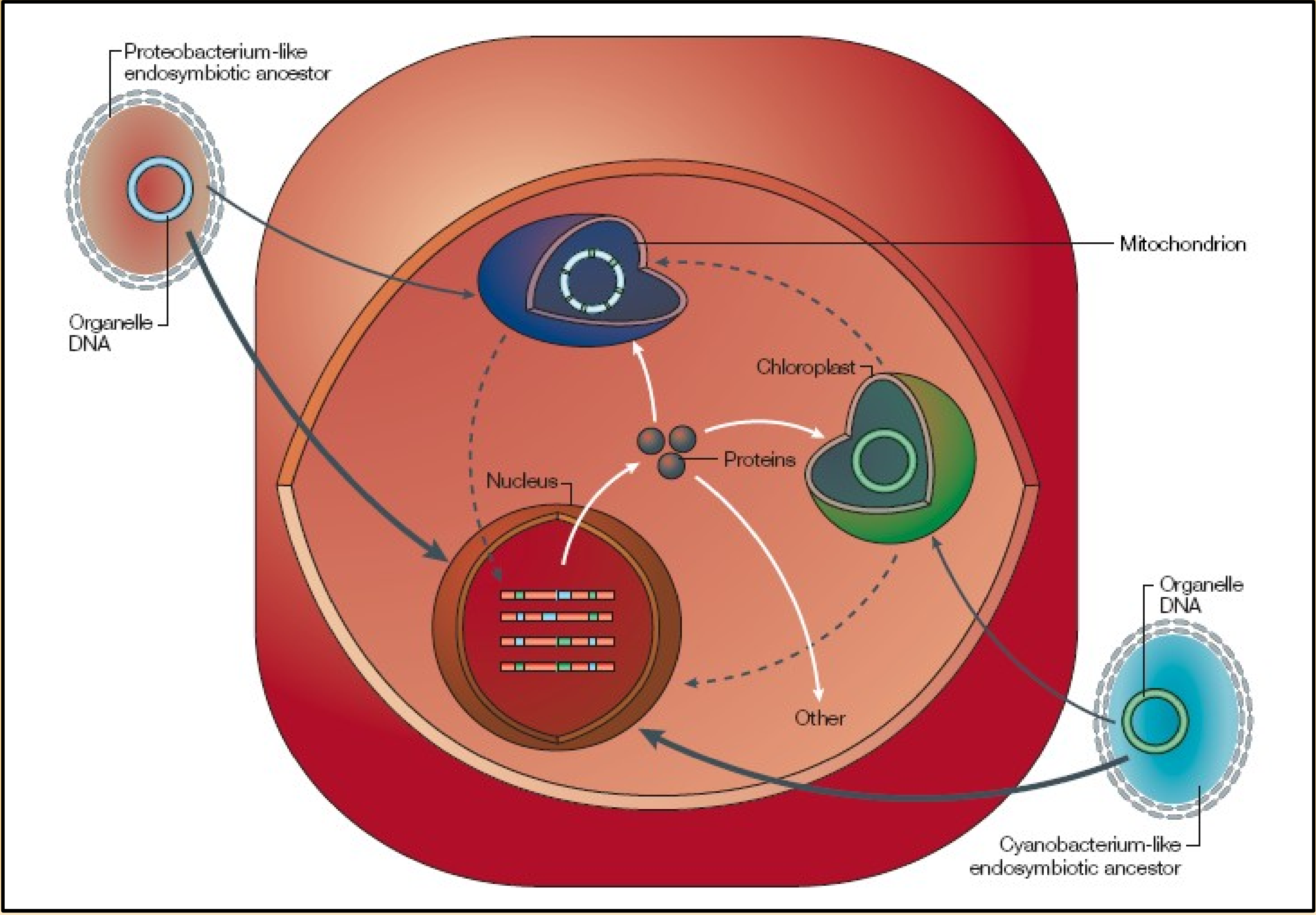

DNA
ribosomes
matrix
outer membrane
inner membrane
intermembrane space
F_0 portion
F_1 portion
cristae
©1998 Encyclopaedia Britannica, Inc.



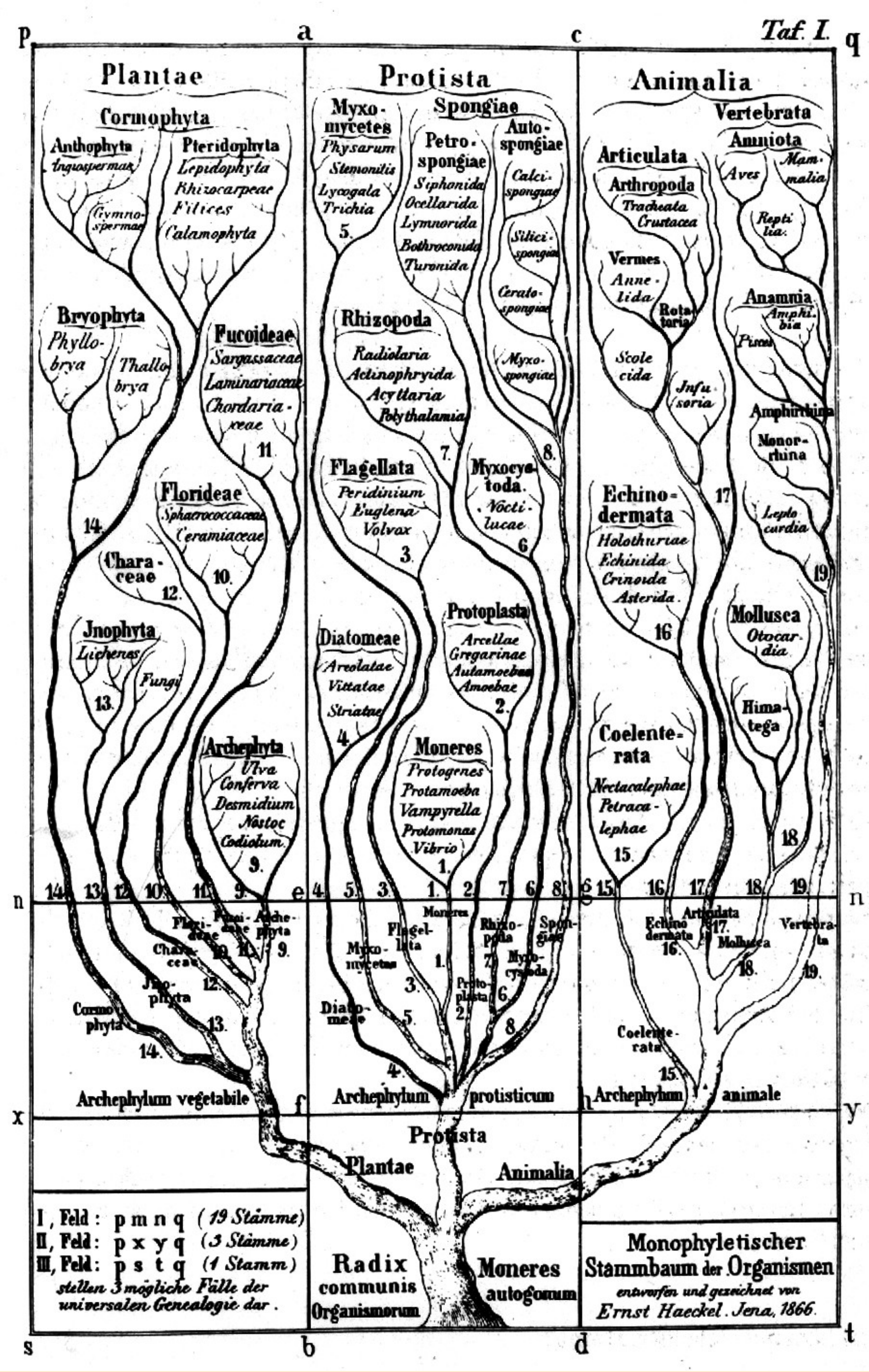
cloroplasto

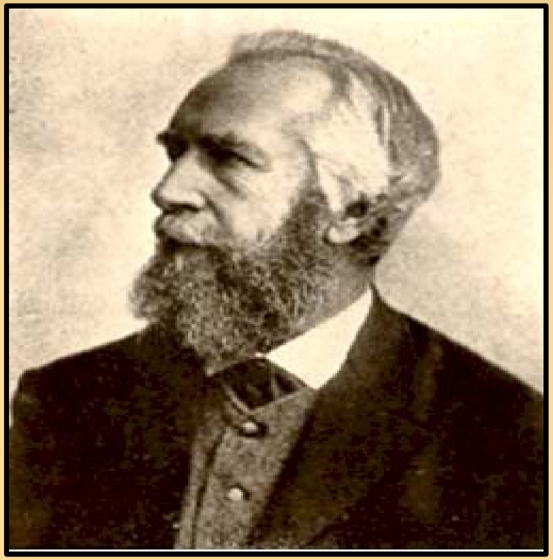

DOUBLE MEMBRANE ENVELOPE
OUTER MEMBRANE
INNER MEMBRANE
RIBOSOMES
STARCH GRAINS
GENETIC MATERIAL
GRANUM
STROMA
THYLAKOIDS
THYLAKOID
© WWW.FTEXPLORING.COM
STROMA LAMELLAE

La “promiscuità”di una cellula eucariote


Proteobacterium-like endosymbiotic ancestor
Organelle DNA
Mitochondrion
Chloroplast
Proteins
Nucleus
Other
Organelle DNA
Cyanobacterium-like endosymbiotic ancestor

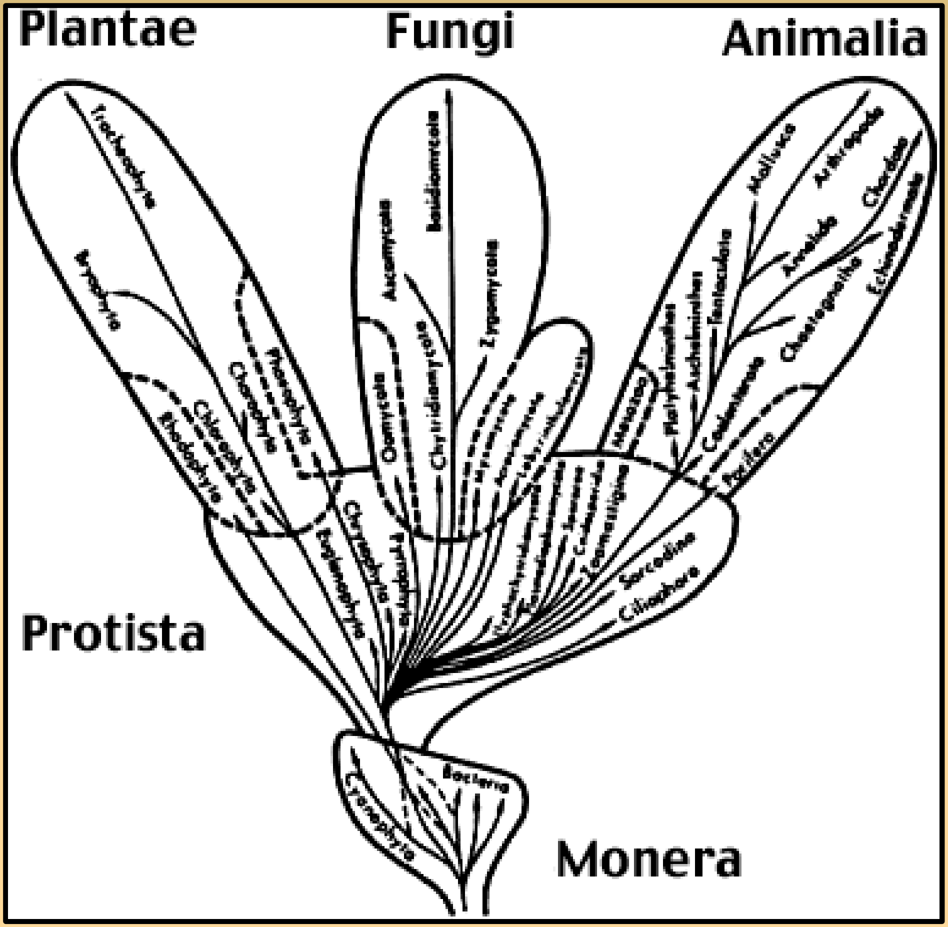
II *Tree of Life*

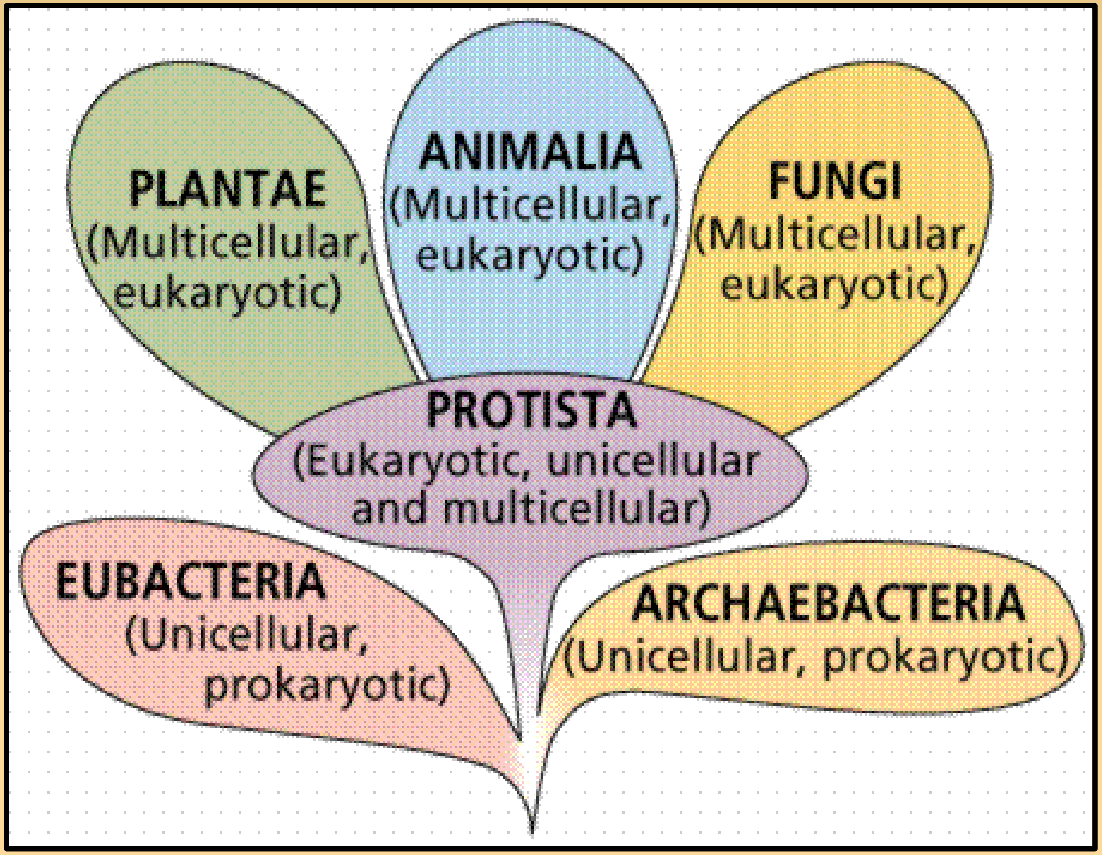

Taf. I.
Plantae
Protista
Animalia
Cormophyta
Anthophyta
Pteridophyta
Bryophyta
Fucoideae
Florideae
Chara-ceae
Jnophyta
Archephyta
Myxo-mycetes
Spongiae
Rhizopoda
Flagellata
Myxocystoda
Diatomeae
Protoplasta
Moneres
Vertebrata
Amniota
Articulata
Arthropoda
Vermes
Anamnia
Amphirhina
Echino-dermata
Mollusca
Coelente-rata
Archephylum vegetabile
Archephylum protisticum
Archephylum animale
Radix communis Organismorum
Moneres autogonum
I, Feld: p m n q (19 Stämme)
II, Feld: p x y q (3 Stämme)
III, Feld: p s t q (1 Stamm)
stellen 3 mögliche Fälle der universalen Genealogie dar.
Monophyletischer Stammbaum der Organismen
entworfen und gezeichnet von Ernst Haeckel. Jena, 1866.



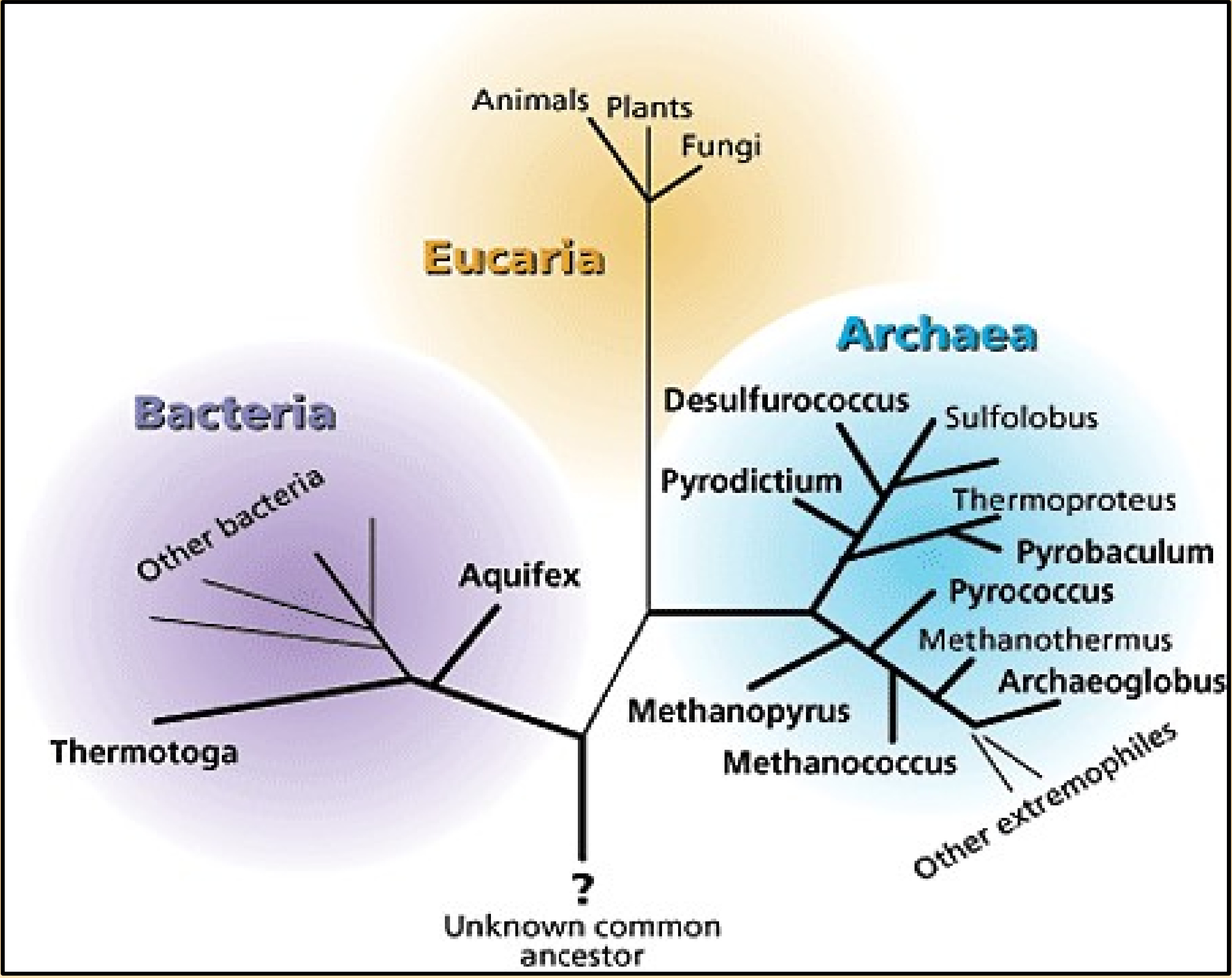
Ernst Haeckel

Il *Tree of Life* – I regni della natura

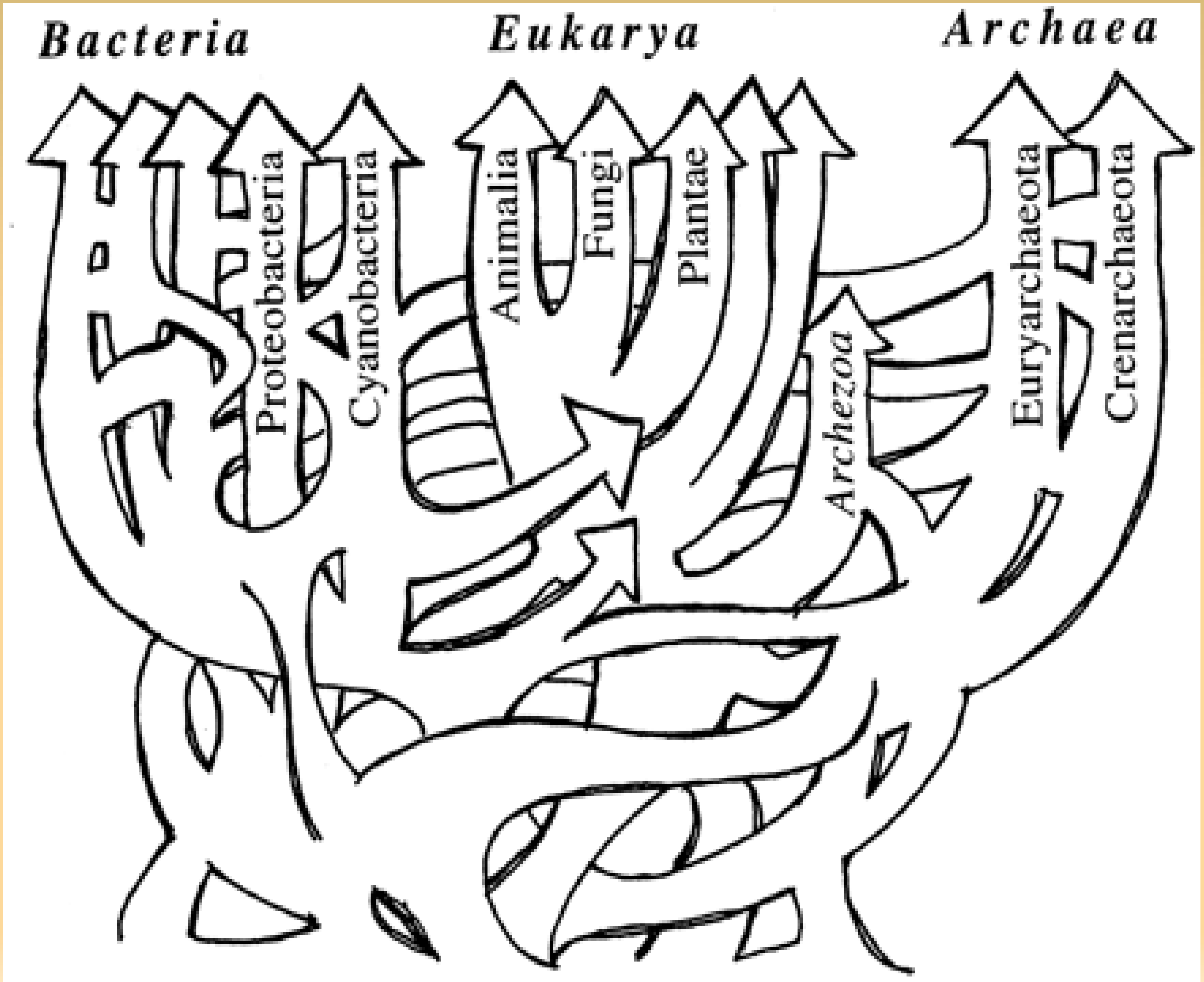

Plantae
Fungi
Animalia
Tracheophyta
Bryophyta
Phaeophyta
Charophyta
Chlorophyta
Rhodophyta
Chrysophyta
Euglenophyta
Pyrrophyta
Oomycota
Chytridiomycota
Ascomycota
Basidiomycota
Zygomycota
Mollusca
Arthropoda
Chordata
Annelida
Echinodermata
Chaetognatha
Tentaculata
Aschelminthes
Platyhelminthes
Mesozoa
Coelenterata
Porifera
Zoomastigina
Sarcodina
Ciliophora
Protista
Bacteria
Cyanophyta
Monera


PLANTAE
(Multicellular, eukaryotic)
ANIMALIA
(Multicellular, eukaryotic)
FUNGI
(Multicellular, eukaryotic)
PROTISTA
(Eukaryotic, unicellular and multicellular)
EUBACTERIA
(Unicellular, prokaryotic)
ARCHAEBACTERIA
(Unicellular, prokaryotic)

Il *Tree of Life* – I domini della natura


Animals
Plants
Fungi
Eucaria
Archaea
Bacteria
Desulfurococcus
Sulfolobus
Pyrodictium
Thermoproteus
Pyrobaculum
Other bacteria
Aquifex
Pyrococcus
Methanothermus
Archaeoglobus
Methanopyrus
Methanococcus
Thermotoga
Other extremophiles
?
Unknown common ancestor

Il *Tree of Life* alla luce delle simbiosi


Bacteria
Eukarya
Archaea
Proteobacteria
Cyanobacteria
Animalia
Fungi
Plantae
Archezoa
Euryarchaeota
Crenarchaeota

Sì, bello, ma in fondo storia, ma in tutto la simbiosi “oggi”?

Numero di batteri ospitati dall’intestino umano:
100.000 miliardi

Numero di cellule dell’uomo:
10.000 miliardi

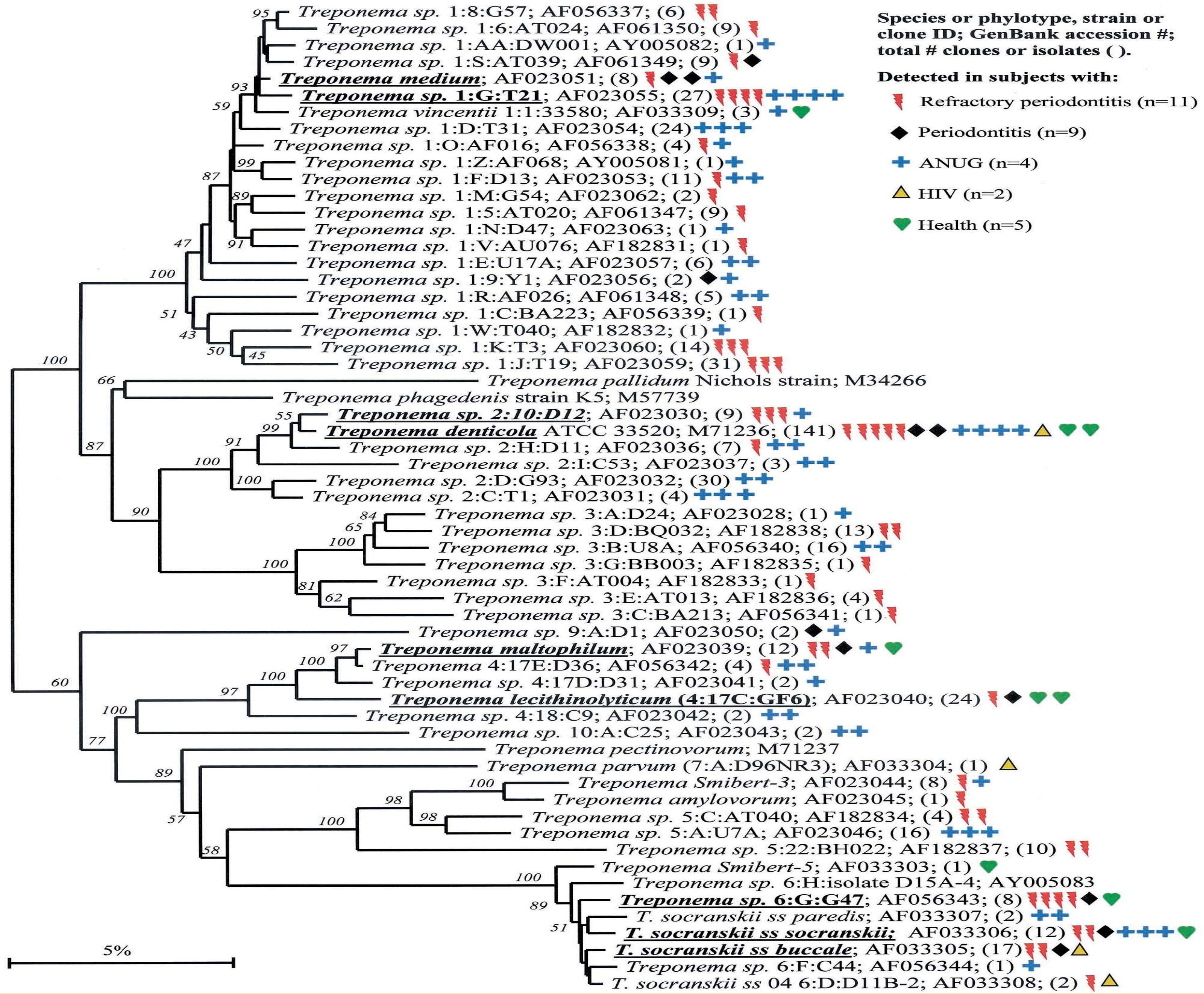
Numero di batteri associati al corpo umano:
150.000 miliardi

Numero di geni batterici nell’intestino umano:
> 300.000

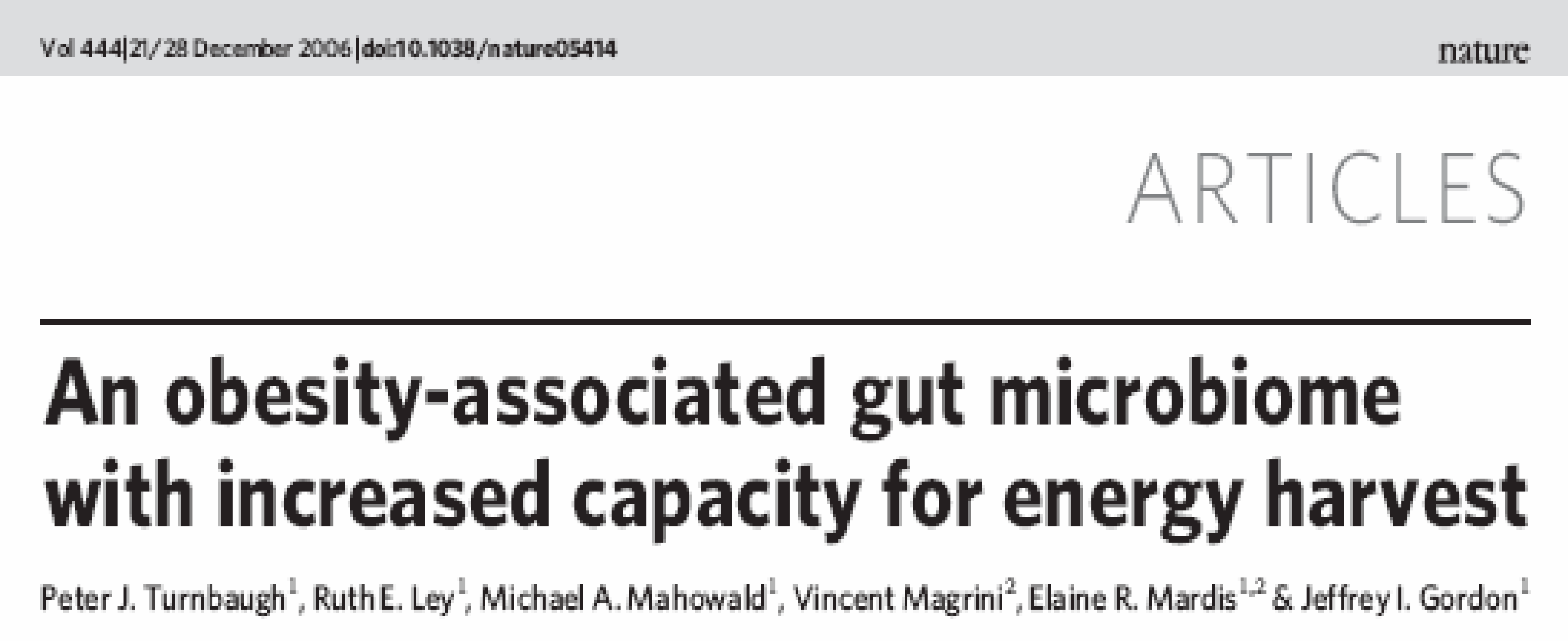
Numero specie batteriche nell’intestino:
Circa 800

Numero di ceppi batterici:
Circa 7000

Batteri associati alla placca gengivale


Treponema sp. 1:8:G57; AF056337; (6) ⚡⚡
Treponema sp. 1:6:AT024; AF061350; (9) ⚡
Treponema sp. 1:AA:DW001; AY005082; (1) ✚
Treponema sp. 1:S:AT039; AF061349; (9) ⚡◆
Treponema medium; AF023051; (8) ⚡◆◆✚
Treponema sp. 1:G:T21; AF023055; (27) ⚡⚡⚡⚡✚✚✚✚✚
Treponema vincentii 1:1:33580; AF033309; (3) ✚♥
Treponema sp. 1:D:T31; AF023054; (24) ✚✚✚
Treponema sp. 1:O:AF016; AF056338; (4) ⚡✚
Treponema sp. 1:Z:AF068; AY005081; (1) ✚
Treponema sp. 1:F:D13; AF023053; (11) ⚡✚✚
Treponema sp. 1:M:G54; AF023062; (2) ⚡
Treponema sp. 1:5:AT020; AF061347; (9) ⚡
Treponema sp. 1:N:D47; AF023063; (1) ✚
Treponema sp. 1:V:AU076; AF182831; (1) ⚡
Treponema sp. 1:E:U17A; AF023057; (6) ✚✚
Treponema sp. 1:9:Y1; AF023056; (2) ◆✚
Treponema sp. 1:R:AF026; AF061348; (5) ✚✚
Treponema sp. 1:C:BA223; AF056339; (1) ⚡
Treponema sp. 1:W:T040; AF182832; (1) ✚
Treponema sp. 1:K:T3; AF023060; (14) ⚡⚡⚡
Treponema sp. 1:J:T19; AF023059; (31) ⚡⚡⚡
Treponema pallidum Nichols strain; M34266
Treponema phagedenis strain K5; M57739
Treponema sp. 2:10:D12; AF023030; (9) ⚡⚡⚡✚
Treponema denticola ATCC 33520; M71236; (141) ⚡⚡⚡⚡⚡◆◆✚✚✚✚✚△♥♥
Treponema sp. 2:H:D11; AF023036; (7) ⚡✚✚
Treponema sp. 2:I:C53; AF023037; (3) ✚✚
Treponema sp. 2:D:G93; AF023032; (30) ✚✚
Treponema sp. 2:C:T1; AF023031; (4) ✚✚✚
Treponema sp. 3:A:D24; AF023028; (1) ✚
Treponema sp. 3:D:BQ032; AF182838; (13) ⚡⚡
Treponema sp. 3:B:U8A; AF056340; (16) ✚✚
Treponema sp. 3:G:BB003; AF182835; (1) ⚡
Treponema sp. 3:F:AT004; AF182833; (1) ⚡
Treponema sp. 3:E:AT013; AF182836; (4) ⚡
Treponema sp. 3:C:BA213; AF056341; (1) ⚡
Treponema sp. 9:A:D1; AF023050; (2) ◆✚
Treponema maltophilum; AF023039; (12) ⚡⚡◆✚♥
Treponema 4:17E:D36; AF056342; (4) ⚡✚✚
Treponema sp. 4:17D:D31; AF023041; (2) ✚
Treponema lecithinolyticum (4:17C:GF6); AF023040; (24) ⚡◆♥♥
Treponema sp. 4:18:C9; AF023042; (2) ✚✚
Treponema sp. 10:A:C25; AF023043; (2) ✚✚
Treponema pectinovorum; M71237
Treponema parvum (7:A:D96NR3); AF033304; (1) △
Treponema Smibert-3; AF023044; (8) ⚡✚
Treponema amylovorum; AF023045; (1) ⚡
Treponema sp. 5:C:AT040; AF182834; (4) ⚡⚡
Treponema sp. 5:A:U7A; AF023046; (16) ✚✚✚
Treponema sp. 5:22:BH022; AF182837; (10) ⚡⚡
Treponema Smibert-5; AF033303; (1) ♥
Treponema sp. 6:H:isolate D15A-4; AY005083
Treponema sp. 6:G:G47; AF056343; (8) ⚡⚡⚡⚡◆♥
T. socranskii ss paredis; AF033307; (2) ✚✚
T. socranskii ss socranskii; AF033306; (12) ⚡⚡◆✚✚✚✚♥
T. socranskii ss buccale; AF033305; (17) ⚡⚡◆△
Treponema sp. 6:F:C44; AF056344; (1) ✚
T. socranskii ss 04 6:D:D11B-2; AF033308; (2) ⚡△
Species or phylotype, strain or clone ID; GenBank accession #; total # clones or isolates ( ).
Detected in subjects with:
⚡ Refractory periodontitis (n=11)
◆ Periodontitis (n=9)
✚ ANUG (n=4)
△ HIV (n=2)
♥ Health (n=5)
5%
95
93
59
99
87
89
47
91
100
51
43
50
45
100
66
55
99
91
87
100
100
90
84
65
100
100
81
62
97
100
100
60
97
100
77
89
100
98
57
98
100
58
100
89
51

“Non sono grasso, sono parassitato”



Vol 444|21/28 December 2006|doi:10.1038/nature05414

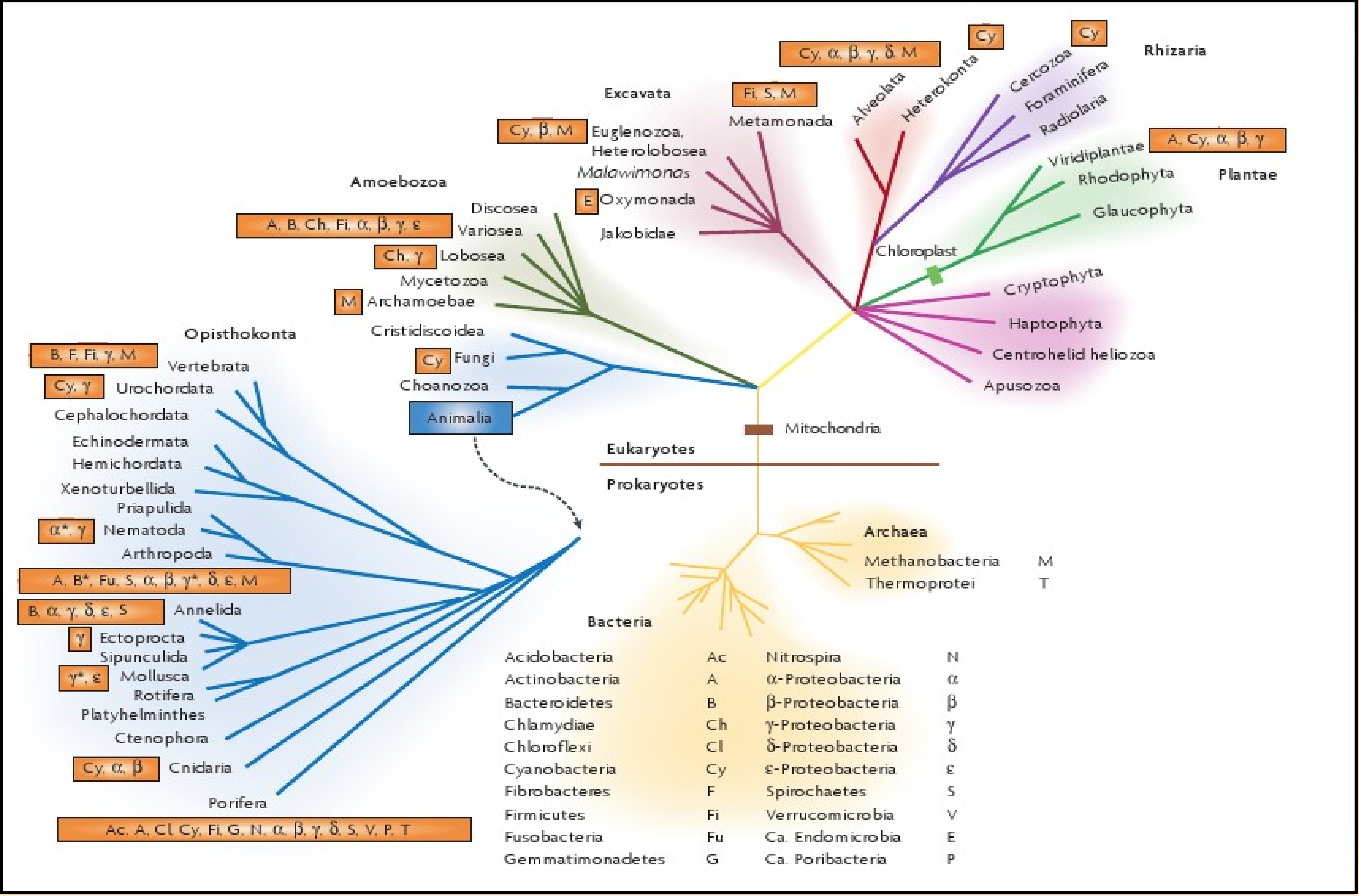
nature

ARTICLES

An obesity-associated gut microbiome with increased capacity for energy harvest

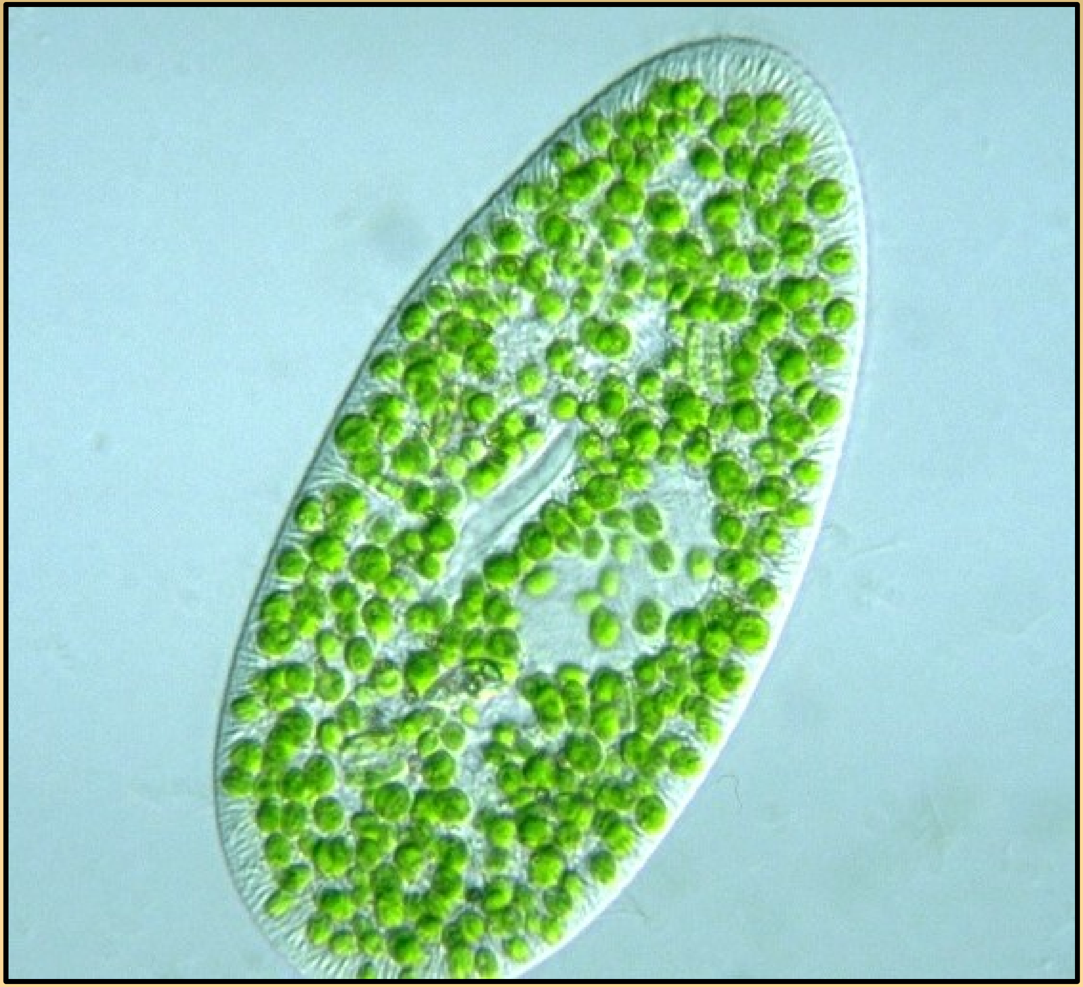
Peter J. Turnbaugh[1], Ruth E. Ley[1], Michael A. Mahowald[1], Vincent Magrini[2], Elaine R. Mardis[1,2] & Jeffrey I. Gordon[1]

Endosimbiosi con “batteri”: una “abitudine” diffusa


Cy, α, β, γ, δ, M
Cy
Cy
Rhizaria
Excavata
Fi, S, M
Alveolata
Heterokonta
Cercozoa
Foraminifera
Radiolaria
Metamonada
Cy, β, M
Euglenozoa,
Heterolobosea
Malawimonas
A, Cy, α, β, γ
Viridiplantae
Rhodophyta
Plantae
E
Oxymonada
Glaucophyta
Jakobidae
Amoebozoa
Discosea
A, B, Ch, Fi, α, β, γ, ε
Variosea
Ch, γ
Lobosea
Chloroplast
Mycetozoa
M
Archamoebae
Cryptophyta
Haptophyta
Centrohelid heliozoa
Apusozoa
Opisthokonta
Cristidiscoidea
B, F, Fi, γ, M
Vertebrata
Cy
Fungi
Cy, γ
Urochordata
Choanozoa
Cephalochordata
Animalia
Echinodermata
Hemichordata
Mitochondria
Eukaryotes
Xenoturbellida
Prokaryotes
Priapulida
α*, γ
Nematoda
Arthropoda
A, B*, Fu, S, α, β, γ*, δ, ε, M
Archaea
Methanobacteria
M
Thermoprotei
T
B, α, γ, δ, ε, S
Annelida
γ
Ectoprocta
Sipunculida
γ*, ε
Mollusca
Rotifera
Platyhelminthes
Ctenophora
Cy, α, β
Cnidaria
Porifera
Ac, A, Cl, Cy, Fi, G, N, α, β, γ, δ, S, V, P, T
Bacteria

Acidobacteria	Ac	Nitrospira	N
Actinobacteria	A	α-Proteobacteria	α
Bacteroidetes	B	β-Proteobacteria	β
Chlamydiae	Ch	γ-Proteobacteria	γ
Chloroflexi	Cl	δ-Proteobacteria	δ
Cyanobacteria	Cy	ε-Proteobacteria	ε
Fibrobacteres	F	Spirochaetes	S
Firmicutes	Fi	Verrucomicrobia	V
Fusobacteria	Fu	Ca. Endomicrobia	E
Gemmatimonadetes	G	Ca. Poribacteria	P

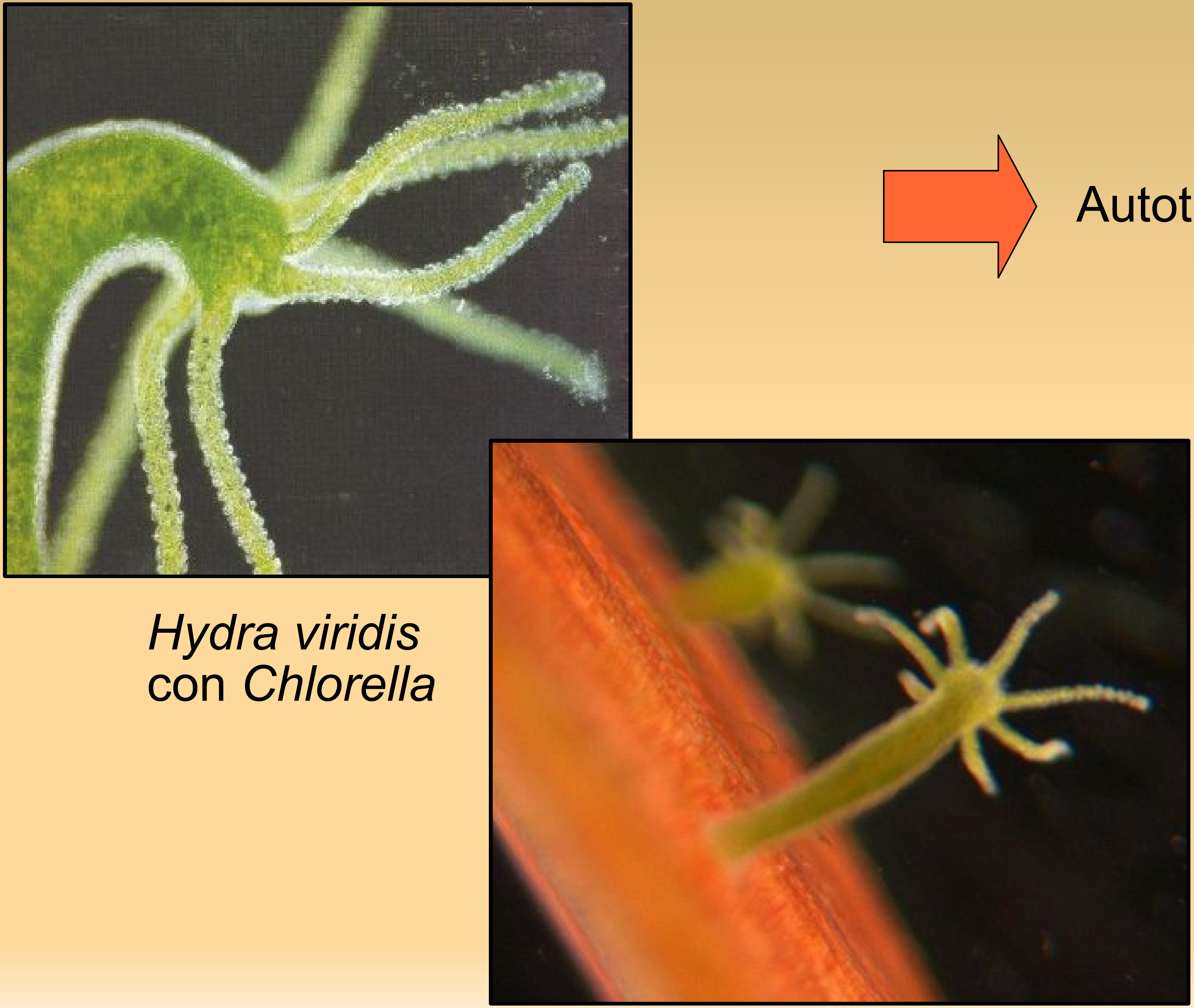
Endosimbiosi – casi particolari



Paramecium bursaria con *Chlorella*

Autotrofo o eterotrofo?

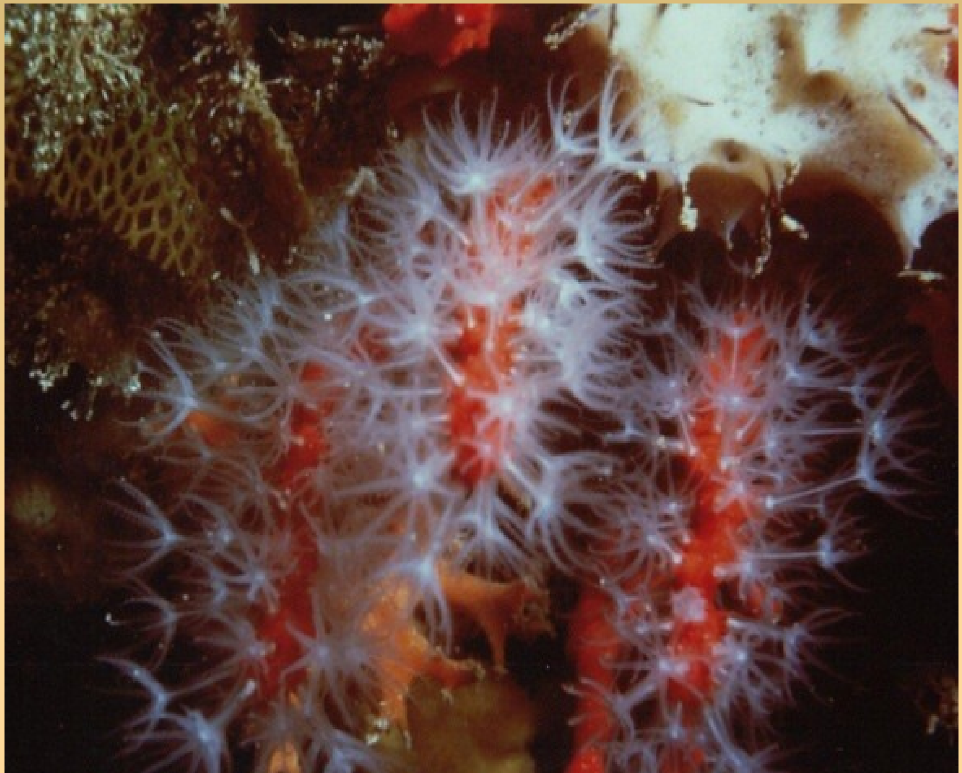
Endosimbiosi – casi particolari

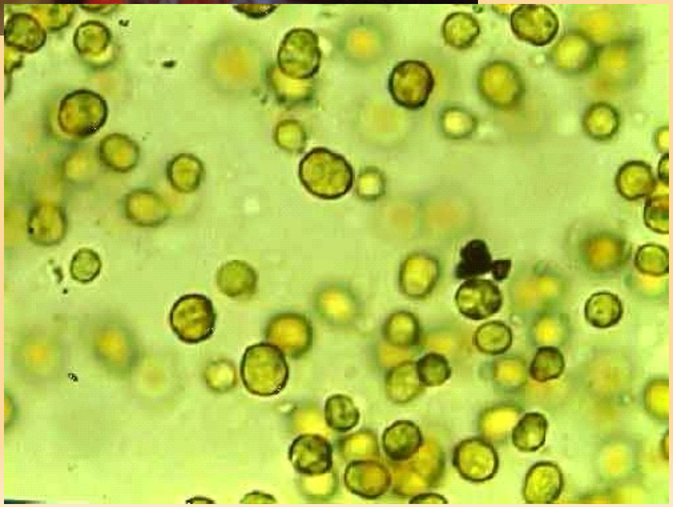


Hydra viridis
con *Chlorella*

→ Autotrofo o eterotrofo?

Endosimbiosi – casi particolari





Autotrofo o eterotrofo?

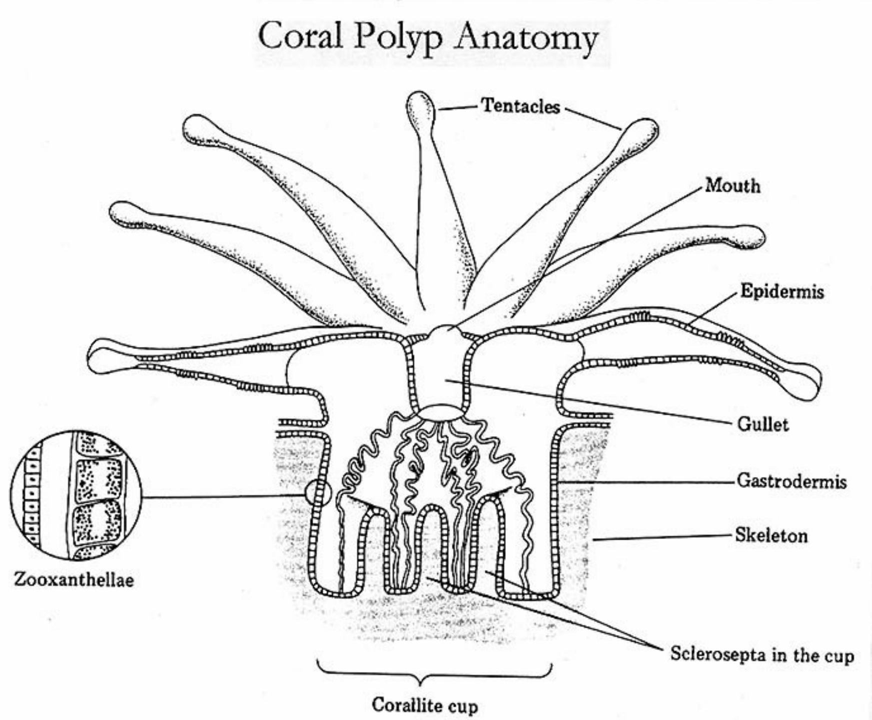
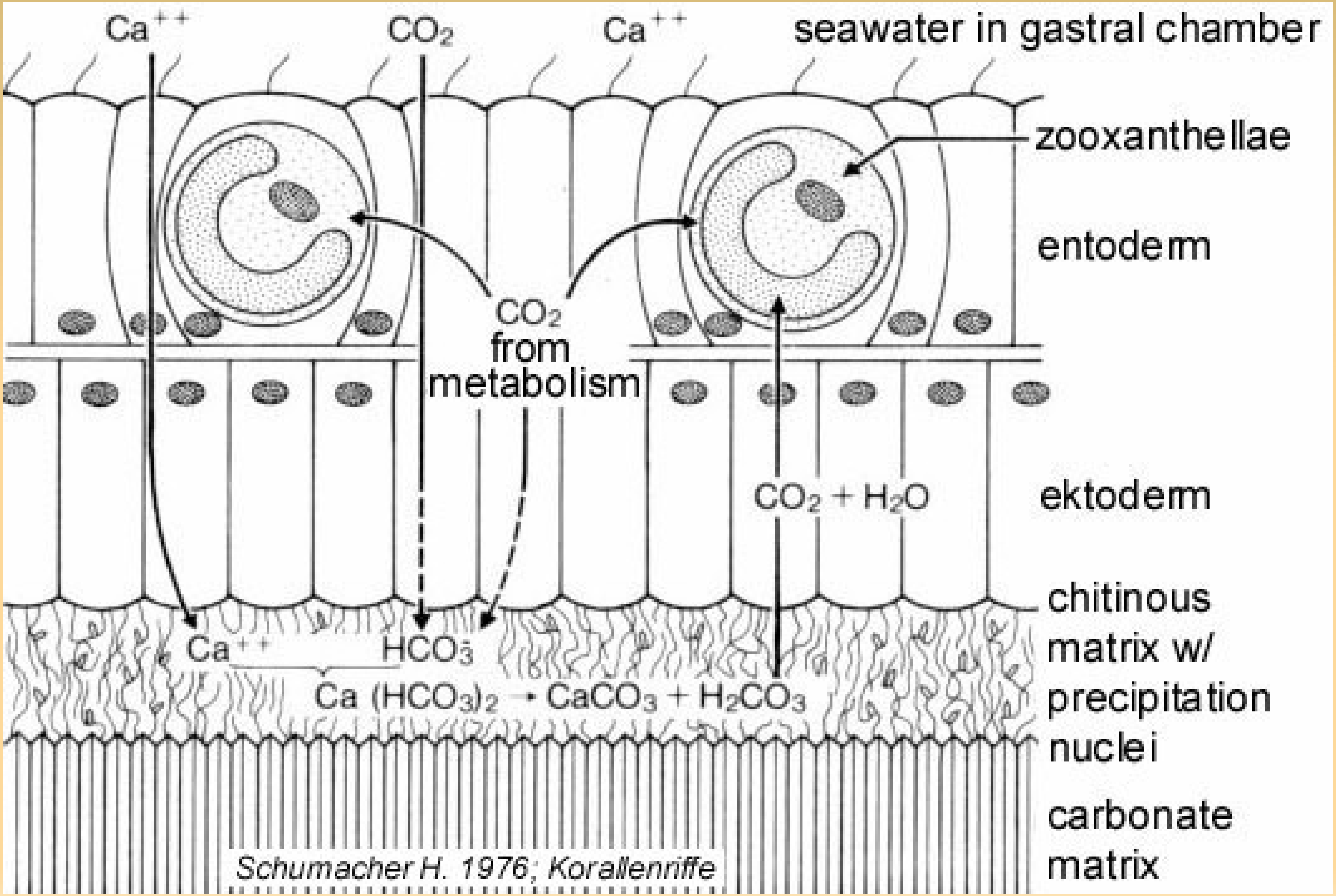

Coral Polyp Anatomy
Tentacles
Mouth
Epidermis
Gullet
Gastrodermis
Skeleton
Zooxanthellae
Sclerosepta in the cup
Corallite cup

Figure 9.3 Anatomy of a coral polyp.

Endosimbiosi – casi particolari


Ca++
CO2
Ca++
seawater in gastral chamber
zooxanthellae
entoderm
CO2 from metabolism
ektoderm
CO2 + H2O
chitinous matrix w/ precipitation nuclei
Ca++
HCO3-
Ca (HCO3)2 → CaCO3 + H2CO3
carbonate matrix

Schumacher H. 1976; Korallenriffe

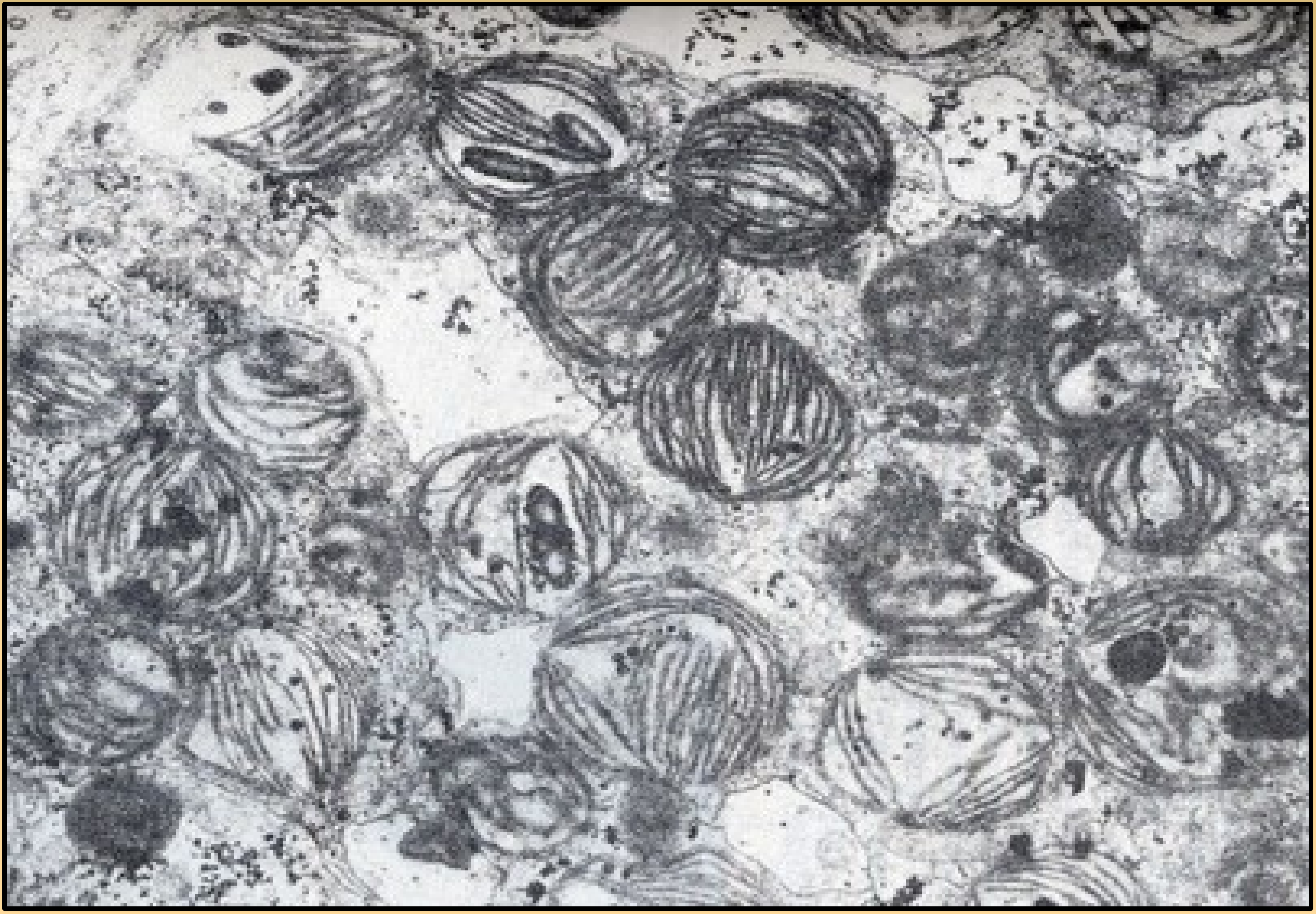
Endosimbiosi – casi particolari

Elysia viridis

Placida dendritica

Plakobranchus sp.

Endosimbiosi – casi particolari

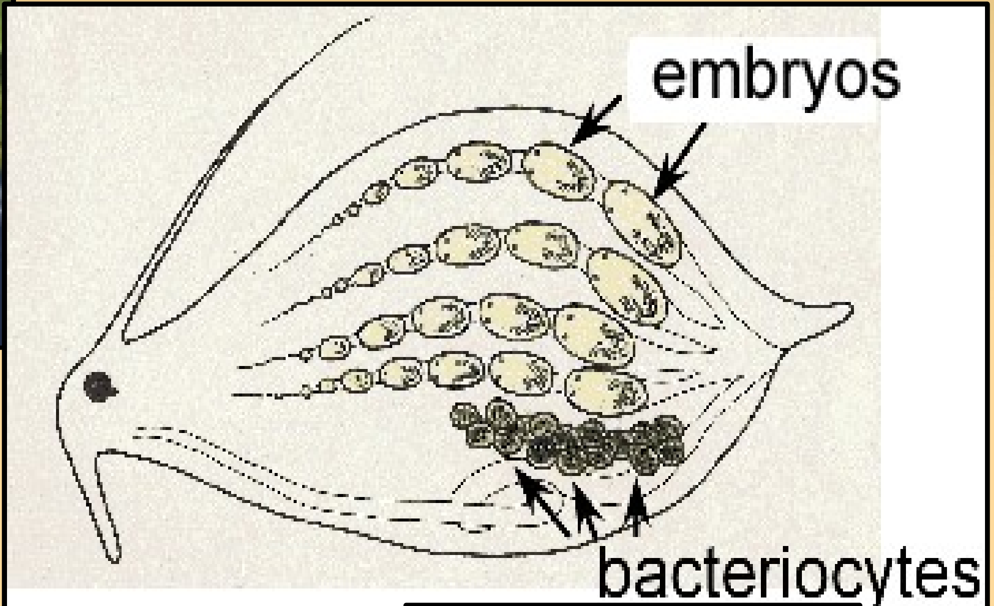


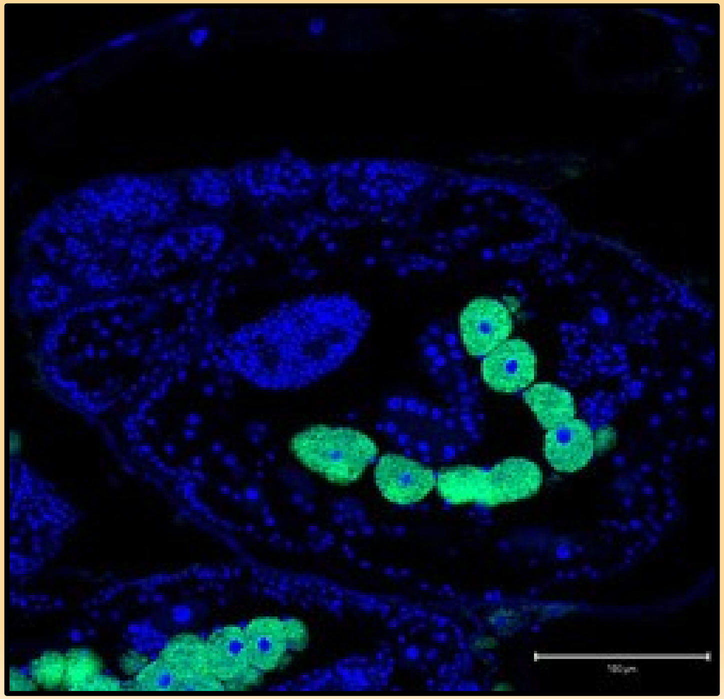
cloroplasti in cellula digestiva di *Elisia viridis*

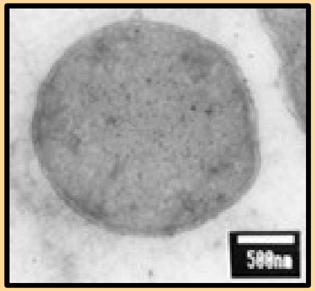
Le simbiosi intracellulari con batteri

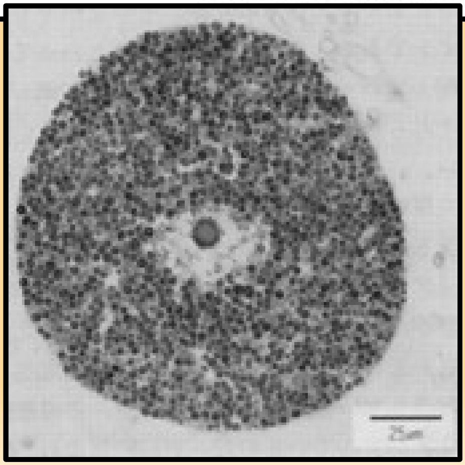
Simbiosi nutrizionali

Buchnera aphidicola e gli afidi

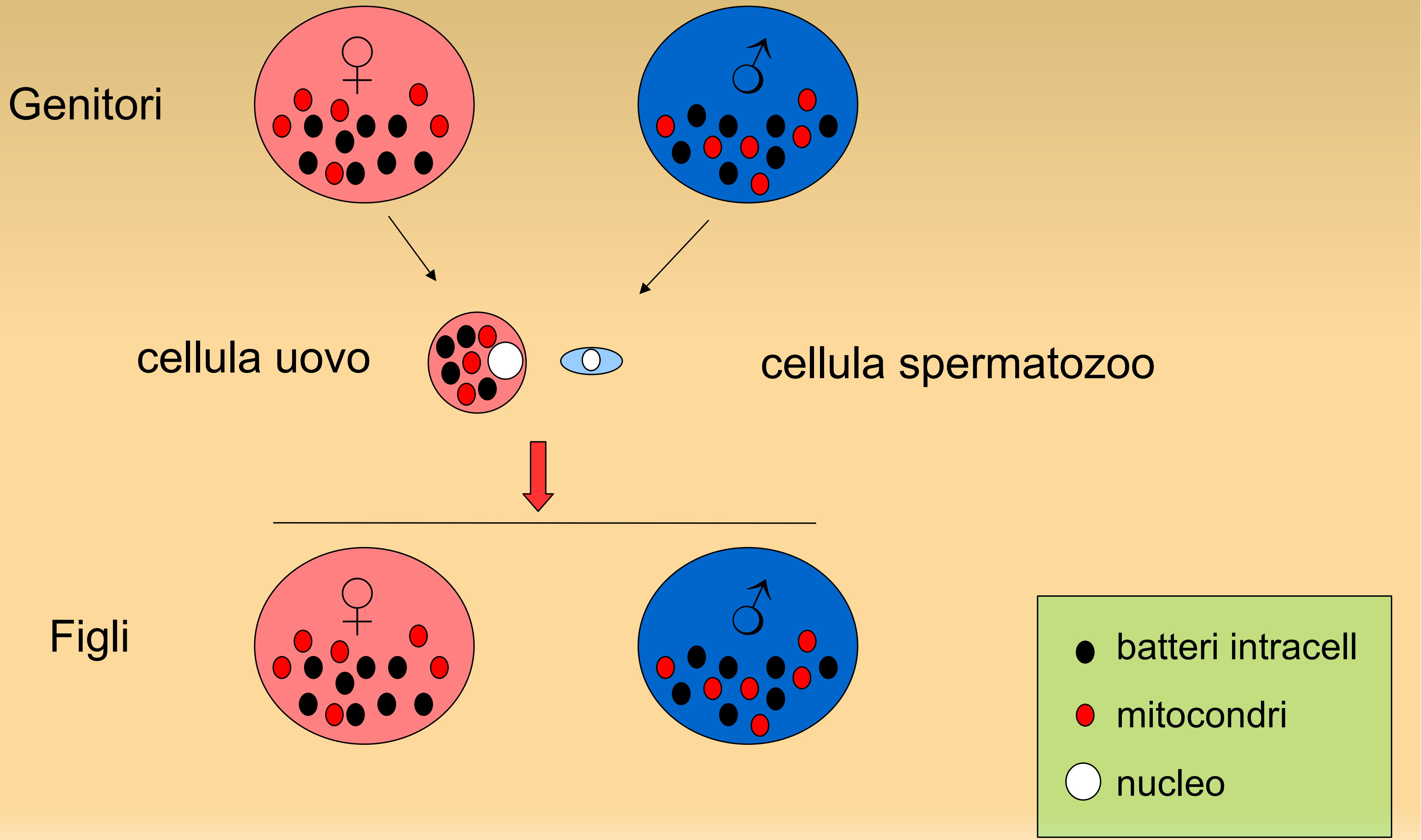

embryos
bacteriocytes







Eredità matrilineare dei simbionti



Genitori

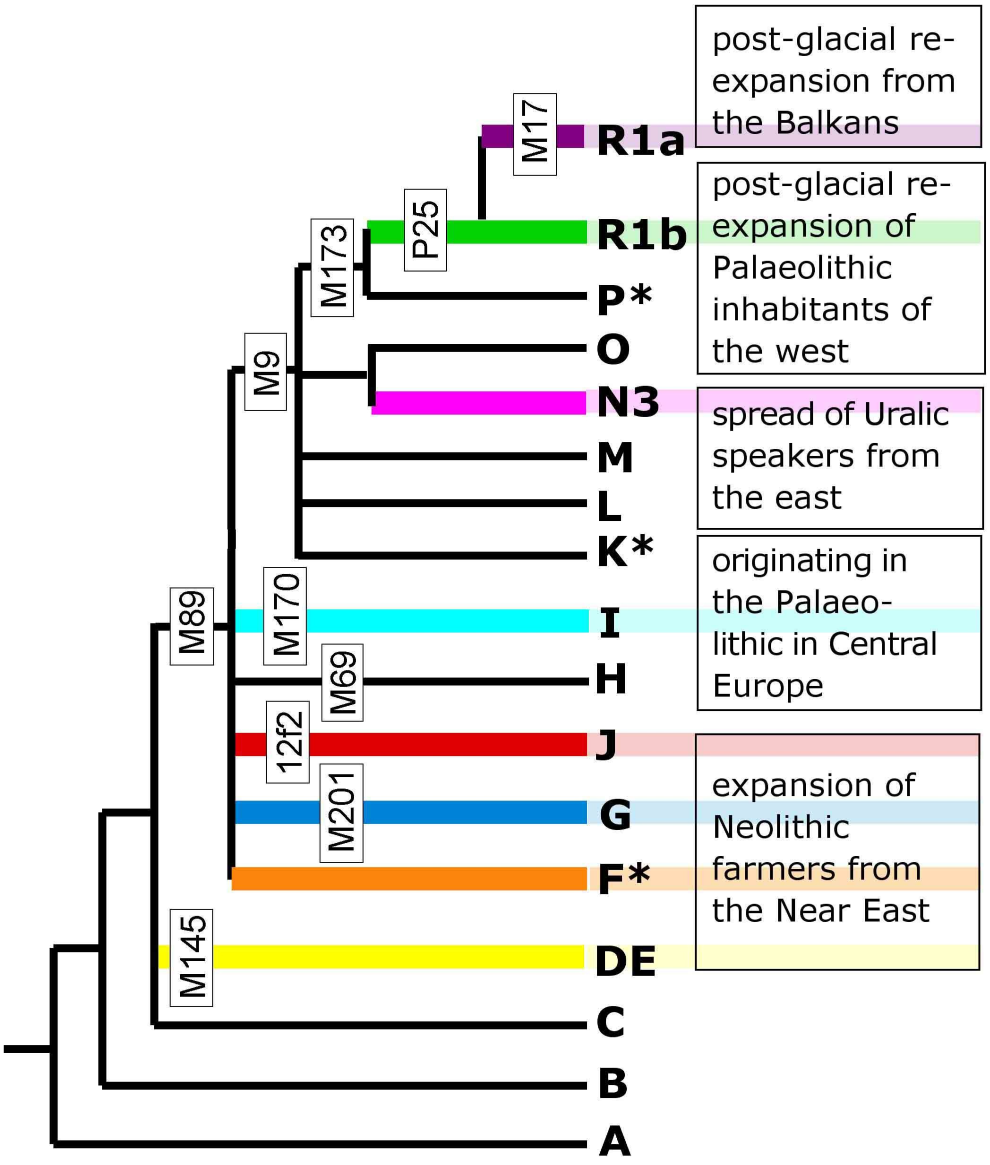
cellula uovo

cellula spermatozoo

Figli

- ● batteri intracell
- 🔴 mitocondri
- ○ nucleo

Utilizzo del DNA mitocondriale per la ricostruzione filogenetica


M17
R1a
P25
R1b
M173
P*
M9
O
N3
M
L
K*
M89
M170
I
M69
H
12f2
J
M201
G
F*
M145
DE
C
B
A

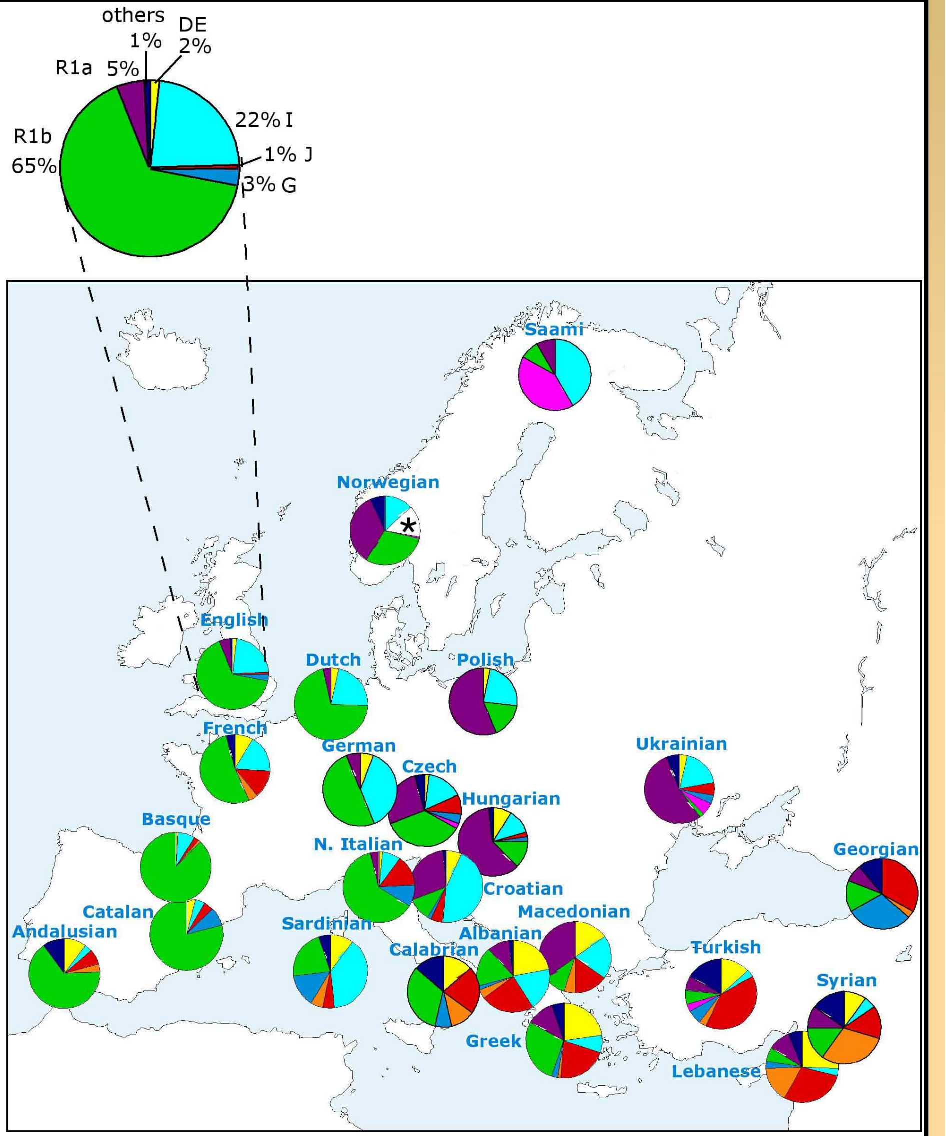
post-glacial re-expansion from the Balkans

post-glacial re-expansion of Palaeolithic inhabitants of the west

spread of Uralic speakers from the east

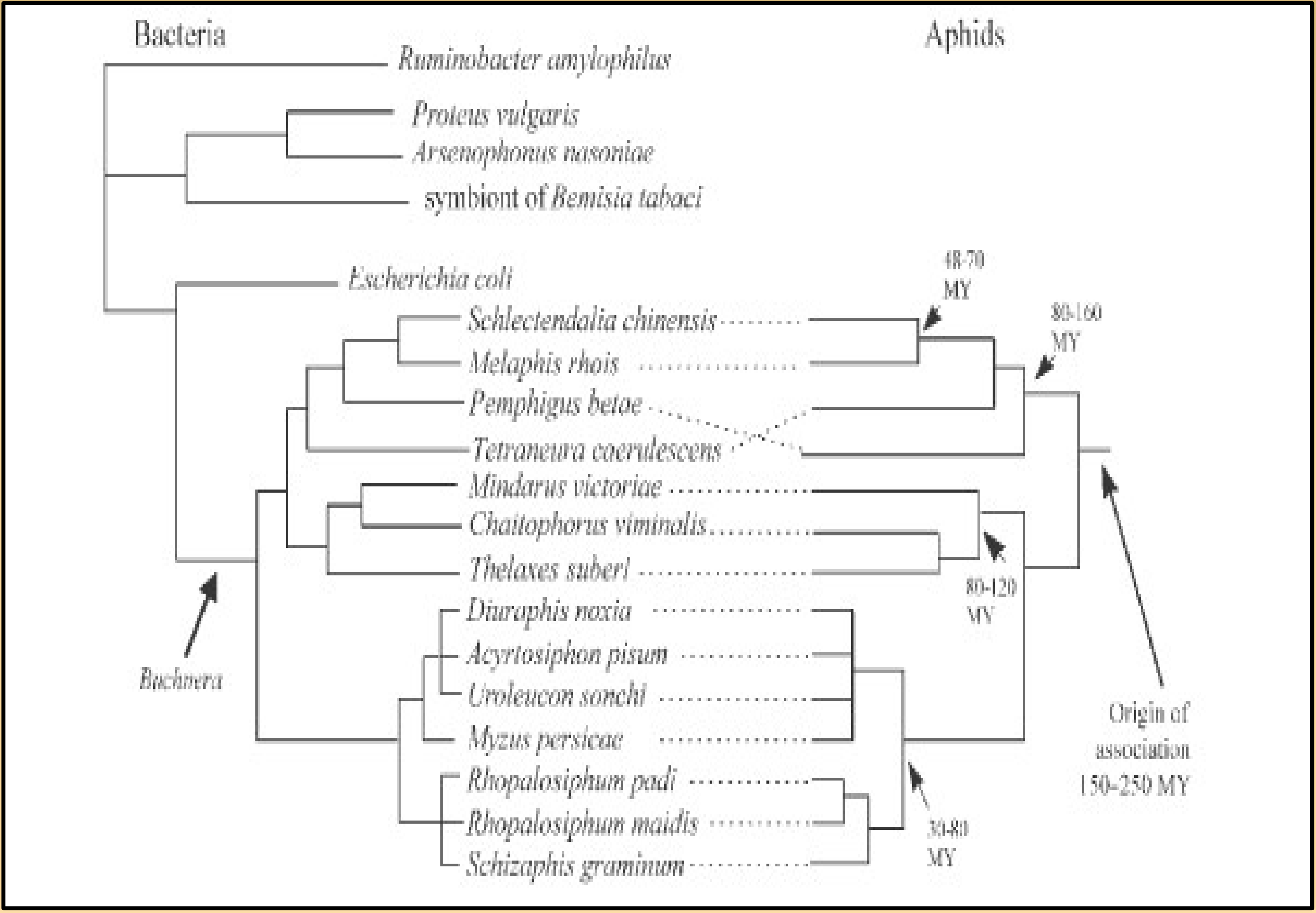
originating in the Palaeolithic in Central Europe

expansion of Neolithic farmers from the Near East

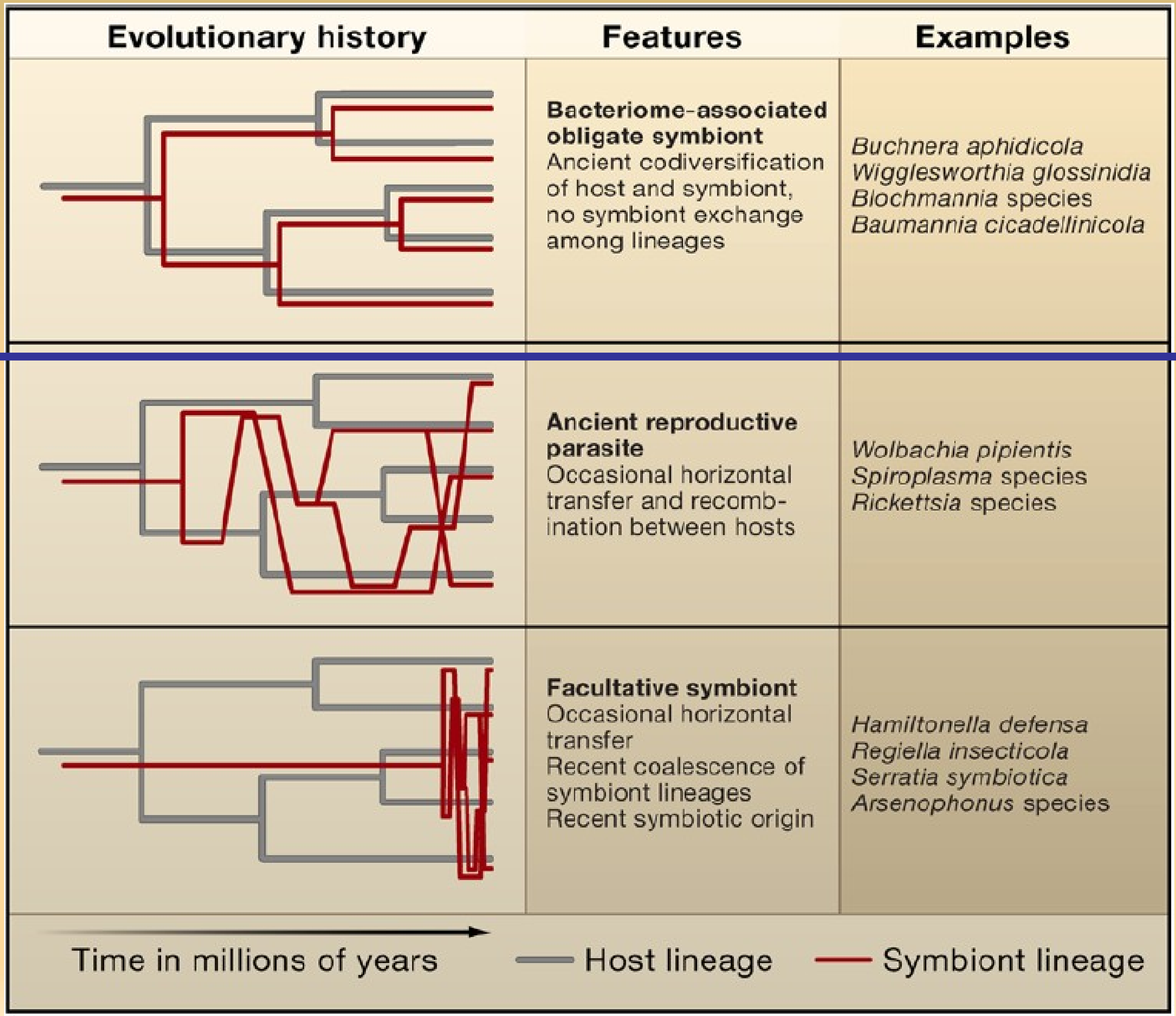

others 1%
DE 2%
R1a 5%
22% I
R1b 65%
1% J
3% G
Saami
Norwegian
*
English
Dutch
Polish
French
German
Czech
Ukrainian
Hungarian
Basque
N. Italian
Georgian
Croatian
Catalan
Macedonian
Andalusian
Sardinian
Albanian
Turkish
Calabrian
Syrian
Greek
Lebanese

Most information from: Semino et al. The genetic legacy of Paleolithic Homo sapiens sapiens in extant Europeans: a Y chromosome perspective. Science 290, 1155-1159 (2000). English sample: our study; Norwegian sample: Capelli et al. A Y chromosome census of the British Isles. Curr. Biol. 13, 979-984 (2003). * Haplogroups F* plus G.

Comparazione filogenetica ospite-simbionte

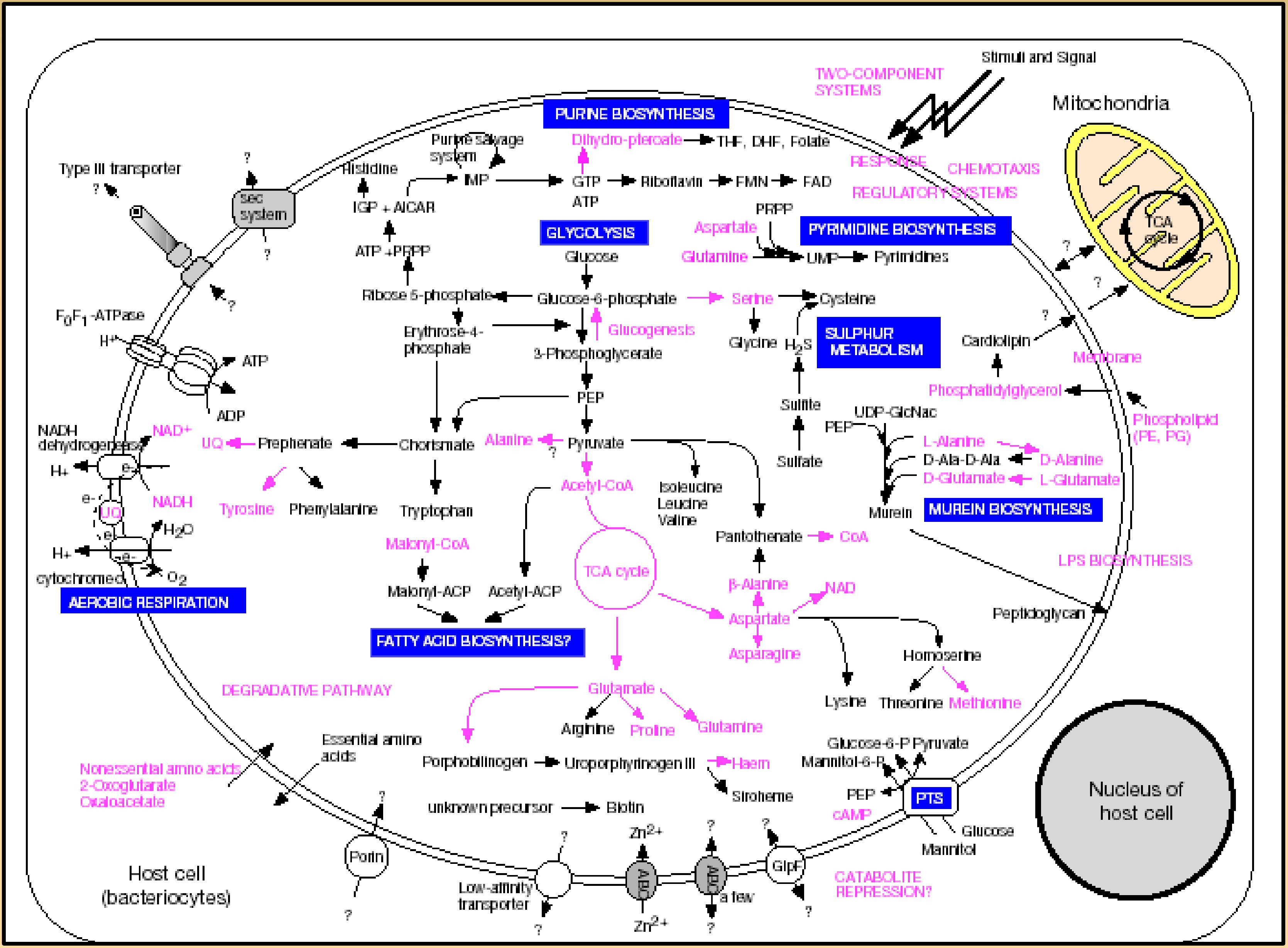

Bacteria
Aphids
Ruminobacter amylophilus
Proteus vulgaris
Arsenophonus nasoniae
symbiont of Bemisia tabaci
Escherichia coli
48-70 MY
Schlectendalia chinensis
80-160 MY
Melaphis rhois
Pemphigus betae
Tetraneura caerulescens
Mindarus victoriae
Chaitophorus viminalis
Thelaxes suberi
80-120 MY
Diuraphis noxia
Acyrtosiphon pisum
Buchnera
Uroleucon sonchi
Myzus persicae
Origin of association 150-250 MY
Rhopalosiphum padi
Rhopalosiphum maidis
30-80 MY
Schizaphis graminum

Le simbiosi intracellulari con i batteri



Evolutionary history	Features	Examples
	Bacteriome-associated obligate symbiont Ancient codiversification of host and symbiont, no symbiont exchange among lineages	*Buchnera aphidicola* *Wigglesworthia glossinidia* *Blochmannia* species *Baumannia cicadellinicola*
	Ancient reproductive parasite Occasional horizontal transfer and recombination between hosts	*Wolbachia pipientis* *Spiroplasma* species *Rickettsia* species
	Facultative symbiont Occasional horizontal transfer Recent coalescence of symbiont lineages Recent symbiotic origin	*Hamiltonella defensa* *Regiella insecticola* *Serratia symbiotica* *Arsenophonus* species

La simbiosi nutrizionale tra *Buchnera aphidicola* e gli afidi


Stimuli and Signal
TWO-COMPONENT SYSTEMS
Mitochondria
TCA cycle
PURINE BIOSYNTHESIS
Dihydro-pteroate
THF, DHF, Folate
Purine salvage system
Histidine
IMP
GTP
ATP
Riboflavin
FMN
FAD
IGP + AICAR
ATP +PRPP
RESPONSE
CHEMOTAXIS
REGULATORY SYSTEMS
Type III transporter
?
sec system
GLYCOLYSIS
Glucose
Aspartate
PRPP
PYRIMIDINE BIOSYNTHESIS
Glutamine
UMP
Pyrimidines
Ribose 5-phosphate
Glucose-6-phosphate
Serine
Cysteine
F_0F_1-ATPase
H^+
ATP
ADP
Erythrose-4-phosphate
Glucogenesis
3-Phosphoglycerate
Glycine
H_2S
SULPHUR METABOLISM
Cardiolipin
Membrane
PEP
Sulfite
Phosphatidylglycerol
NADH dehydrogenase
NAD+
UQ
Prephenate
Chorismate
Alanine
Pyruvate
Sulfate
UDP-GlcNac
PEP
L-Alanine
D-Ala-D-Ala
D-Alanine
D-Glutamate
L-Glutamate
Phospholipid (PE, PG)
H+
e-
NADH
Tyrosine
Phenylalanine
Tryptophan
Acetyl-CoA
Isoleucine
Leucine
Valine
Murein
MUREIN BIOSYNTHESIS
UQ
H_2O
H+
cytochromed
O_2
Malonyl-CoA
TCA cycle
Pantothenate
CoA
LPS BIOSYNTHESIS
AEROBIC RESPIRATION
Malonyl-ACP
Acetyl-ACP
β-Alanine
NAD
Aspartate
Peptidoglycan
FATTY ACID BIOSYNTHESIS?
Asparagine
Homoserine
DEGRADATIVE PATHWAY
Glutamate
Lysine
Threonine
Methionine
Arginine
Proline
Glutamine
Essential amino acids
Porphobilinogen
Uroporphyrinogen III
Haem
Glucose-6-P
Pyruvate
Mannitol-6-P
Nonessential amino acids
2-Oxoglutarate
Oxaloacetate
Siroheme
PEP
PTS
cAMP
unknown precursor
Biotin
Zn^{2+}
Nucleus of host cell
Porin
Glucose
Mannitol
GlpF
Host cell (bacteriocytes)
Low-affinity transporter
ABC
ABC
a few
CATABOLITE REPRESSION?
Zn^{2+}

La riduzione del genoma di *Buchnera aphidicola*

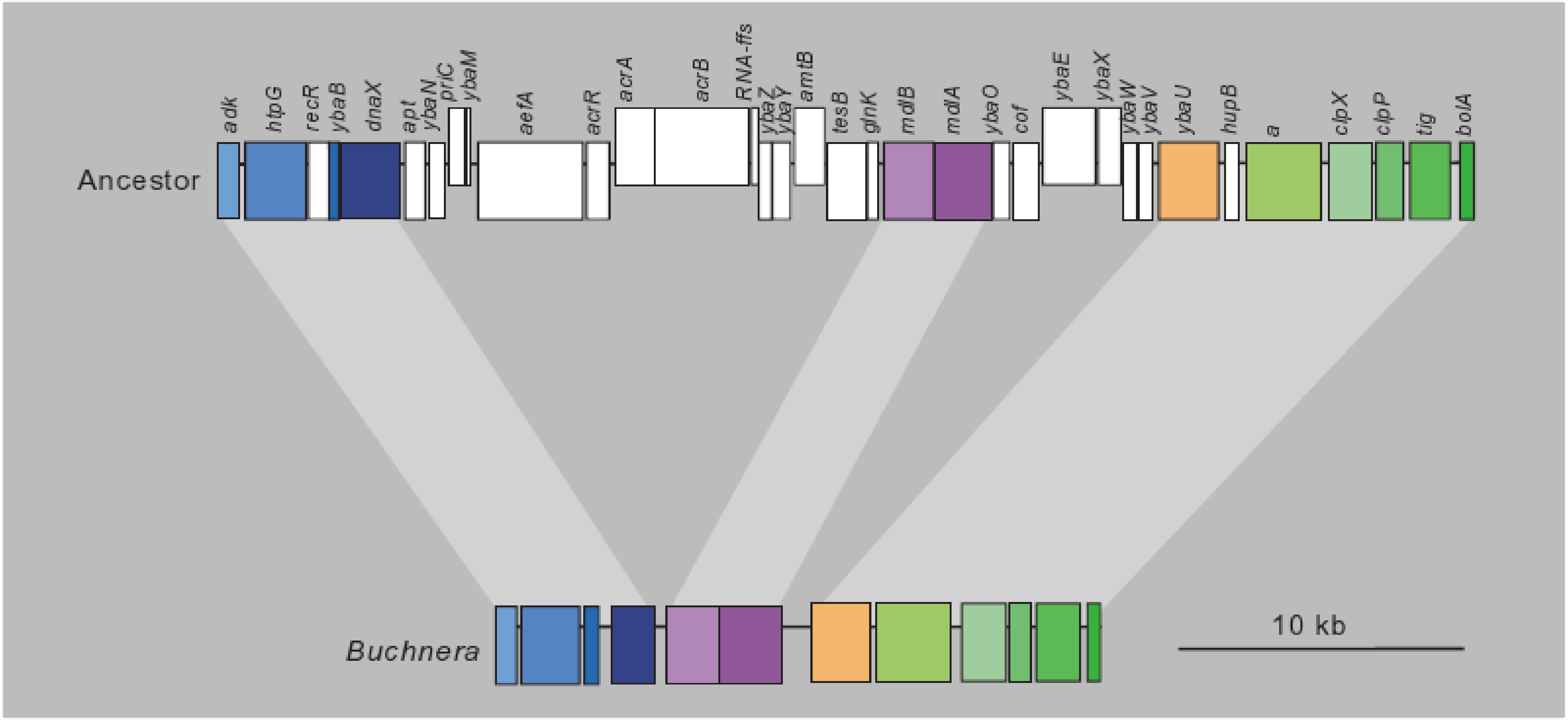

adk
htpG
recR
ybaB
dnaX
apt
ybaN
priC
ybaM
aefA
acrR
acrA
acrB
RNA-ffs
ybaZ
ybaY
amtB
tesB
glnK
mdlB
mdlA
ybaO
cof
ybaE
ybaX
ybaW
ybaV
ybaU
hupB
a
clpX
clpP
tig
bolA
Ancestor
Buchnera
10 kb

Figure 2
Part of a syntenic fragment from *Buchnera* and the ancestor (same as *E. coli* for this region). Deleted loci are white in the ancestor; orthologous genes are color-coded. Genes shifted up in the figure are oriented forward in the genome; genes shifted down are oriented backwards.

La riduzione del genoma di *Buchnera aphidicola*

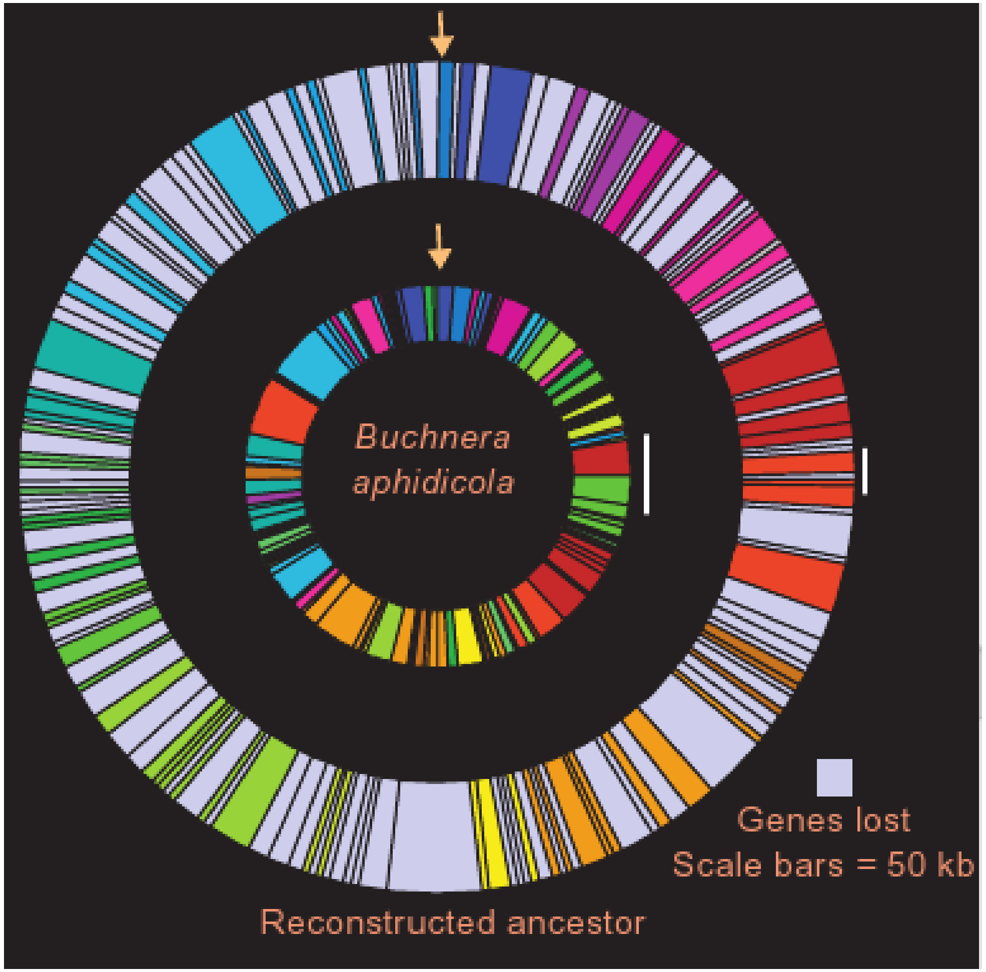
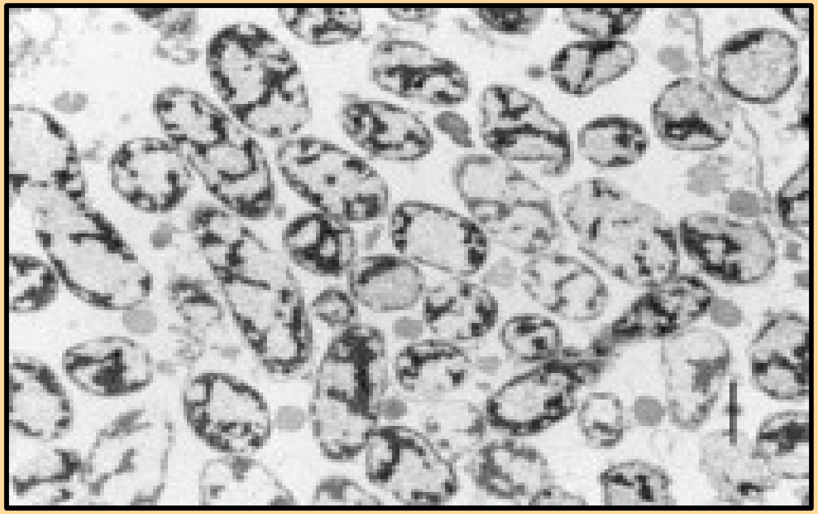

Buchnera aphidicola
Genes lost
Scale bars = 50 kb
Reconstructed ancestor

Figure 3
Graphic depiction of syntenic fragments and lost regions in the genome of the reconstructed ancestor and in *Buchnera*. Syntenic fragments are color-coded based on position in the ancestor. Lost regions occurring between syntenic fragments are gray.

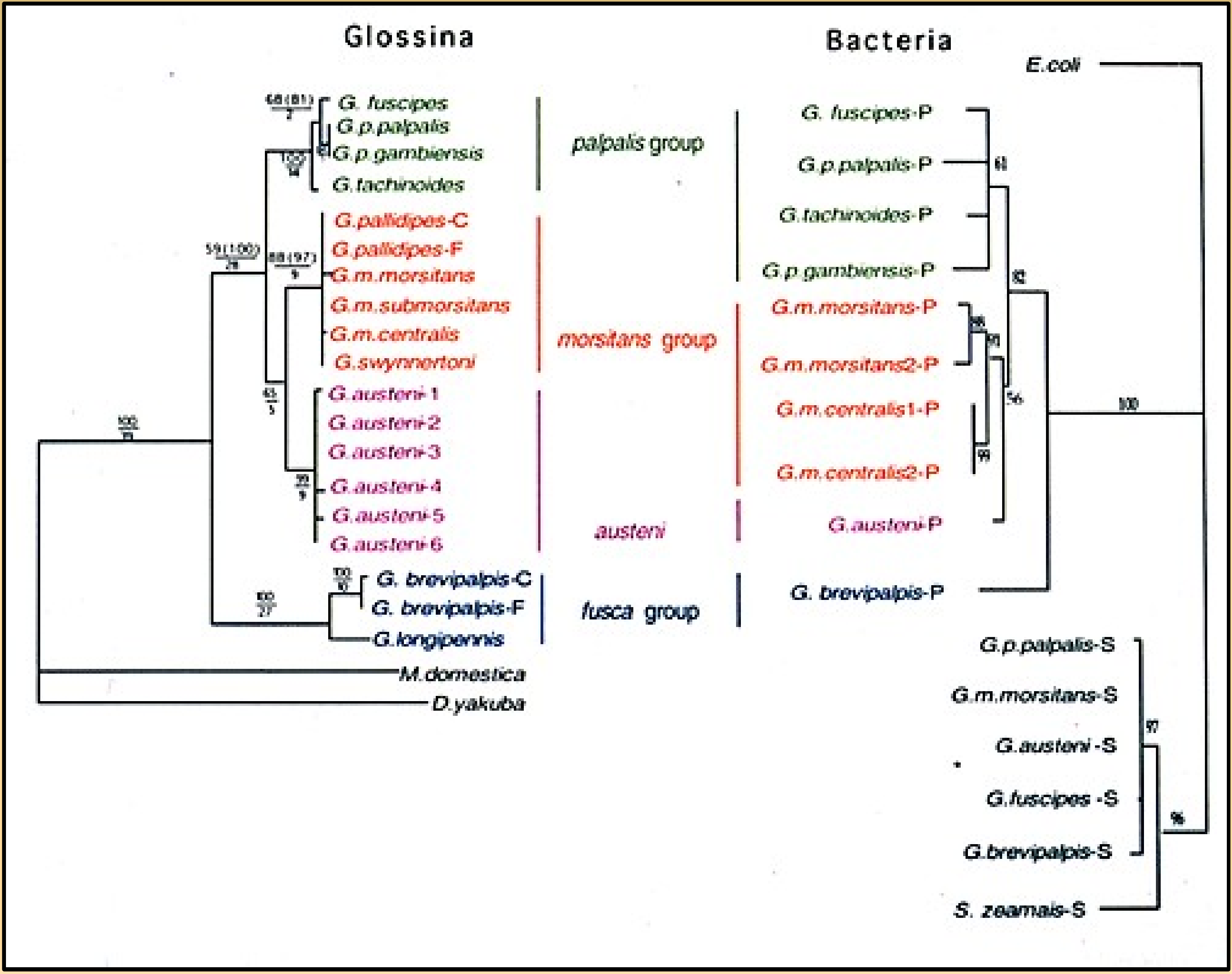
Le mosche tsè-tsè e *Wigglesworthia glossinidia*

Glossina spp.



Eye of Science/Photoresearchers

Le mosche tsè-tsè e *Wigglesworthia glossinidia*


Glossina
Bacteria
G. fuscipes
G.p.palpalis
G.p.gambiensis
G.tachinoides
G.pallidipes-C
G.pallidipes-F
G.m.morsitans
G.m.submorsitans
G.m.centralis
G.swynnertoni
G.austeni-1
G.austeni-2
G.austeni-3
G.austeni-4
G.austeni-5
G.austeni-6
G. brevipalpis-C
G. brevipalpis-F
G.longipennis
M.domestica
D.yakuba
palpalis group
morsitans group
austeni
fusca group
E.coli
G. fuscipes-P
G.p.palpalis-P
G.tachinoides-P
G.p.gambiensis-P
G.m.morsitans-P
G.m.morsitans2-P
G.m.centralis1-P
G.m.centralis2-P
G.austeni-P
G. brevipalpis-P
G.p.palpalis-S
G.m.morsitans-S
G.austeni -S
G.fuscipes -S
G.brevipalpis-S
S. zeamais-S
100
97
96
82
56
99

Le mosche tsè-tsè e *Wigglesworthia glossinidia*

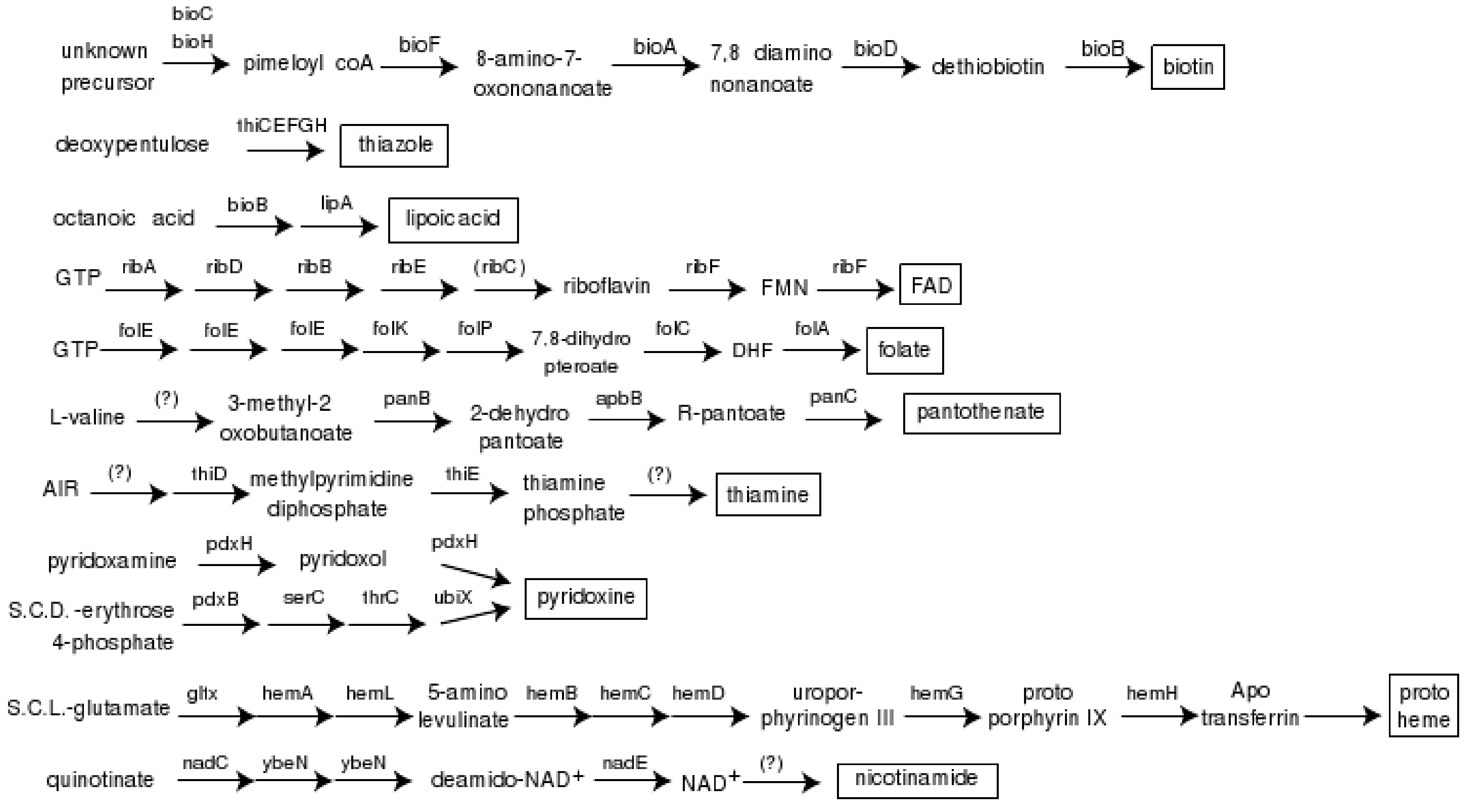

unknown precursor
bioC bioH
pimeloyl coA
bioF
8-amino-7-oxononanoate
bioA
7,8 diamino nonanoate
bioD
dethiobiotin
bioB
biotin
deoxypentulose
thiCEFGH
thiazole
octanoic acid
bioB
lipA
lipoic acid
GTP
ribA
ribD
ribB
ribE
(ribC)
riboflavin
ribF
FMN
ribF
FAD
GTP
folE
folE
folE
folK
folP
7,8-dihydro pteroate
folC
DHF
folA
folate
L-valine
(?)
3-methyl-2 oxobutanoate
panB
2-dehydro pantoate
apbB
R-pantoate
panC
pantothenate
AIR
(?)
thiD
methylpyrimidine diphosphate
thiE
thiamine phosphate
(?)
thiamine
pyridoxamine
pdxH
pyridoxol
pdxH
pyridoxine
S.C.D.-erythrose 4-phosphate
pdxB
serC
thrC
ubiX
S.C.L.-glutamate
gltx
hemA
hemL
5-amino levulinate
hemB
hemC
hemD
uropor-phyrinogen III
hemG
proto porphyrin IX
hemH
Apo transferrin
proto heme
quinotinate
nadC
ybeN
ybeN
deamido-NAD+
nadE
NAD+
(?)
nicotinamide

Fig. 2 Cofactor biosynthetic pathways in *W. glossinidia* deduced from the gene set. The sequential pathways are represented by arrows, each indicating one step catalyzed by the enzyme named. The end product of each reaction is boxed. The question markes indicate steps for which no genes were found in the *W. glossinidia* genome. The *W. glossinidia* genome encodes the potential to synthesize biotin, thiazole, lipoic acid, FAD (riboflavin, B2), folate, pantothenate, thiamine (B1), pyridoxine (B6), protoheme and nicotinamide.

Le mosche tsè-tsè e *Wigglesworthia glossinidia*

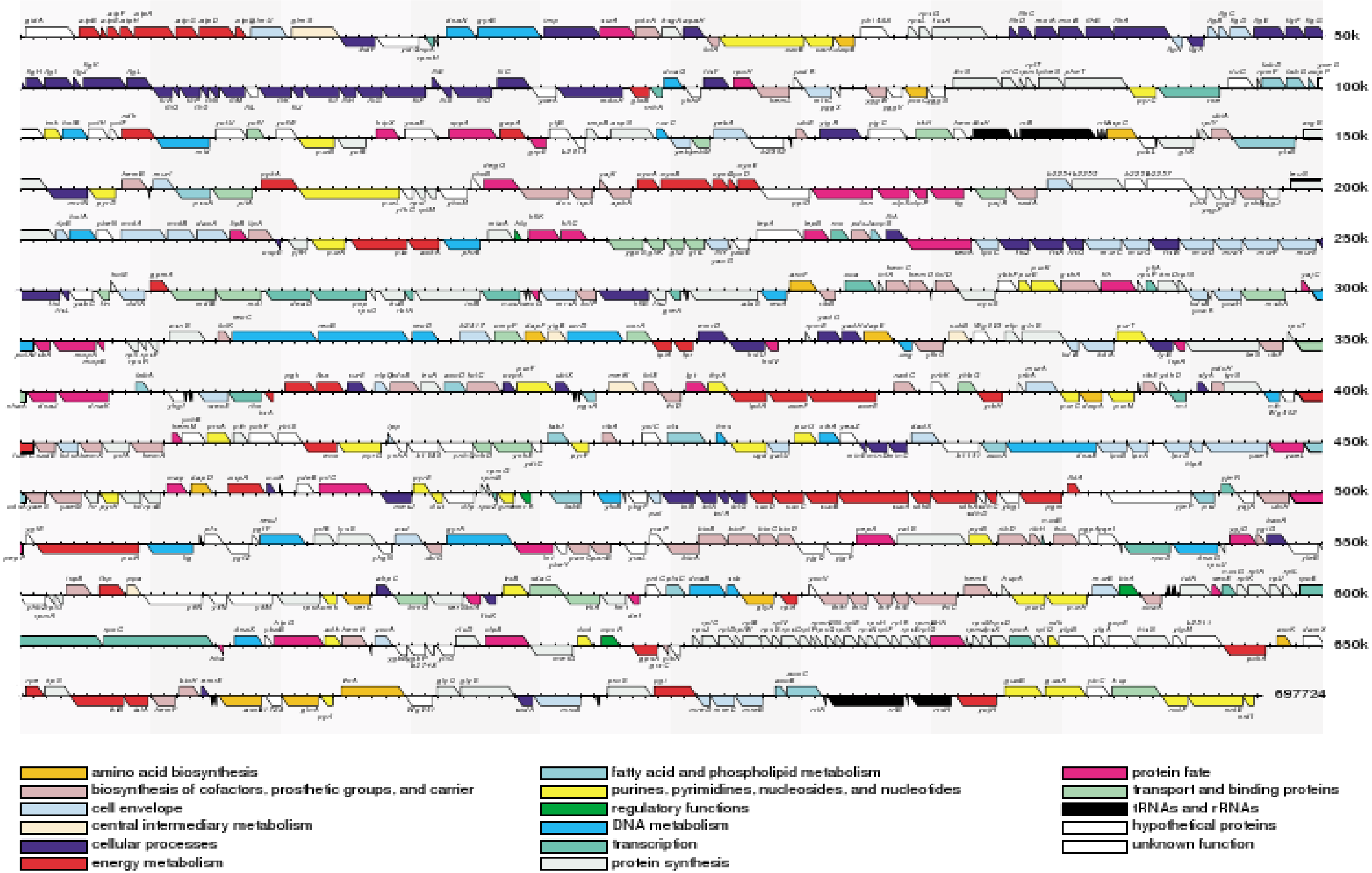
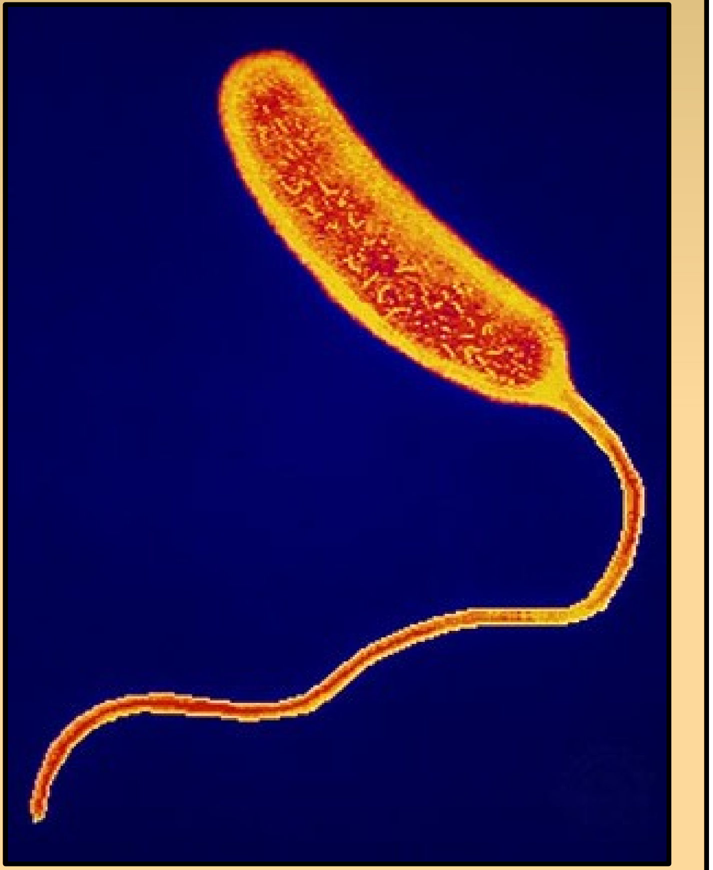

50k
100k
150k
200k
250k
300k
350k
400k
450k
500k
550k
600k
650k
697724
amino acid biosynthesis
biosynthesis of cofactors, prosthetic groups, and carrier
cell envelope
central intermediary metabolism
cellular processes
energy metabolism
fatty acid and phospholipid metabolism
purines, pyrimidines, nucleosides, and nucleotides
regulatory functions
DNA metabolism
transcription
protein synthesis
protein fate
transport and binding proteins
tRNAs and rRNAs
hypothetical proteins
unknown function

Fig. 1 Linear representation of the *W. glossinidia* chromosome illustrating the location of each predicted coding sequences and RNA gene. The predicted coding sequences were compared with a non-redundant protein database for assignment of putative functions. In addition, pWig1 encodes spermidine N1-acetyltransferase, three putative membrane proteins with similarities to a mechano-sensitive channel protein (*yggB*), a putative transmembrane protein of *Salmonella typhimurium* and a cation-transport inhibitor protein of *Neisseria meningitidis* (stomatin/Mec-2 family), respectively. Another of its predicted coding sequences products is homologous to TraT of the F incompatibility group plasmids. A small heat shock protein (ibp) is also encoded by the *Buchnera* plasmid.

Le mosche tsè-tsè e *Wigglesworthia glossinidia*



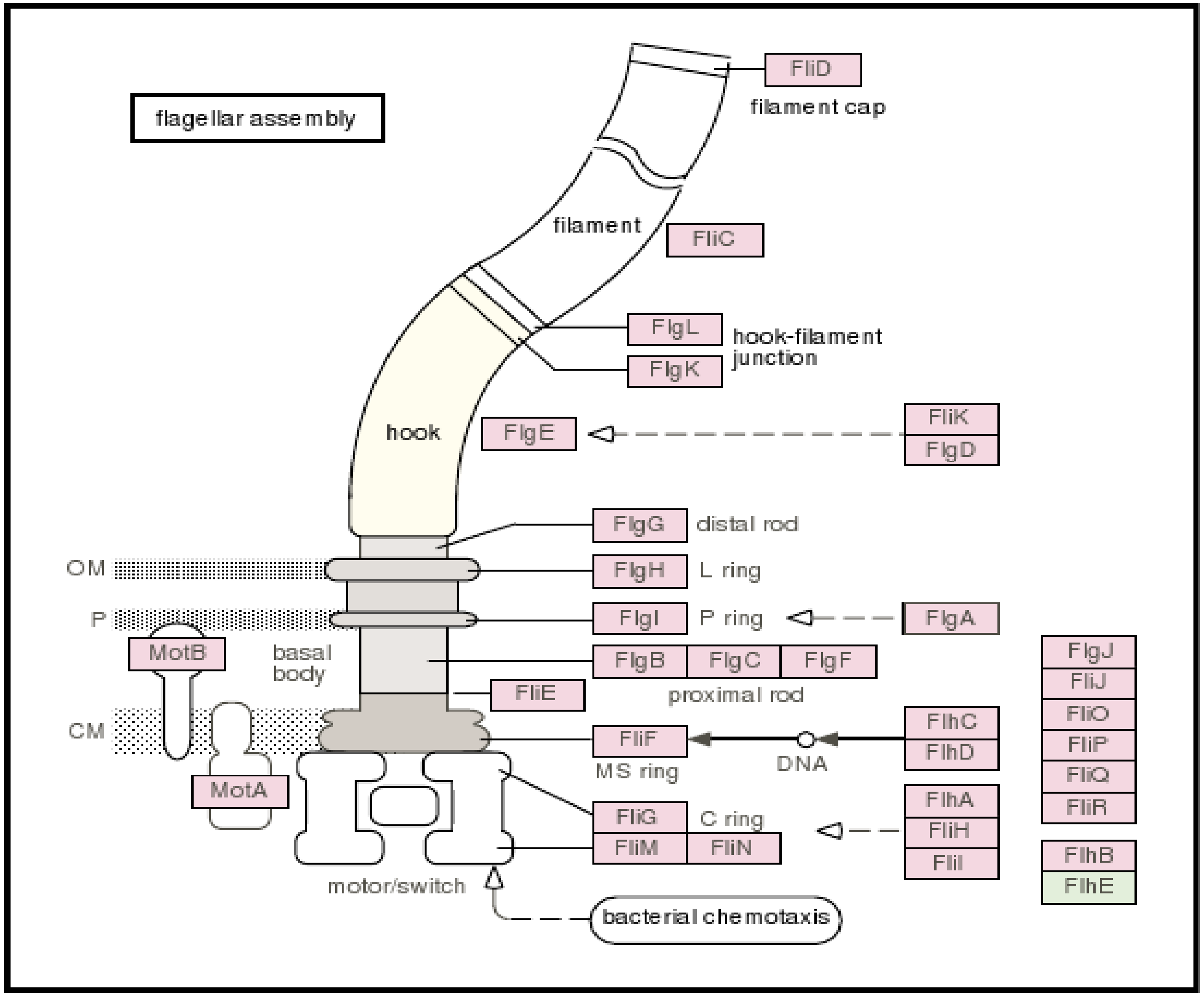

flagellar assembly
FliD
filament cap
filament
FliC
FlgL
FlgK
hook-filament junction
hook
FlgE
FliK
FlgD
FlgG
distal rod
OM
FlgH
L ring
P
FlgI
P ring
FlgA
MotB
basal body
FlgB
FlgC
FlgF
FliE
proximal rod
FlgJ
FliJ
FliO
FliP
FliQ
FliR
CM
FliF
MS ring
DNA
FlhC
FlhD
MotA
FliG
C ring
FliM
FliN
FlhA
FliH
FliI
FlhB
FlhE
motor/switch
bacterial chemotaxis

Fig. 3 Genes involved in the synthesis of flagellar assembly of *E. coli* K12 MG1655. The pink boxes denote homologs present in the *W. glossinidia* genome and the green boxes show genes that are not present in *W. glossinidia*. *W. glossinidia* has retained genes encoding flagellar functions, including the basal body, hook, filament, filament cap regions and the integral membrane proteins required for motility functions, *motA* and *motB*. OM, outer membrane; P, periplasmic space; CM, cell membrane. Region III within the flagellar *fli* operon of *E. coli* and *S. typhimurium* is composed of two regions, IIIa and IIIb, with a disruption consisting of DNA unrelated to the flagellar system[29]. The disruption is ancient, having taken place approximately 150 million years ago[30]. The organization of the IIIa and IIIb region genes in *W. glossinidia* is continuous, however, suggesting that *W. glossinidia* predates the divergence of the two free-living bacteria.

Le mosche tsè-tsè e *Sodalis glossinidius*

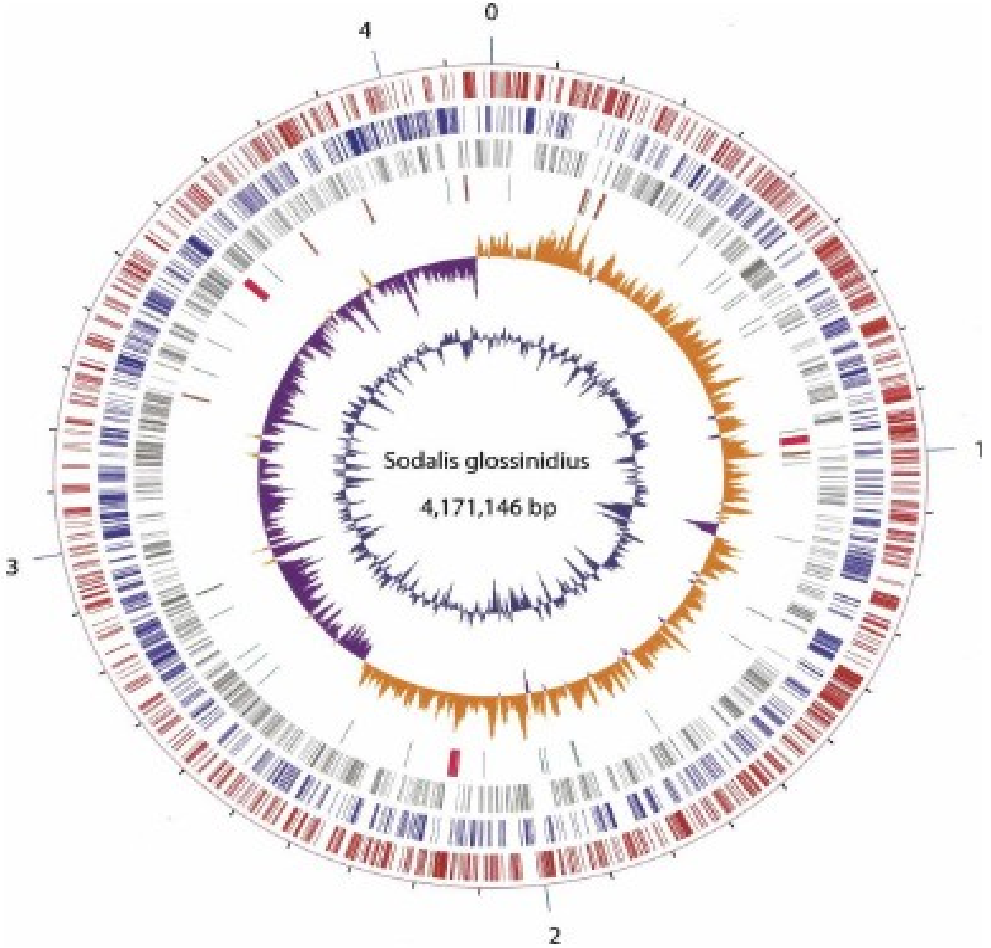
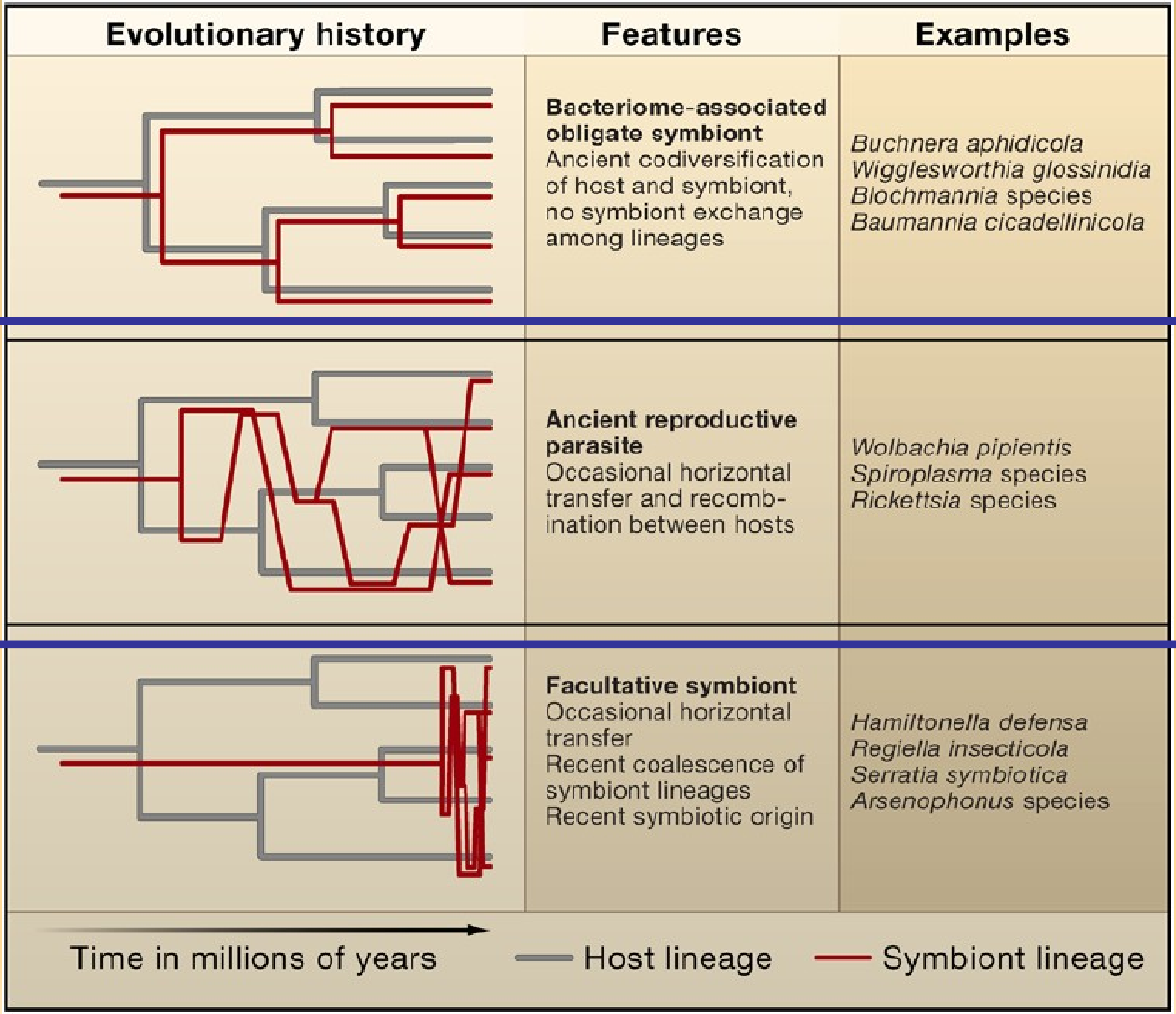


Figure 1. Circular representation of the *Sodalis glossinidius* chromosome. The outer scale (indicated by numbers 1–4) is shown in megabases. From the outside in: circle 1, positive strand CDSs (red); circle 2, negative strand CDSs (blue); circle 3, pseudogenes (gray); circle 4, tRNA genes (green), rRNA genes (brown), genes for type III secretion systems (pink); circle 5, GC skew ([G − C]/[G+C]; khaki indicates values >0; purple indicates values <0); and circle 6, G+C content (higher values outward).

... ma erosione

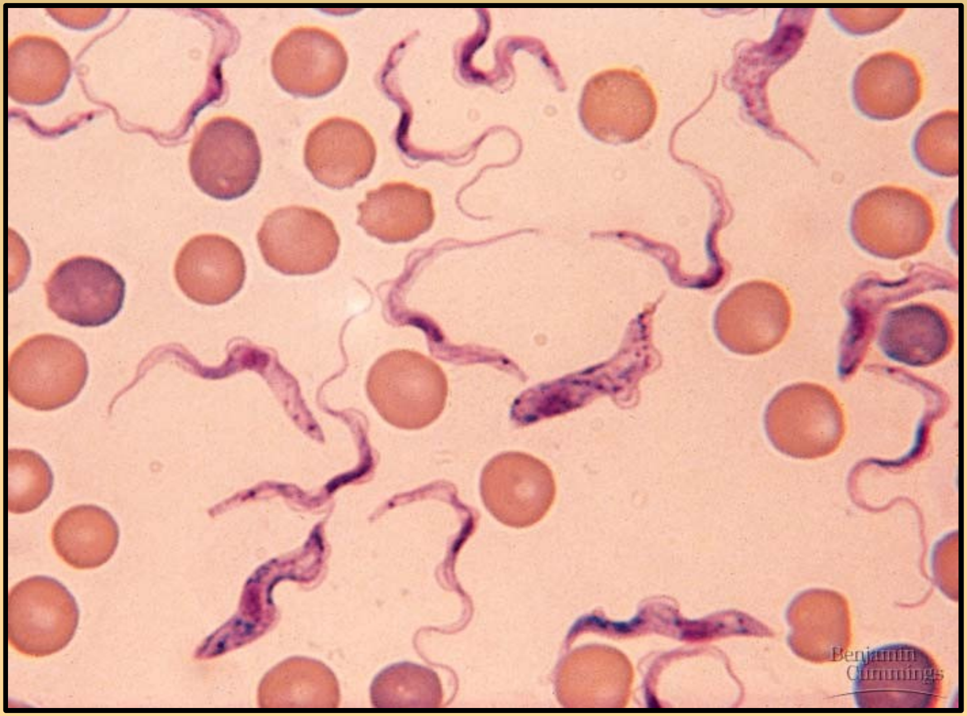
Le simbiosi intracellulari con i batteri



Evolutionary history	Features	Examples
	Bacteriome-associated obligate symbiont Ancient codiversification of host and symbiont, no symbiont exchange among lineages	*Buchnera aphidicola* *Wigglesworthia glossinidia* *Blochmannia* species *Baumannia cicadellinicola*
	Ancient reproductive parasite Occasional horizontal transfer and recombination between hosts	*Wolbachia pipientis* *Spiroplasma* species *Rickettsia* species
	Facultative symbiont Occasional horizontal transfer Recent coalescence of symbiont lineages Recent symbiotic origin	*Hamiltonella defensa* *Regiella insecticola* *Serratia symbiotica* *Arsenophonus* species

Le mosche tsè-tsè e *Sodalis glossinidius*

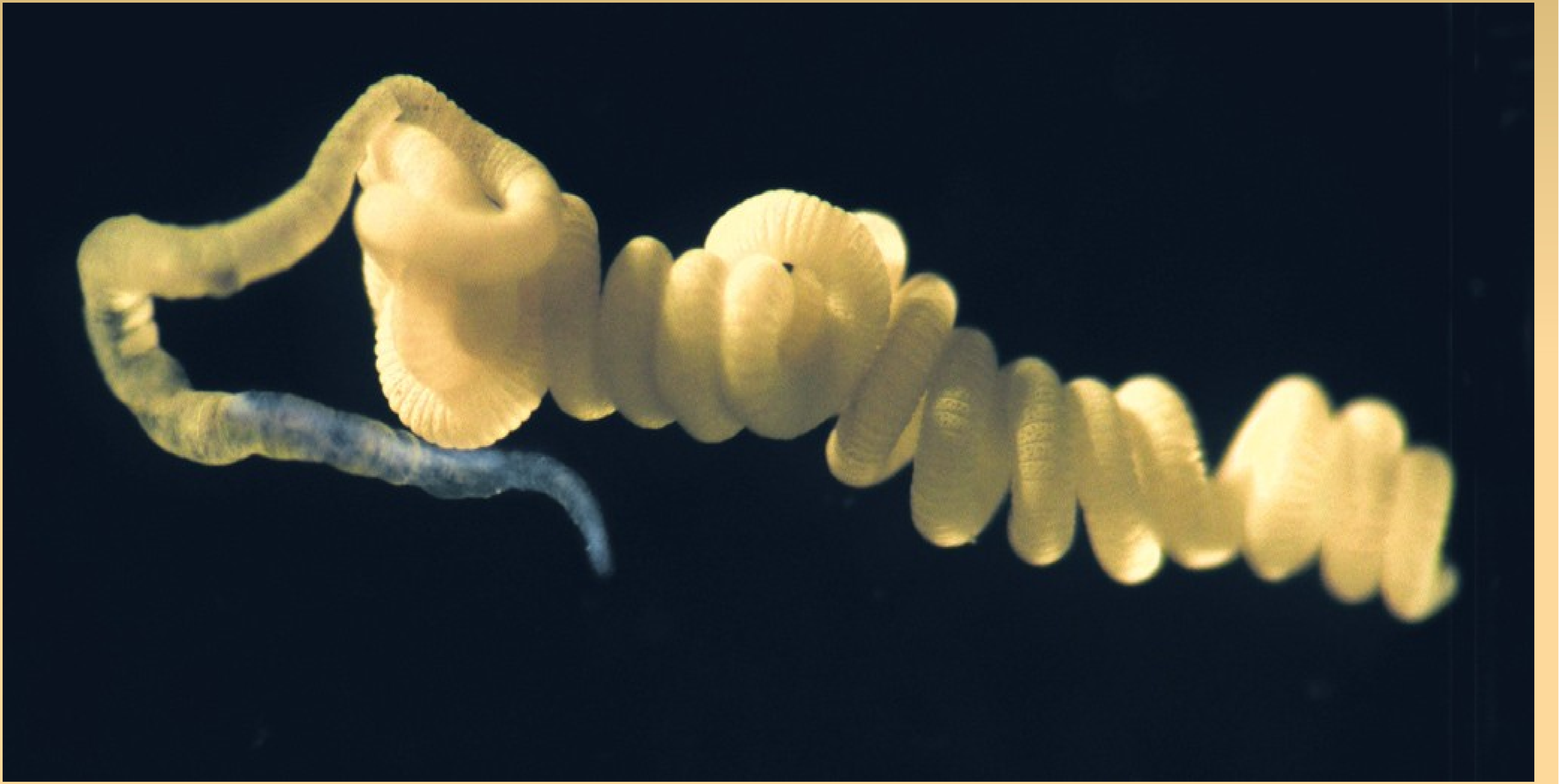
S. glossinidius e
Trypanosoma spp.


Benjamin Cummings

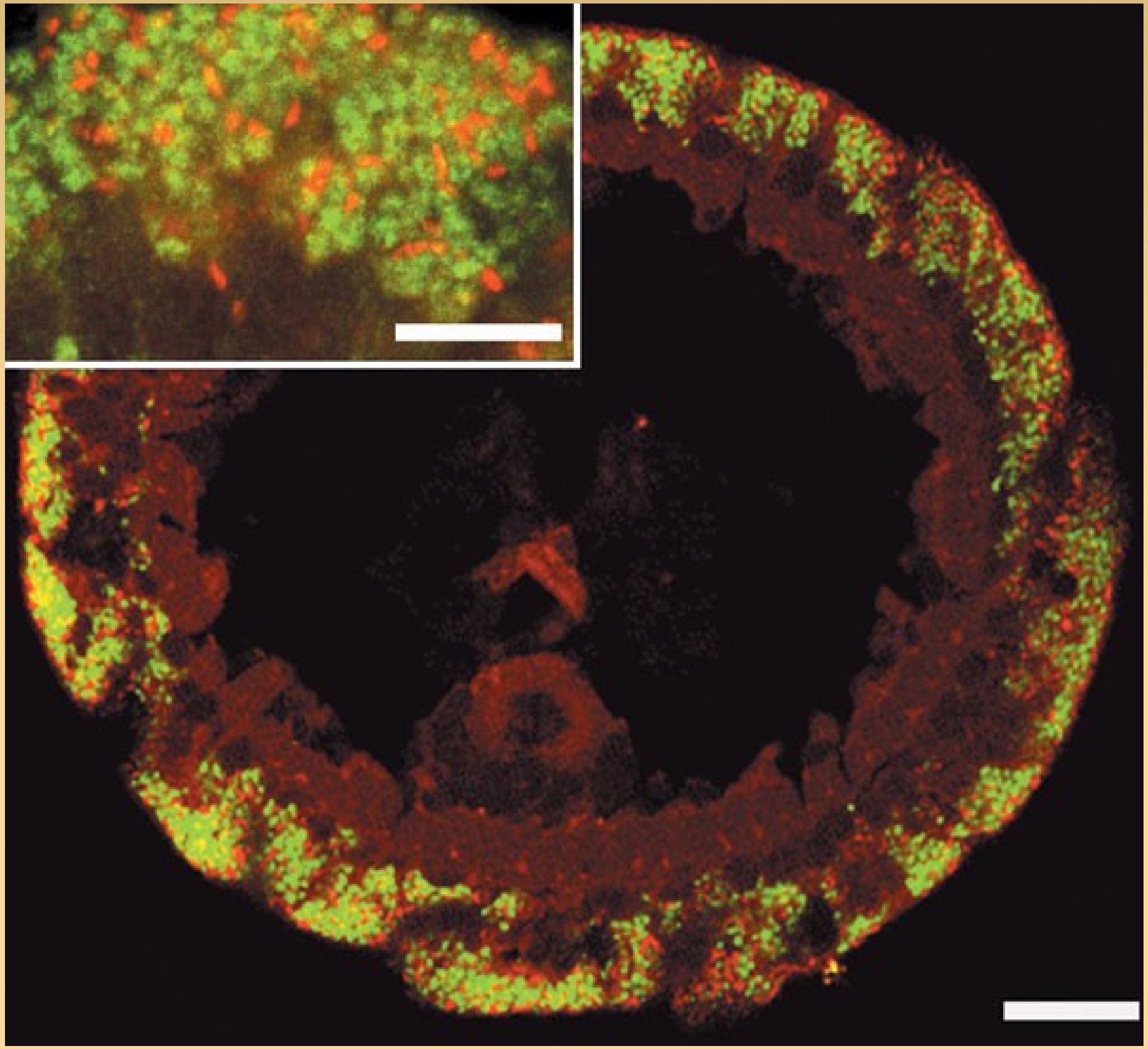
Anellidi: *Olavius algarvensis*

Isola d'Elba

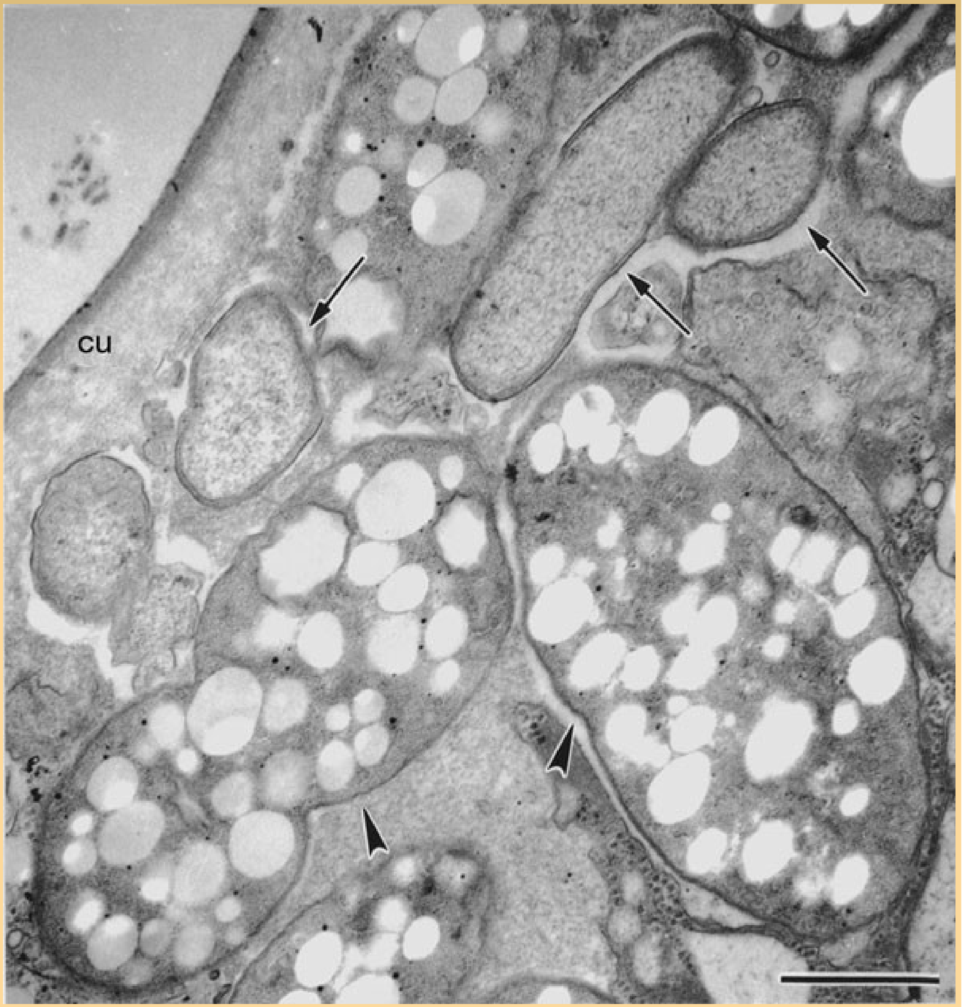
Anellidi: *Olavius algarvensis*



La simbiosi tra *Olavius algarvensis* e due batteri

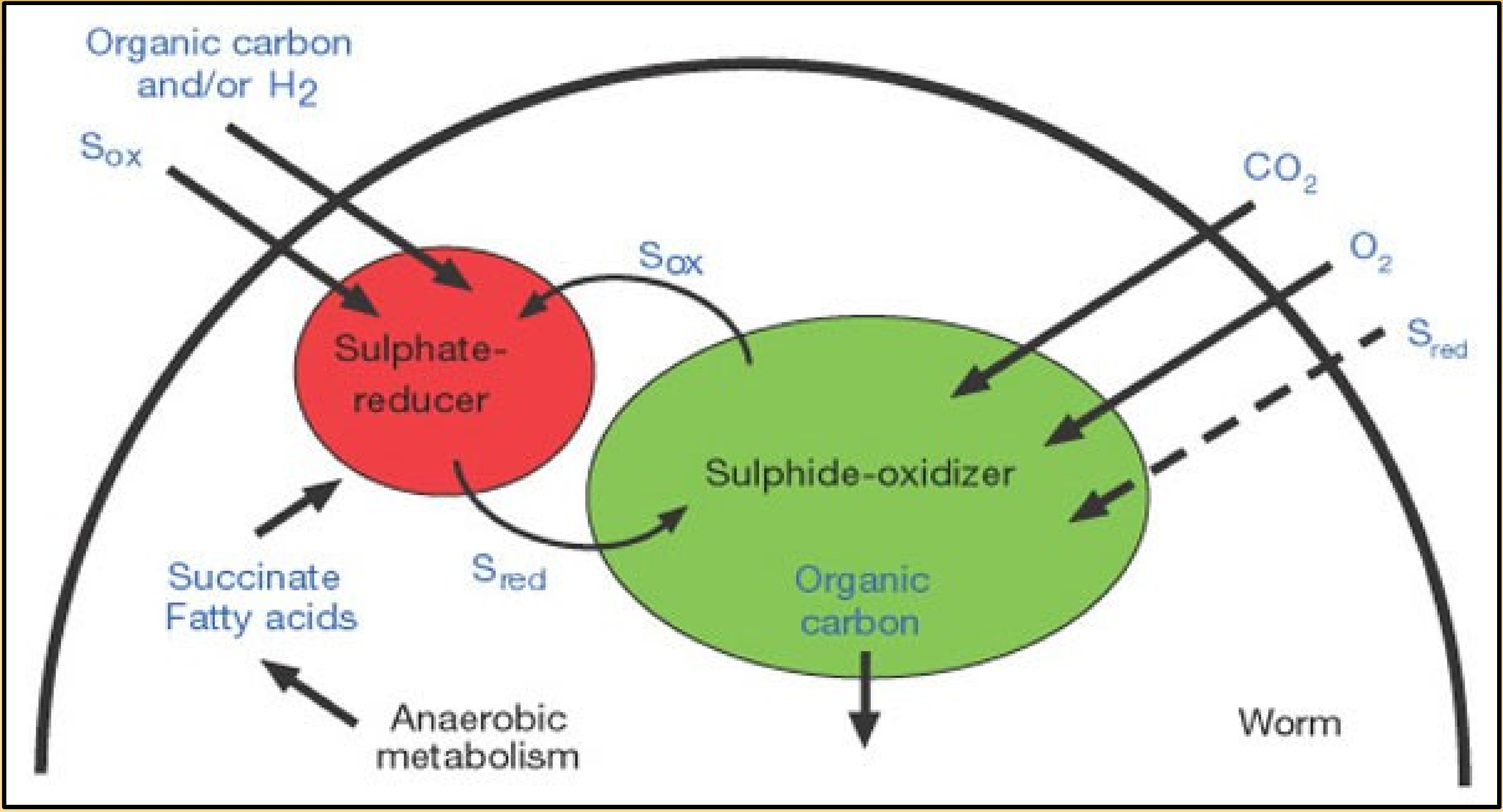


in verde: γ proteobatterio
in rosso: δ proteobatterio



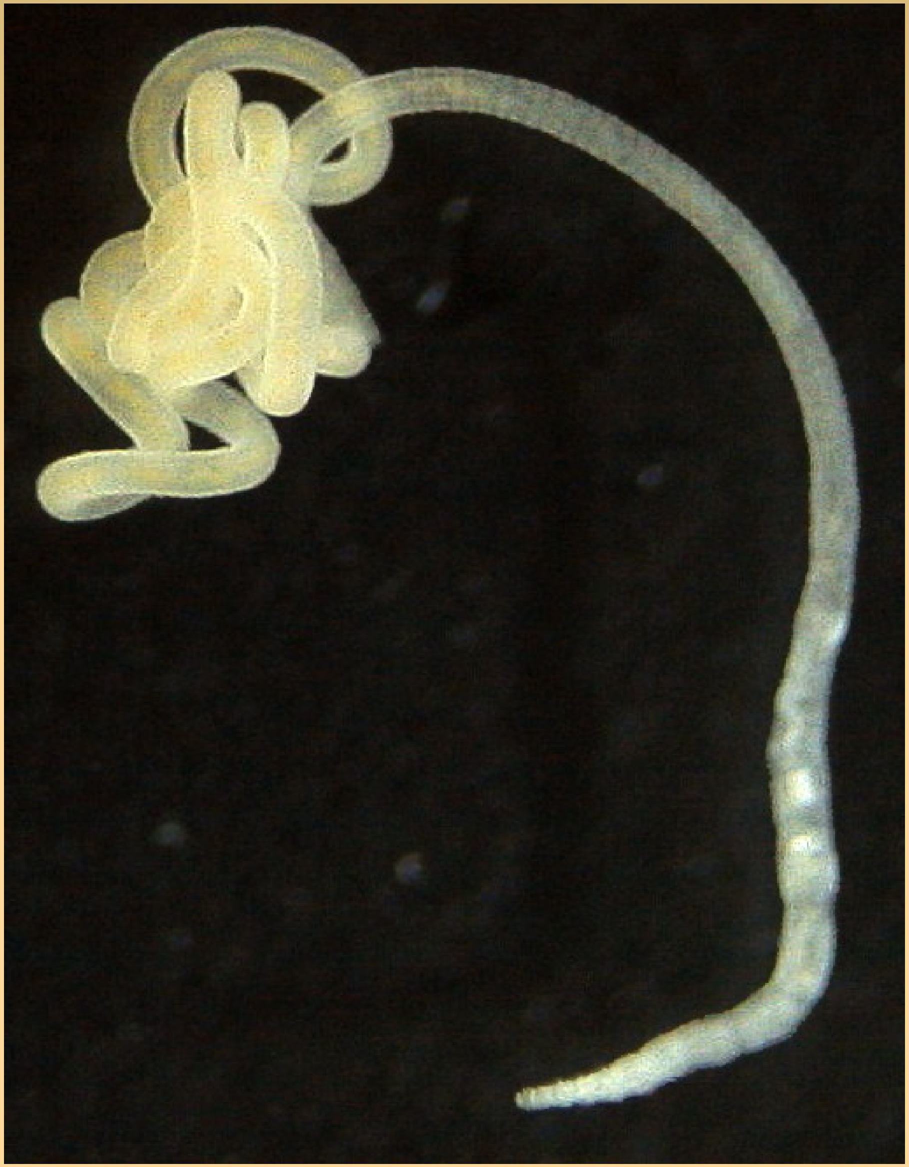
testa di freccia: γ proteobatterio
freccia: δ proteobatterio

La simbiosi tra *Olavius algarvensis* e due batteri


Organic carbon and/or H_2
S_{ox}
S_{ox}
CO_2
O_2
S_{red}
Sulphate-reducer
Sulphide-oxidizer
Succinate Fatty acids
S_{red}
Organic carbon
Anaerobic metabolism
Worm

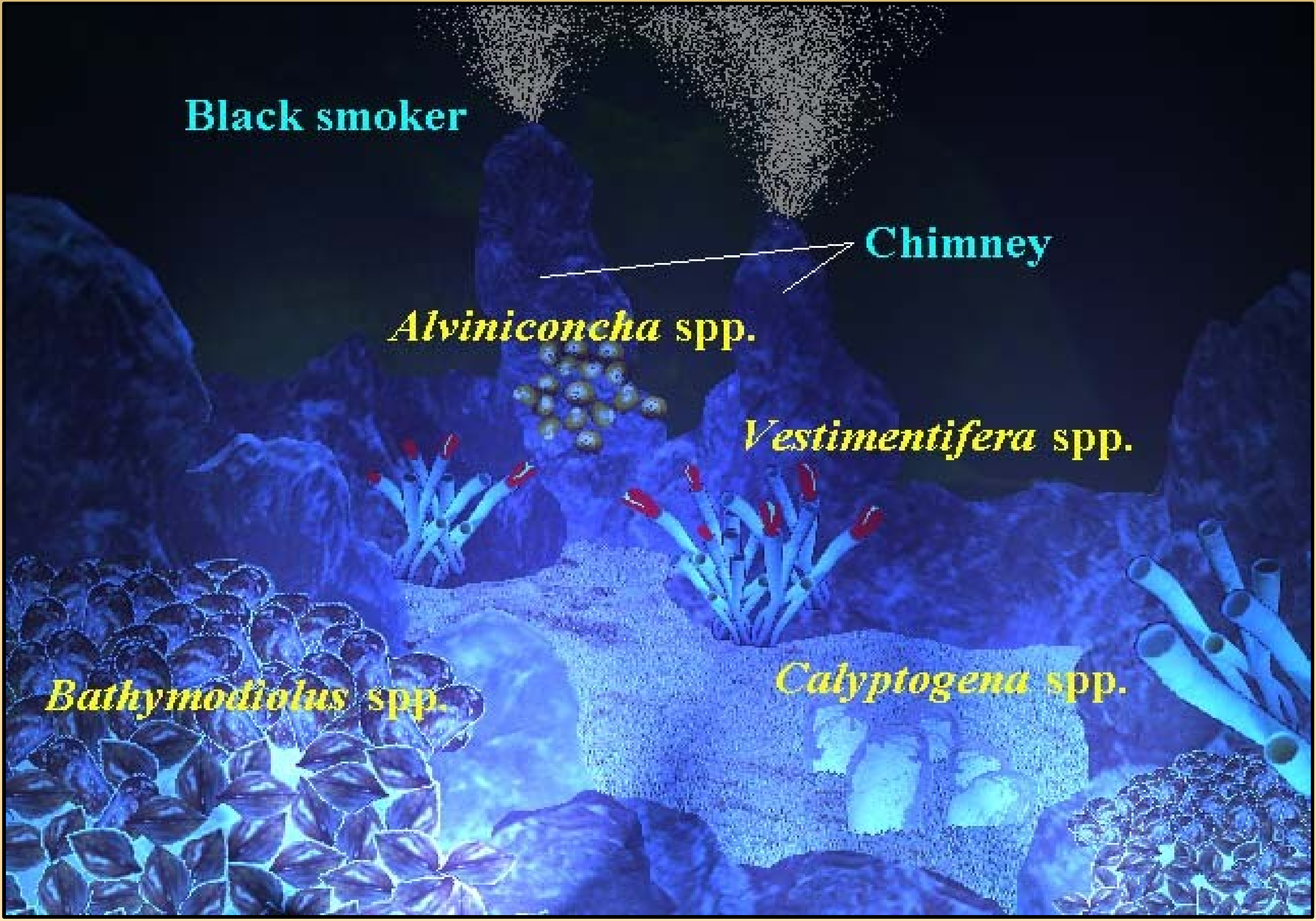
in verde: γ proteobatterio
in rosso: δ proteobatterio

Olavius algarvensis

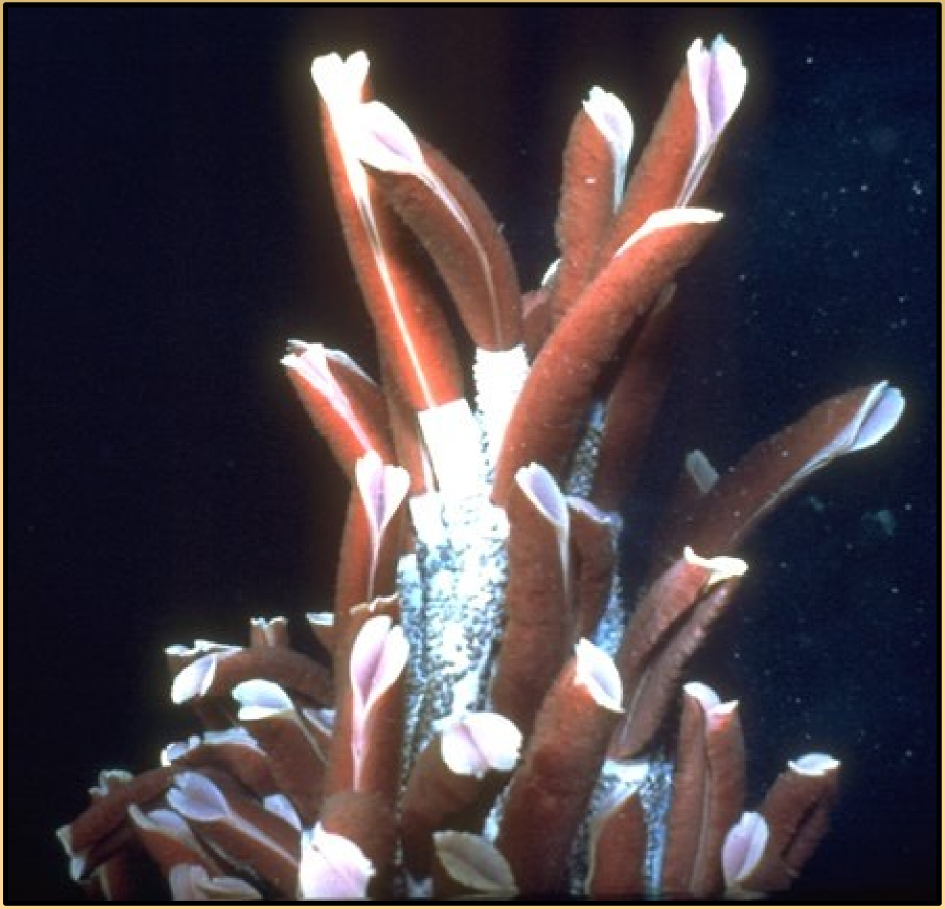


Autotrofo o eterotrofo?

Le simbiosi delle sorgenti idrotermali di profondità


Black smoker
Chimney
Alviniconcha spp.
Vestimentifera spp.
Calyptogena spp.
Bathymodiolus spp.

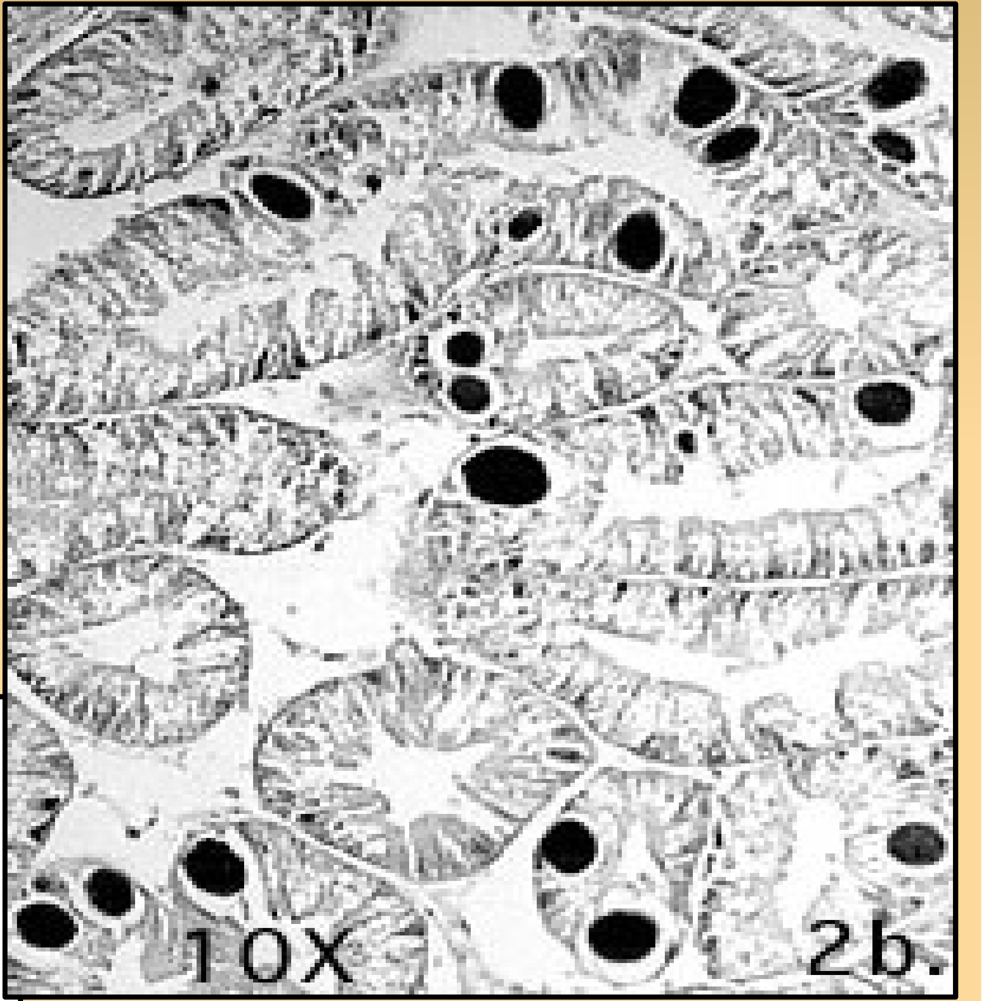
Pogonofori: *Riftia pachyptila*

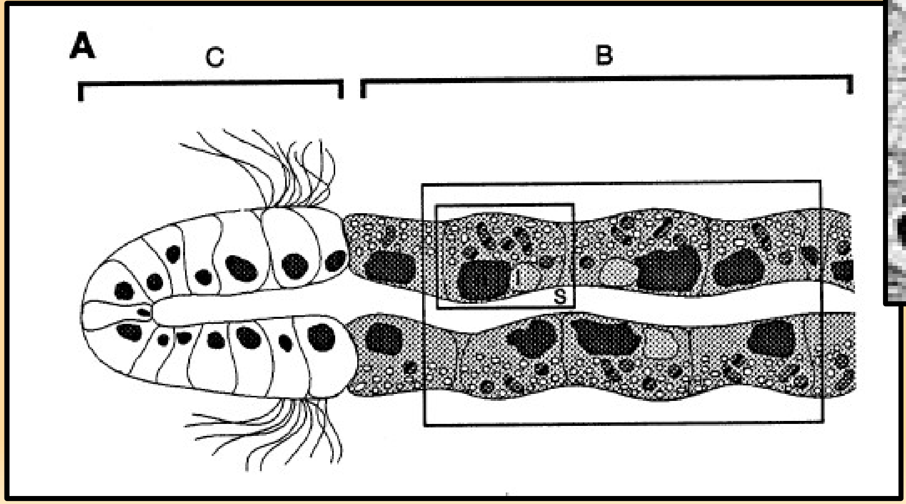


CO_2

Molluschi: *Bathymodiolus* sp.

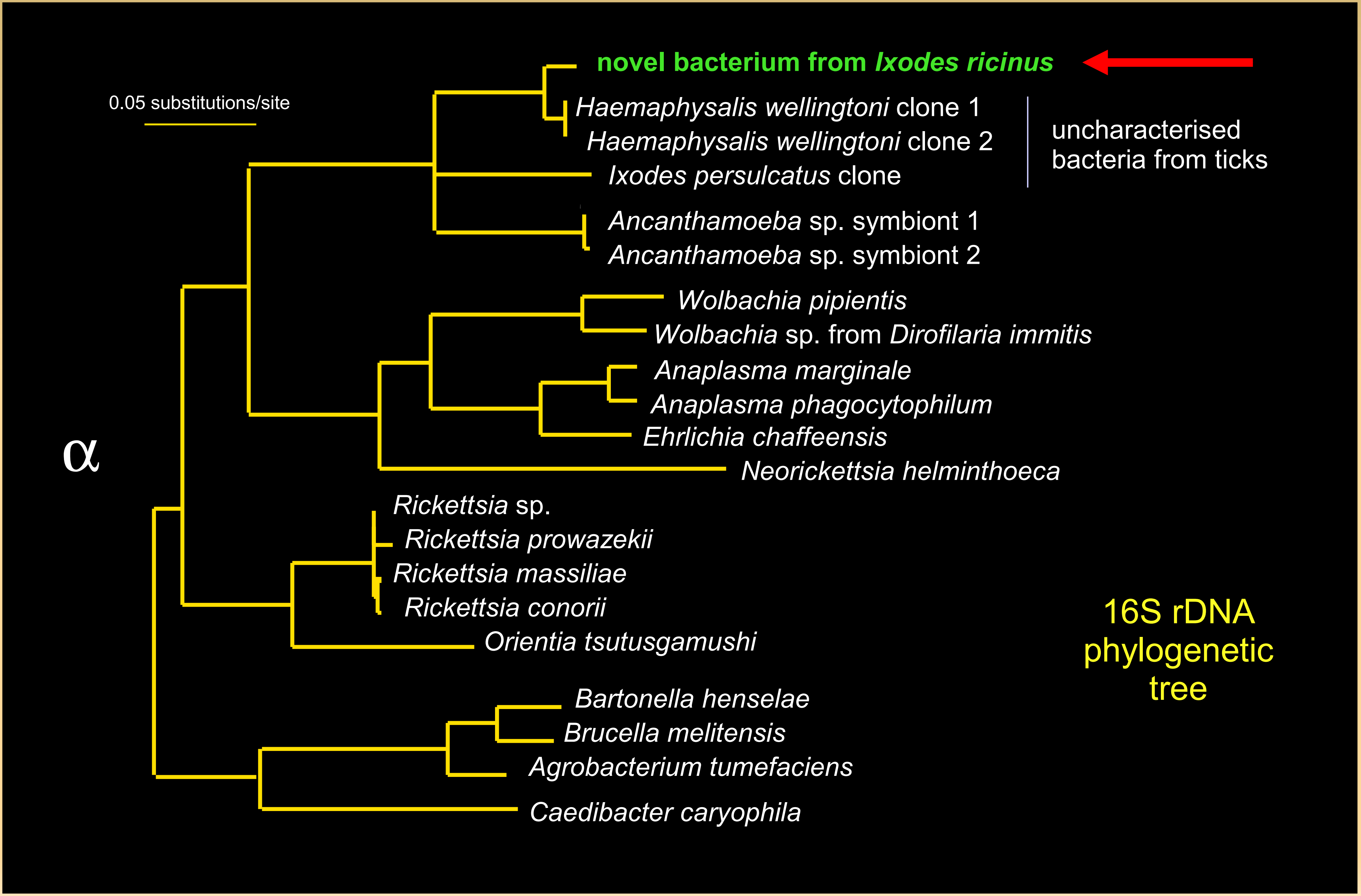
CH_4





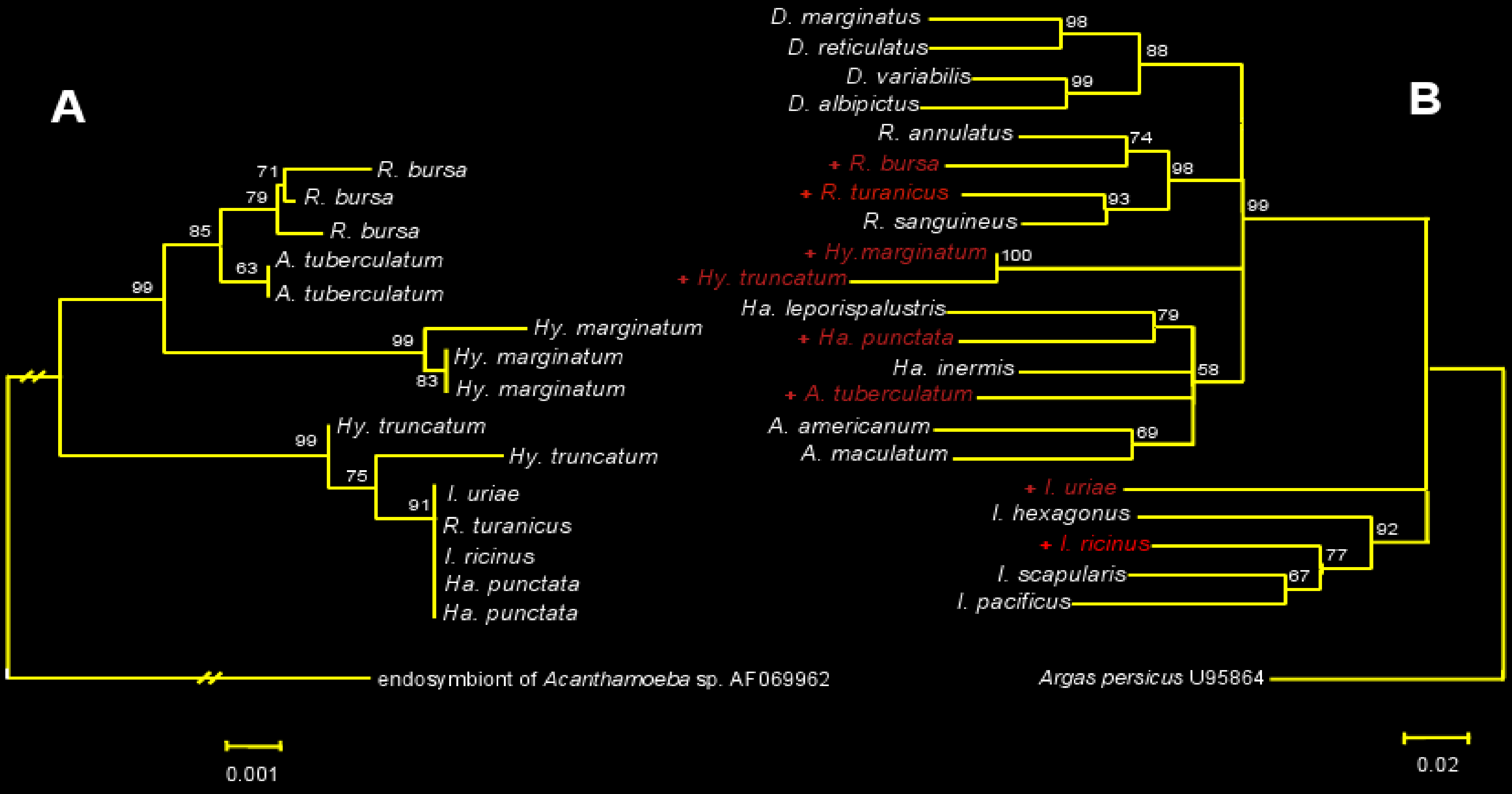
Artropodi: *Ixodes ricinus* e le zecche

Artropodi: *Ixodes ricinus* e le zecche


0.05 substitutions/site
α
novel bacterium from *Ixodes ricinus*
Haemaphysalis wellingtoni clone 1
Haemaphysalis wellingtoni clone 2
Ixodes persulcatus clone
uncharacterised bacteria from ticks
Ancanthamoeba sp. symbiont 1
Ancanthamoeba sp. symbiont 2
Wolbachia pipientis
Wolbachia sp. from *Dirofilaria immitis*
Anaplasma marginale
Anaplasma phagocytophilum
Ehrlichia chaffeensis
Neorickettsia helminthoeca
Rickettsia sp.
Rickettsia prowazekii
Rickettsia massiliae
Rickettsia conorii
Orientia tsutusgamushi
Bartonella henselae
Brucella melitensis
Agrobacterium tumefaciens
Caedibacter caryophila

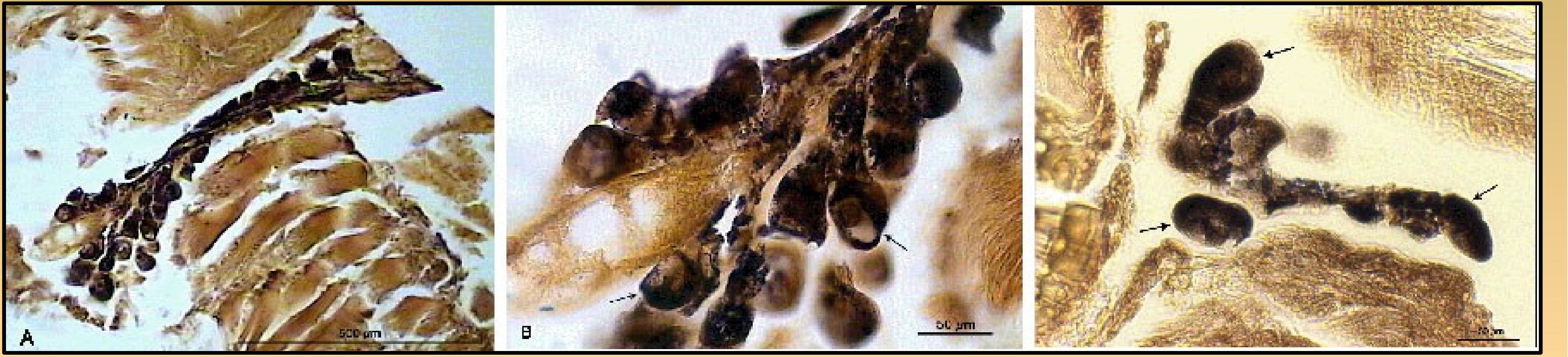
16S rDNA phylogenetic tree

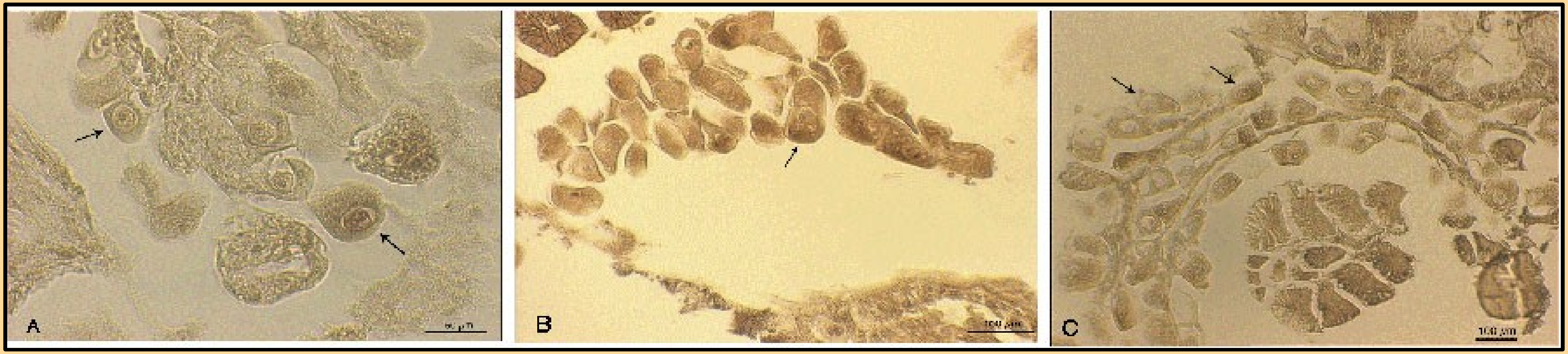
Artropodi: *Ixodes ricinus* e le zecche


A
71
R. bursa
79
R. bursa
85
R. bursa
63
A. tuberculatum
A. tuberculatum
99
99
Hy. marginatum
Hy. marginatum
83
Hy. marginatum
Hy. truncatum
99
Hy. truncatum
75
I. uriae
91
R. turanicus
I. ricinus
Ha. punctata
Ha. punctata
endosymbiont of *Acanthamoeba* sp. AF069962
0.001
B
D. marginatus
98
D. reticulatus
88
D. variabilis
99
D. albipictus
R. annulatus
74
+ R. bursa
98
+ R. turanicus
93
R. sanguineus
99
+ Hy. marginatum
100
+ Hy. truncatum
Ha. leporispalustris
79
+ Ha. punctata
Ha. inermis
58
+ A. tuberculatum
A. americanum
69
A. maculatum
+ I. uriae
I. hexagonus
92
+ I. ricinus
77
I. scapularis
67
I. pacificus
Argas persicus U95864
0.02

Confronto tra le filogenesi di *Midichloria* (A) e delle zecche ospiti (B). → Non c'è corrispondenza → Possibile trasferimento orizzontale

Artropodi: *Ixodes ricinus* e le zecche


A
500 µm
B
50 µm


A
B
100 µm
C
100 µm

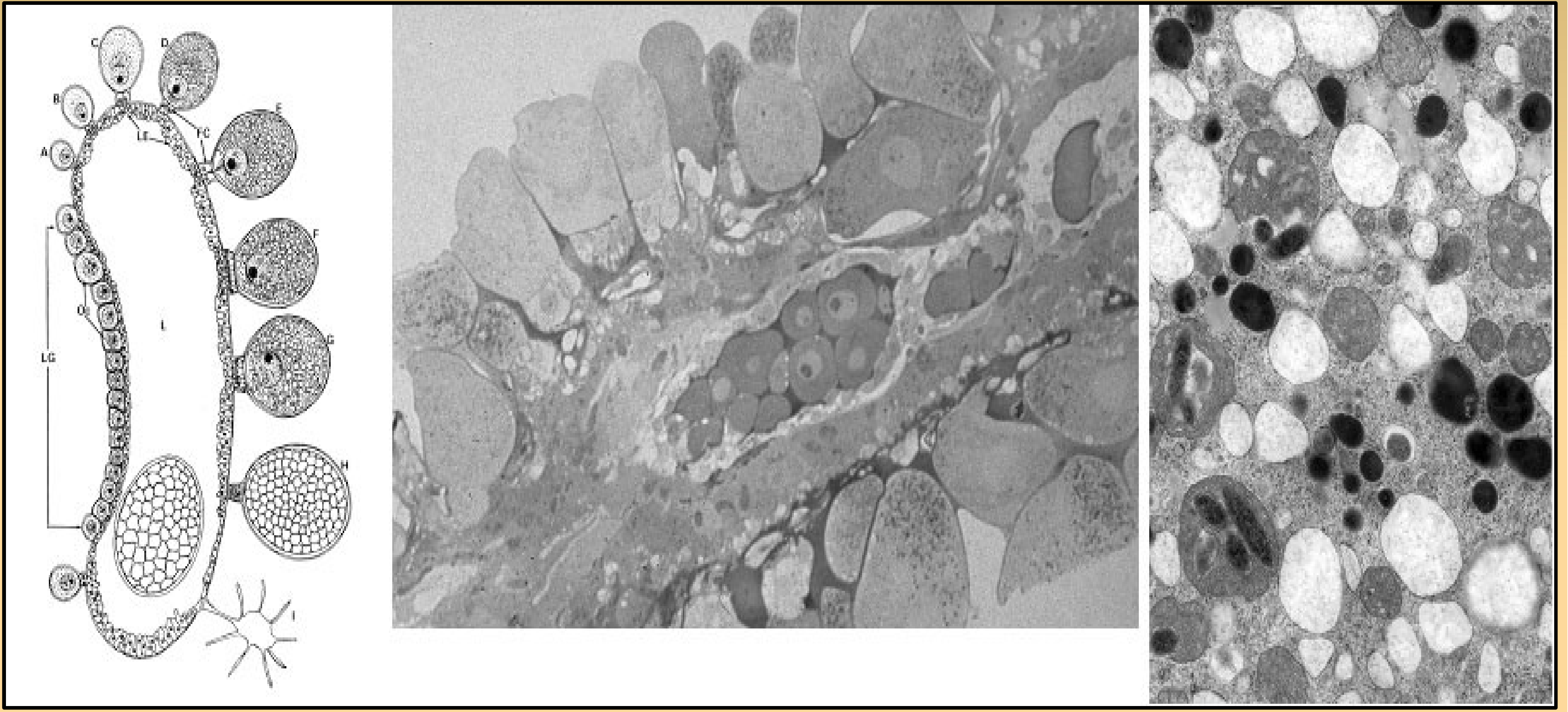
(No probe)

(Gamma-proteobacteria specific probe)

(RNase control)

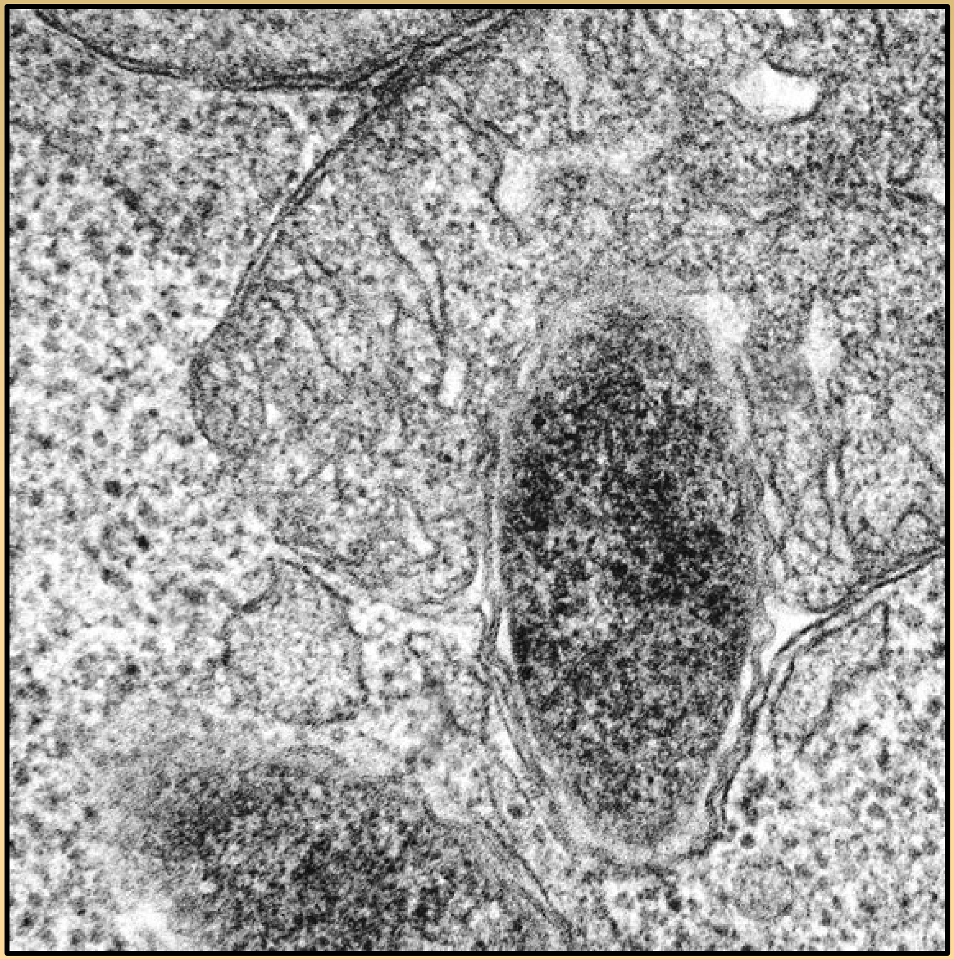
Il batterio è specifico degli ovari delle zecche

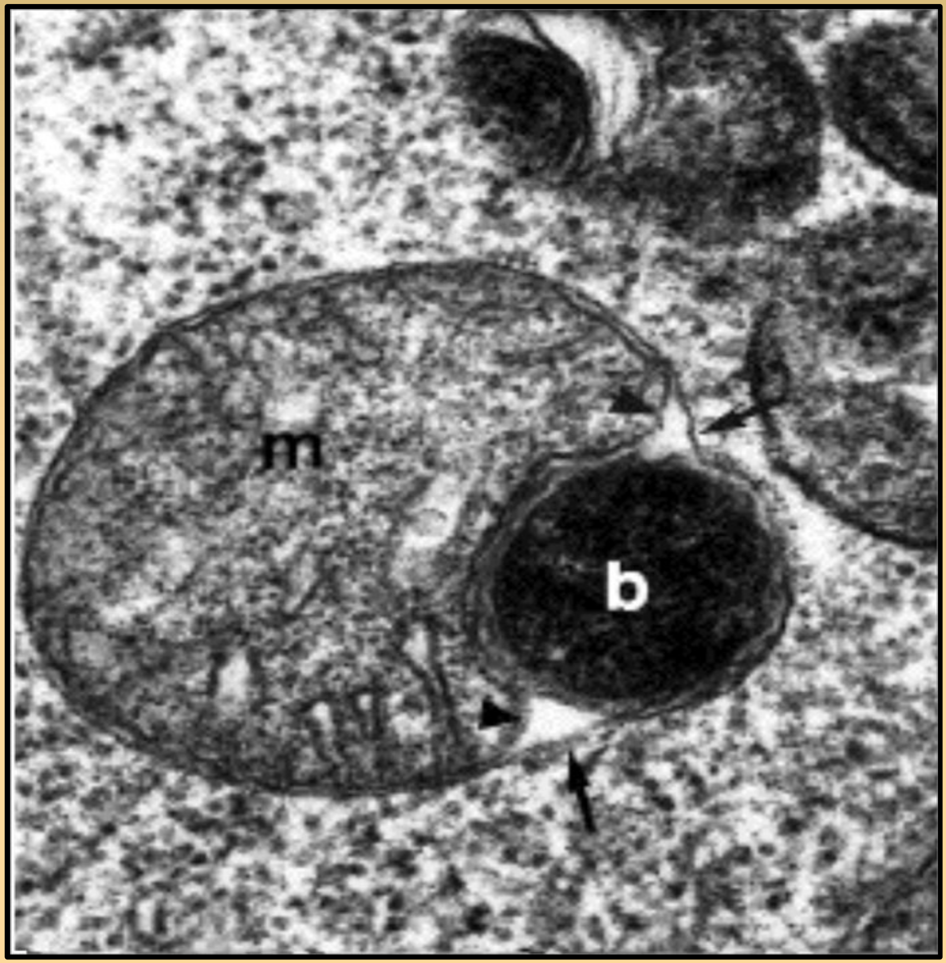
Artropodi: *Ixodes ricinus* e le zecche


C
D
B
LE
FC
E
A
F
O
LG
L
G
H
I

- Il batterio è trasmesso per via transovarica

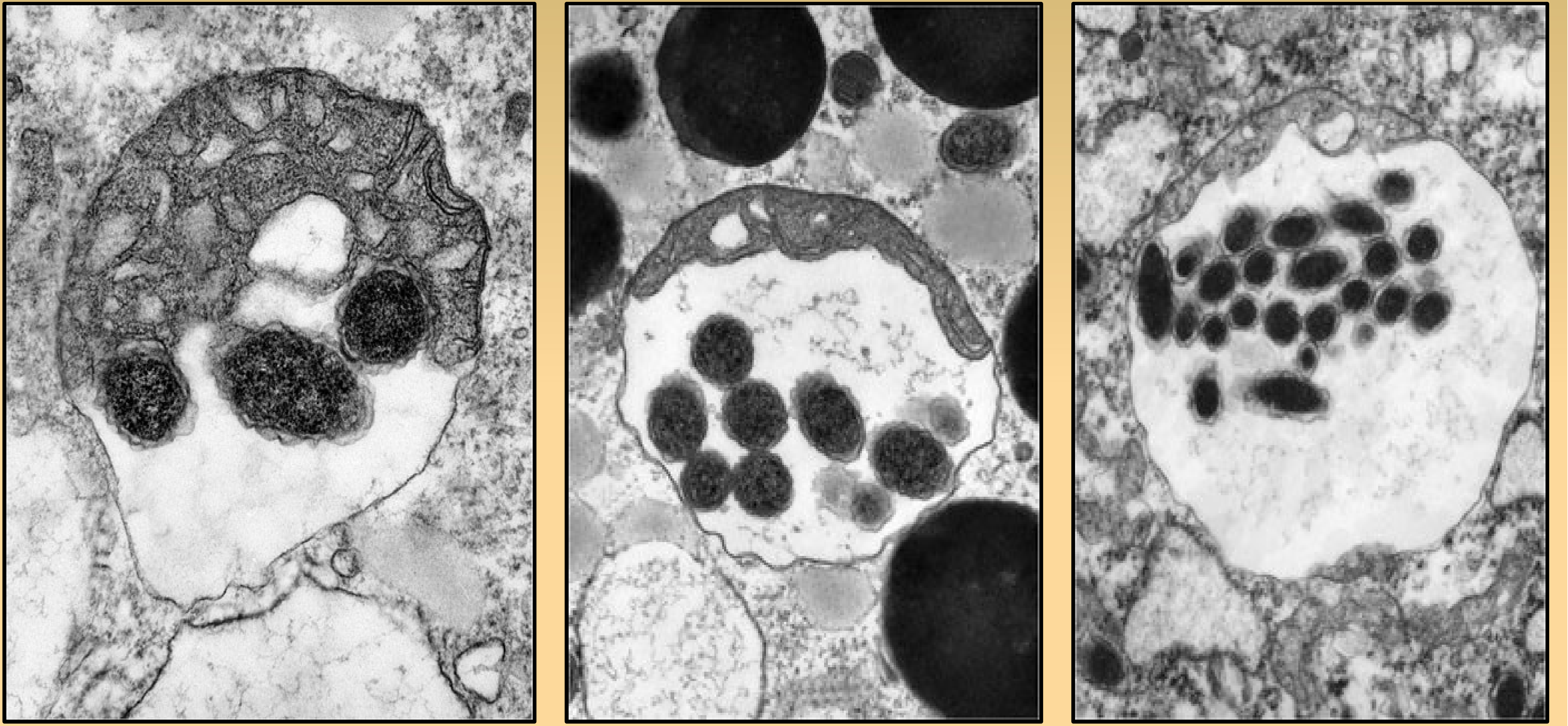
Artropodi: *Ixodes ricinus* e le zecche





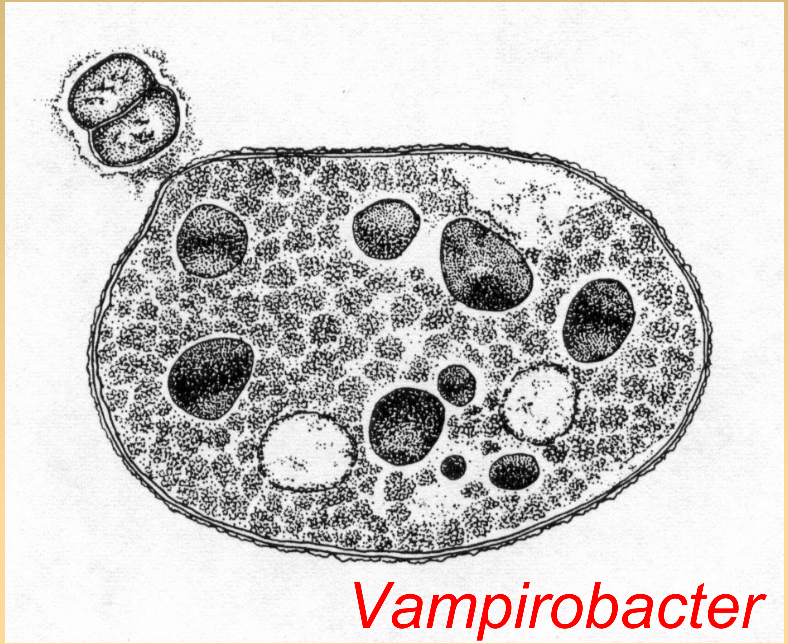
➡ Il batterio invade i mitocondri...

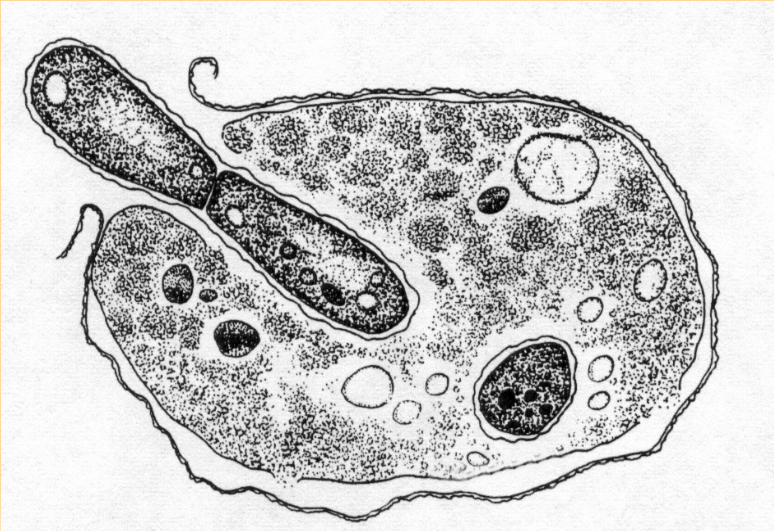
Artropodi: *Ixodes ricinus* e le zecche

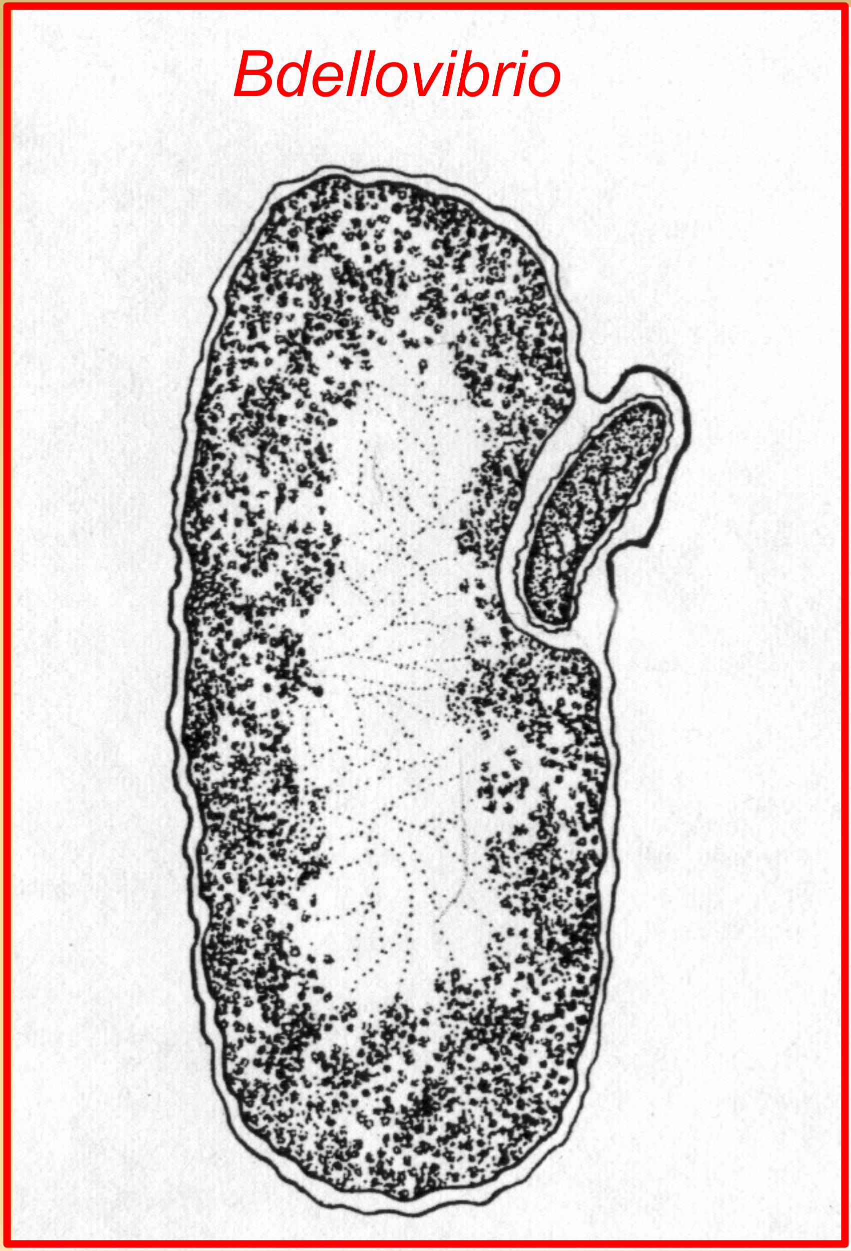


.... e li degrada

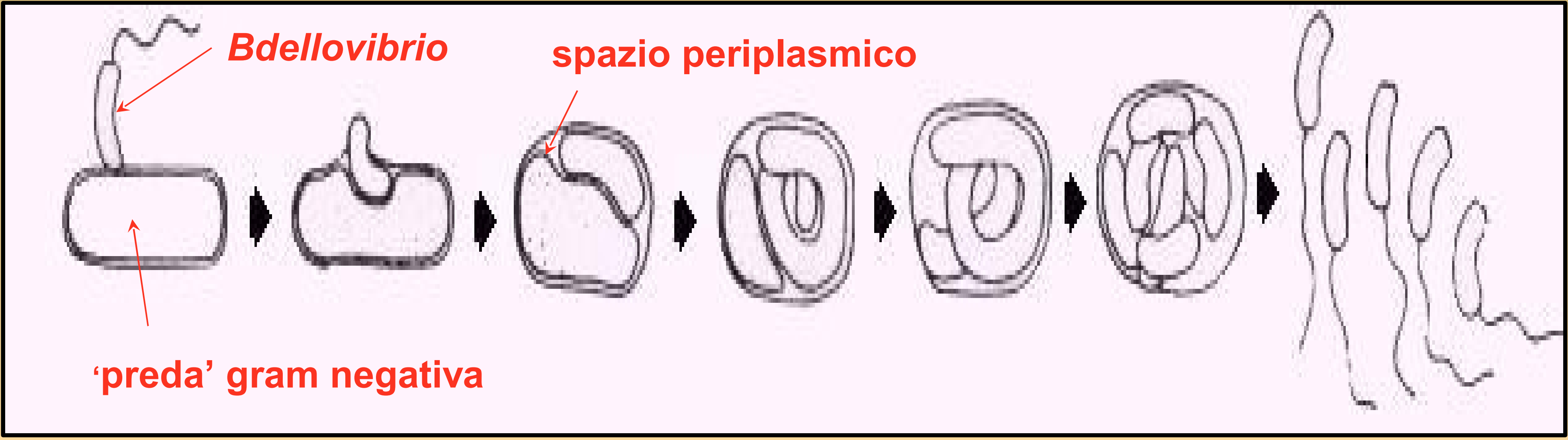
In natura esistono batteri “predatori”

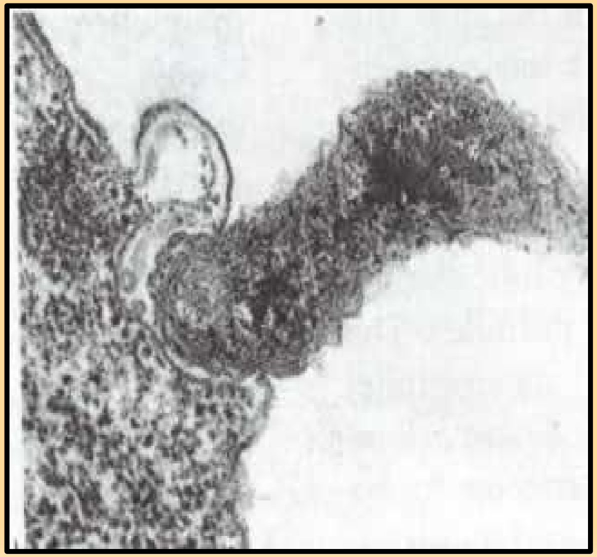

Vampirobacter

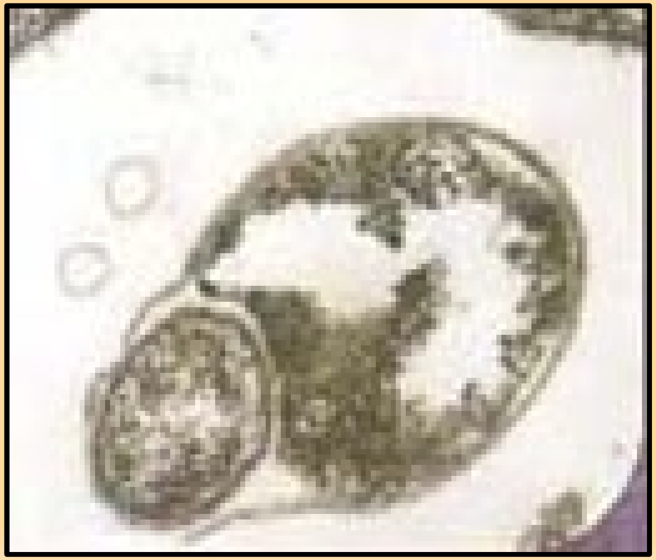


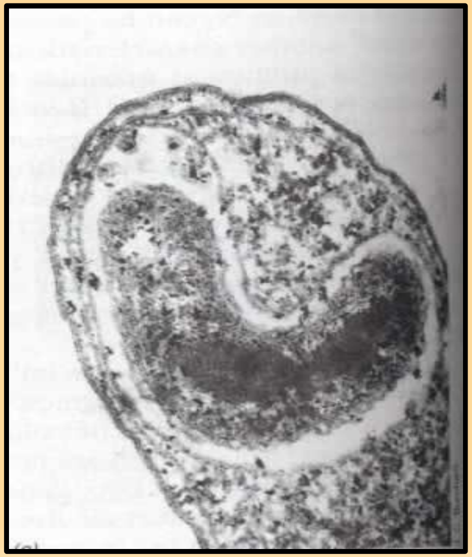

Bdellovibrio

Similarità con il ciclo vitale di *Bdellovibrio* spp.

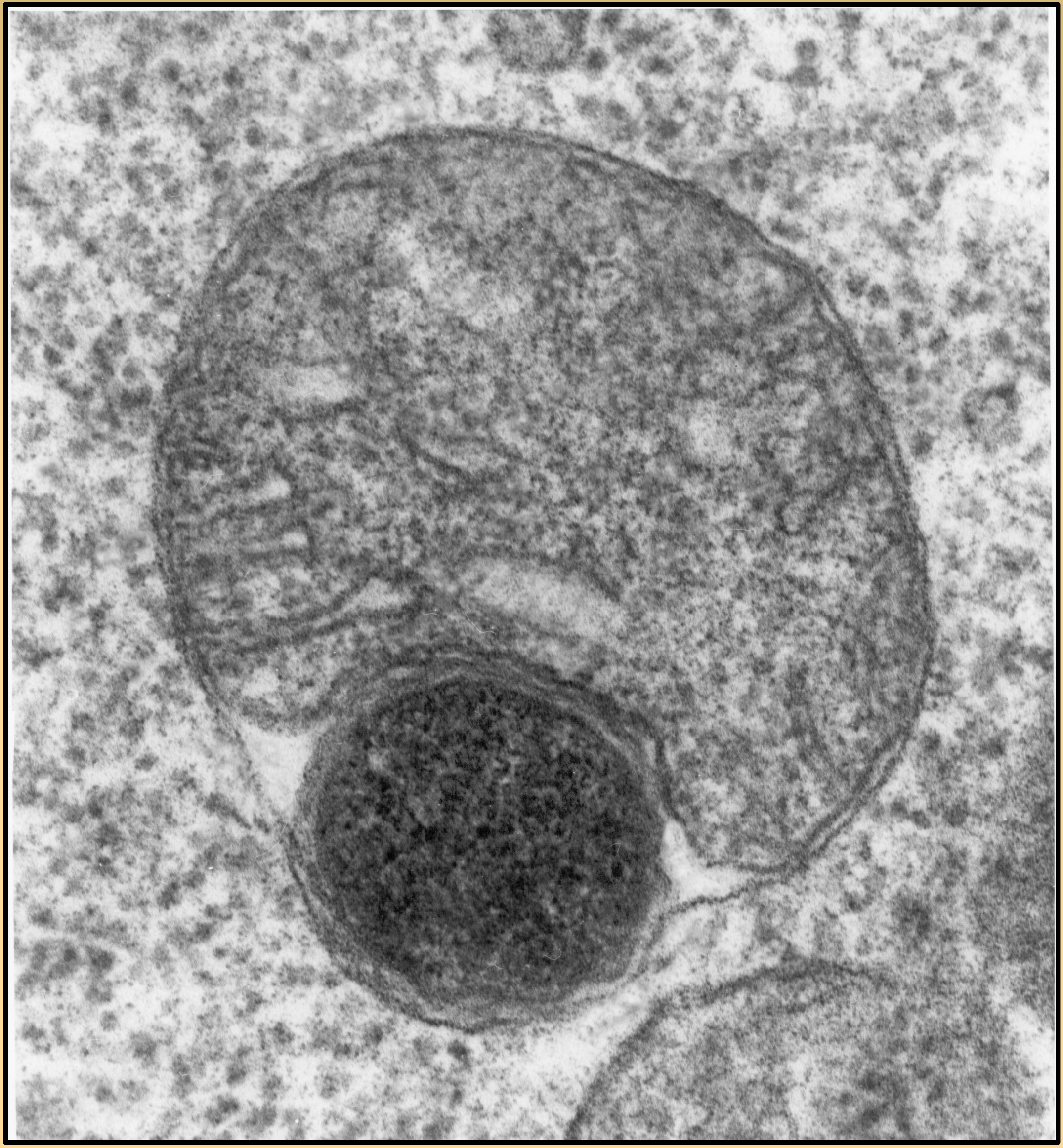

Bdellovibrio
spazio periplasmico
'preda' gram negativa



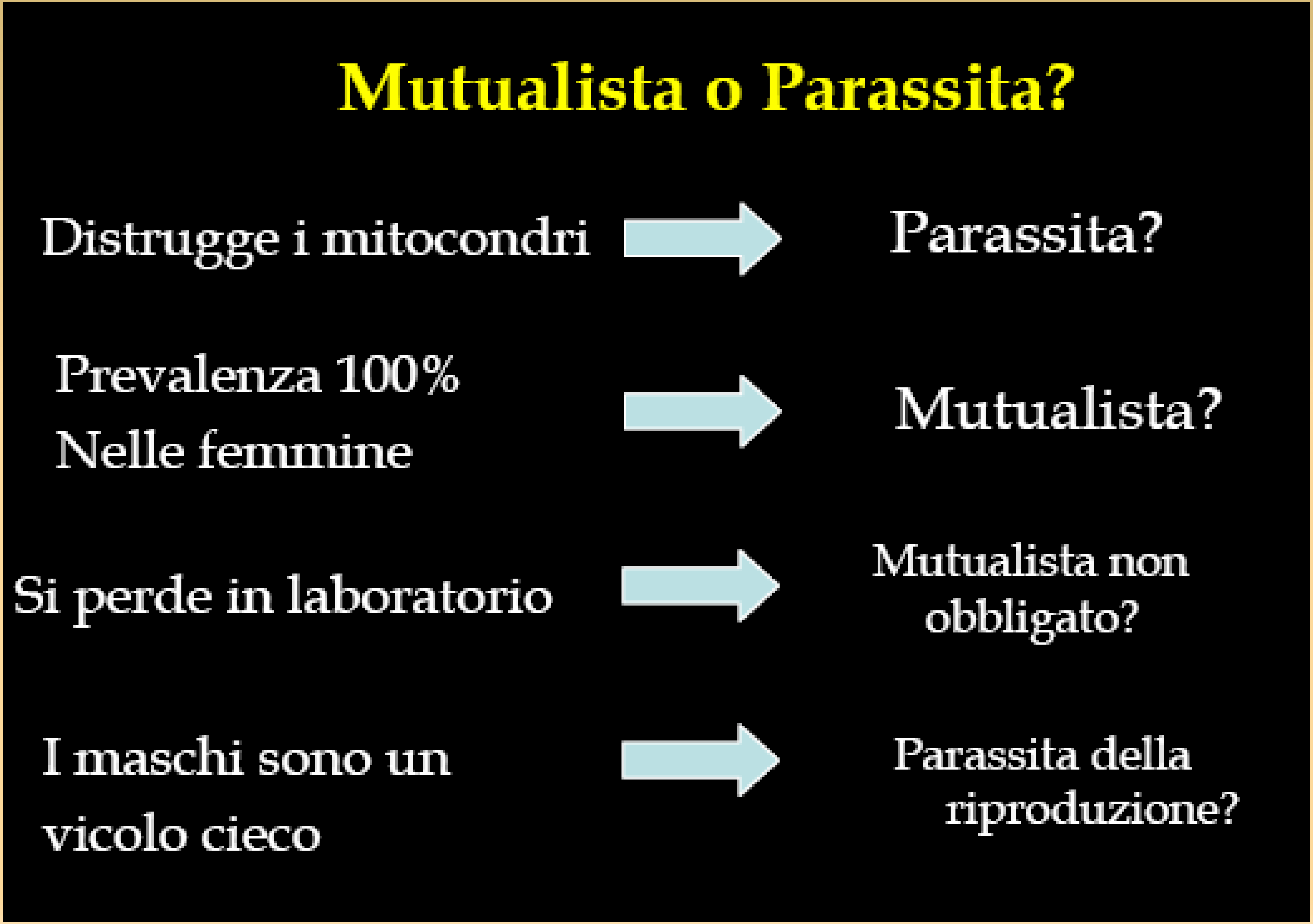




Ixodes ricinus e *Midichloria mitochondrii*



Ruolo di *Midichloria mitochondrii*



Mutualista o Parassita?

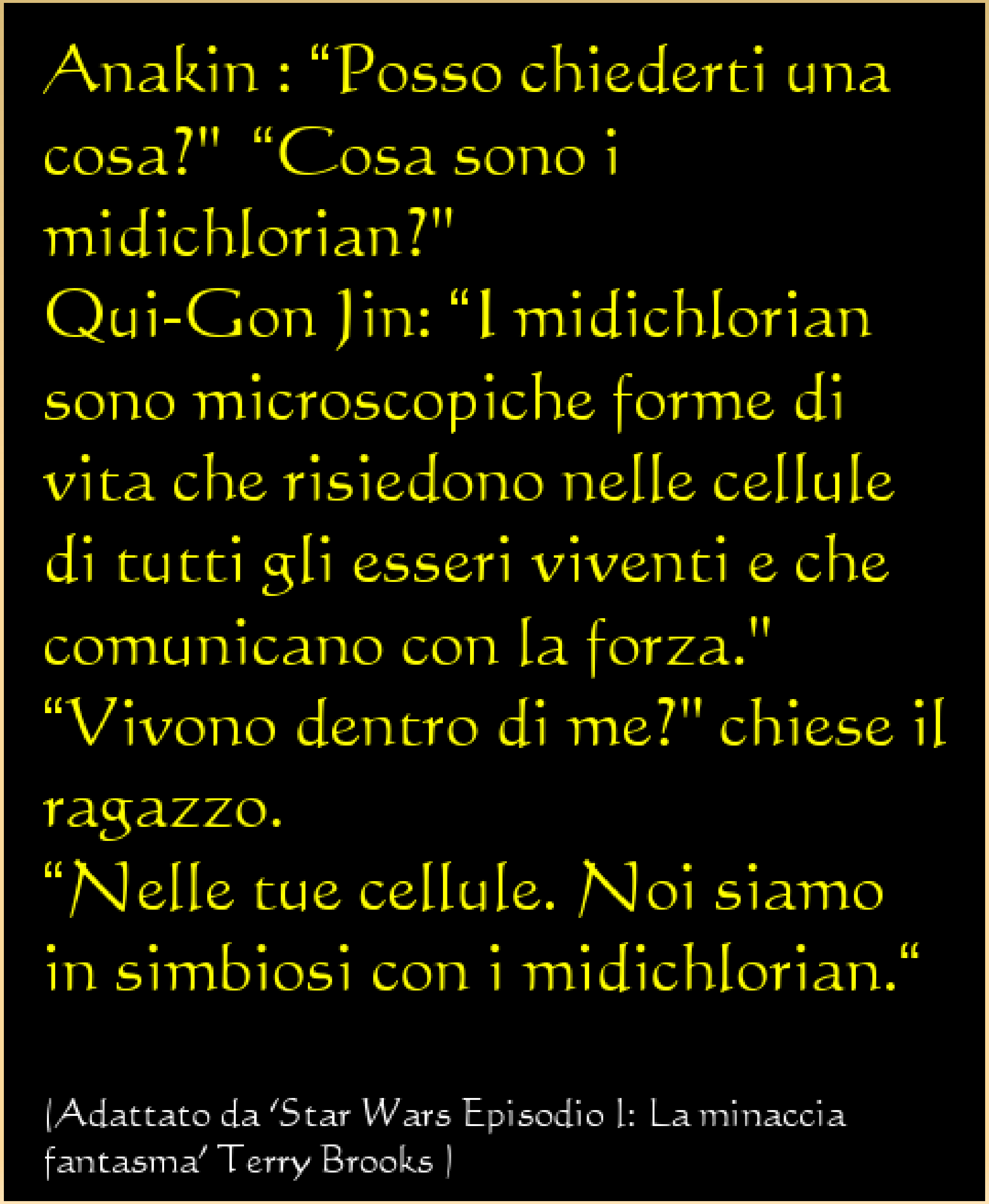
Distrugge i mitocondri → Parassita?

Prevalenza 100%
Nelle femmine → Mutualista?

Si perde in laboratorio → Mutualista non obbligato?

I maschi sono un vicolo cieco → Parassita della riproduzione?

Ixodes ricinus e *Midichloria mitochondrii*



Anakin : “Posso chiederti una cosa?" “Cosa sono i midichlorian?"
Qui-Gon Jin: “I midichlorian sono microscopiche forme di vita che risiedono nelle cellule di tutti gli esseri viventi e che comunicano con la forza."
“Vivono dentro di me?" chiese il ragazzo.
“Nelle tue cellule. Noi siamo in simbiosi con i midichlorian.“

(Adattato da ‘Star Wars Episodio I: La minaccia fantasma’ Terry Brooks)

Midichlorian count

- Obi-Wan Kenobi 13.400

- Luke Skywalker 14.500

- Yoda 17.700

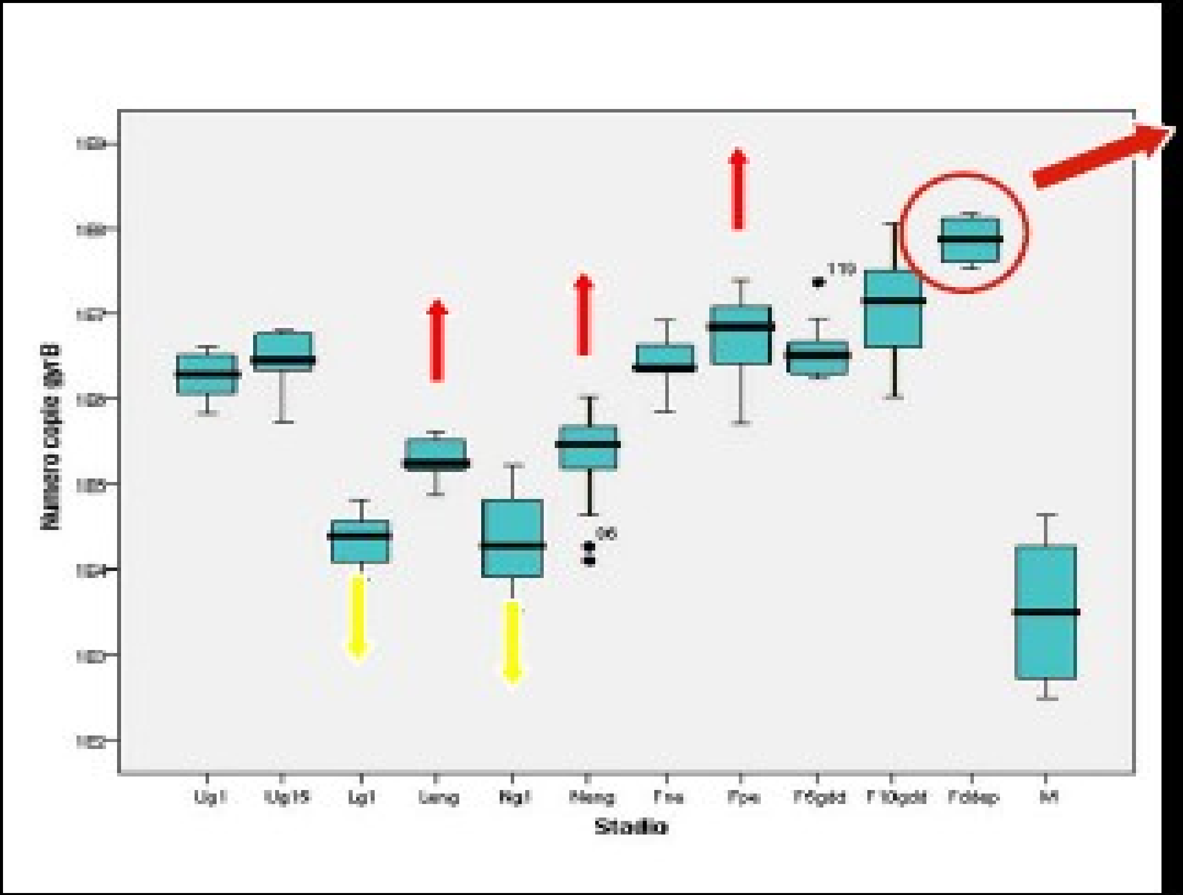
- Darth Vader 27.700

(Darth Fener)

Midichlorian count

- *Ixodes ricinus* 1.000.000!!

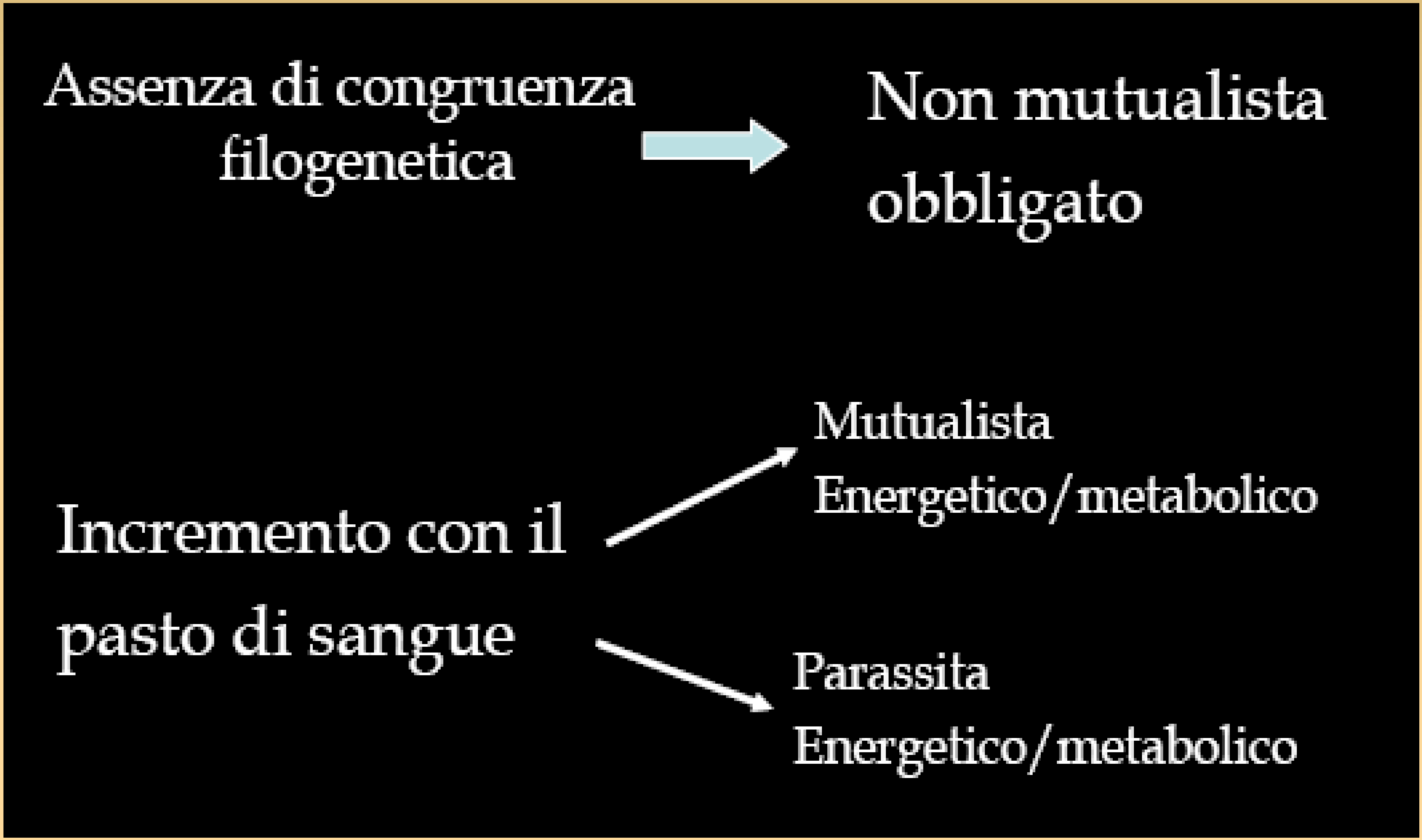
Midichlorian count



valore massimo
$1,5 \times 10^8$

- Forte aumento del simbionte dopo il pasto di sangue
- Diminuzione drastica dopo il passaggio da uno stadio all’altro, tranne nella muta ninfa/adulto

Ruolo di *Midichloria mitochondrii*



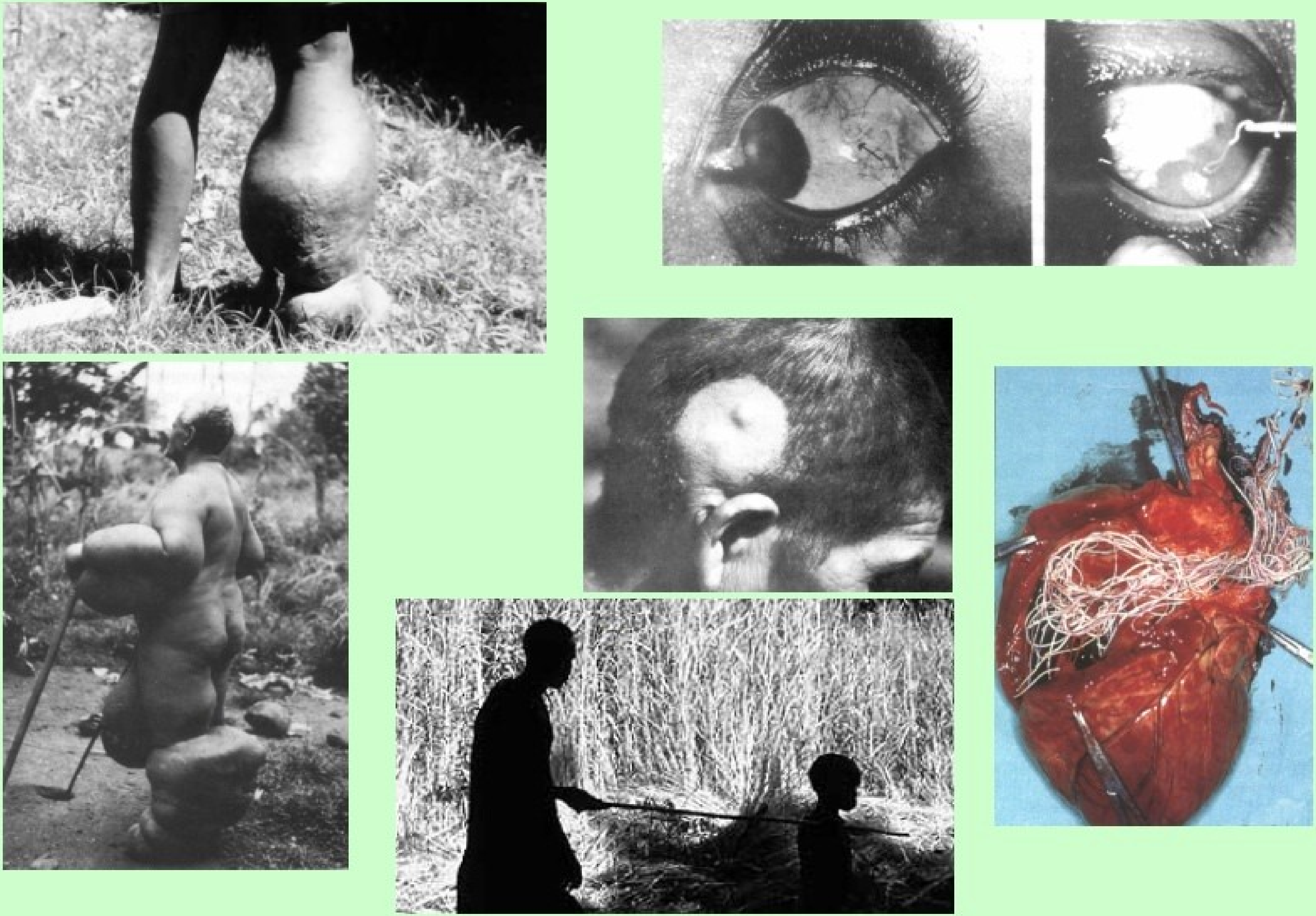
Assenza di congruenza filogenetica → Non mutualista obbligato

Incremento con il pasto di sangue → Mutualista Energetico/metabolico

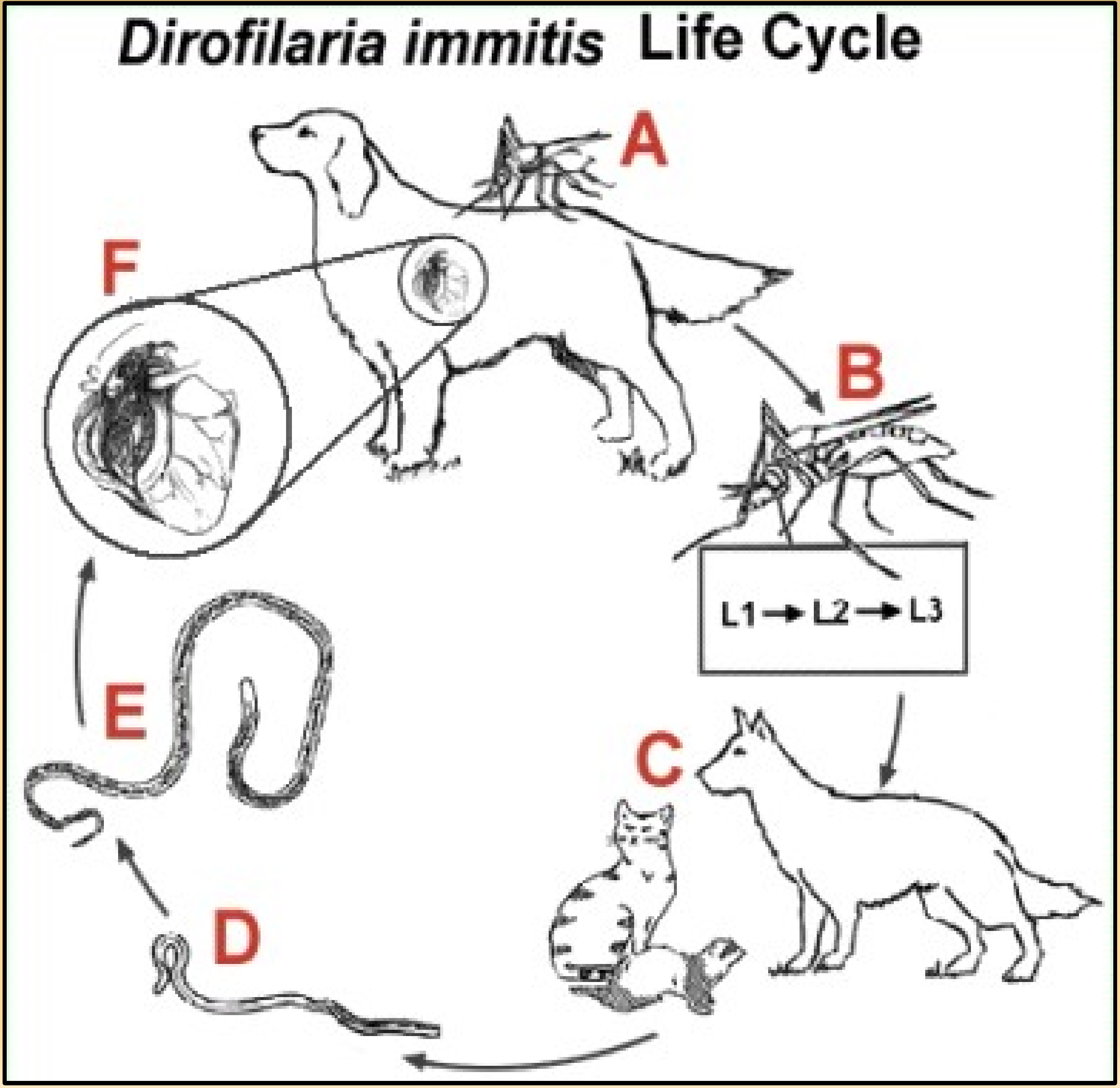
Incremento con il pasto di sangue → Parassita Energetico/metabolico

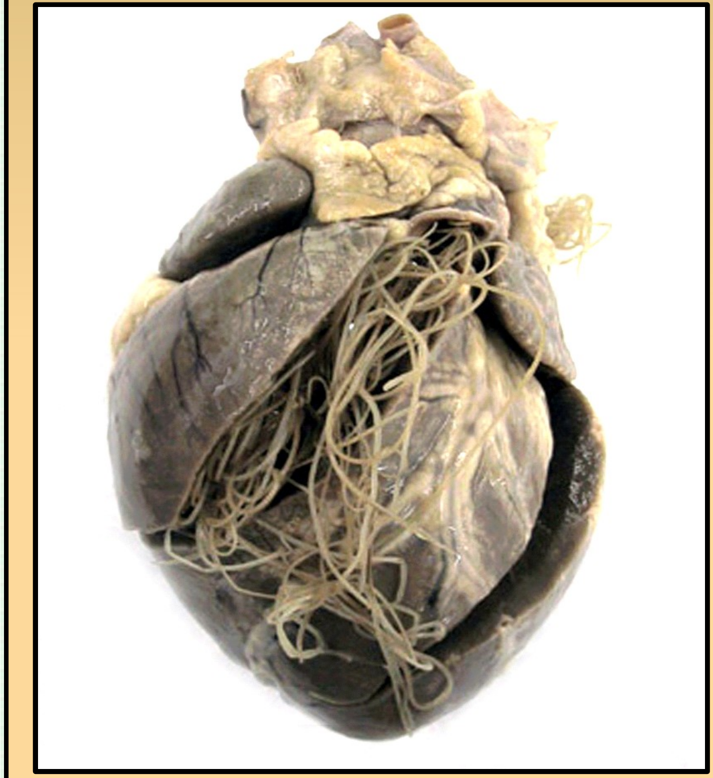
Artropodi e nematodi – *Wolbachia pipientis*

Le filarie

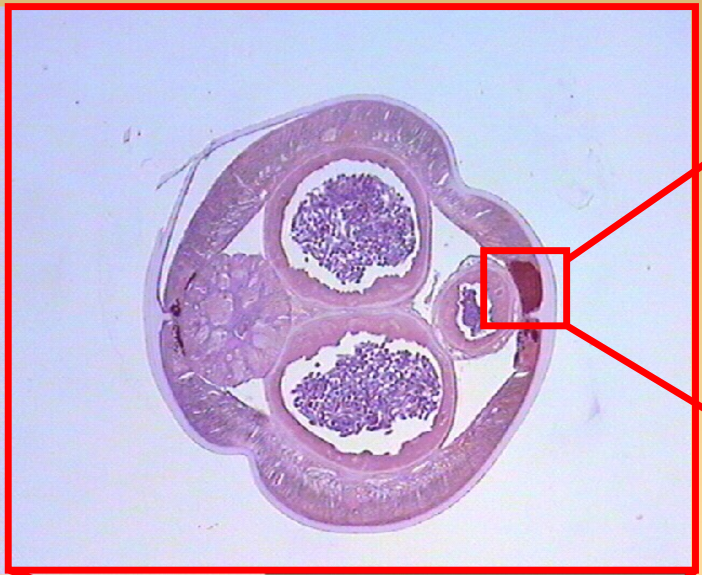


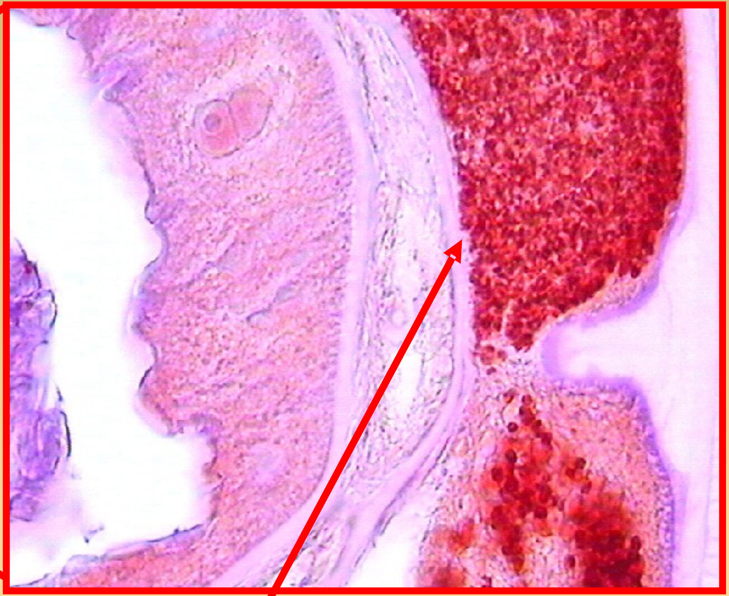
Ciclo vitale di *Dirofilaria immitis*

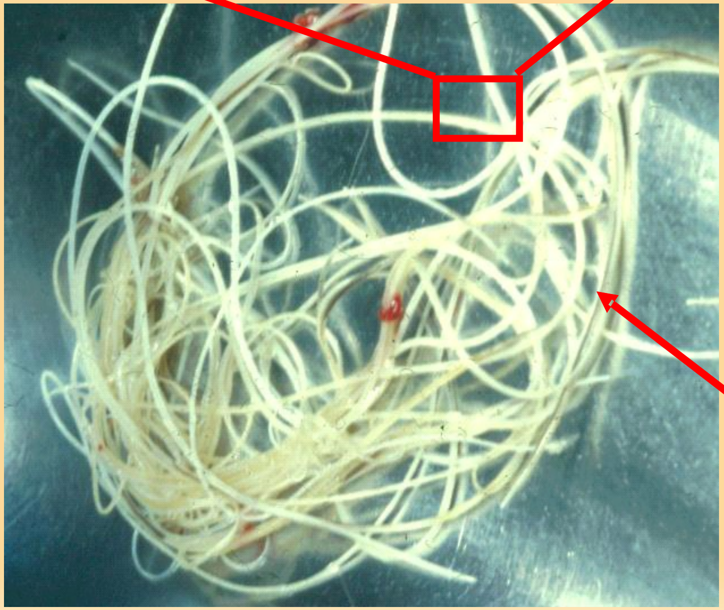

Dirofilaria immitis Life Cycle
A
B
L1 → L2 → L3
C
D
E
F



Le filarie e *Wolbachia pipientis*





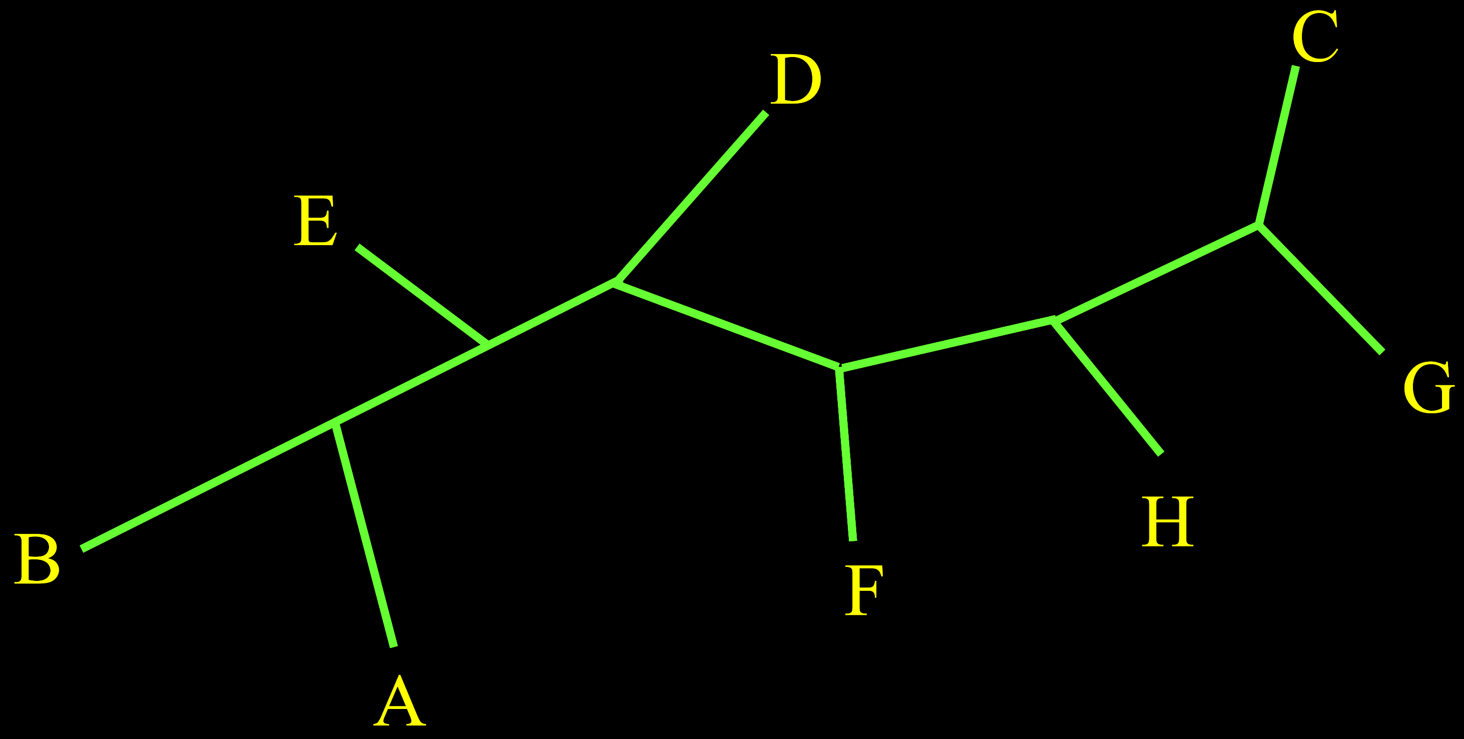


W. pipientis **nelle corde laterali**

Dirofilaria immitis

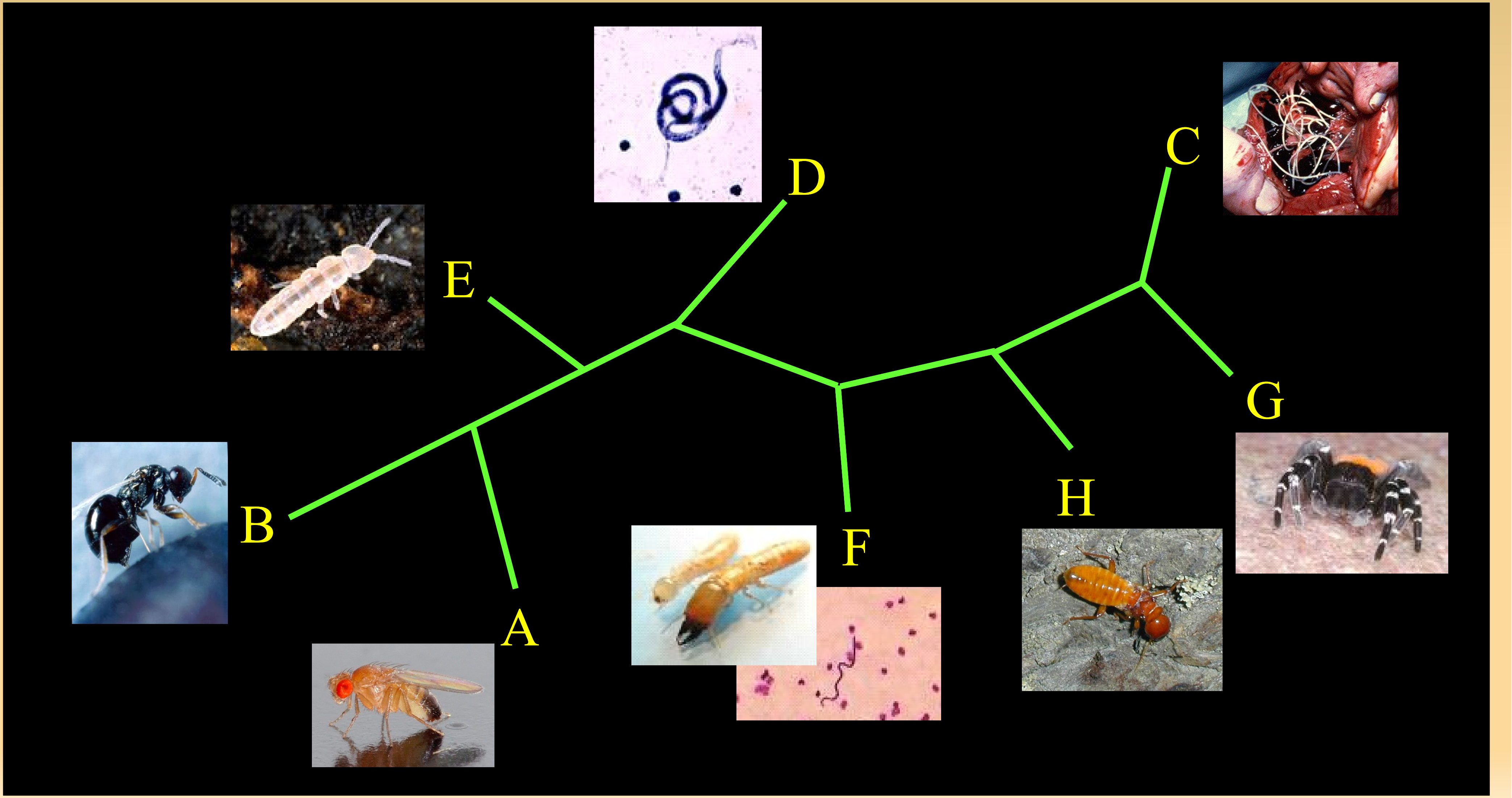
Wolbachia pipientis

Assenza di una tassonomia "sicura": supergruppi



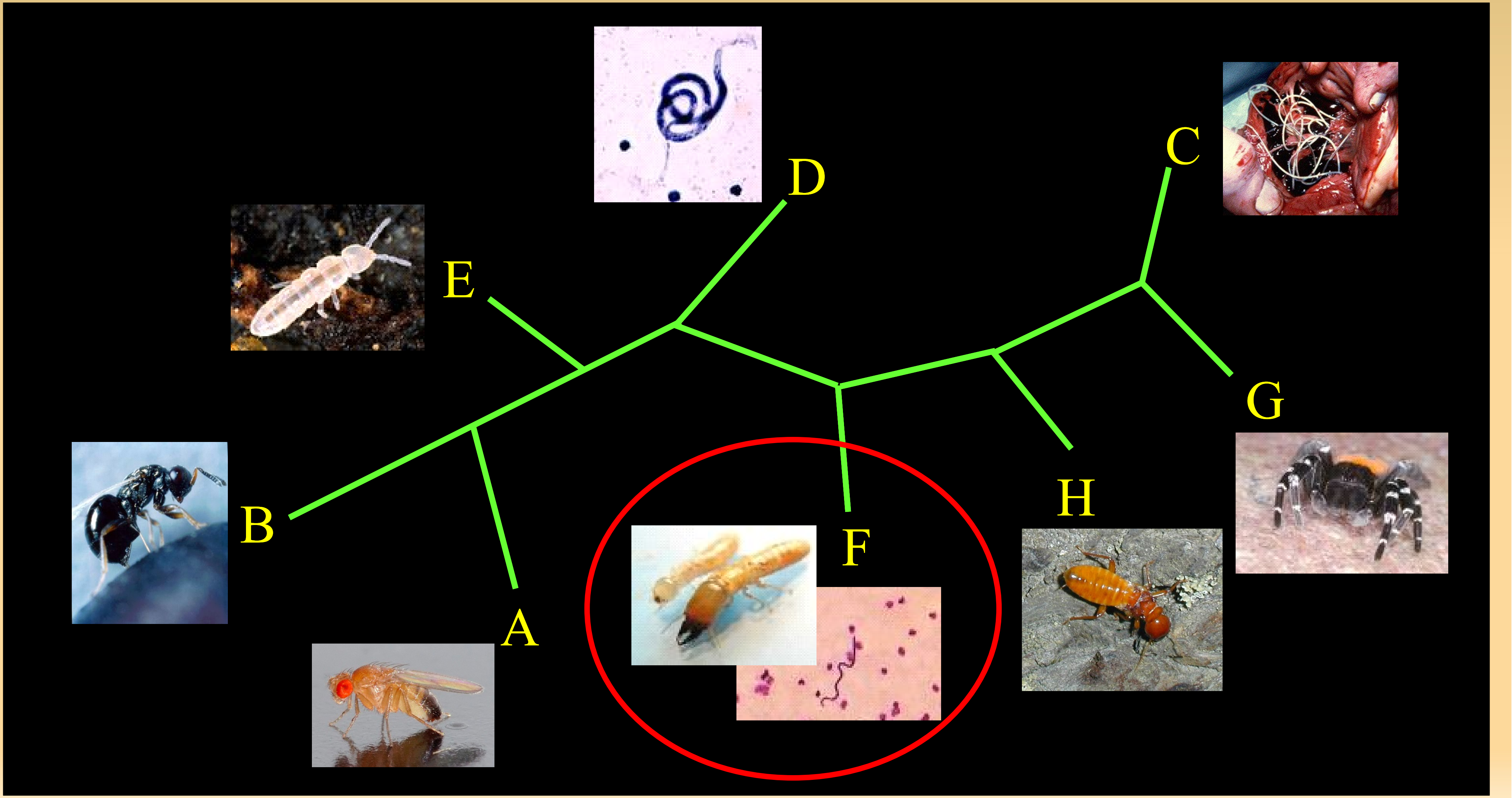
Wolbachia pipientis

Assenza di una tassonomia “sicura”: supergruppi

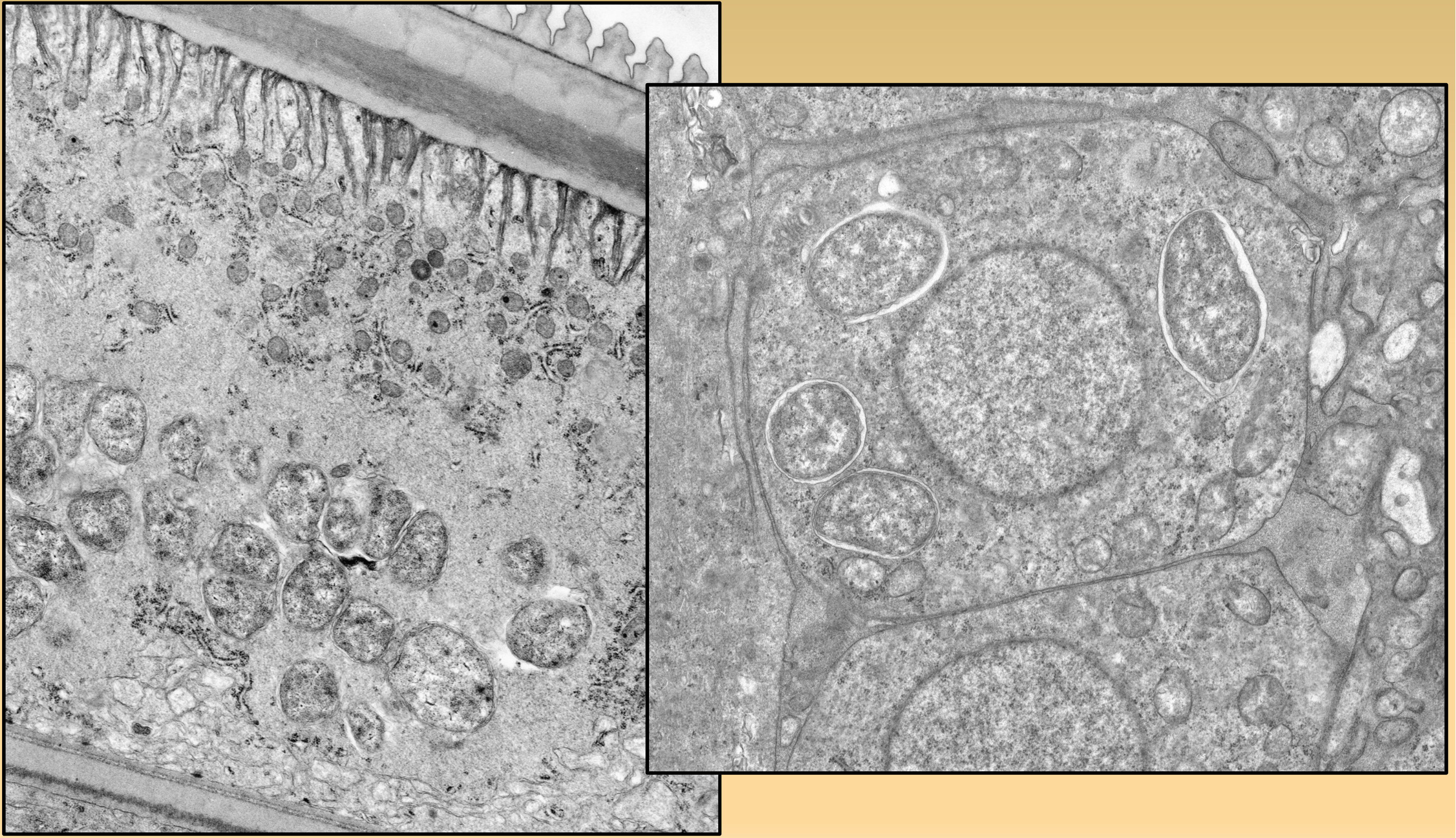


Wolbachia pipientis

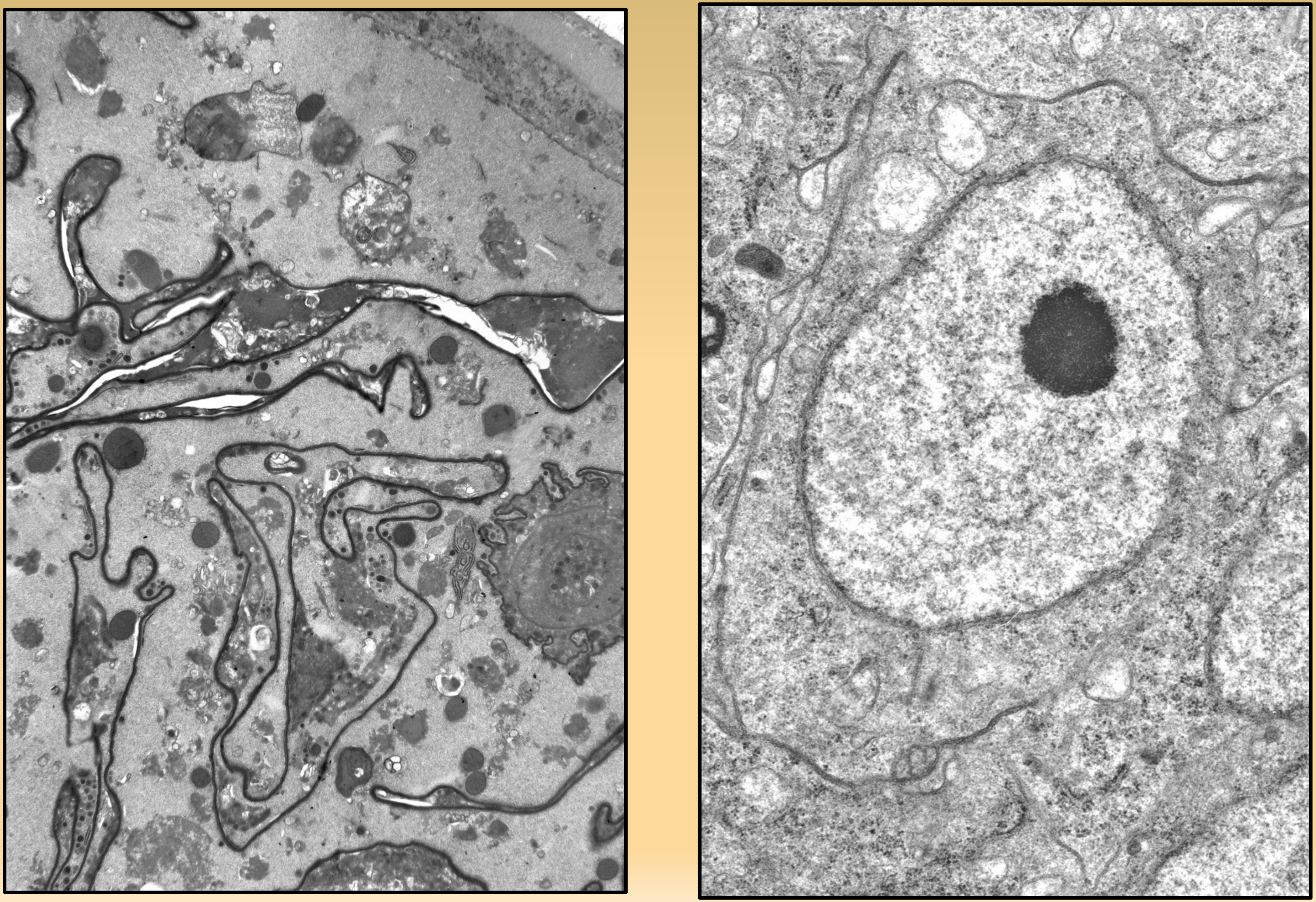
Assenza di una tassonomia "sicura": supergruppi



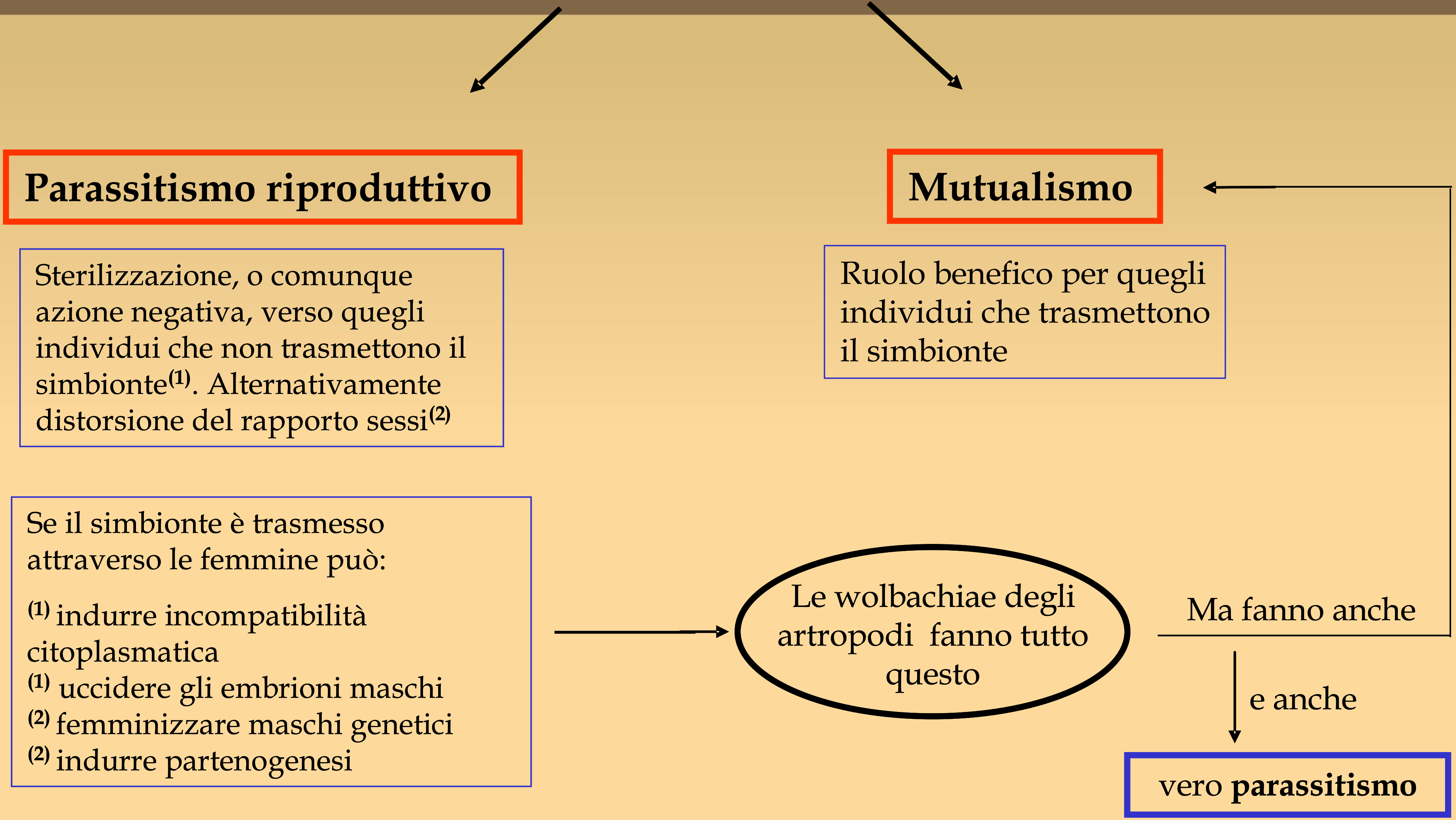
Wolbachia pipientis nelle filarie



Wolbachia pipientis: cure antibiotiche



Un simbionte trasmesso per via verticale ha due possibili opzioni evolutive:



Parassitismo riproduttivo

Sterilizzazione, o comunque azione negativa, verso quegli individui che non trasmettono il simbionte(1). Alternativamente distorsione del rapporto sessi(2)

Se il simbionte è trasmesso attraverso le femmine può:

(1) indurre incompatibilità citoplasmatica
(1) uccidere gli embrioni maschi
(2) femminizzare maschi genetici
(2) indurre partenogenesi

Mutualismo

Ruolo benefico per quegli individui che trasmettono il simbionte

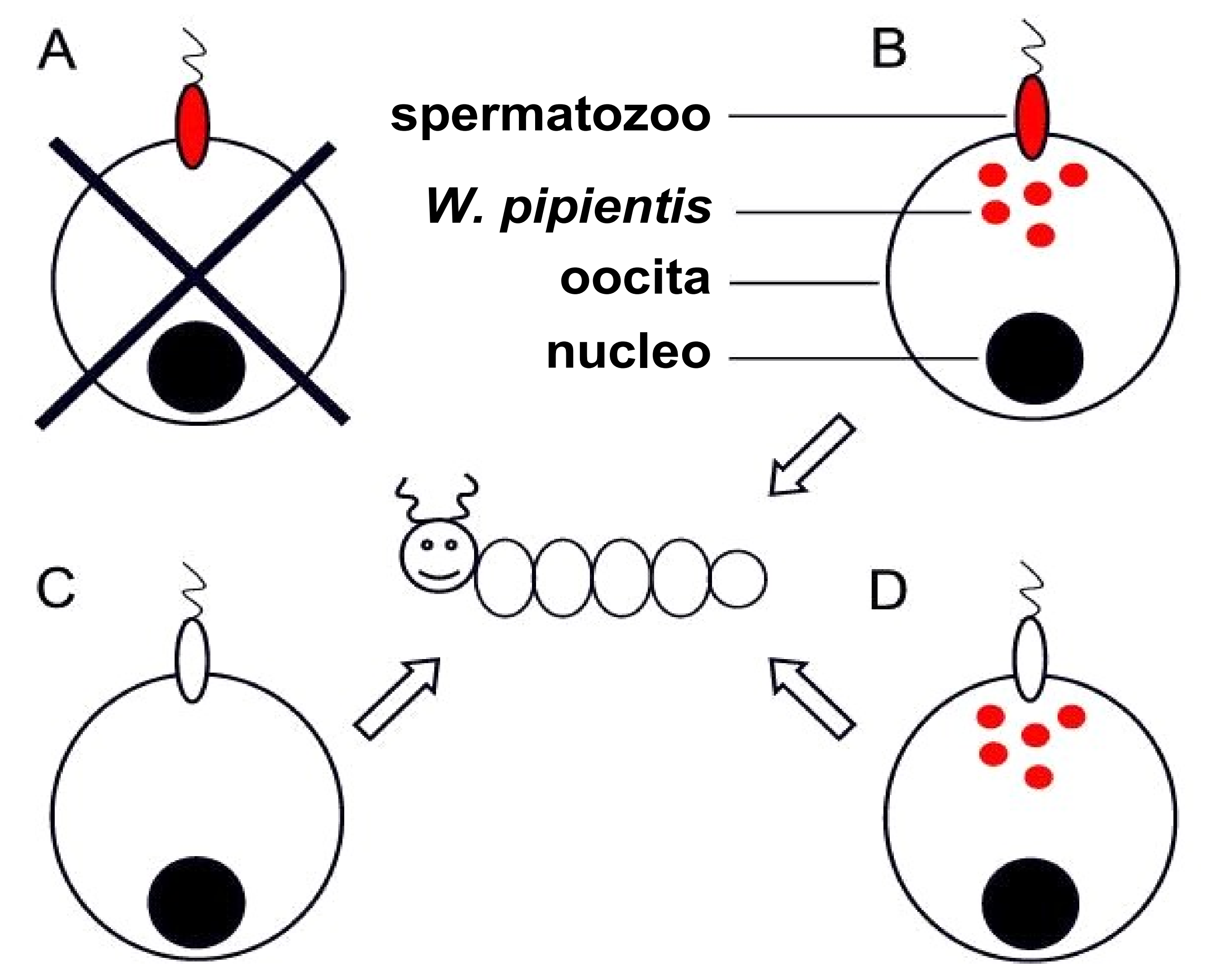
Le wolbachiae degli artropodi fanno tutto questo

Ma fanno anche

e anche

vero **parassitismo**

W. pipientis: incompatibilità citoplasmatica


A
B
spermatozoo
W. pipientis
oocita
nucleo
C
D

Le simbiosi: parassitismo *vs* mutualismo

“Secondo me la domanda più importante da porsi a proposito di qualunque **parassita** è questa:

i suoi geni sono trasmessi alle generazioni successive per mezzo degli stessi veicoli usati dai geni dell’ospite?

Se non lo sono, mi aspetto che il parassita **danneggi** l’ospite, in un modo o nell’altro; ma se invece lo sono, il parassita farà tutto ciò che può per **aiutare** l’ospite, non solo a sopravvivere ma anche a riprodursi. Nel corso dell’evoluzione cesserà di essere un parassita, coopererà con l’ospite e alla fine potrà anche fondersi con i suoi tessuti e diventare **del tutto irriconoscibile** come parassita. Forse […] le nostre cellule hanno affrontato problemi simili molto tempo fa e noi tutti siamo derivati da antiche fusioni di parassiti.”

da ‘Il gene egoista’ di Richard Dawkins (2ª edizione, 1989)