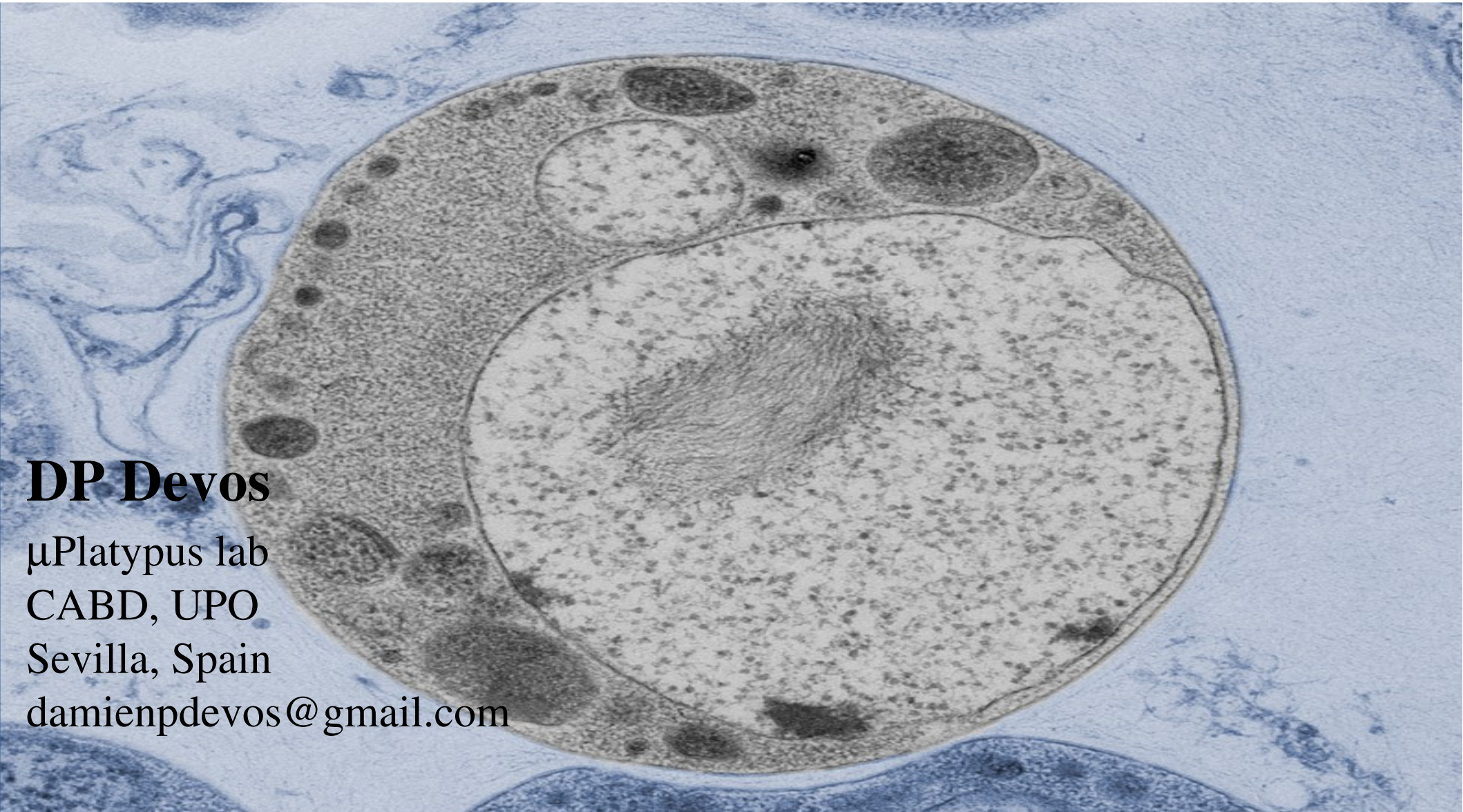
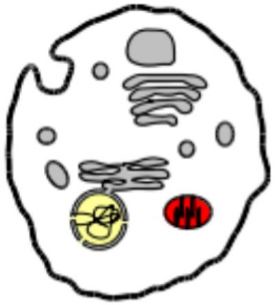
Evolutionary Cell Biology of the eukaryotic endomembrane system, of division mode, and µbiology's platypus



DP Devos

µPlatypus lab
CABD, UPO
Sevilla, Spain
damienpdevos@gmail.com



TOP
Eukaryotes

Top-Down approach

OPH (Dacks & Field)

PCH (Devos, Rout & Sali)

Eukaryotic Realm

Radiation

Point of origin

LECA

Big jumps as opposed to stepwise

Prokaryotic Realm

Eukaryogenesis

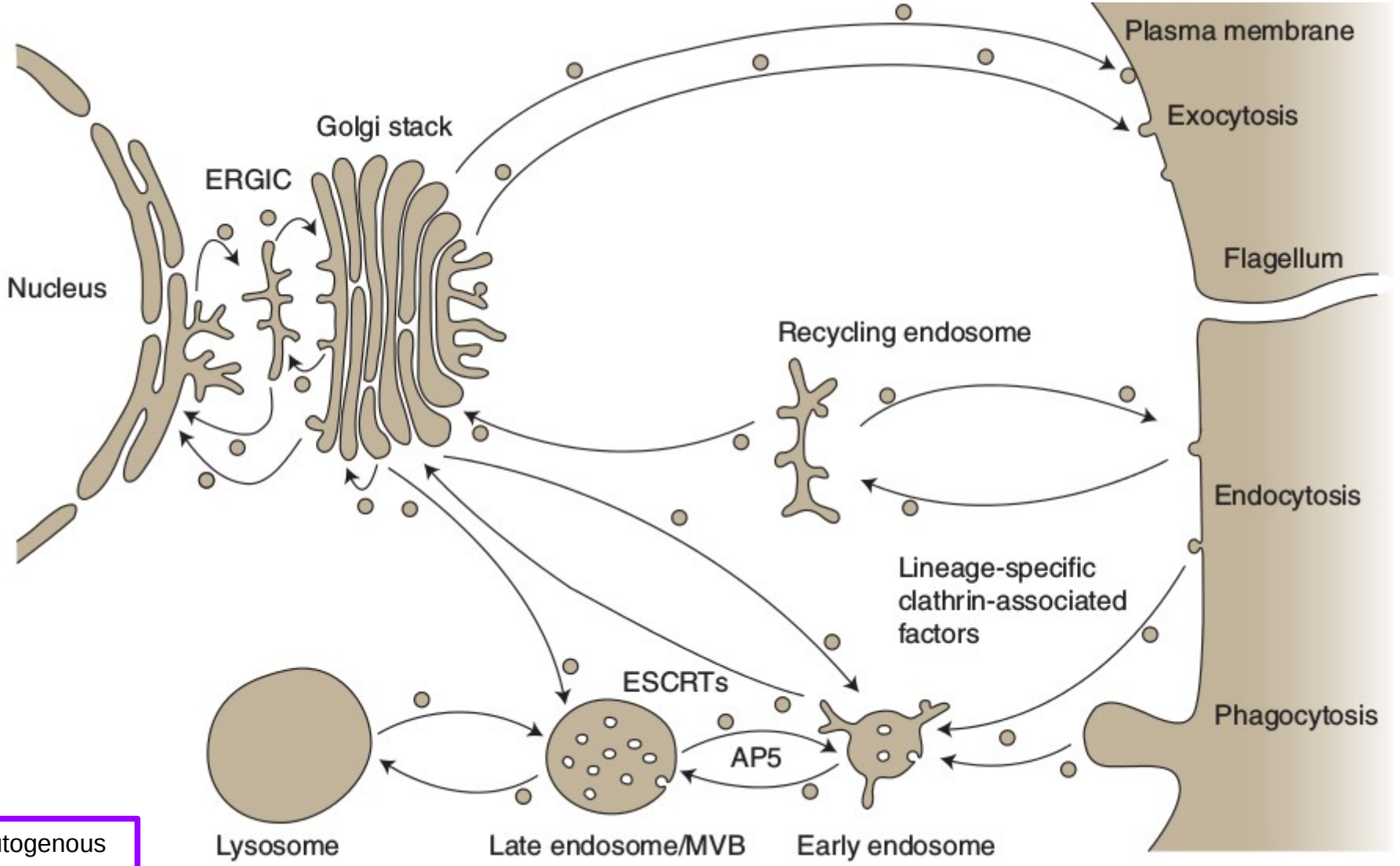
Point of beginning

µPlatypus (Devos & Reynaud)

Bottom-Up approach

Prokaryotes
BOTTOM

The eukaryotic endomembrane system



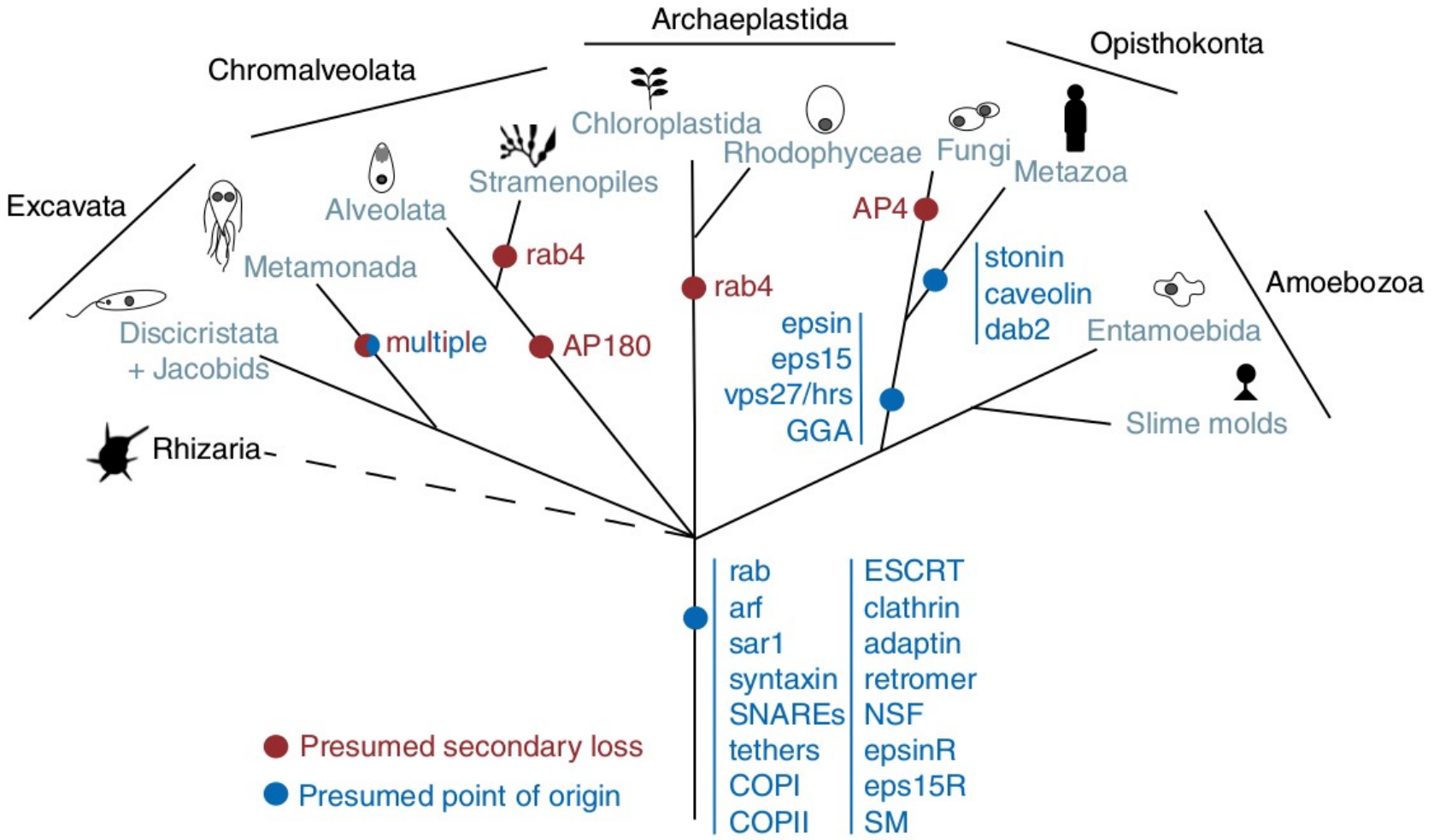
Autogenous
vs
endosymbiotic

Mitochondria

Chloroplast

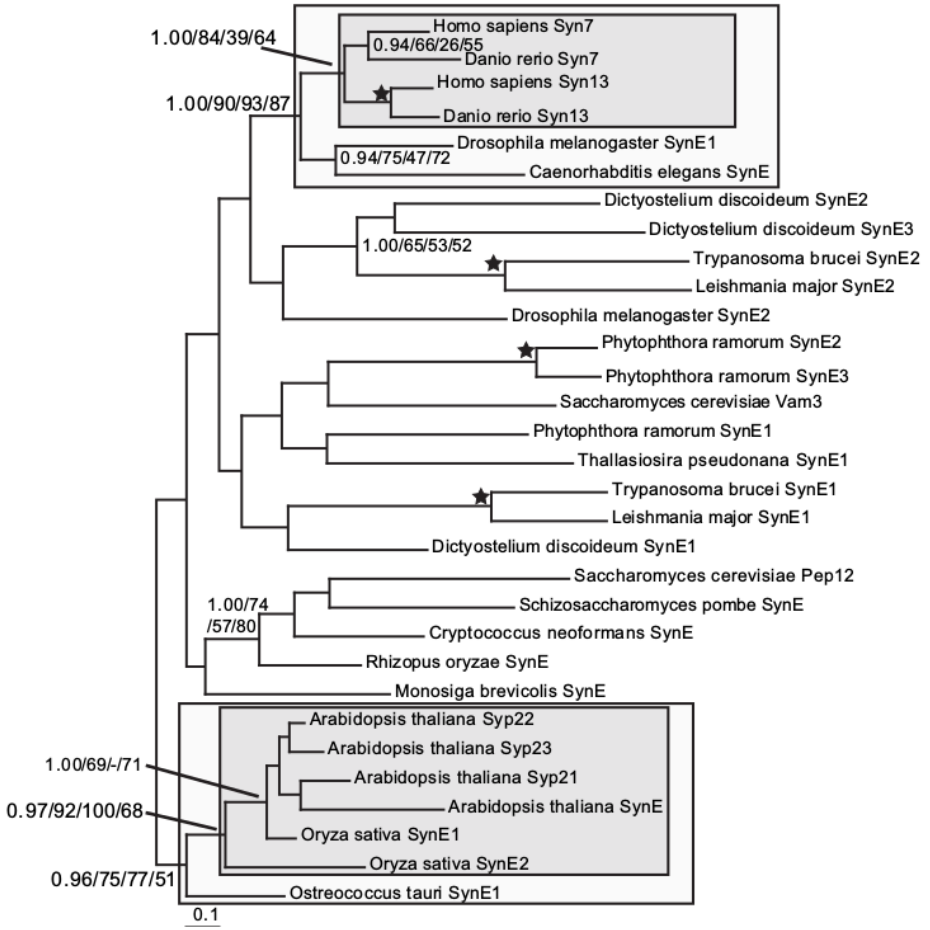
Wideman *et al.*, CSF Perspect Biol 2014

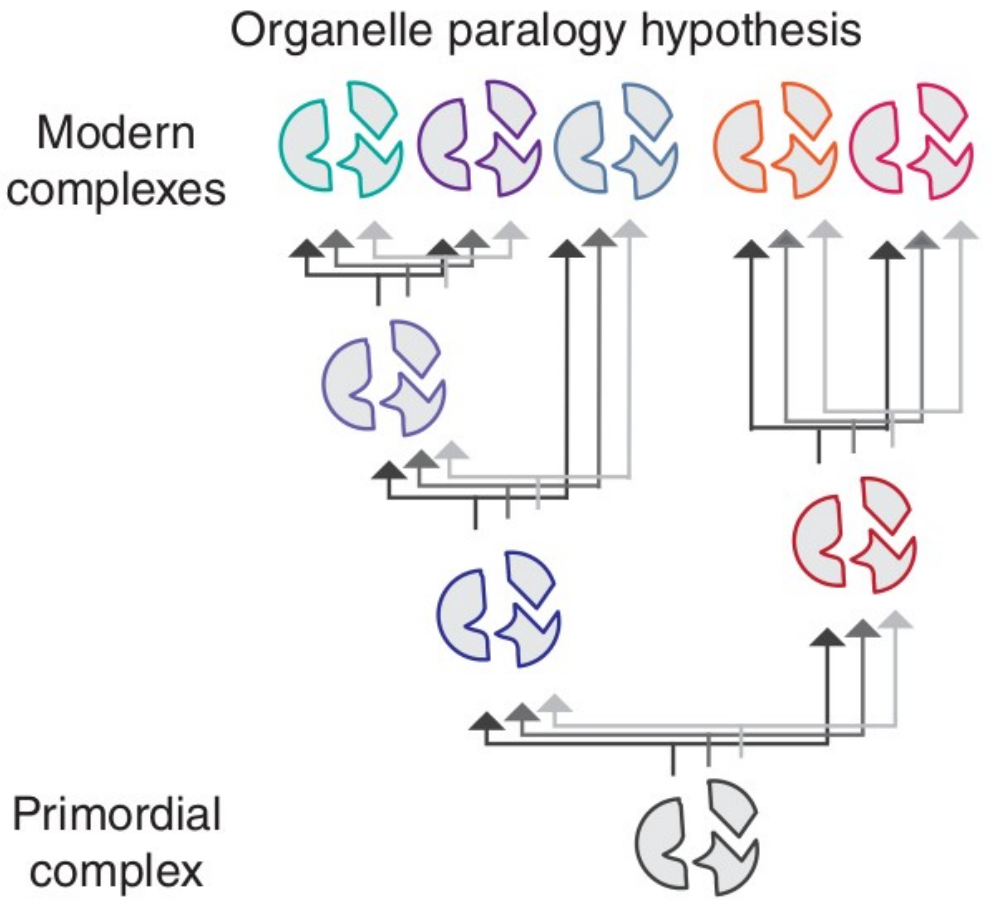
Ancestral eukaryote had a developed MS



Dacks & Field, JCS 2007

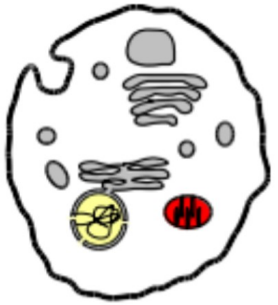
The organelles paralogy hypothesis





The organelle paralogy hypothesis (OPH) proposes that the increase in complexity was caused by iterative gene **duplications**, followed by sequence **divergence** and neofunctionalization in multiple interacting proteins encoding organelle identity and pathway specificity.

Dacks & Field, JCS 2007; Dacks *et al.*, PNAS 2008



TOP
Eukaryotes

Top-Down approach

OPH (Dacks & Field)

PCH (Devos, Rout & Sali)

Eukaryotic Realm

Divergence
Radiation

Point of origin

LECA

Sequence signal barrier

> 1/2rd of euk genes/proteins

Structure is more conserved than sequence

Prokaryotic Realm

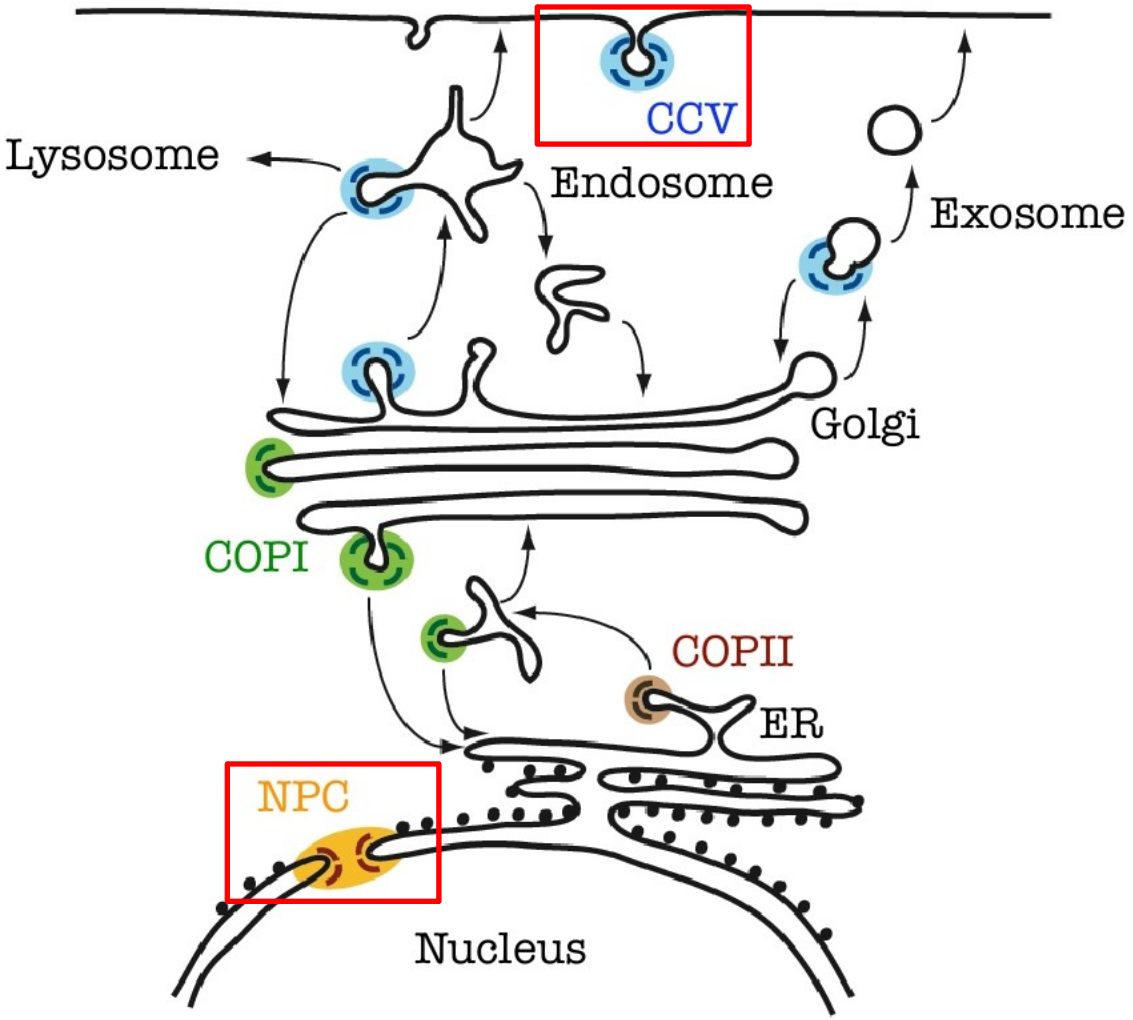
Point of beginning

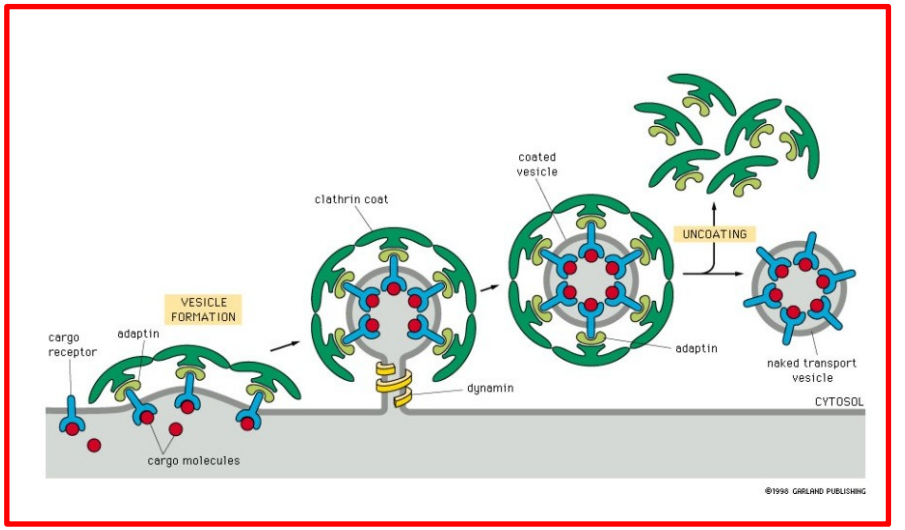
µPlatypus (Devos & Reynaud)

Bottom-Up approach

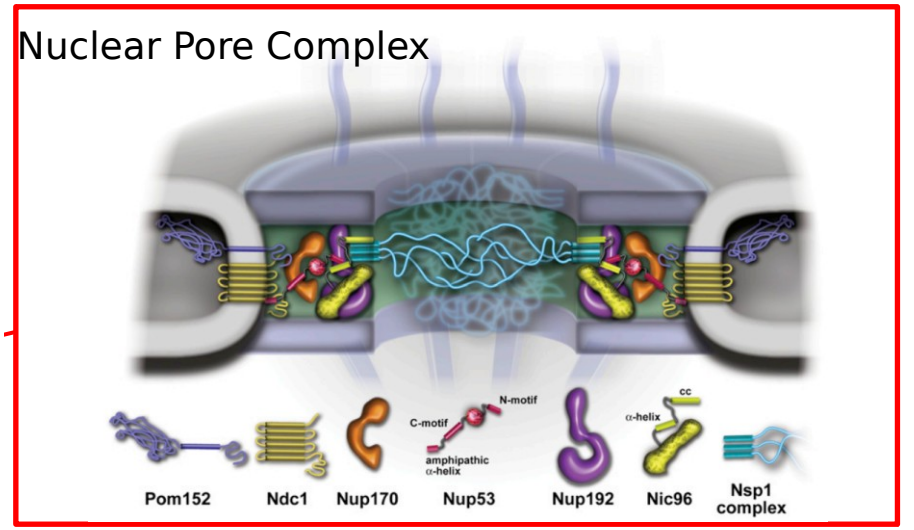
Prokaryotes
BOTTOM

Membrane coating systems



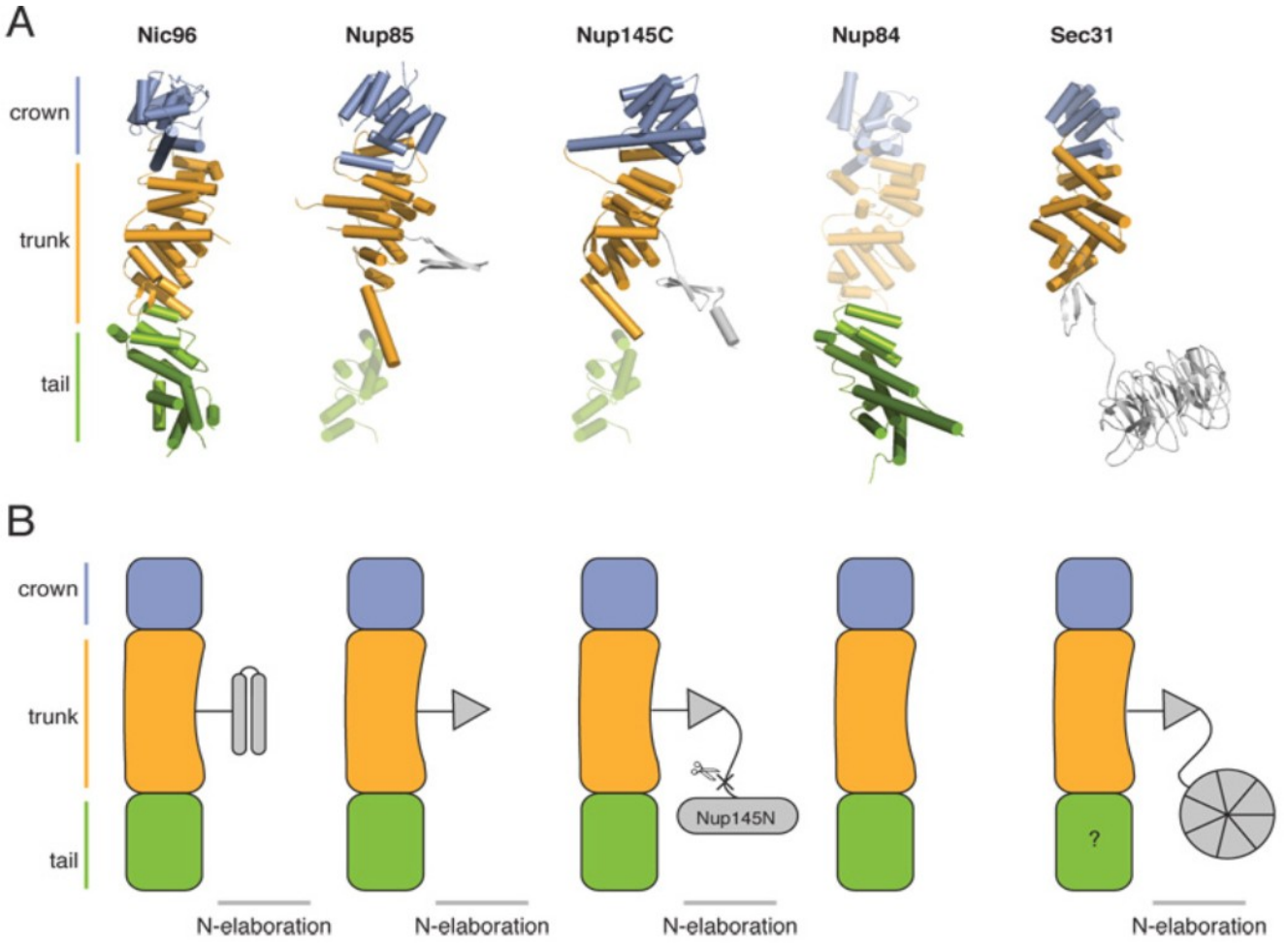


Nuclear Pore Complex



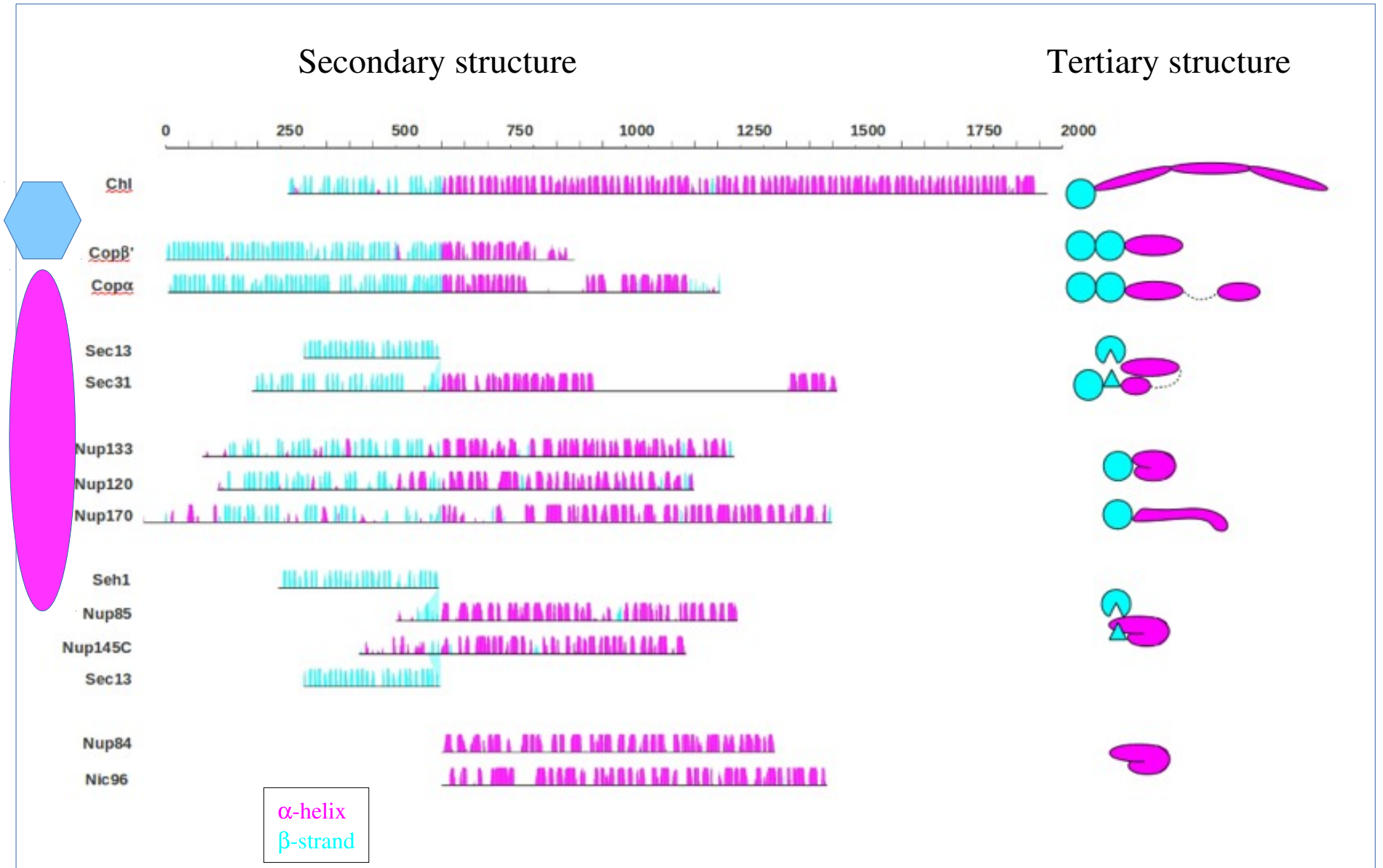
Amlacher *et al.*, Cell 2011

Structural similarity of the euk MCs



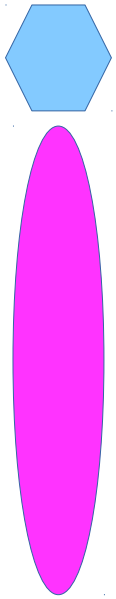
Brohawn *et al.*, Science 2008

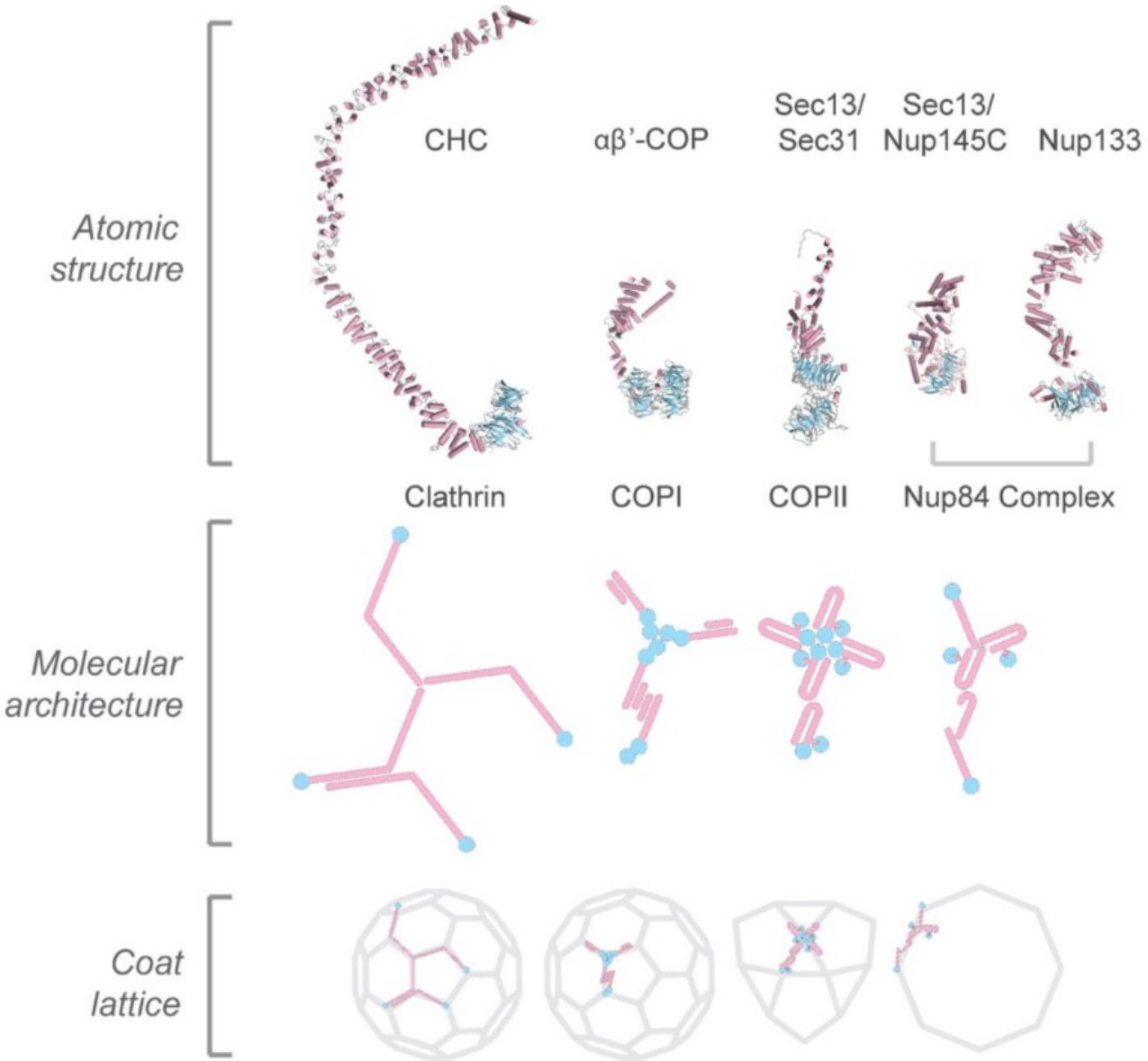
Membrane coat (MC) architecture



Devos *et al.*, PLoS B 2004

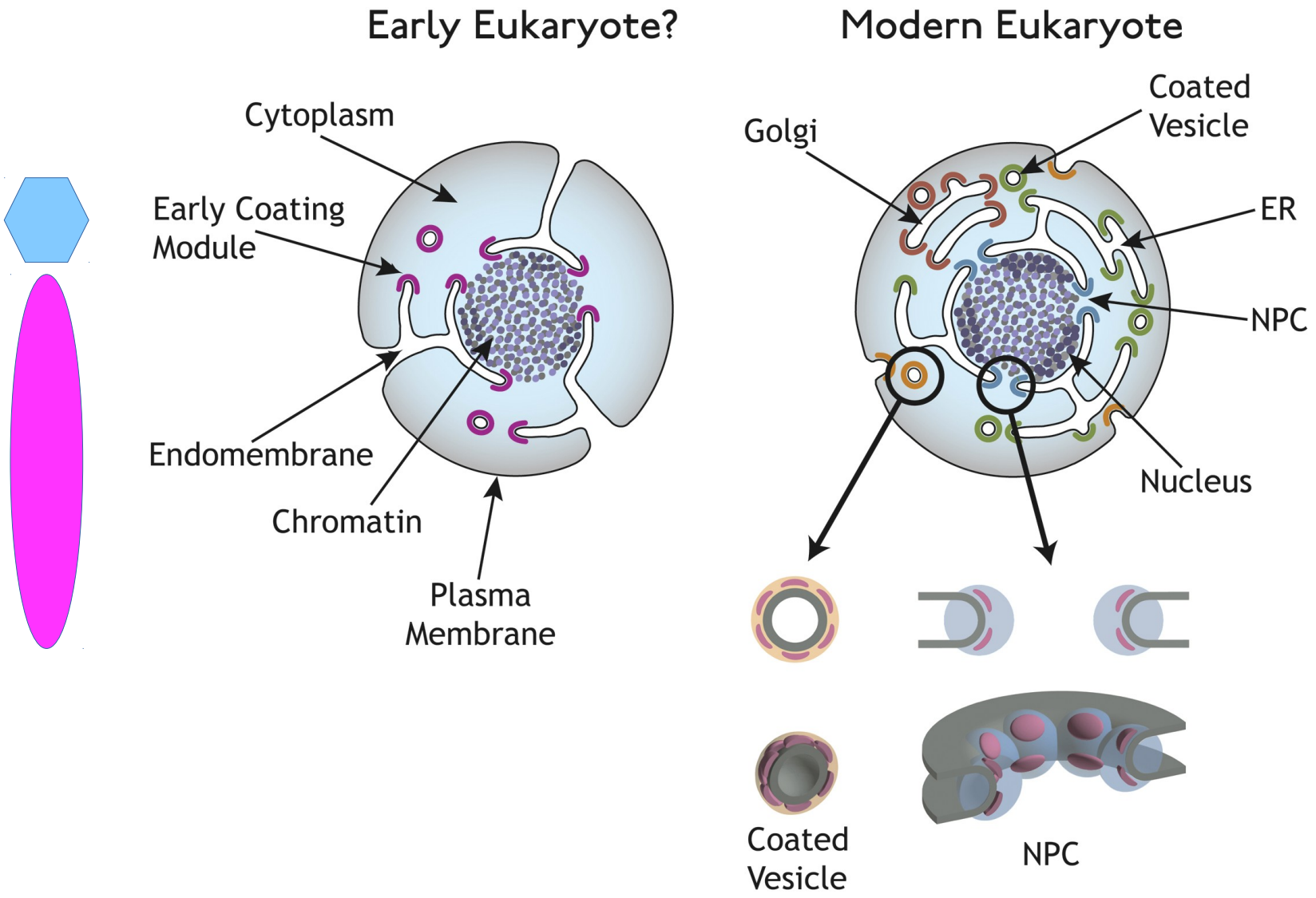
MC diversity





Field *et al.*, JCB 2011

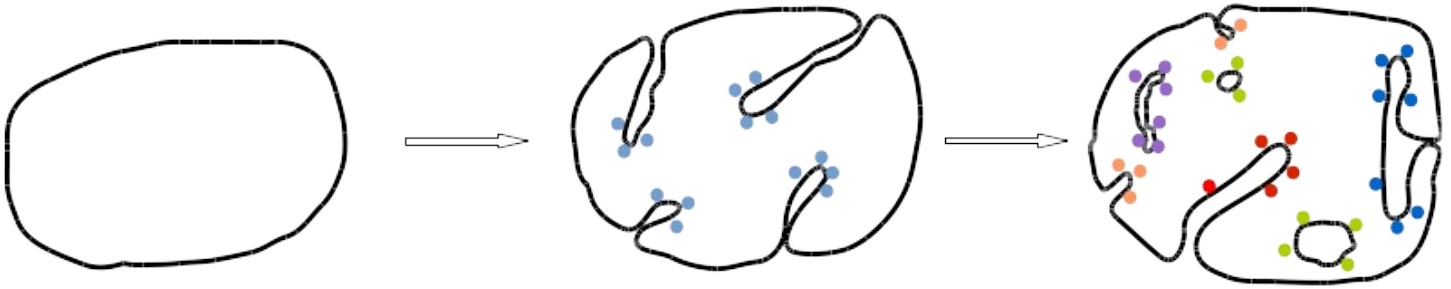
The protocoatomer hypothesis

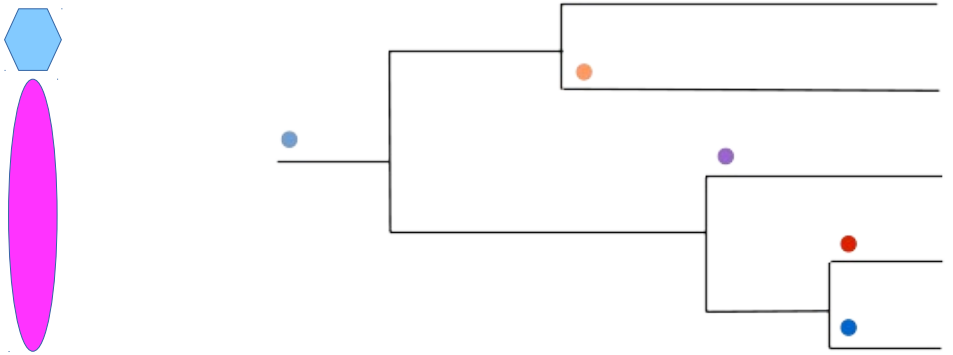


Devos *et al.*, PLoS B 2004

Evolution of the EMS: origin, tempo and mode.

Intermediary state might have been
a non-differentiated, multi-functional network of tubules and vesicles

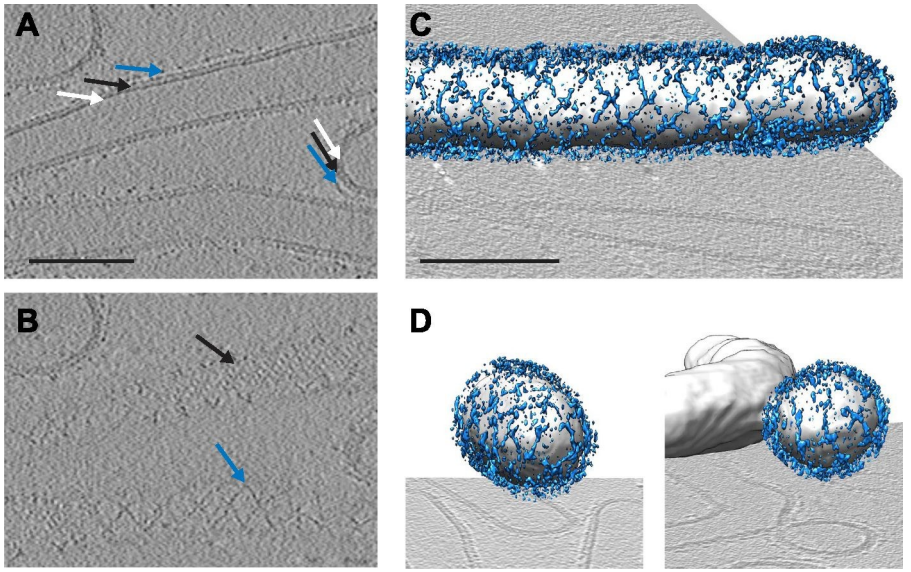




Devos *et al.,* PLoS B 2004; Dacks *et al.,* PNAS 2008; Gonzalez-Sanchez *et al.*, Biology 2015

Ancestral multifunctional TVN support (I)

Vesicle forming components, such as copII, also forms tubular structures



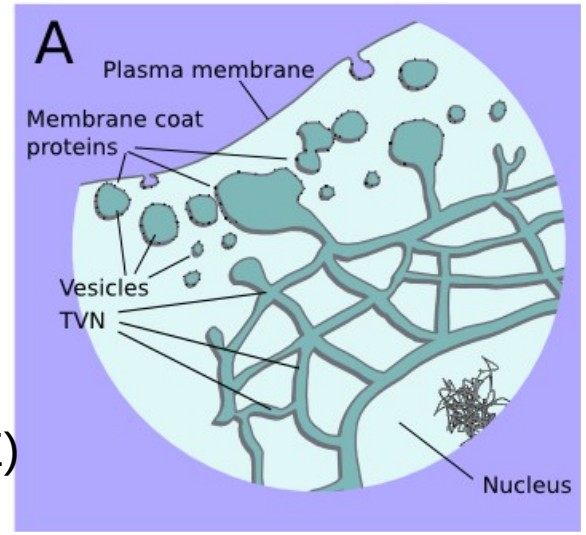
Cryo-electron tomograms of a reconstituted COPII budding reaction. Scale bars = 100 nm.(A) A slice through a tomogram showing two coat layers arranged around tubular and spherical membranes. White, black and blue arrows point to the membrane, inner, and outer coat layers respectively. (B) A slice through the top of the tubes in panel A, showing repeating features in the coat layers. (C) A surface rendering of a COPII-coated tube. The membrane and inner coat are in grey, the outer coat in blue. (D) Surface renderings of spherically curved regions of membrane, coloured as in panel C.

Zanetti *et al*., eLIFE 2013

Ancestral multifunctional TVN support (II)

Reduced eukaryotic ES are multifunctional TVN

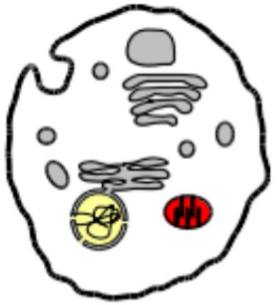
G. lamblia (E)



- Microsporidia: Golgi-derived branching or varicose tubules, as a tubular network (Beznoussenko *et al*., JCS 2007).

- *E. histolytica*: ER-derived continuous reticular network (Teixeira & Huston, Eukaryot. Cell 2008; Vaithilingam *et al*., CIB 2008).

- *G. lamblia*: Contiguous ER and endosome/lysosome compartment continuous with the nuclear envelope.“an ER-like tubulovesicular compartment, which itself can dynamically communicate with clathrin-containing vacuoles at the periphery of the cell to receive endocytosed proteins”. In addition, the TVN of *G. lamblia* serves as a site of protein synthesis but also of degradation of material from the outside (Abodeely *et al*., Eukaryot. Cell 2009).



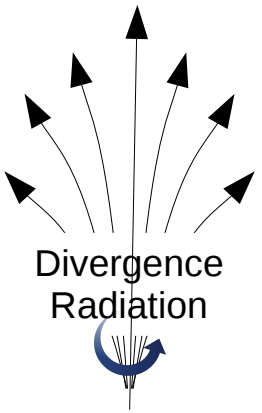
TOP
Eukaryotes

Top-Down approach

OPH (Dacks & Field)

PCH (Devos, Rout & Sali)

Eukaryotic
Realm



Divergence
Radiation

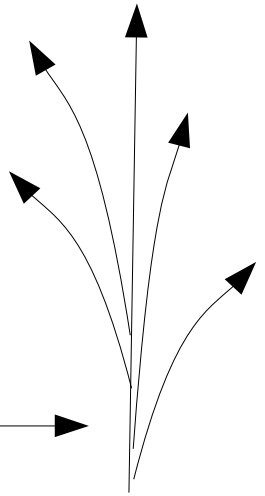
Undifferentiated
multifunctional TVN
as ancestral eukaryotic EMS

Point of origin

LECA

Sequence signal barrier

Prokaryotic
Realm



Point of beginning

µPlatypus (Devos & Reynaud)

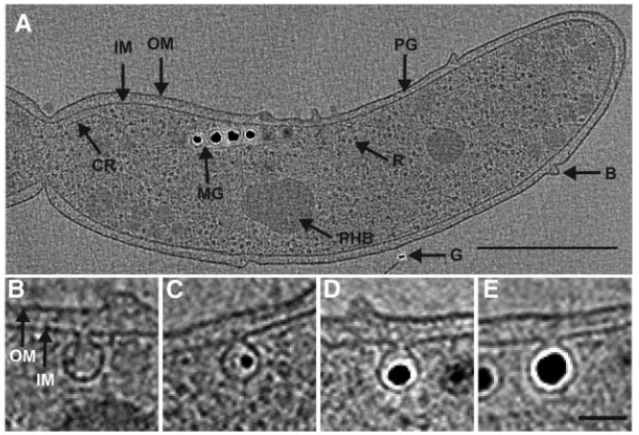
Bottom-Up approach

Prokaryotes
BOTTOM

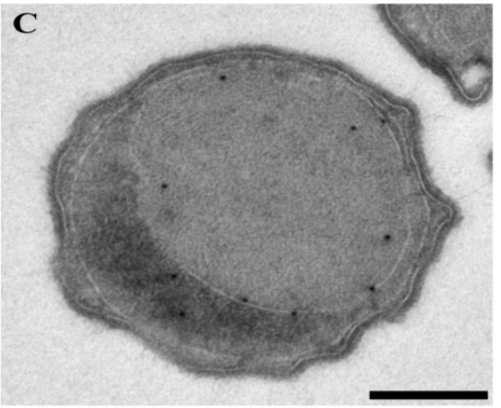
Prokaryotic membrane organisation

Centro Andaluz de Biología del Desarrollo

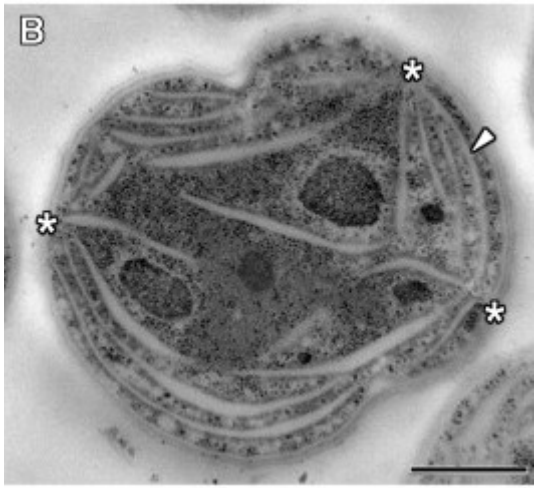
Magnetosomes



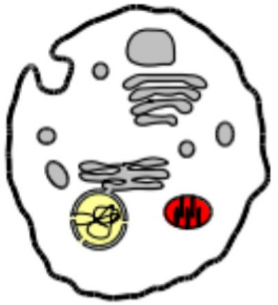
Anammoxosome



Thylakoids



Komeili *et al*., Science 2005; van de Meene *et al.,* BBA 2012; van Niftrik & Jetten MMBR 2012



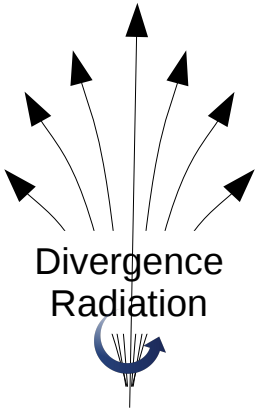
TOP
Eukaryotes

Top-Down approach

OPH (Dacks & Field)

PCH (Devos, Rout & Sali)

Eukaryotic
Realm



Divergence
Radiation

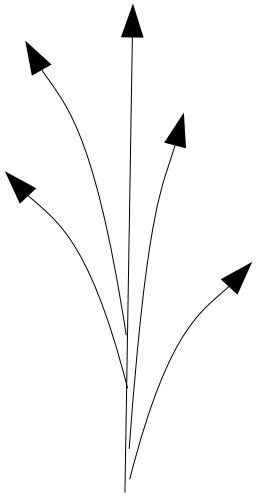
Undifferentiated
multifunctional TVN
as ancestral eukaryotic EMS

Point of origin

LECA

Sequence signal barrier

Prokaryotic
Realm

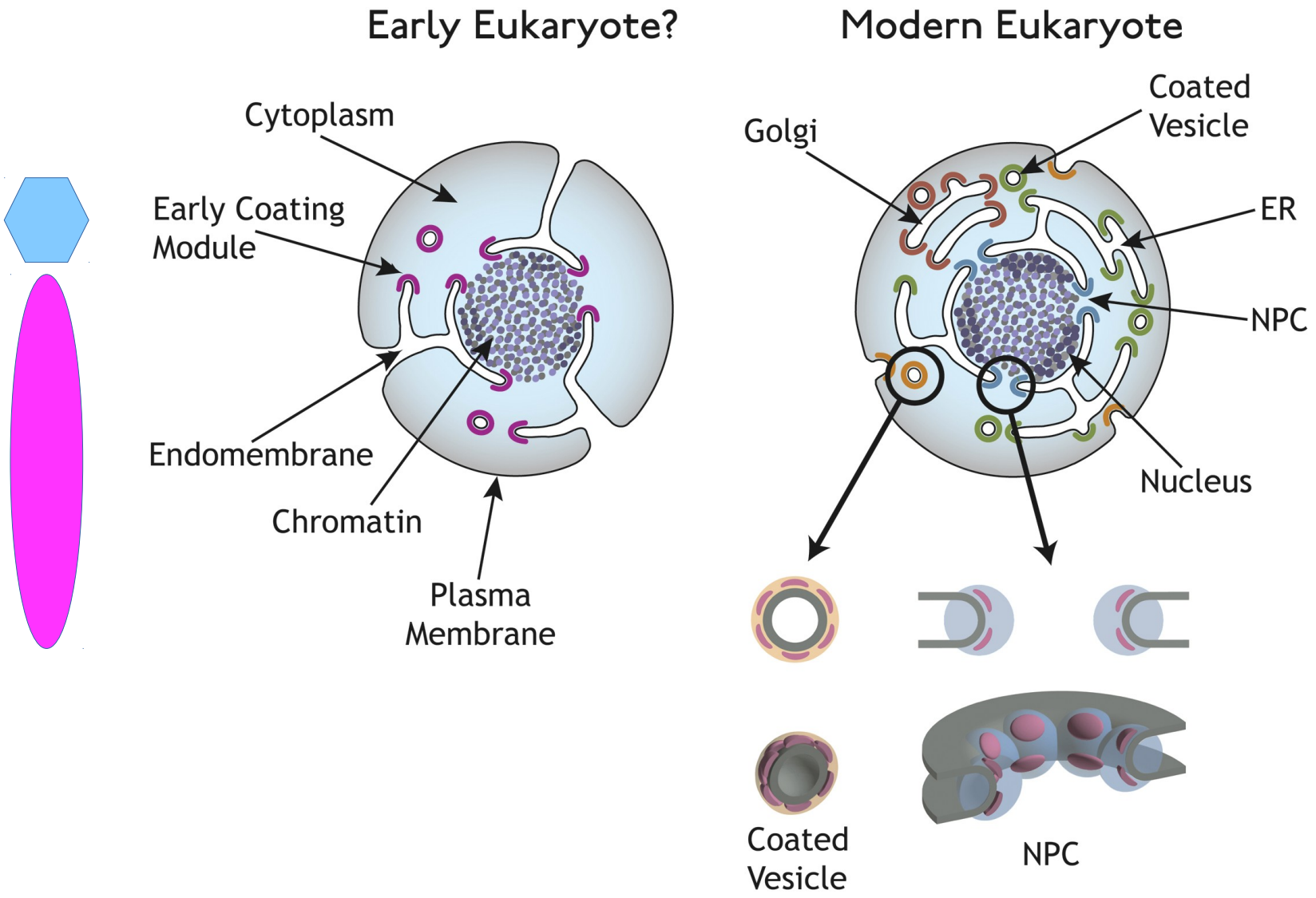


µPlatypus (Devos & Reynaud)

Bottom-Up approach

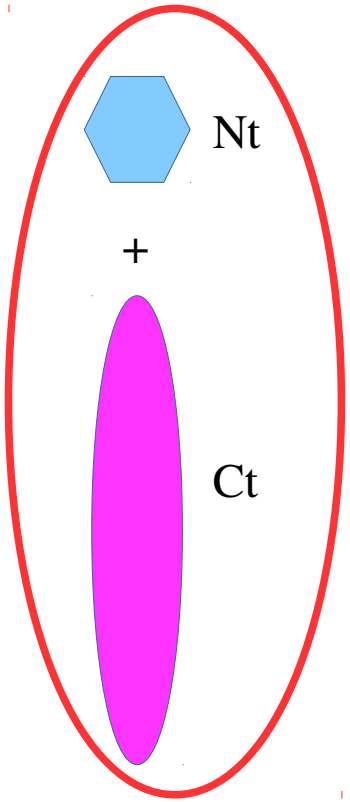
Prokaryotes
BOTTOM

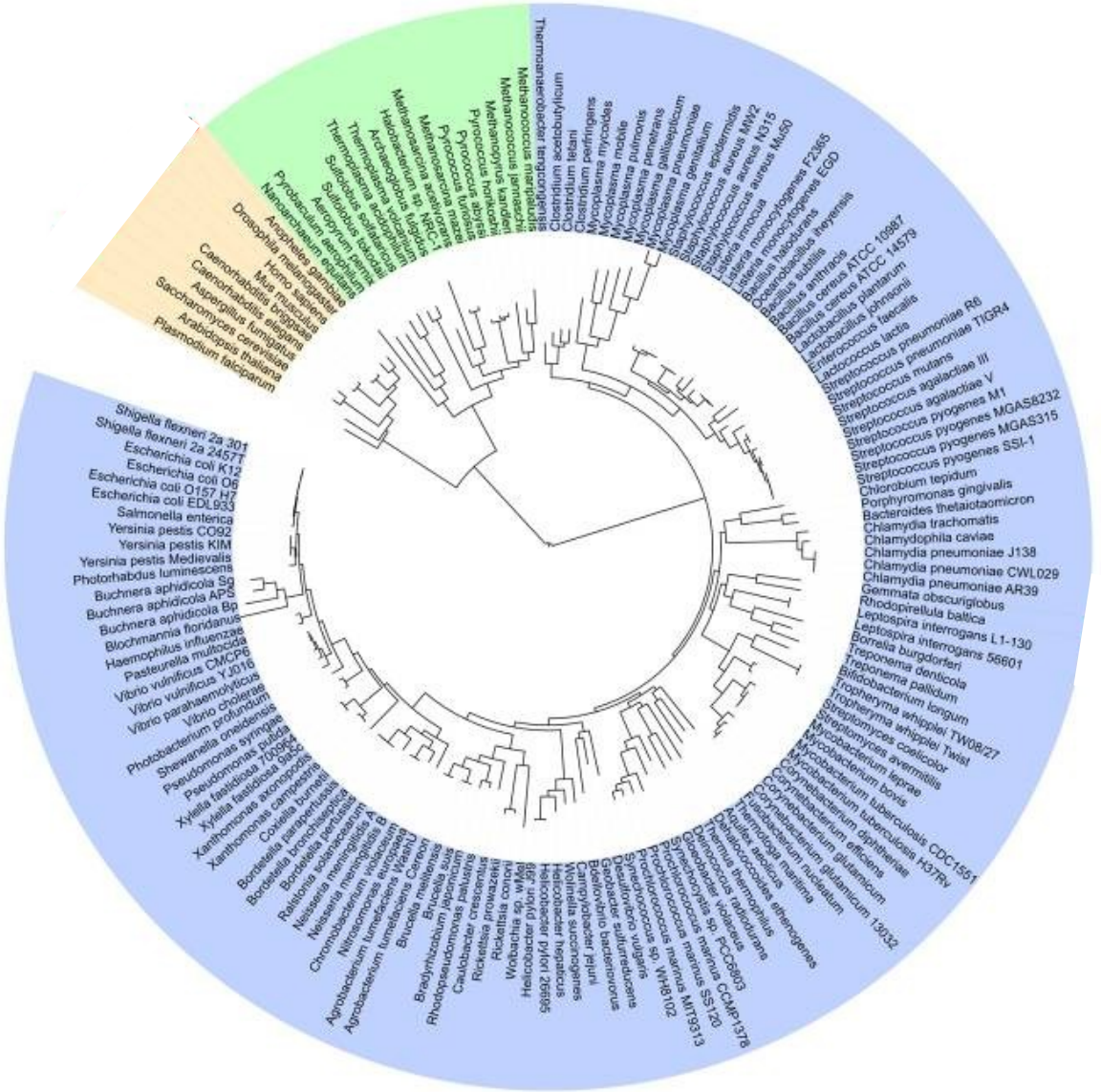
Origin of the MC proteins?



MCs in the tree of life

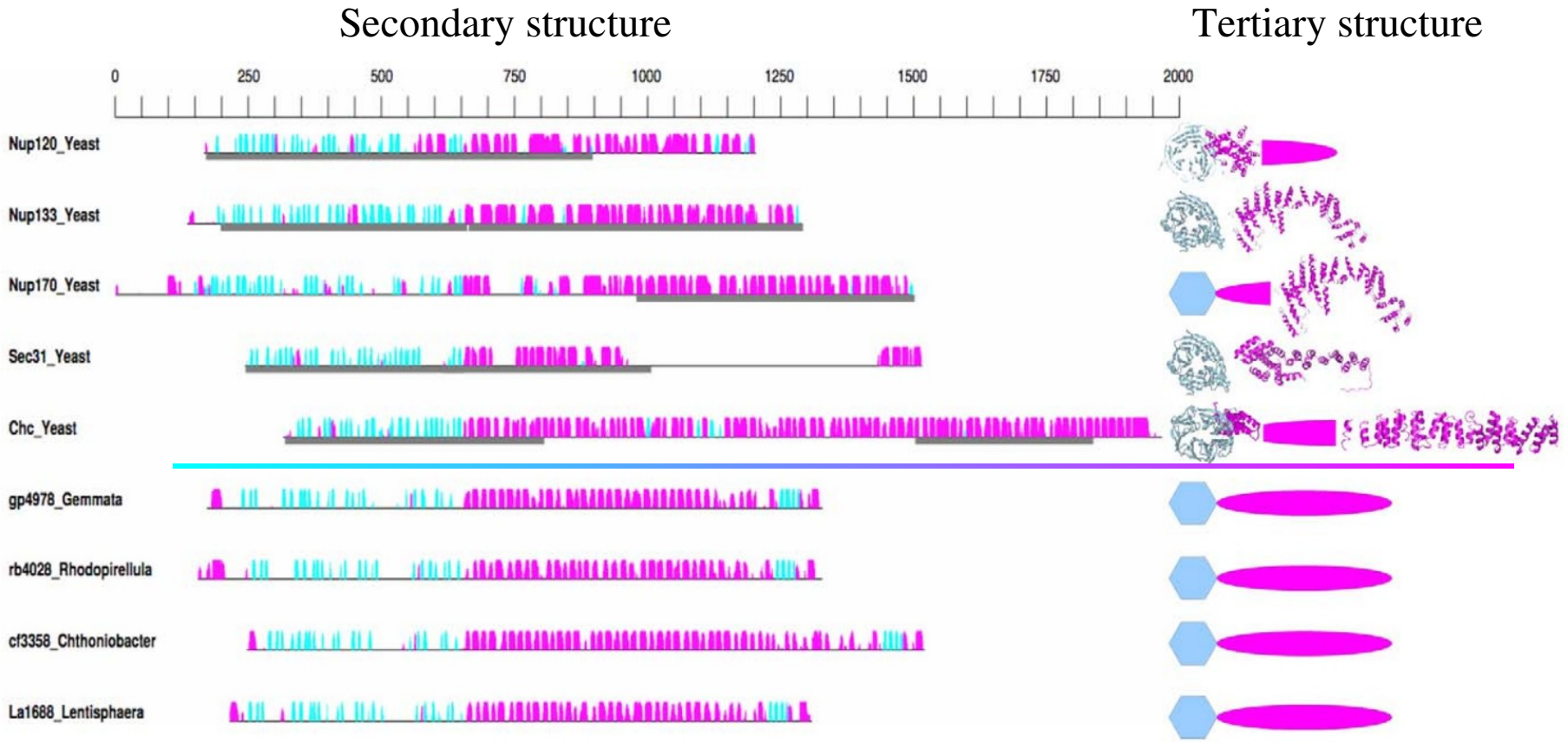
HHSearch
>200 genomes
>1.5 10^9 Seq





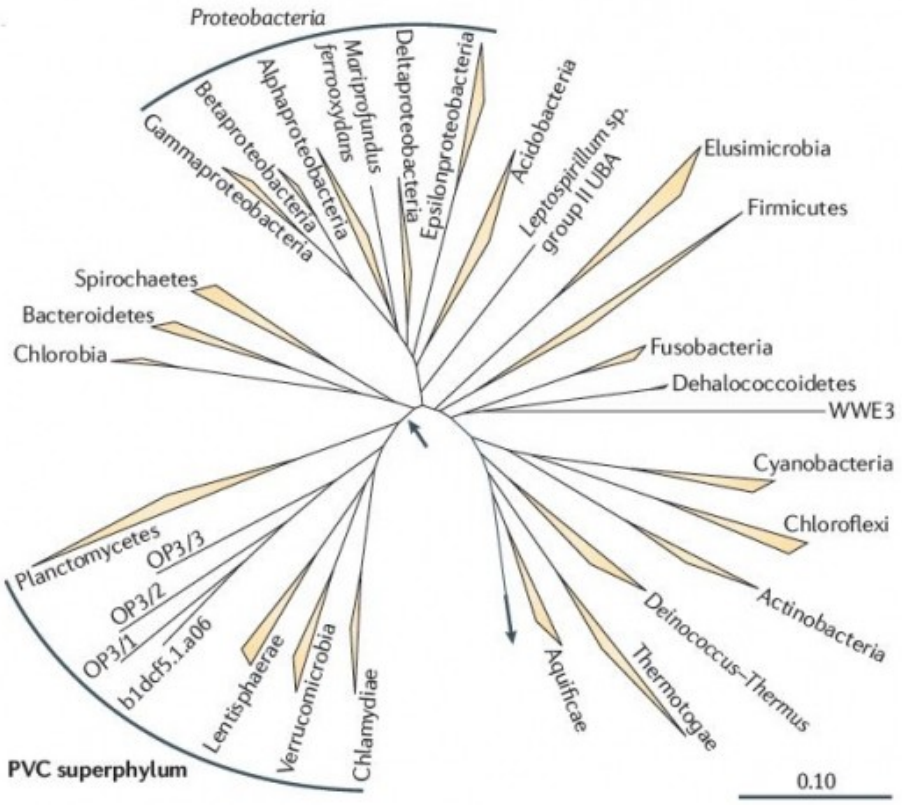
Santarella *et al.*, PLoS B 2010

Prokaryotic MCs



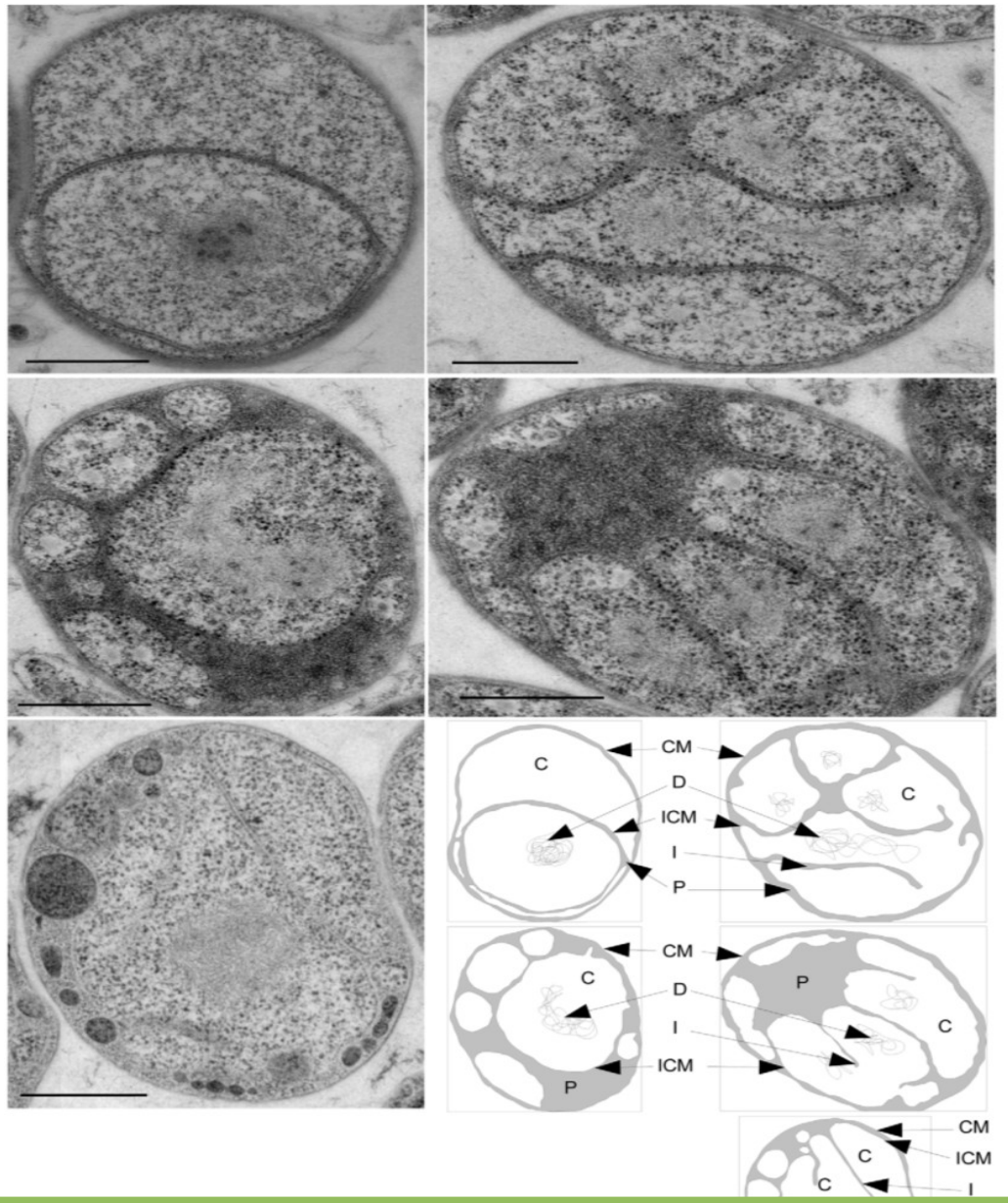
Santarella *et al.*, PLoS B 2010

The PVC bacteria superphylum



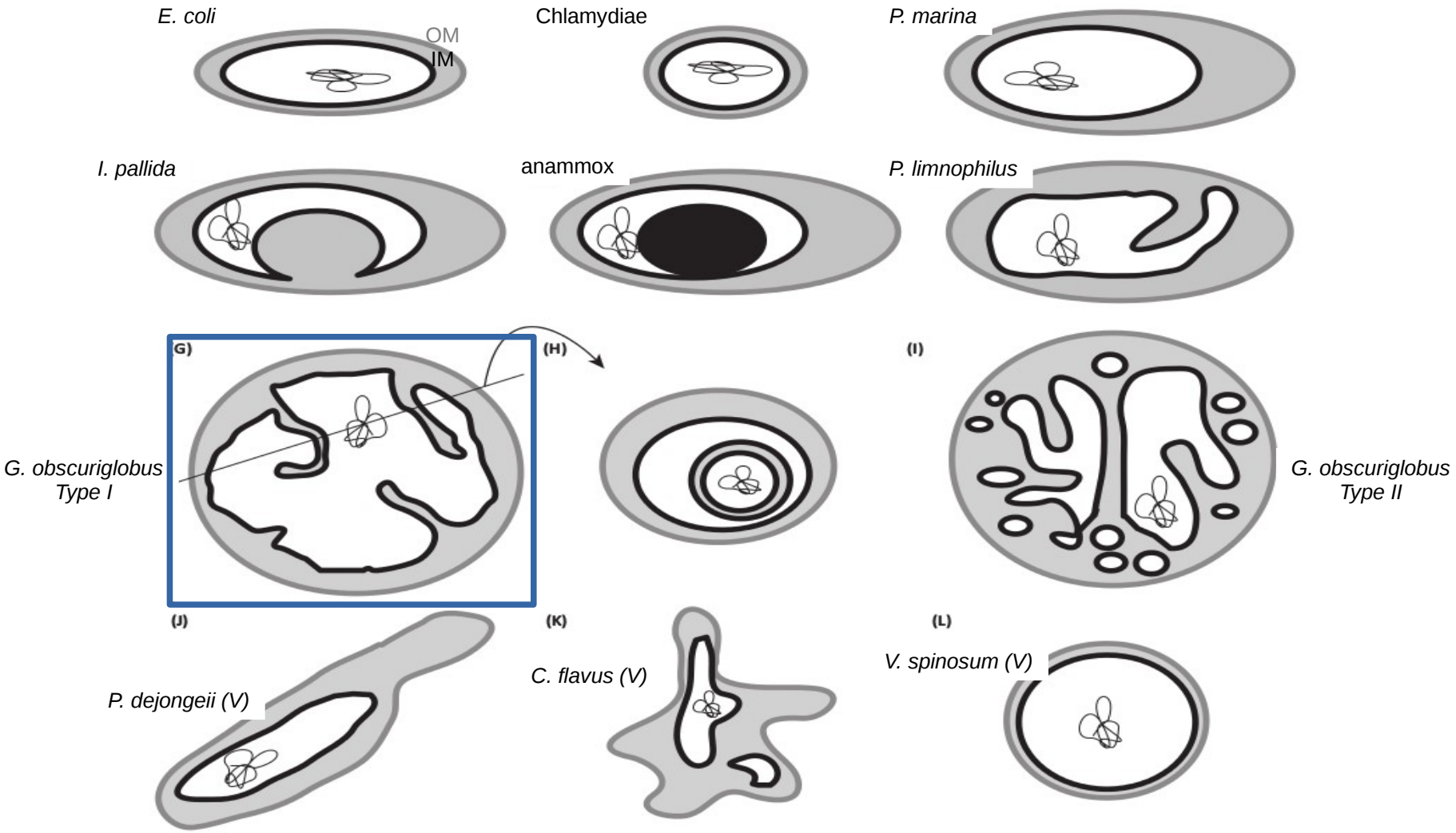
Fuerst & Sagulenko, Nature Review Microbiol 2011

Gemmata obscuriglobus



Santarella *et al.*, PLoS B 2010

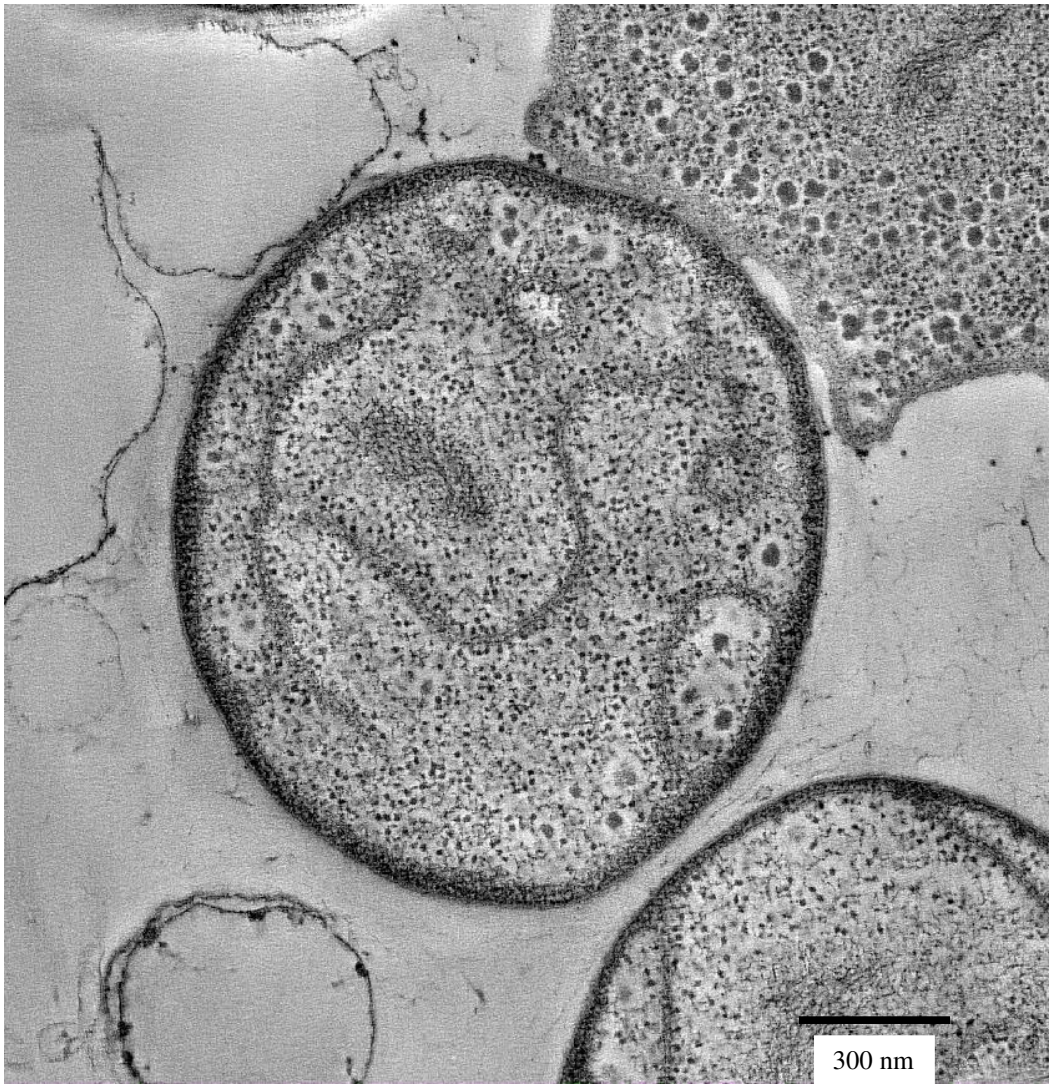
PVC endomembrane system



Developed prokaryotic ES

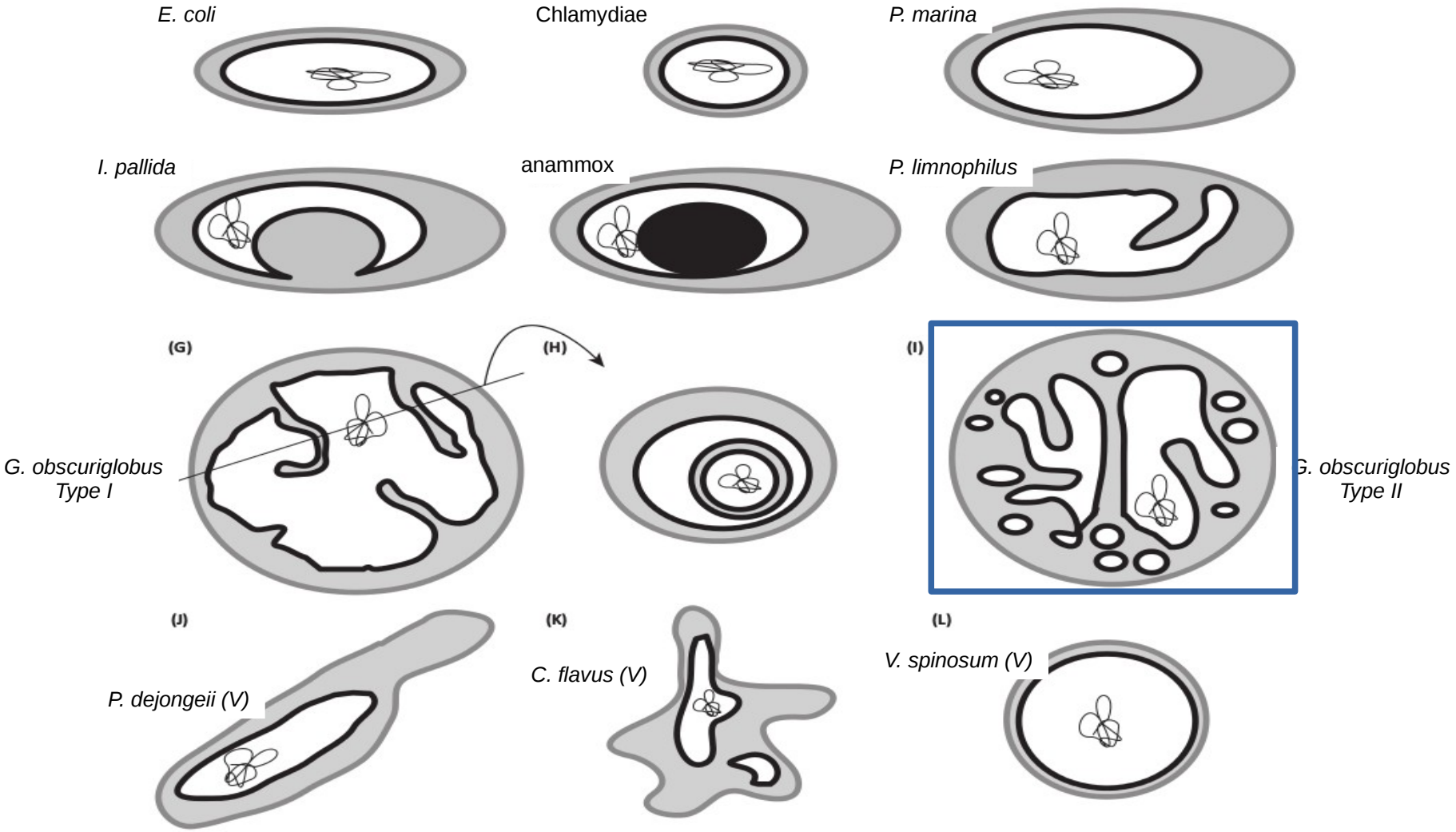
Centro Andaluz de Biología del Desarrollo

Sections 250nm
Technai F30 300kv (FEI)
Dual axis tilt series
IMOD
1130 slices/5



Santarella *et al.*, PLoS B 2010

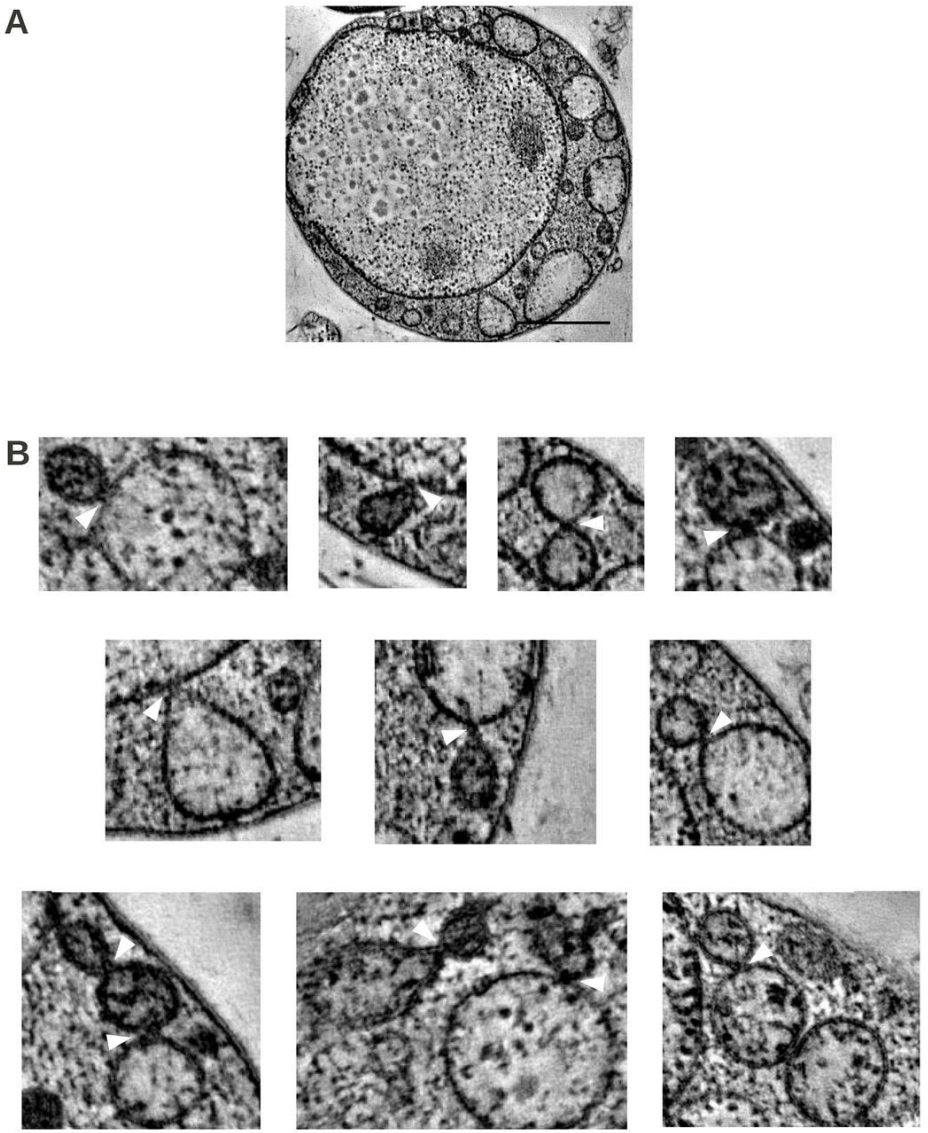
Complex endomembrane system in prokaryote

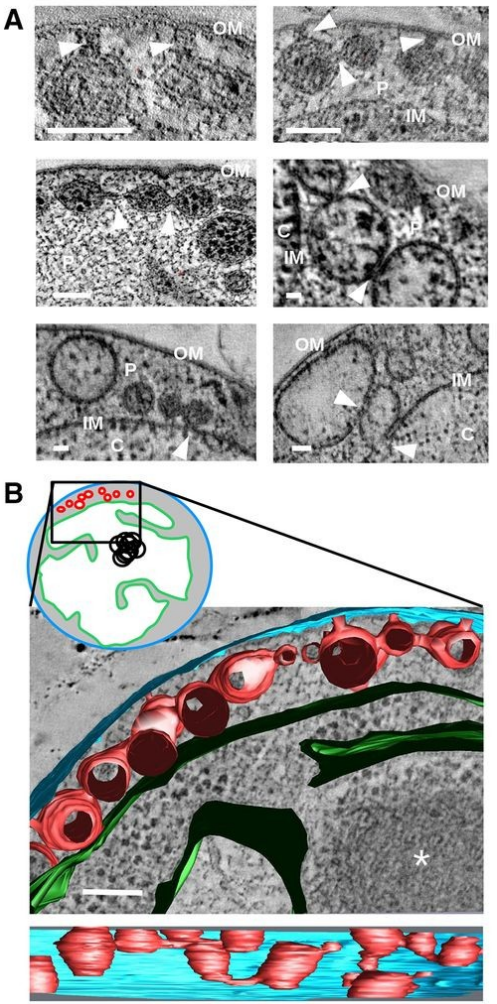


Prokaryotic periplasmic vesicles

Acehan *et al*., JCS 2014

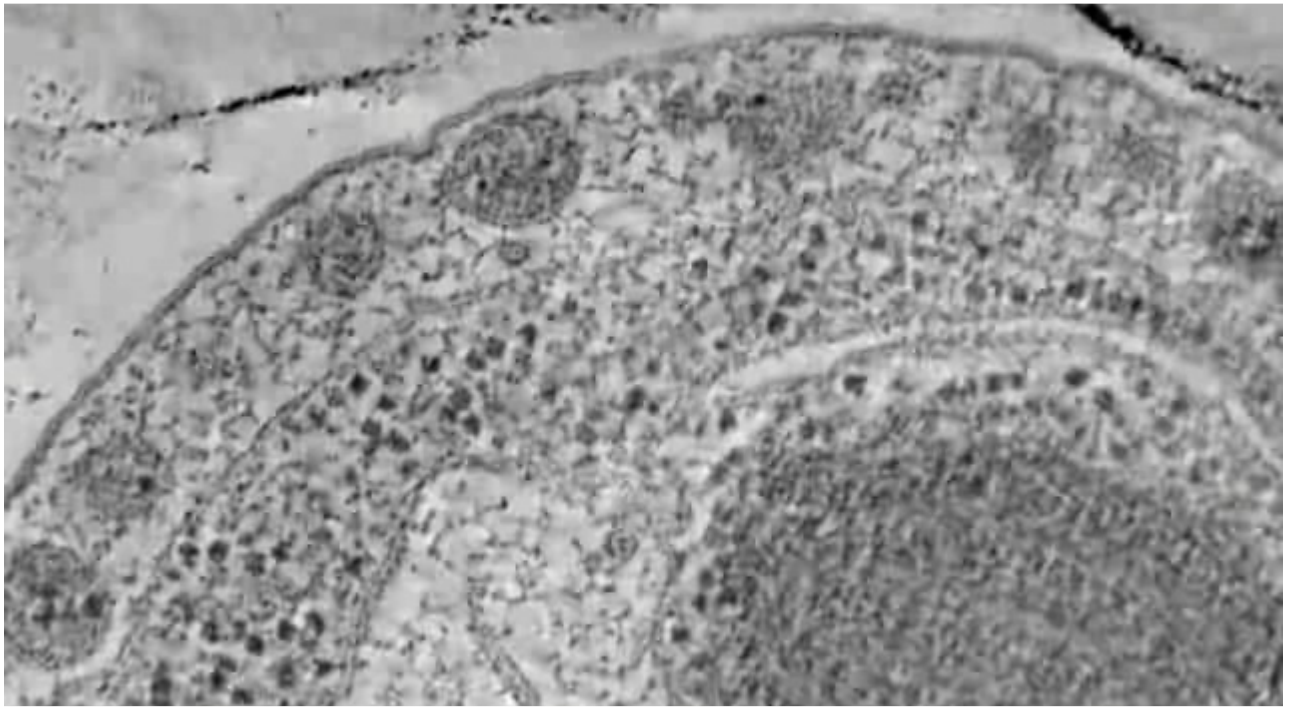
Prokaryotic connected vesicles





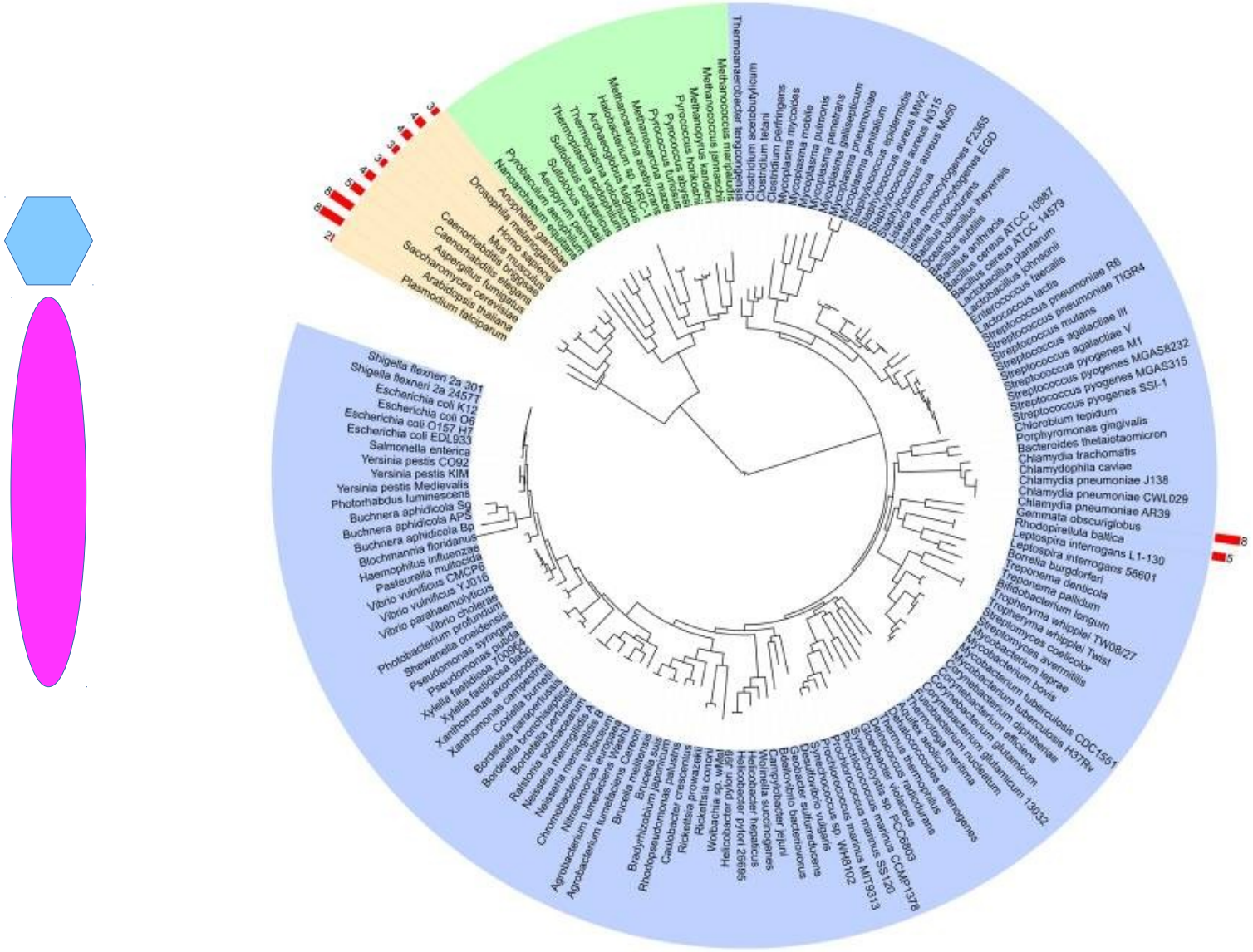
Acehan *et al*., JCS 2014

Tubulovesicular network in bacteria



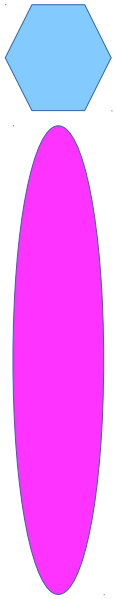
Acehan *et al*., JCS 2014

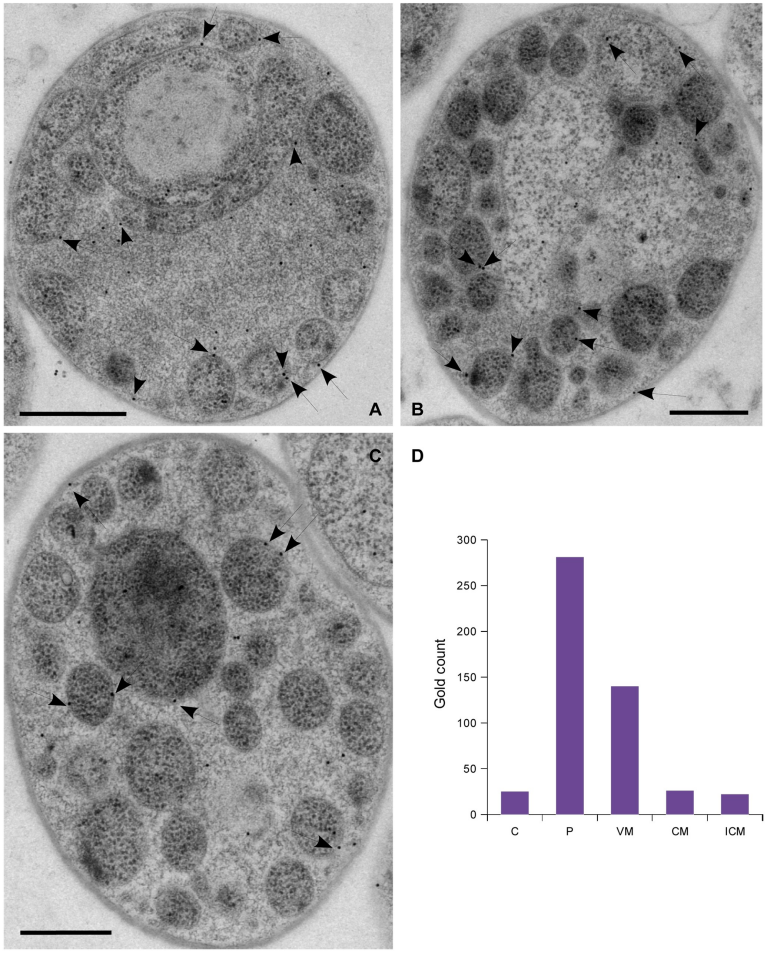
MCs in the tree of life

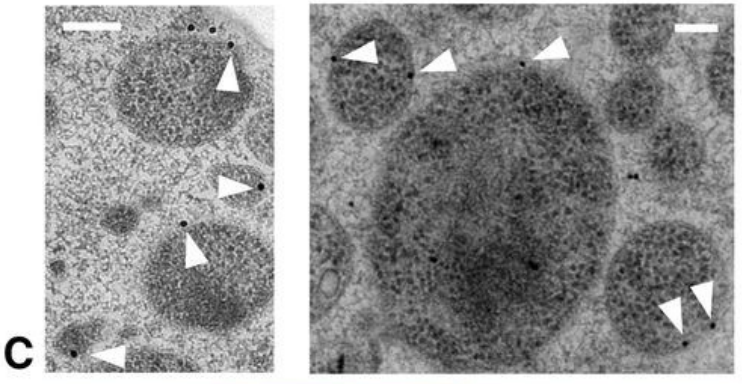


Santarella *et al.*, PLoS B 2010

Prokaryotic MC localization



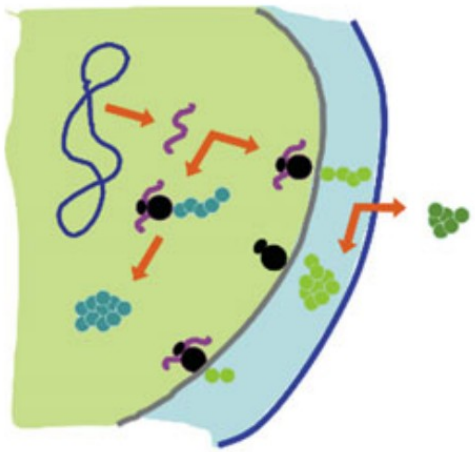




Santarella *et* al., PLoS B 2010; Acehan *et al*., JCS 2014

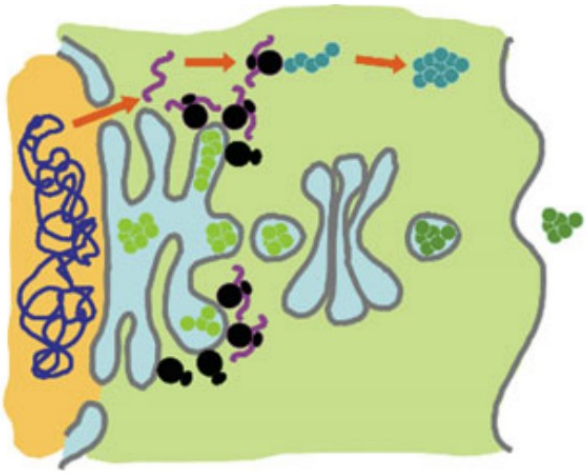
Periplasm internalization at the origin of eukaryotic ES (de Duve; Blobel)

(a) Diderm bacteria



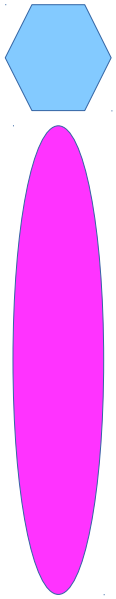
Protein import mechanisms
Chaperones
Unfolded protein response
Outer membrane vesicles
Multi-drug resistance efflux pumps
Kinases

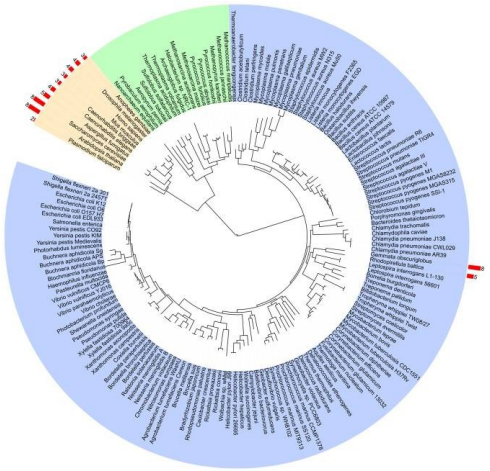
(c) Eukaryote

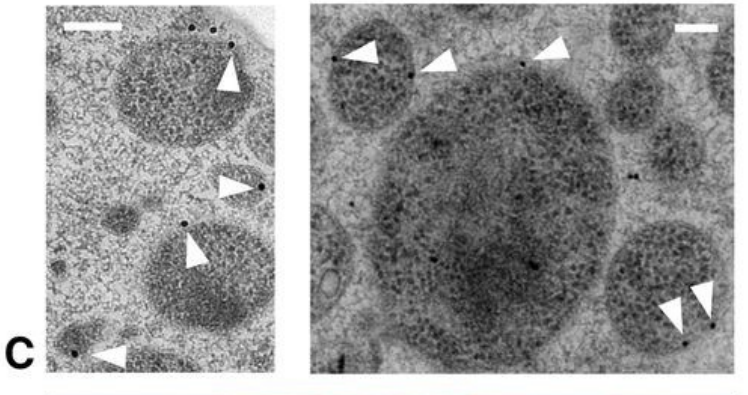


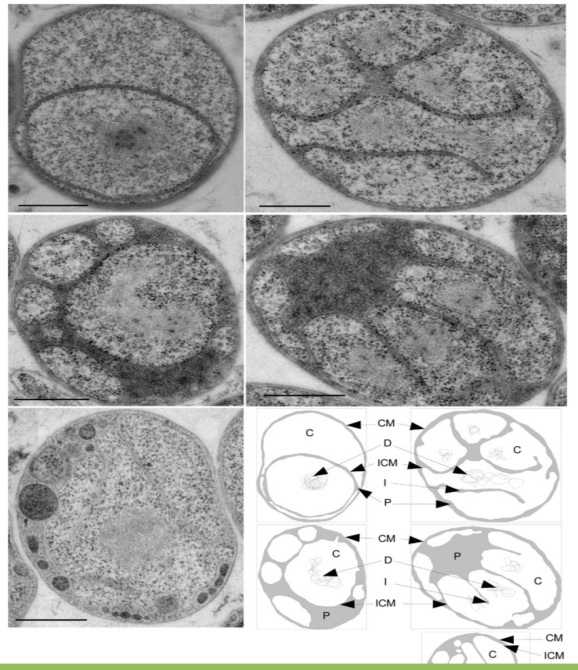
Devos & Reynaud Science2010; Reynaud and Devos PRSCB 2011

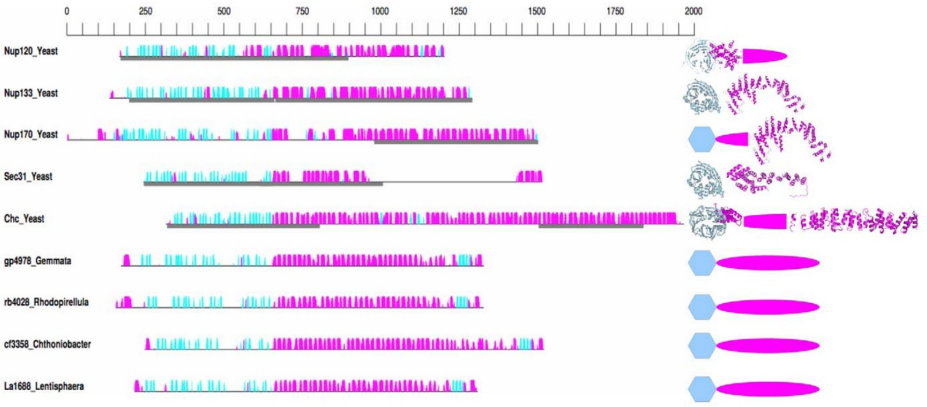
The PVC bacteria superphylum **could have** contributed to the origin of the eukaryotic endomembrane.



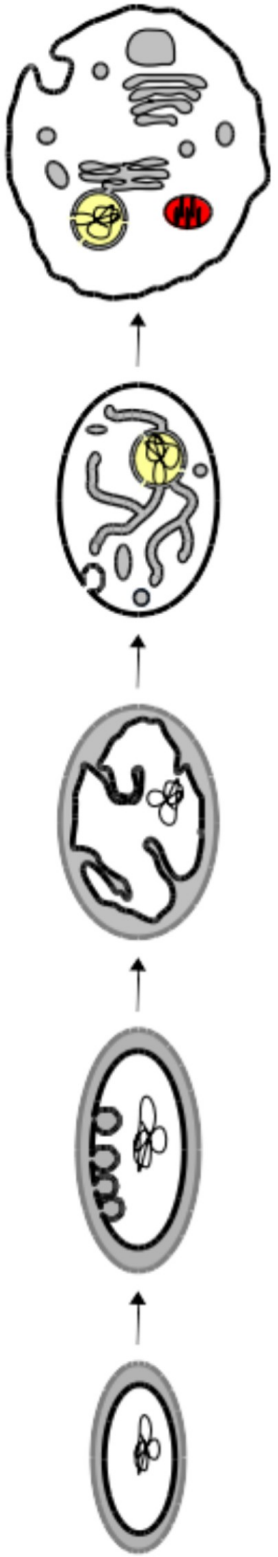








Santarella *et* al., PLoS B 2010; Acehan *et al*., JCS 2014



Eukaryotic Realm

Prokaryotic Realm

TOP
Eukaryotes

Divergence
Radiation

LECA

Sequence signal barrier

Prokaryotes
BOTTOM

Top-Down approach

OPH (Dacks & Field)

PCH (Devos, Rout & Sali)

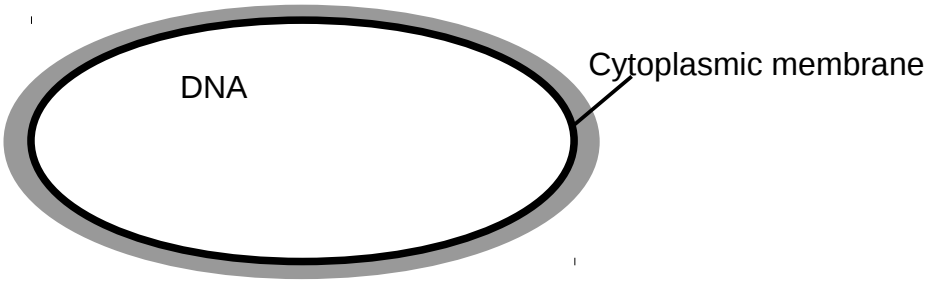
Undifferentiated
multifunctional TVN
as ancestral eukaryotic EMS

Planctomycetes might have
contributed to eukaryotic
EMS development

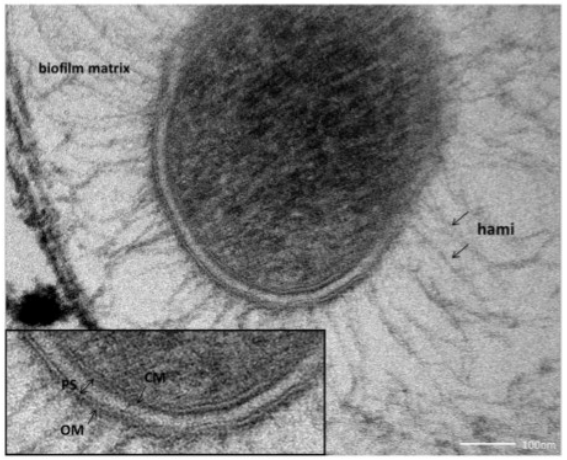
µPlatypus (Devos & Reynaud)

Bottom-Up approach

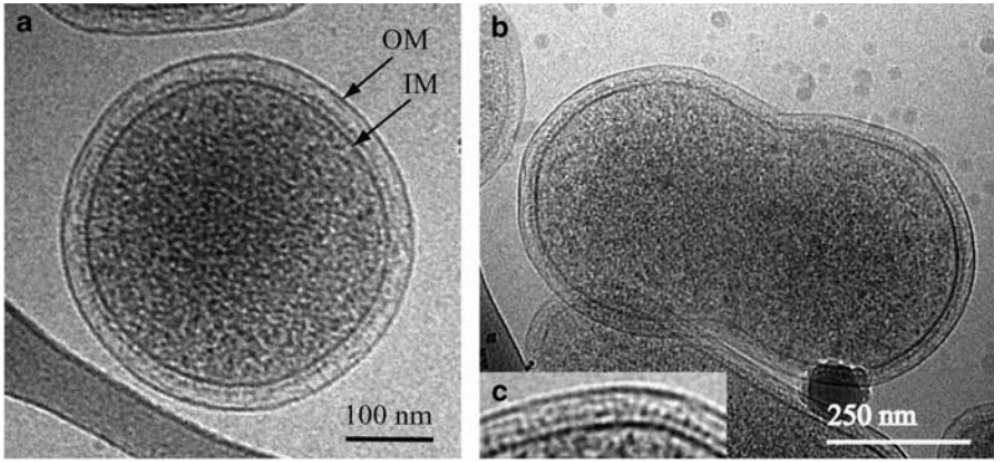
Archaea



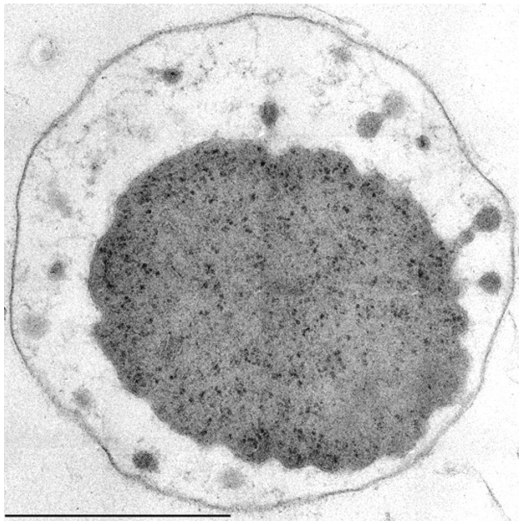
Archaeal OM/IM & TVN



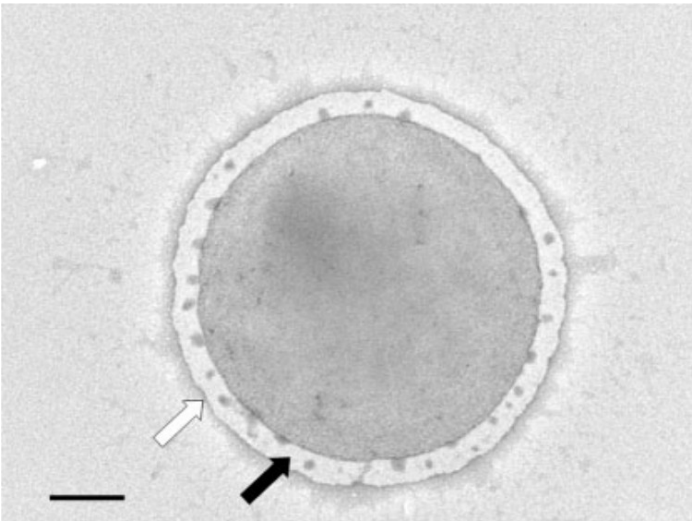
SM1
(Euryarchaeota)



ARMAN
(Unclear Crenar/Eury)



Ignicoccus hospitalis
(Crenarchaeota)

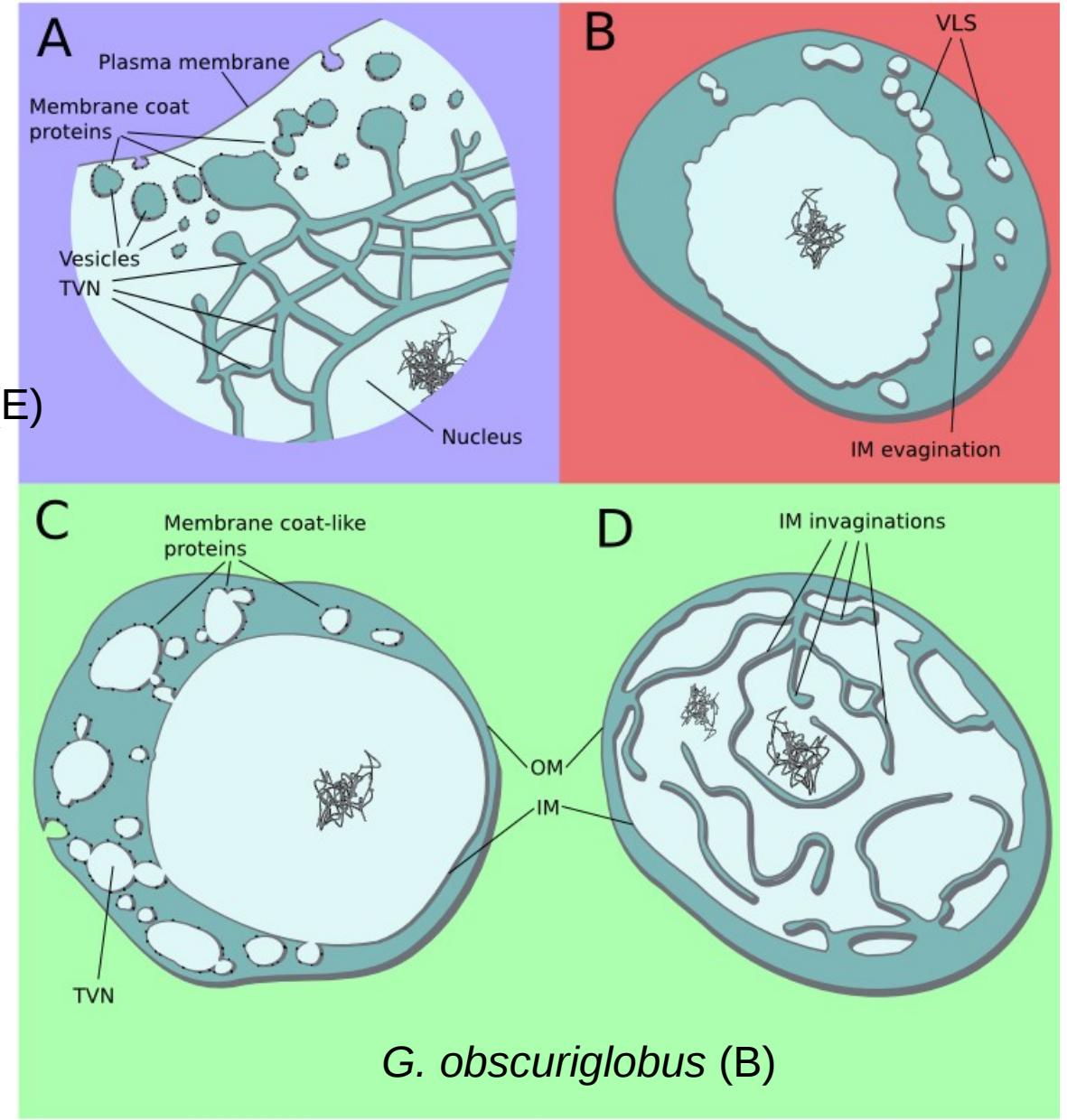


Methanomassiliicoccus luminyensis
(Euryarchaeota)

Perras *et al.,* Frontiers Microbiol 2014; Comolli *et al.,* ISME J 2009*;* Huber *et al.,* PNAS 2008; Dridi *et al.,* IJ Sys Evol Microb 2012

Reduced eukaryotic ES

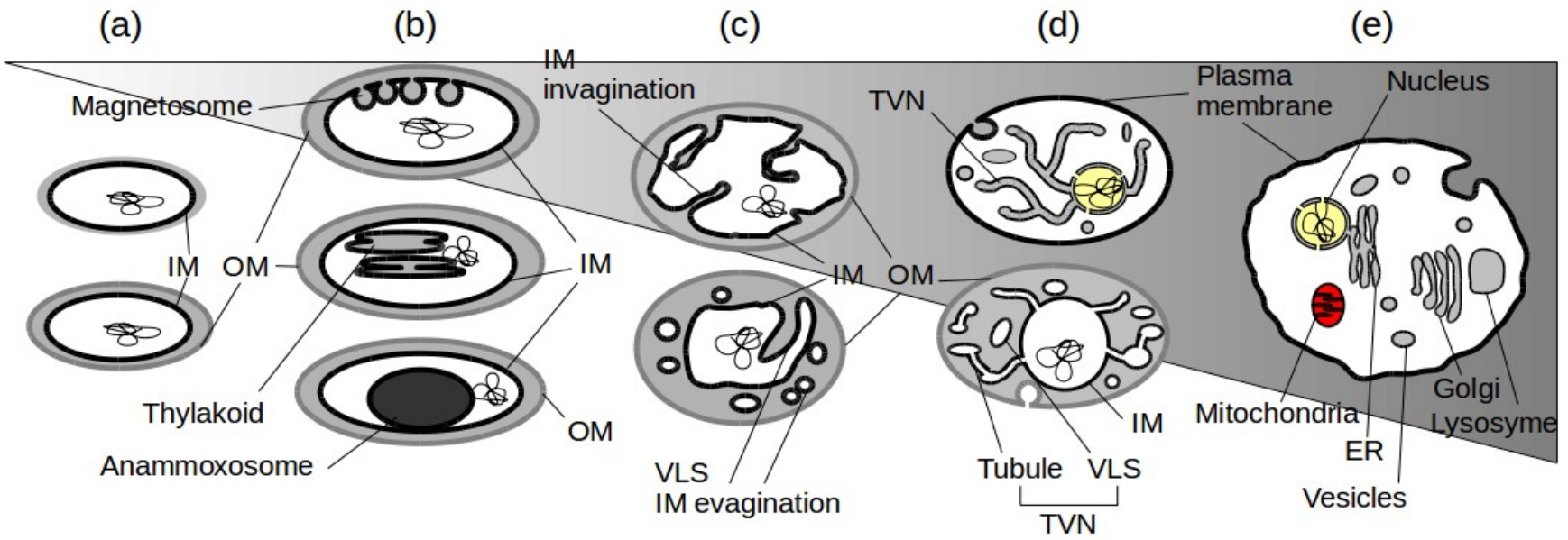
G. lamblia (E)



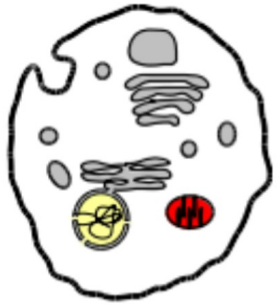
I. hospitalis (A)

G. obscuriglobus (B)

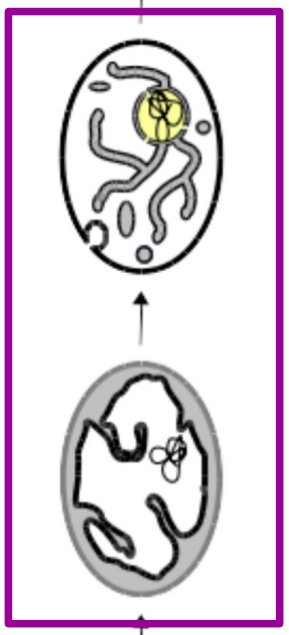
Intermediary membrane organisation



Gonzalez-Sanchez *et al.*, Biology 2015

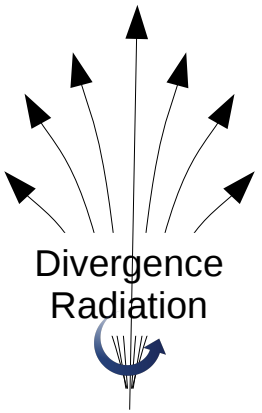


Eukaryotic Realm



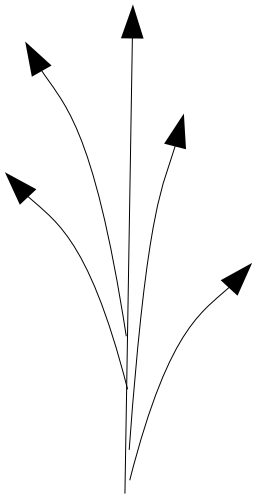
Prokaryotic Realm

TOP
Eukaryotes



Divergence
Radiation

LECA



Prokaryotes
BOTTOM

Top-Down approach

OPH (Dacks & Field)

PCH (Devos, Rout & Sali)

Undifferentiated
multifunctional TVN
as ancestral eukaryotic EMS

Structure more conserved than sequence

Planctomycetes might have
contributed to eukaryotic
EMS development

µPlatypus (Devos & Reynaud)

Bottom-Up approach

PVC euk/arch features

PVC Superphylum		
Features	**Specific to**	**Found in**
Compartmentalized cell plan (*20*)	Eu	Pl, Ve
Condensed DNA (*22*)	Eu	Pl
Division by budding (*24*)***	Eu	Pl
Membrane coats (*11*)	Eu	Pl
Sterol (*25*)	Eu	Pl, Ch
Proteic cell wall (*27*)	Eu	Pl
Ester and ether lipids (*28*)	Ar	Pl
FtsZ loss (*7*)	Eu, Ar**	Pl, Ch
Tubulin (*8, 9*)	Eu	Ve
C1 transfer (*29, 30*)	Ar	Pl
Endocytosis (*15*)	Eu	Pl

- Few molecular actors known
- Lack of sequence similarity
(doesn't imply lack of homology MreB/Actin & FtsZ/Tubulin)
- HGT (no signs of, too complex, too many)
- Convergence (too many)
- Similarity of features (tertiary structure and function)

The bacterial PVC superphylum might have lain on the path of the origin of the eukaryotic features

Devos & Reynaud *Science* 2010

Microbiology's platypus

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PVC Superphylum		
Features	**Specific to**	**Found in**
Compartmentalized cell plan (*20*)	Eu	Pl, Ve
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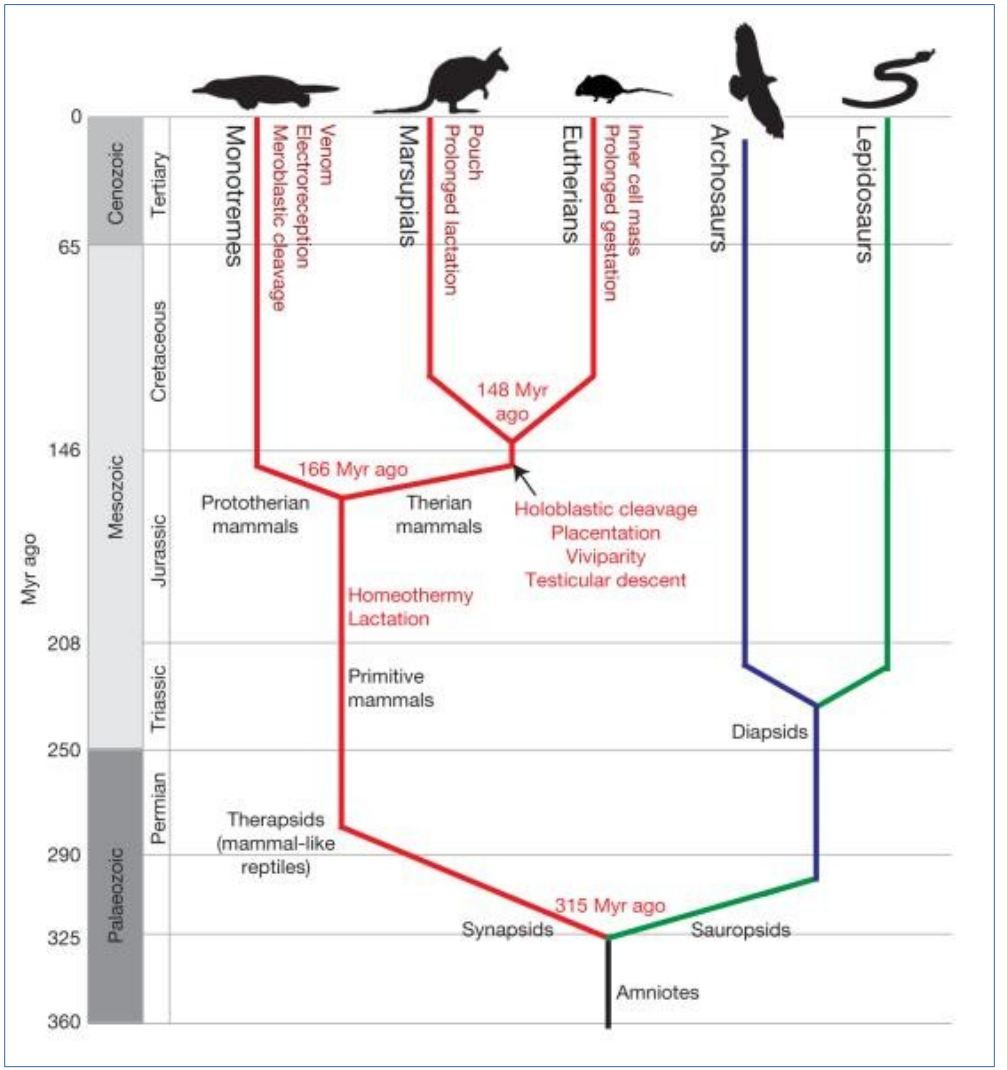

Warren *et* al.,Nature 2008

PVC bacteria

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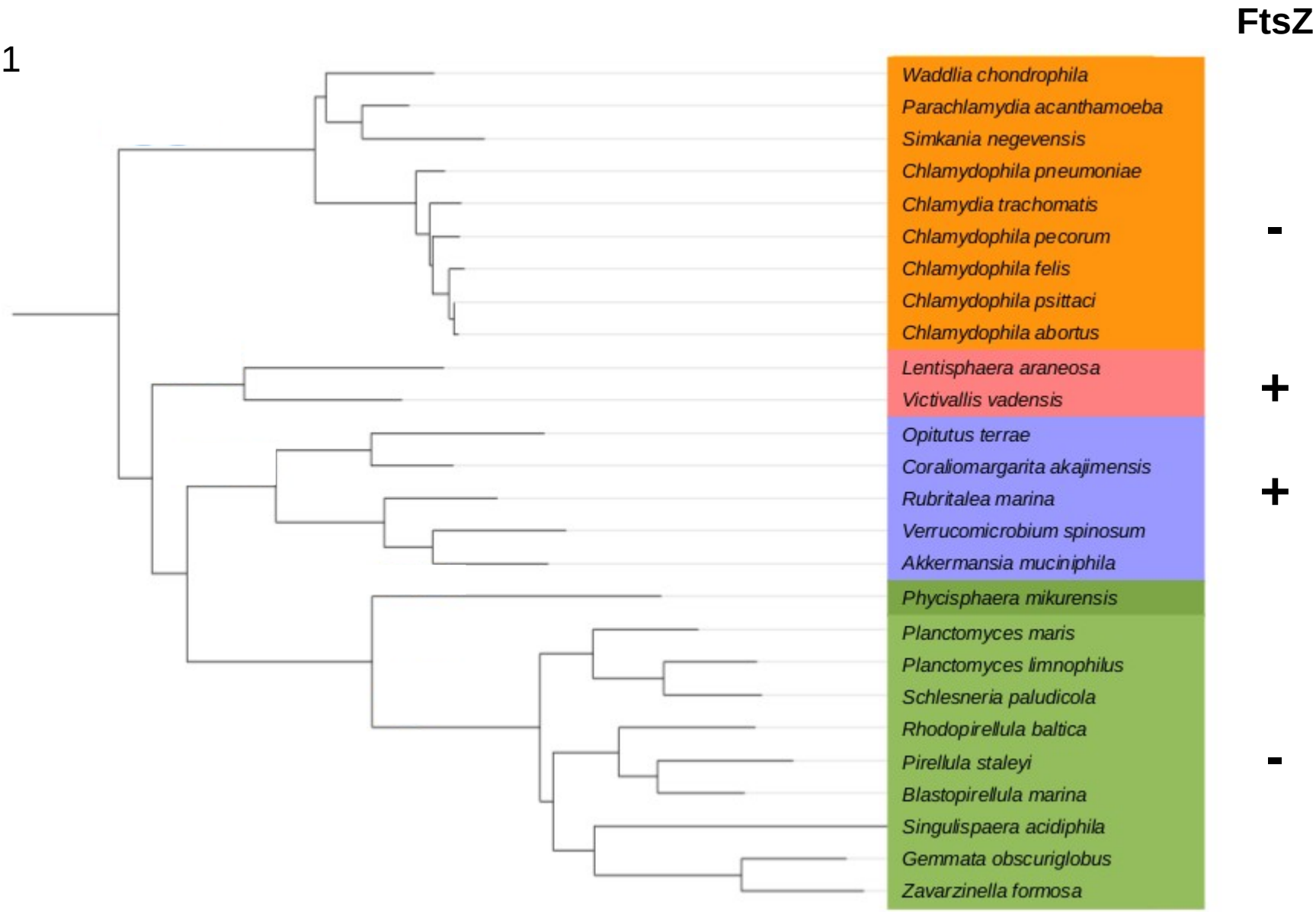
Fig. 1



Rivas *et al.*, *submitted*

PVC division modes

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Fig. 2

Rivas *et al.*, *submitted*

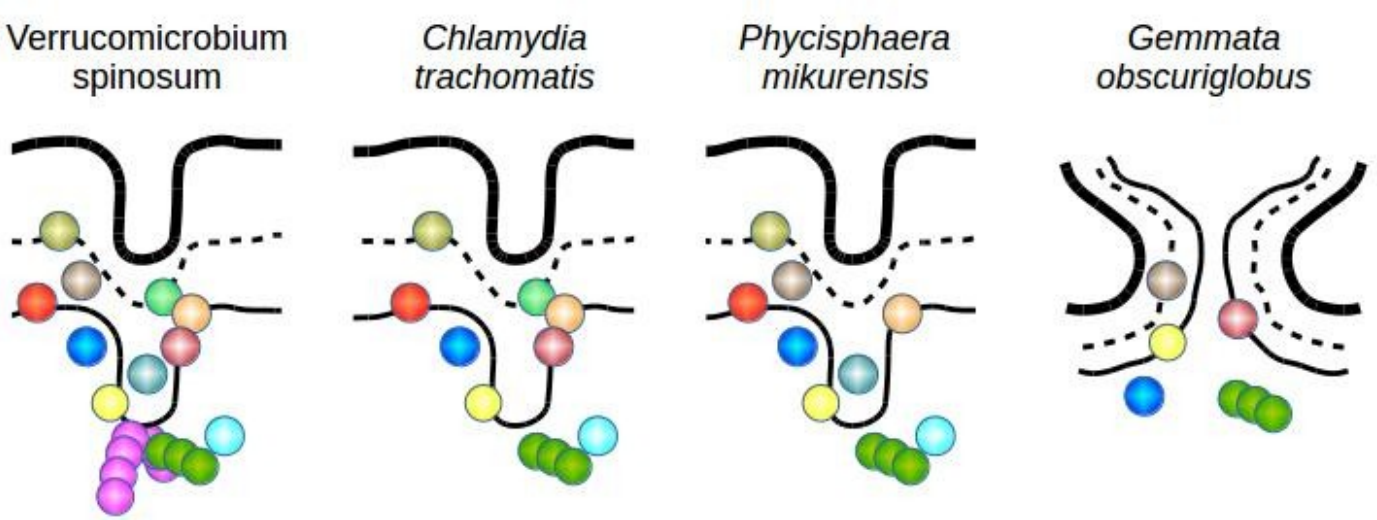
PVC *dcw* cluster conservation

Table 1

Proteins	V	L	C	P	Pbudding	Pfission
Alr1	10	1	3	14	11	3
AmiA	10	0	10	0	0	0
AmiB	10	0	10	0	0	0
AmiC	10	0	10	0	0	0
DacC	9	1	10	7	6	1
DapA	10	1	10	14	11	3
DapB	10	1	10	14	11	3
DapF	10	1	10	14	11	3
DapL	10	1	10	14	11	3
DdlB	10	1	10	14	11	3
MraY	10	1	10	13	10	3
MurA	10	1	10	14	11	3
MurB	10	1	10	14	11	3
MurC	10	1	10	14	11	3
MurD	10	1	10	14	11	3
MurE	10	1	10	14	11	3
MurF	10	1	10	14	11	3
MurG	10	1	10	14	11	3
MurI	3	0	4	2	0	2
MurJ	10	1	10	14	11	3
TolA	8	1	10	14	11	3
TolB	8	1	10	14	11	3
TolQ	10	1	10	14	11	3
TolR	10	1	10	14	11	3
Pal	10	1	10	13	10	3
Pbp2	10	1	10	7	4	3
MreB	10	1	10	14	11	3
MreC	9	1	10	7	4	3
MreD	0	0	0	0	0	0
NlpD	10	1	10	12	9	3
RodZ	9	1	10	13	11	2
EnvC	9	1	9	14	11	3
FtsA	10	1	10	14	11	3
FtsE	10	1	10	14	11	3
FtsK	10	1	10	14	11	3
FtsI	10	1	10	7	4	3
FtsW	10	1	10	7	4	3
FtsP	6	0	2	9	6	3
FtsZ	9	1	0	0	0	0
FtsB	0	0	0	0	0	0
FtsL	0	0	0	0	0	0
FtsN	0	0	0	0	0	0
FtsQ	0	0	0	0	0	0
FtsX	0	0	0	0	0	0
Total species	10	1	10	14	11	3

Rivas *et al.*, *submitted*

ECB division mode



MurA-G
FtsZ
Pbp2
AmiABC
MreB
MreC
NlpD
RodZ
EnvC
FtsAEK
FtsIW
FtsP

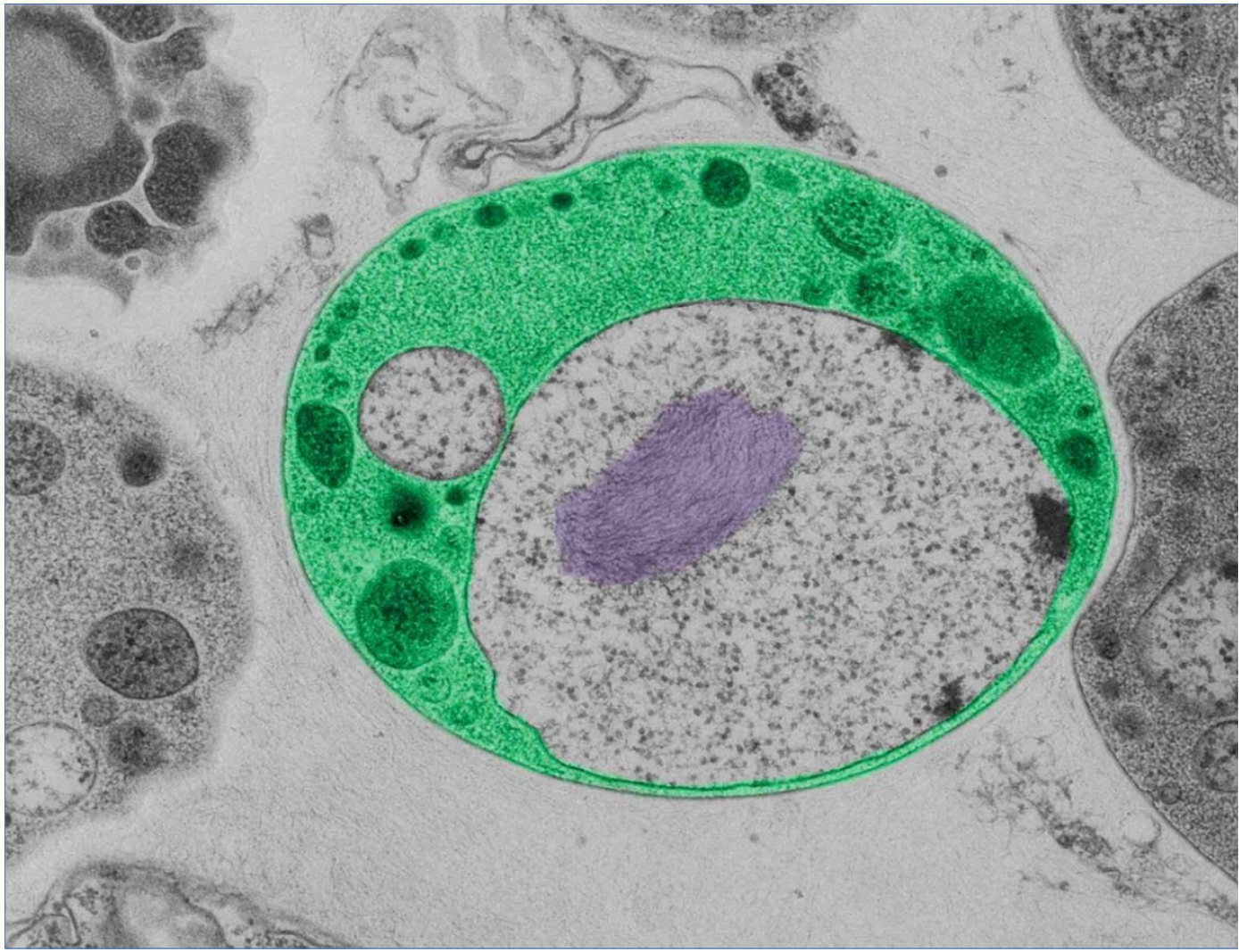
Thanks!

Centro Andaluz de Biología del Desarrollo

A Sali (UCSF, SF)
M Rout (Rockefeller U, NY)
I Mattaj (EMBL, HD)
R Santarella (EMBL, HD)

J Fuerst (Queensland U, Au)
J Wittbrodt (HD U, D)

The µplatypus lab
I Irastorza
I Ibarra
N Bordin
E Rivas

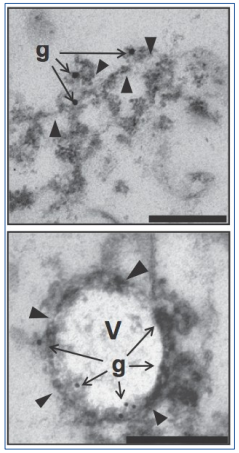


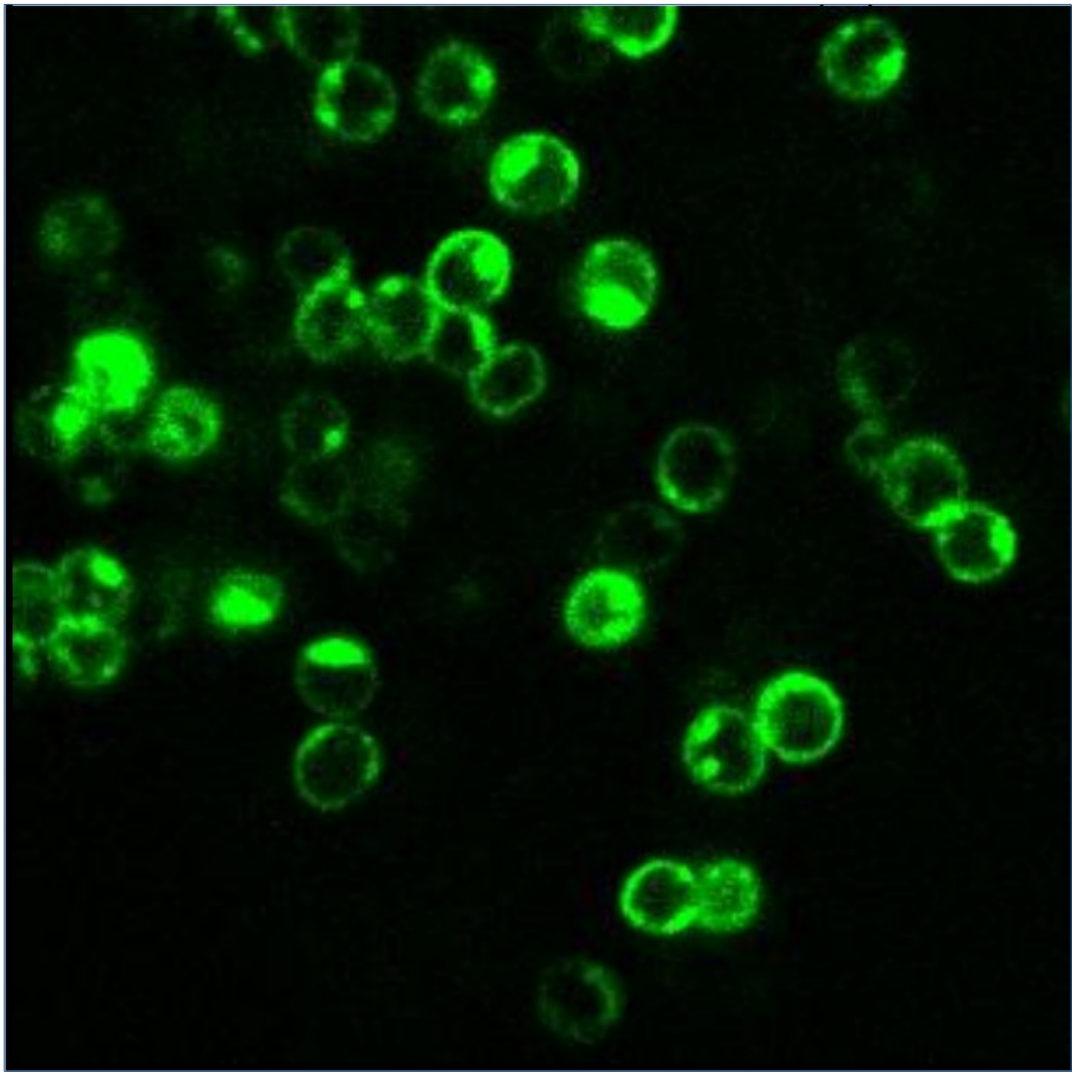
JUNTA DE ANDALUCIA

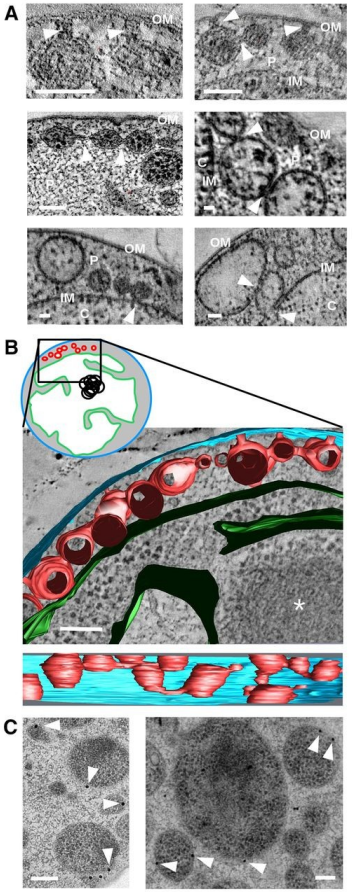
UNIVERSIDAD PABLO DE OLAVIDE SEVILLA AÑO 1997

MARIE CURIE ACTIONS

Prokaryotic endocytosis?







Lonhienne *et* al., PNAS 2010