

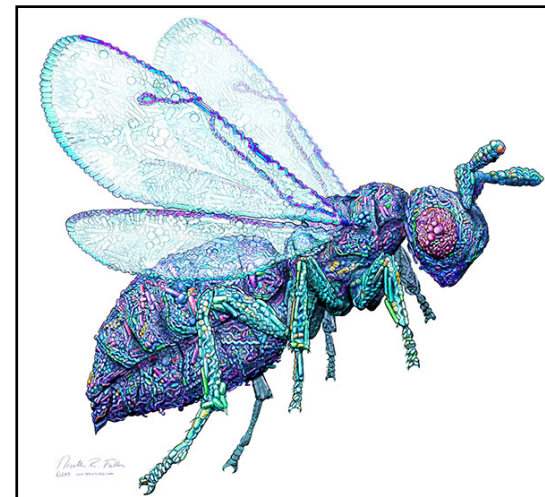
The Economist

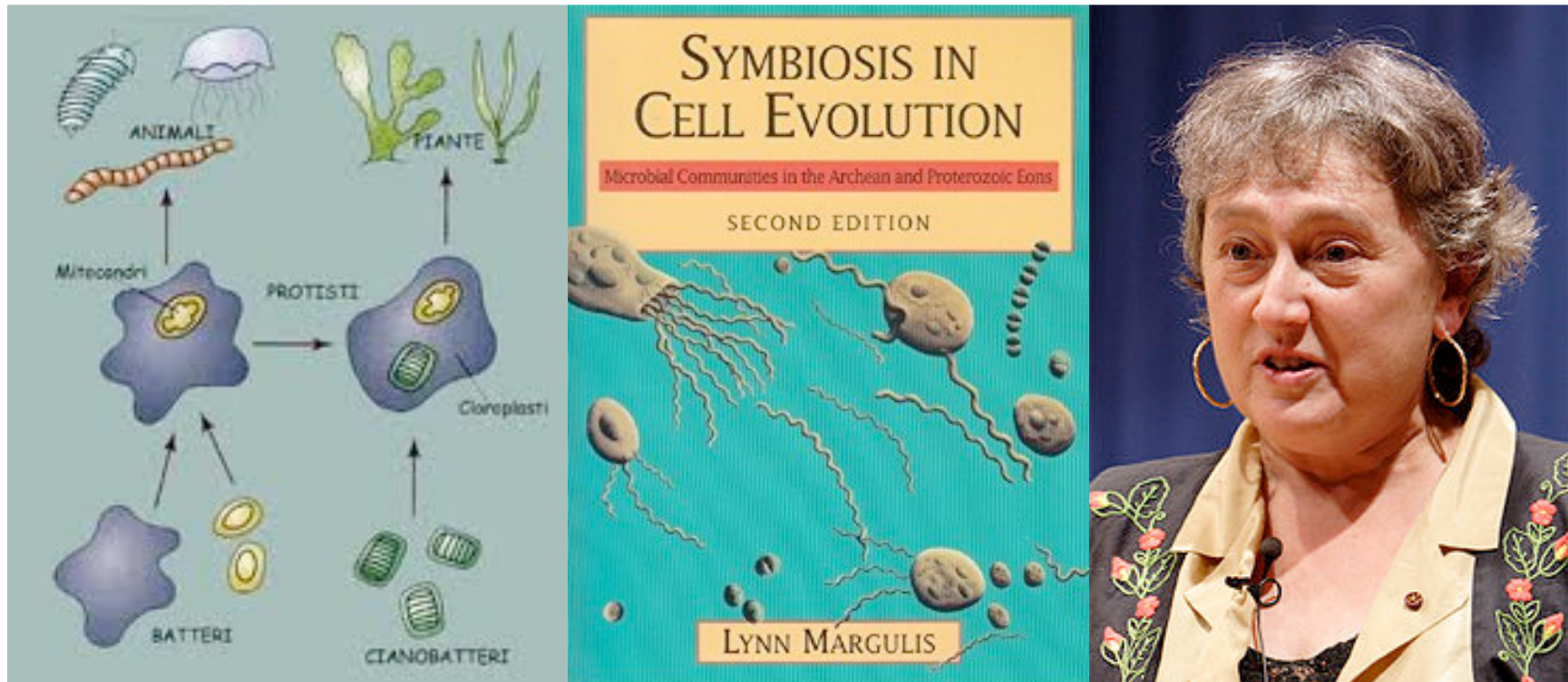
AUGUST 18TH-24TH 2012

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The Catholic church's unholy mess
 Paul Ryan: the man with the plan
 Generation Xhausted
 China, victim of the Olympics?
 On the origin of specie

Microbes maketh man





"Life did not take over the globe by combat, but by networking"



A SYMBIOTIC VIEW OF LIFE: WE HAVE NEVER BEEN INDIVIDUALS

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KEYWORDS

symbionts, symbiosis, individuality, evolution, holobiont

ABSTRACT

The notion of the "biological individual" is crucial to studies of genetics, immunology, evolution, development, anatomy, and physiology. Each of these biological subdisciplines has a specific conception of individuality, which has historically provided conceptual contexts for integrating newly acquired data. During the past decade, nucleic acid analysis, especially genomic sequencing and high-throughput RNA techniques, has challenged each of these disciplinary definitions by finding significant interactions of animals and plants with symbiotic microorganisms that disrupt the boundaries that heretofore had characterized the biological individual. Animals cannot be considered individuals by anatomical or physiological criteria because a diversity of symbionts are both present and functional in completing metabolic pathways and serving other physiological functions. Similarly, these new studies have shown that animal development is incomplete without symbionts. Symbionts also constitute a second mode of genetic inheritance, providing selectable genetic variation for natural selection. The immune system also develops, in part, in dialogue with symbionts and





From bacterial bleaching to the hologenome theory of evolution

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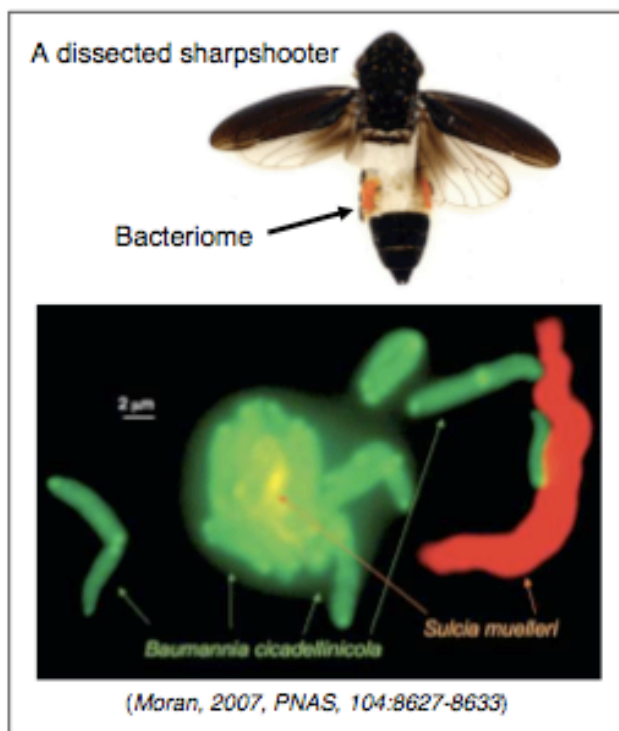
Abstract. Extensive bleaching of the coral *Oculina patagonica* in the eastern Mediterranean Sea occurs every summer when the seawater temperature exceeds 25°C. The infection by *Vibrio shiloi* and subsequent bleaching occurred only above 25°C because several of the bacterial virulence factors, superoxide dismutase, adhesion and toxin P, are only expressed above 25°C. Starting in 2002, the corals developed resistance to *V. shiloi*. Attempts to explain the resistance led to the Coral Probiotic Hypothesis, which posits that corals can adapt to their environment, including resistance to pathogens, by changing their symbiotic bacteria. The hologenome theory considers the holobiont a unit of natural selection. The hologenome is defined as the sum of the genetic information of the host and its microbiota. The theory is based on four well documented generalizations: (1) All animals and plants establish symbiotic relationships with microorganisms. (2) Symbiotic microorganisms are transmitted between generations. (3) The association between host and symbiont affects the fitness of the holobiont. (4) Under environmental stress, the symbiotic microbial community can change rapidly. These points taken together suggest that the genetic wealth of diverse microbial symbionts can play an important role both in adaptation and in evolution of higher organisms.

Keywords: Coral bleaching; *Vibrio*; holobiont, hologenome, evolution



PRIMARY SYMBIONTS

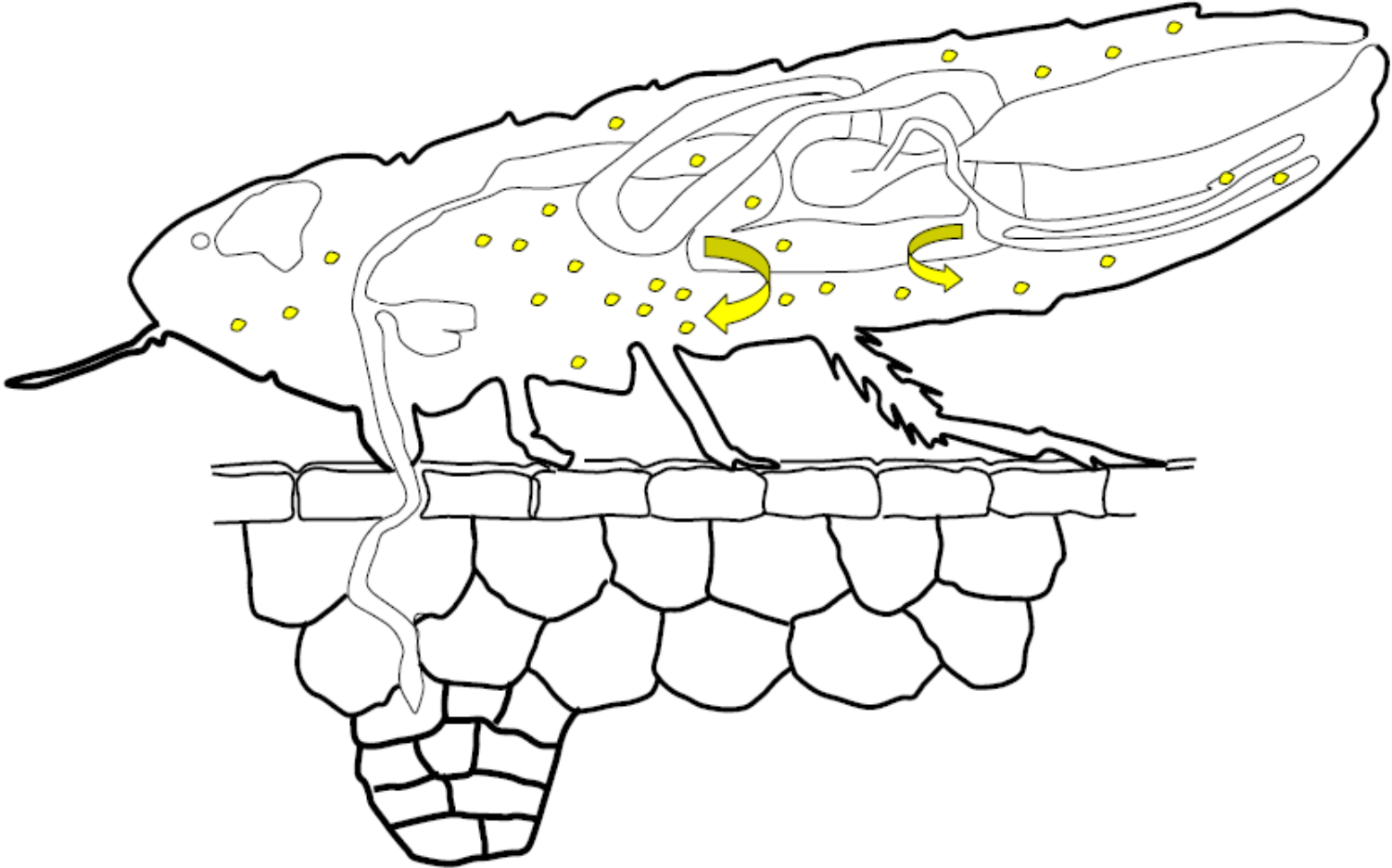
They provide to the host essential factors that are lacking in the natural diet (Dale & Moran 2006, *Cell* 126:453-465)



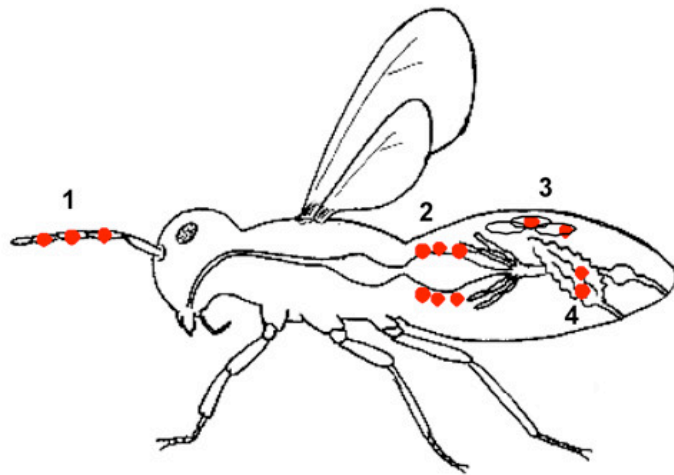
Xylem sap: amino acids, organic acids, and sugars; primarily aspartate, asparagine, glutamate, glutamine, malate, and glucose



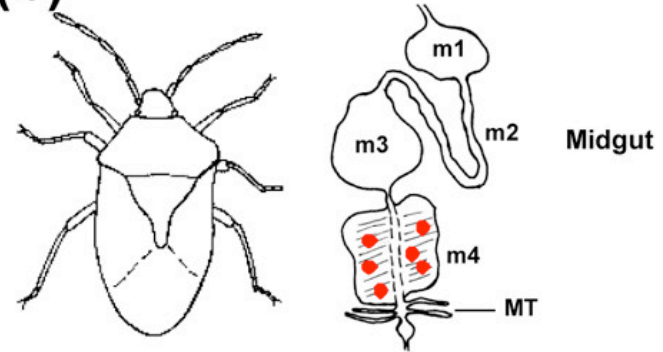
Secondary symbionts



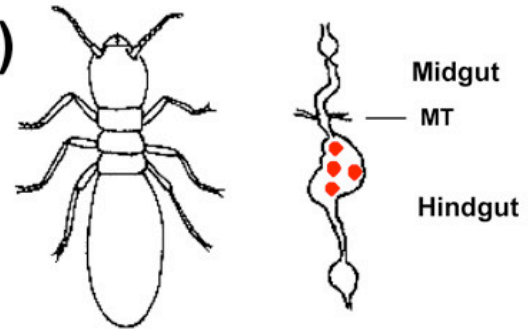
(a)



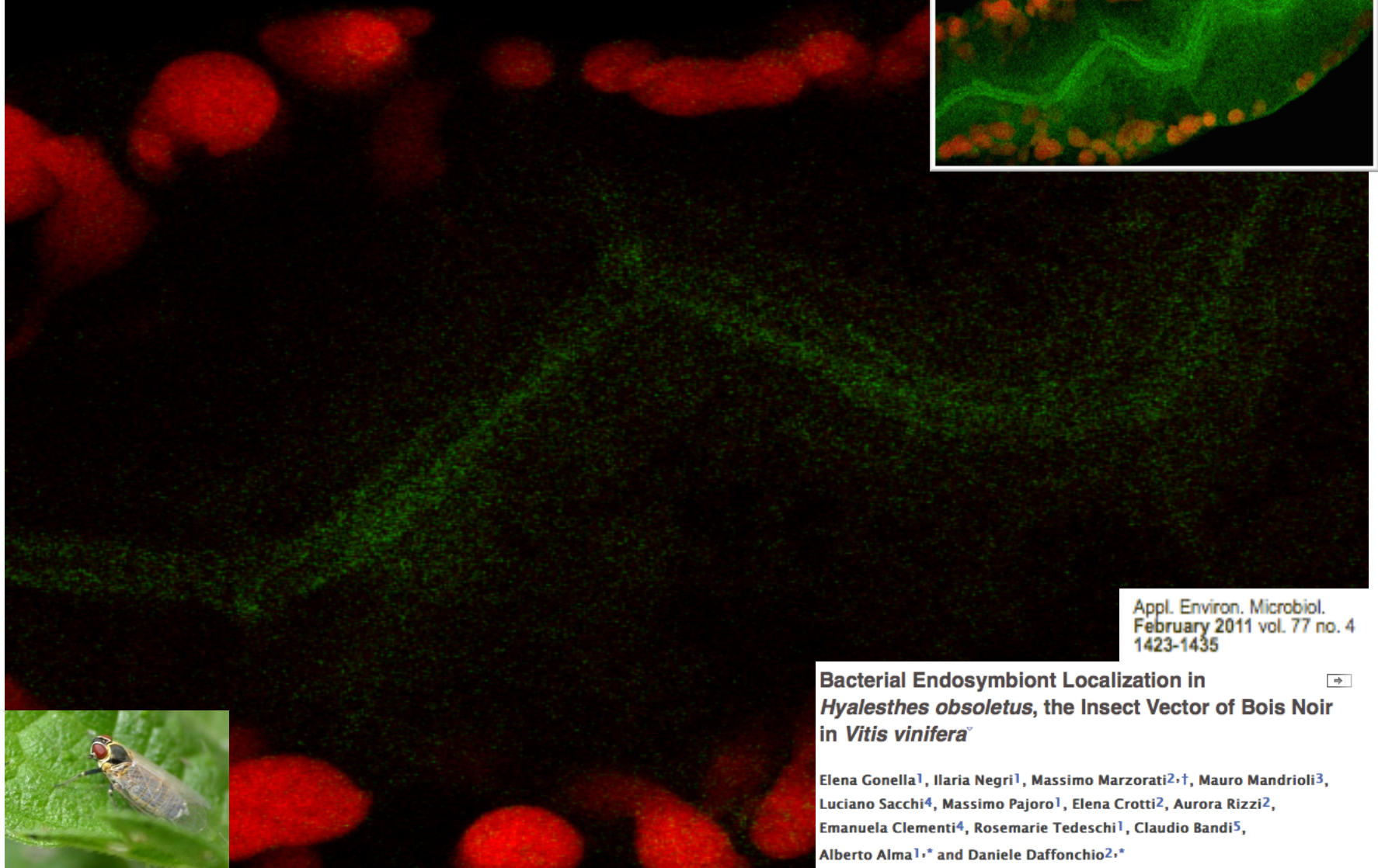
(b)



(c)



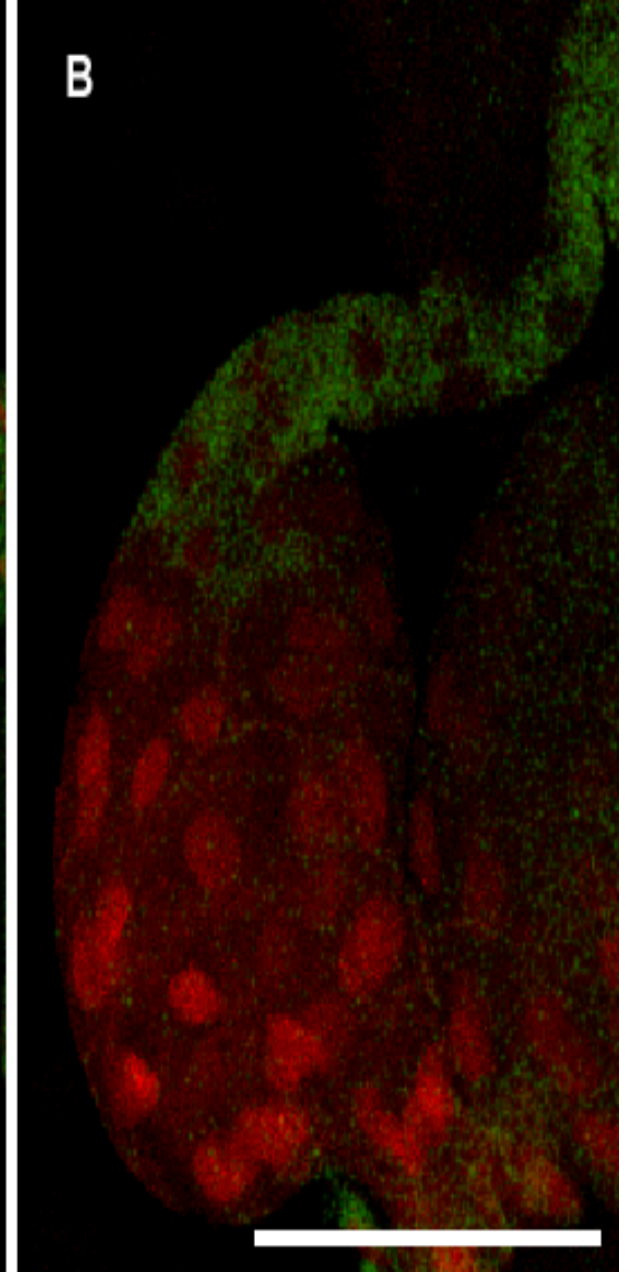
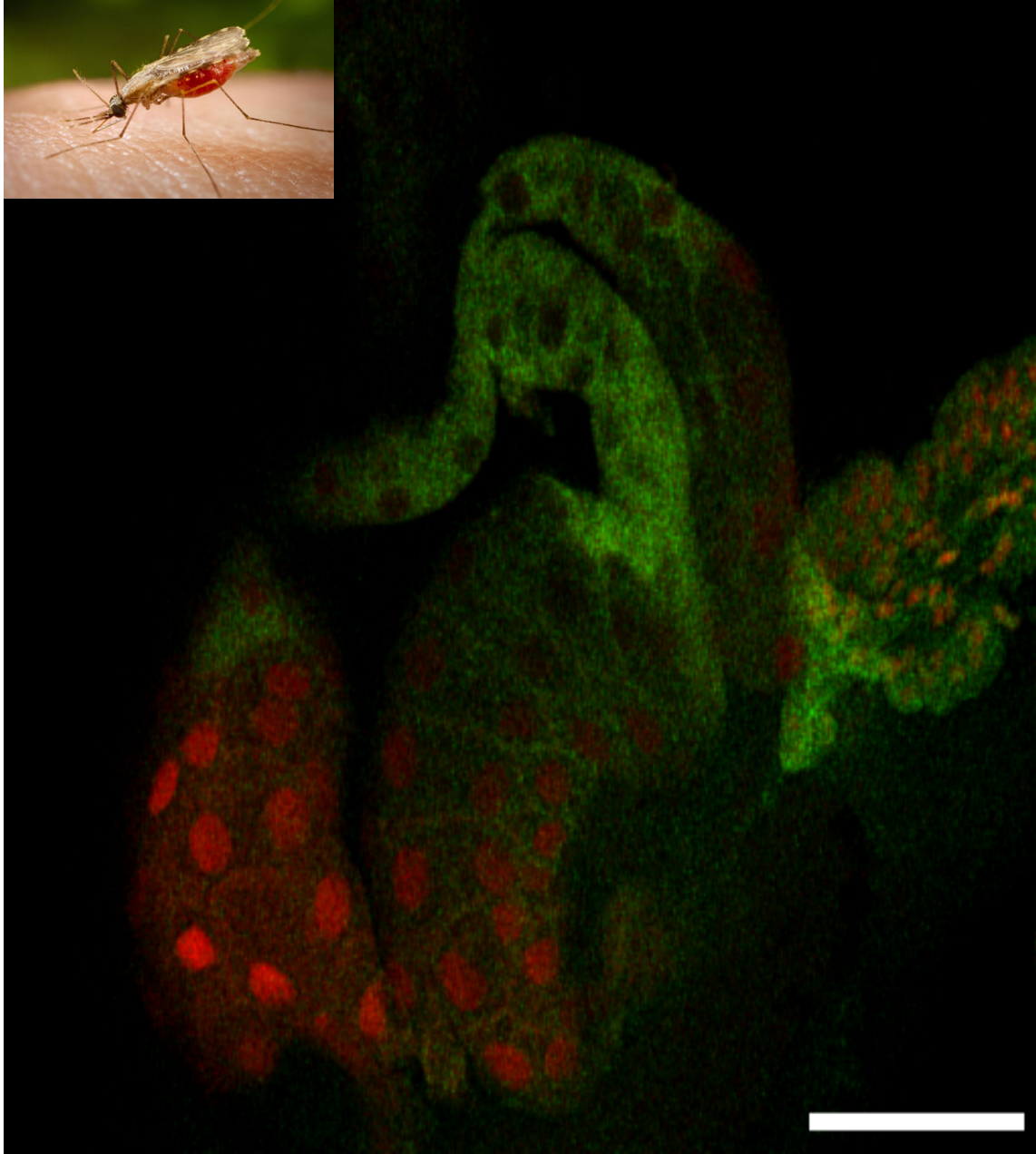
Phytoplasma in the salivary glands of the insect *H. obsoletus*.

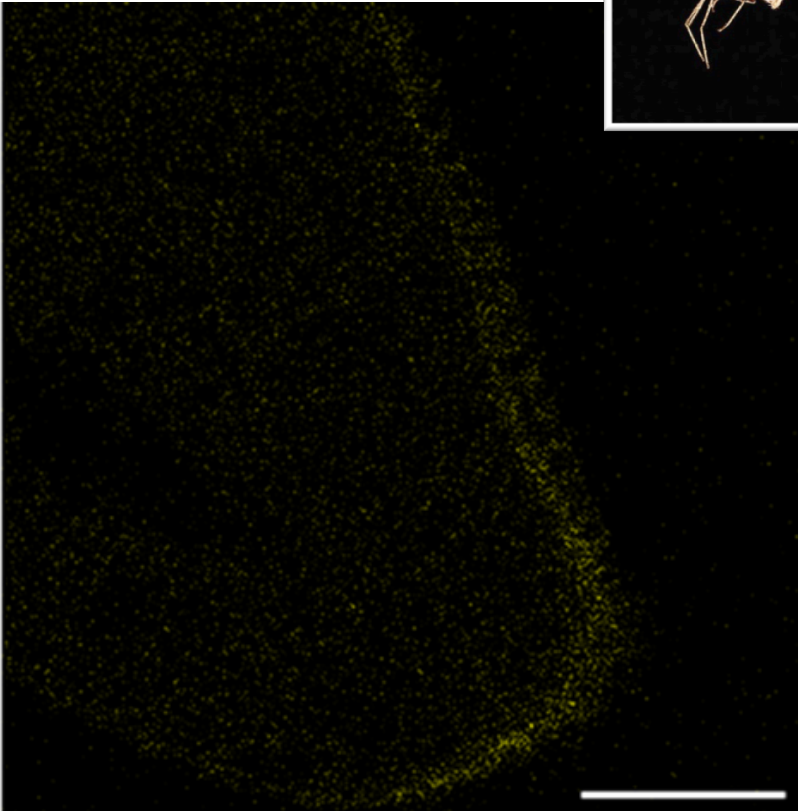
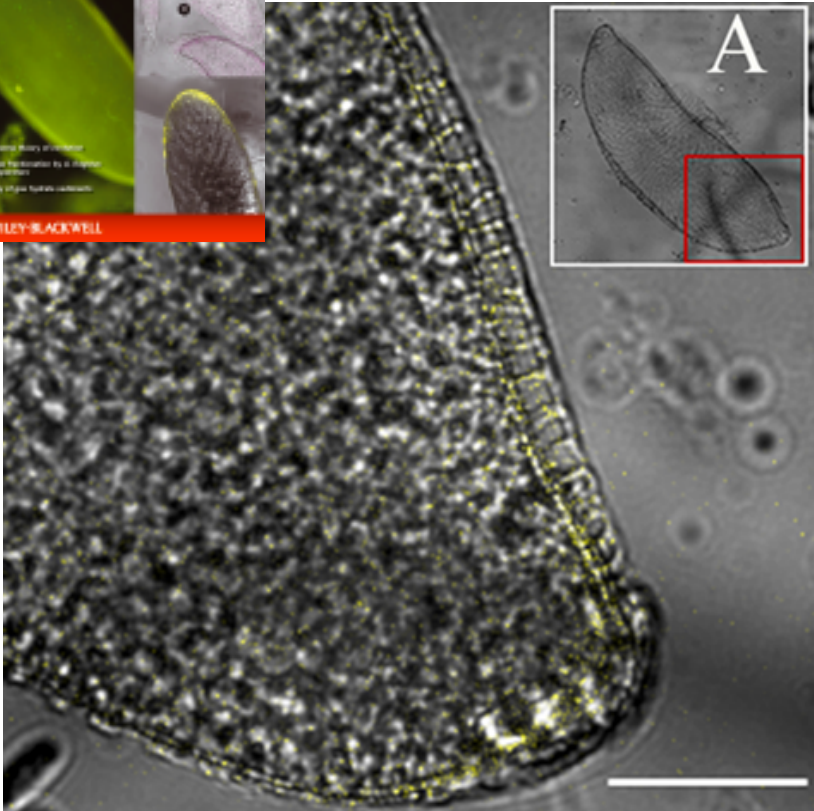


Appl. Environ. Microbiol.
February 2011 vol. 77 no. 4
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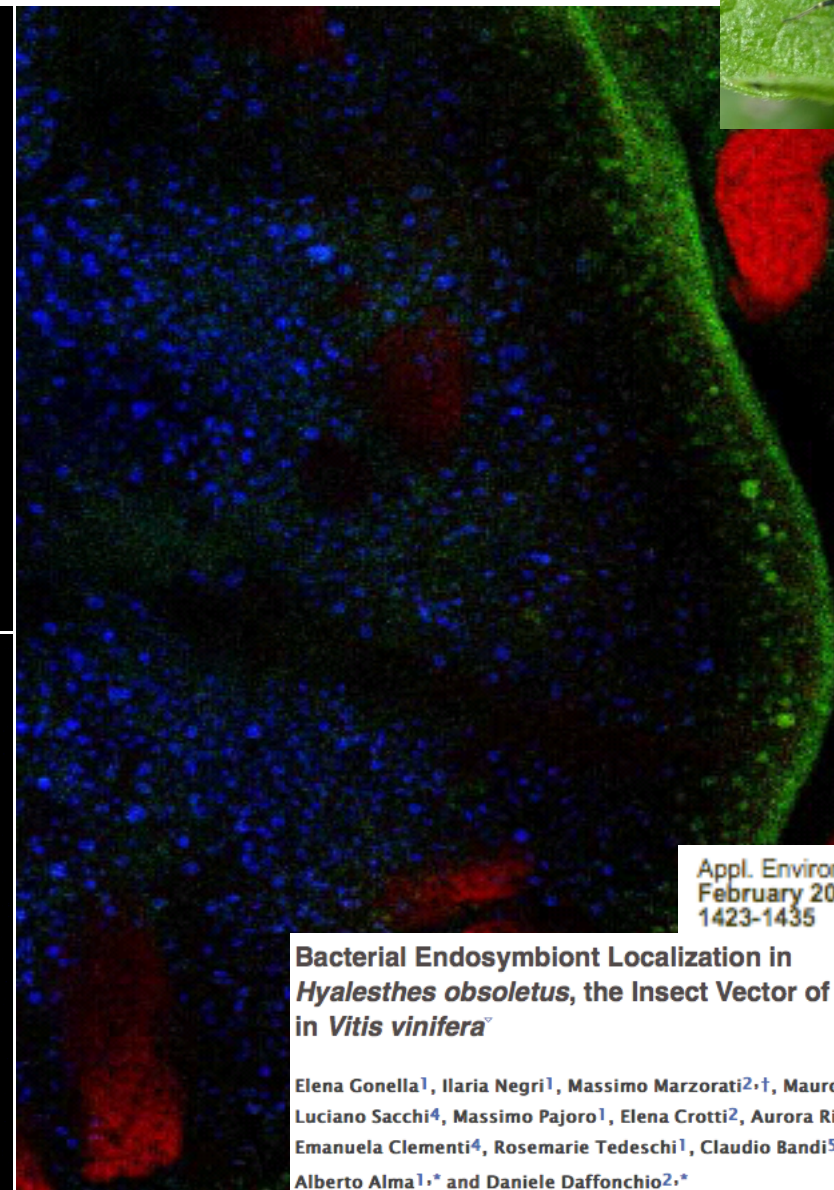
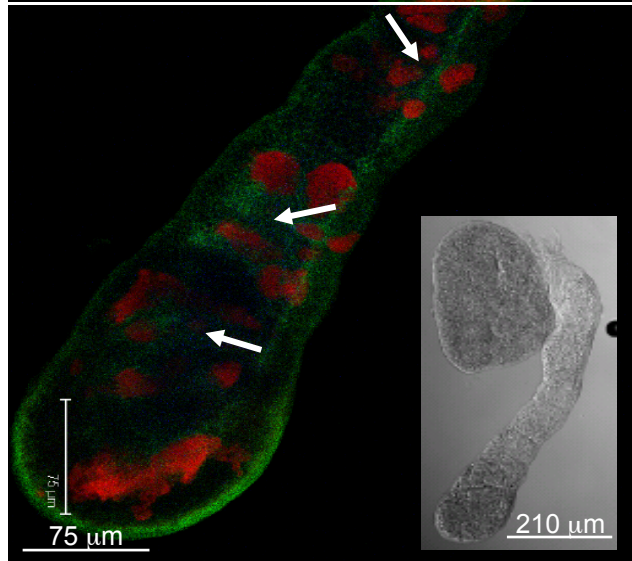
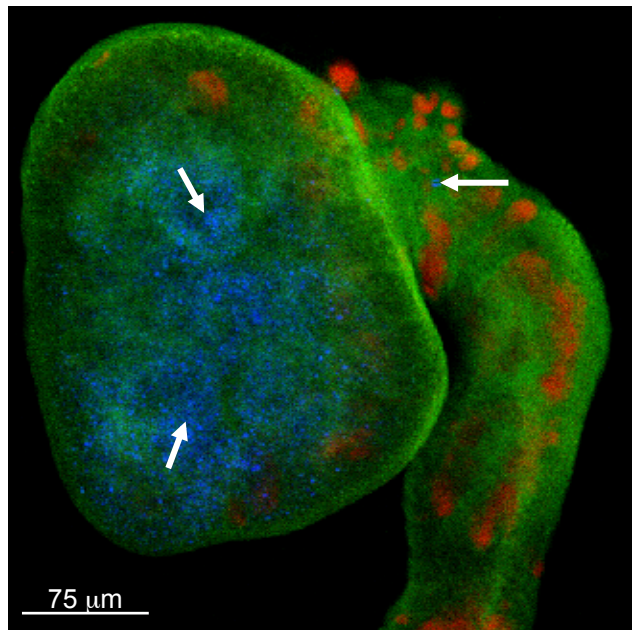
Bacterial Endosymbiont Localization in 
***Hyalesthes obsoletus*, the Insect Vector of Bois Noir**
in *Vitis vinifera*

Elena Gonella¹, Ilaria Negri¹, Massimo Marzorati^{2,†}, Mauro Mandrioli³,
Luciano Sacchi⁴, Massimo Pajoro¹, Elena Crotti², Aurora Rizzi²,
Emanuela Clementi⁴, Rosemarie Tedeschi¹, Claudio Bandi⁵,
Alberto Alma^{1,*} and Daniele Daffonchio^{2,*}





Cy3-labeled *Sulcia* FITC-labeled *Bacteroidetes*



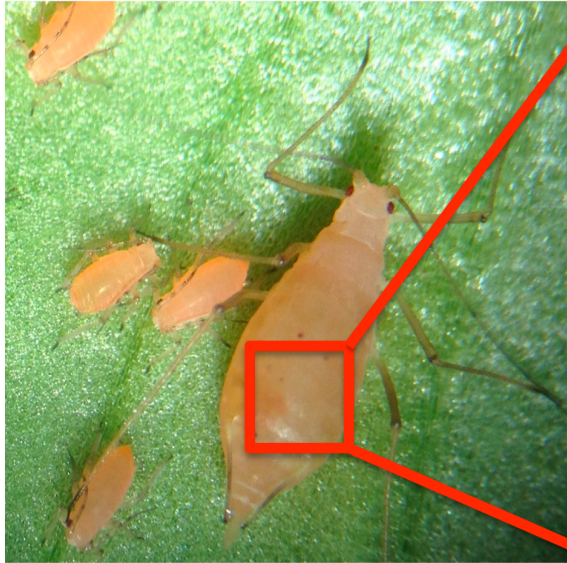
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Alberto Alma^{1,*} and Daniele Daffonchio^{2,*}

Symbionts (both primary and secondary) may be intracellular...

Pea aphids



Bacteriocytes

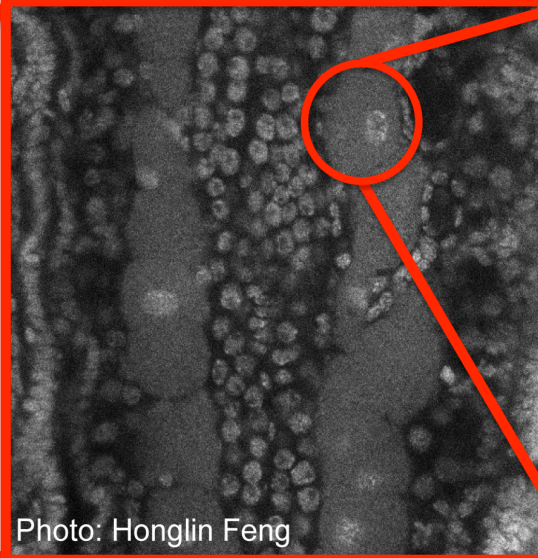


Photo: Honglin Feng

Buchnera

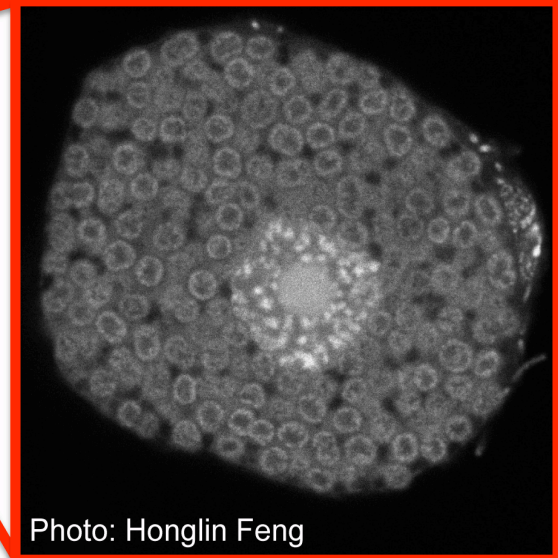
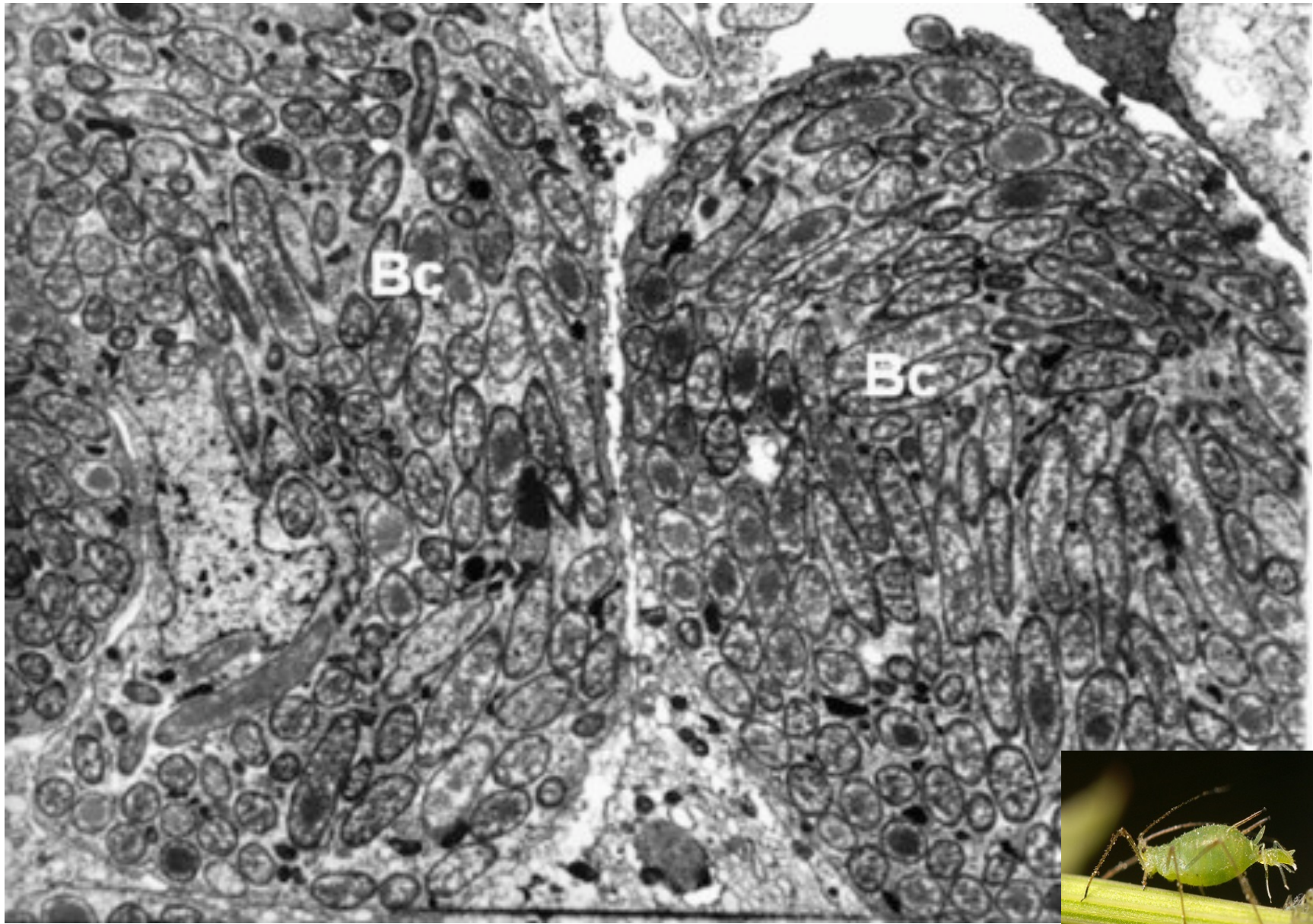
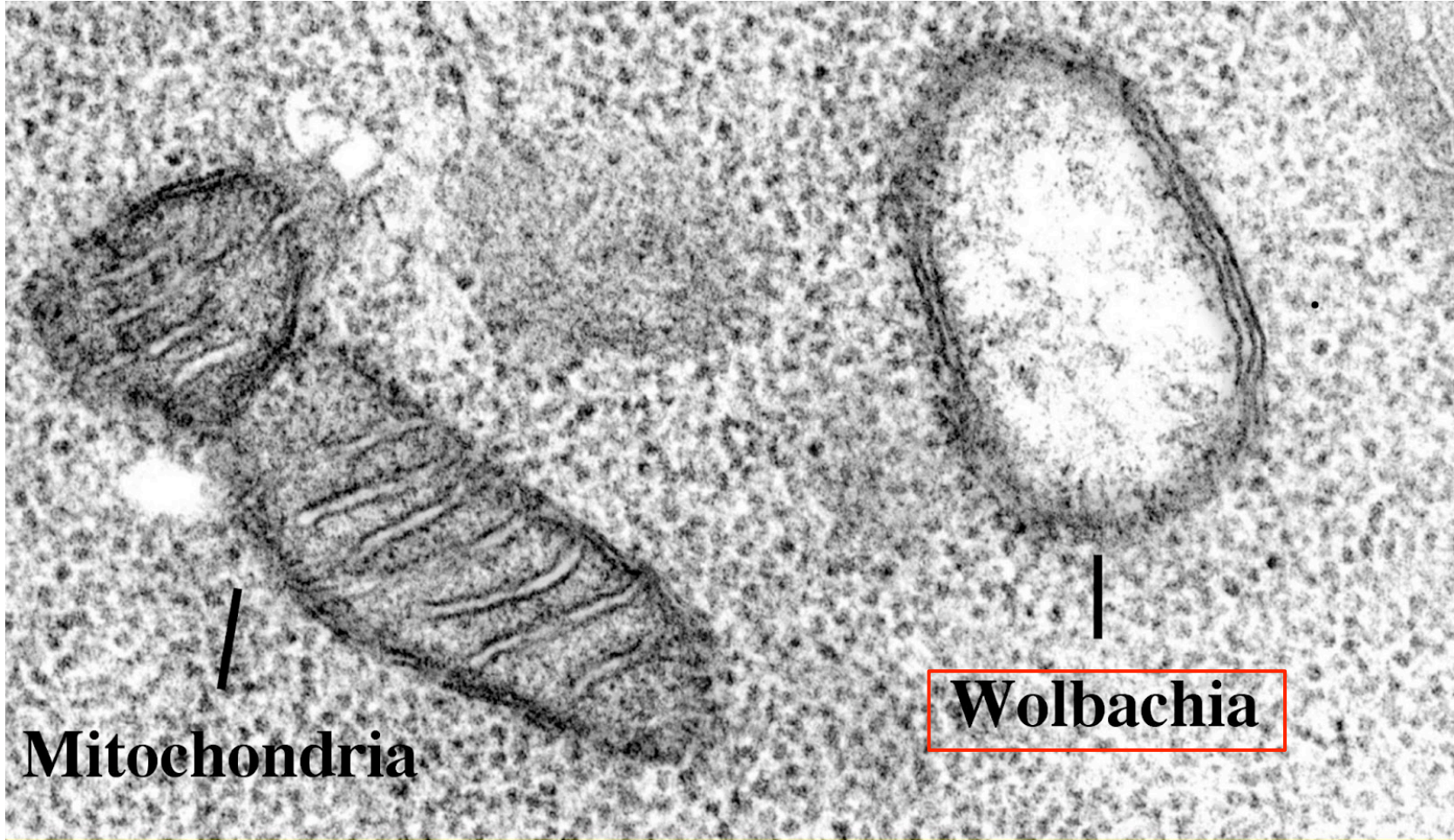


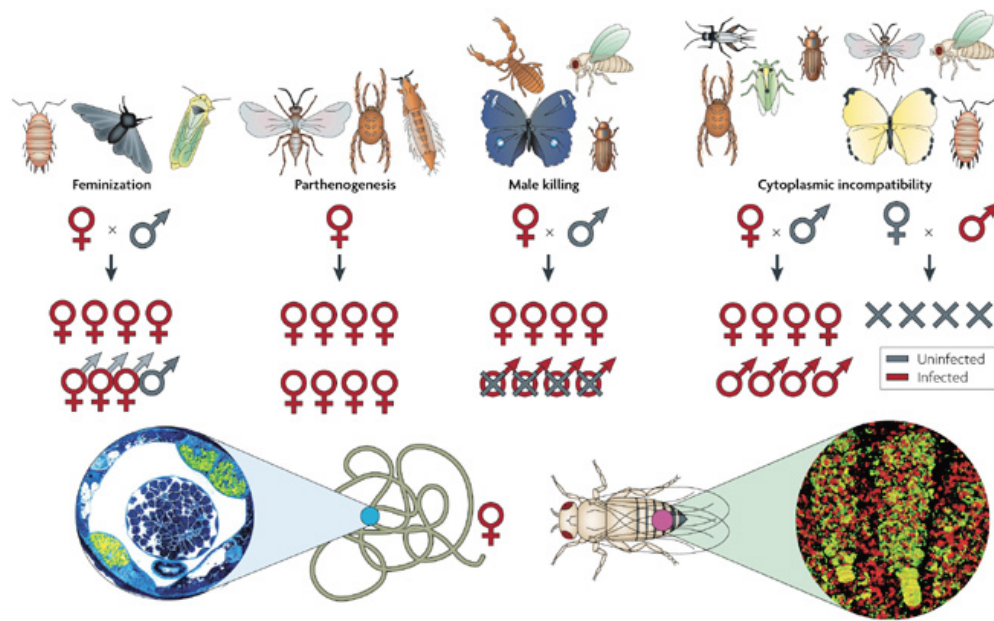
Photo: Honglin Feng





Mitochondria

Wolbachia



Nature Reviews | Microbiology

Strain	Host	Supergroup	Phenotype [†]	Genome size (Mb)	Status	Refs or project leaders
wMel	<i>Drosophila melanogaster</i>	A	Cytoplasmic incompatibility	1.27	Complete	94
wBm ⁶	<i>Brugia malayi</i>	D	Mutualist	1.08	Complete	18
wMelPop	<i>D. melanogaster</i>	A	Cytoplasmic incompatibility	1.3	Assembled	S. O'Neill
wPip	<i>Culex pipiens</i>	B	Cytoplasmic incompatibility	1.48	Assembled	J. Parkhill and S. Sinkins
wRi	<i>Drosophila simulans</i>	A	Cytoplasmic incompatibility	1.44	Assembled	S. Andersson, R. Garrett and K. Bourtzis
wAna	<i>Drosophila ananassae</i>	A	Cytoplasmic incompatibility	Unknown	Unfinished	19
wSim	<i>D. simulans</i>	A	Cytoplasmic incompatibility presumed	Unknown	Unfinished	19
wAu	<i>D. simulans</i>	A	Not cytoplasmic incompatibility	Unknown	Unfinished	S. O'Neill
wWill	<i>Drosophila willistoni</i>	A	Unknown	Unknown	Unfinished	J. Craig Venter Institute
wViTA	<i>Nasonia vitripennis</i>	A	Cytoplasmic incompatibility	Unknown	In progress	J. Werren and S. Richards
wUni	<i>Muscidifurax uniraptor</i>	A	Parthenogenesis	Unknown	In progress	S. Anderson and K. Bourtzis
wBo1	<i>Hypolimnas bolina</i>	B	Male killing	~1.6	In progress	A. Duplouy and S. O'Neill
wVu1	<i>Armadillidium vulgare</i>	B	Feminization	~1.7	In progress	R. Garrett, P. Greve, D. Bouchon and K. Bourtzis
None designated	<i>Diaphorina citri</i>	B	Unknown	Unknown	In progress	W. Hunter, Y. Ping Duan, R. Shatters and D. Hall
wDim	<i>Dirofilaria immitis</i>	C	Mutualist	~1.0	In progress	C. Bandi and B. Slatko
wOv	<i>Onchocerca volvulus</i>	C	Mutualist	~1.1	In progress	M. Taylor, M. Blaxter and B. Slatko

Encarsia parasitic wasps



Molecular Ecology (2004) 13, 2009–2016

doi: 10.1046/j.1365-294X.2004.02203.x

Distribution of the bacterial symbiont *Cardinium* in arthropods

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†Department of Entomology, University of Arizona, Tucson, USA

A *Cardinium*-like symbiont in the proturan *Acerella muscorum* (Hexapoda)

R. Dallai*, D. Mercati, F. Giusti, M. Gottardo, A. Carapelli

Department of Evolutionary Biology, University of Siena, I-53100 Siena, Italy

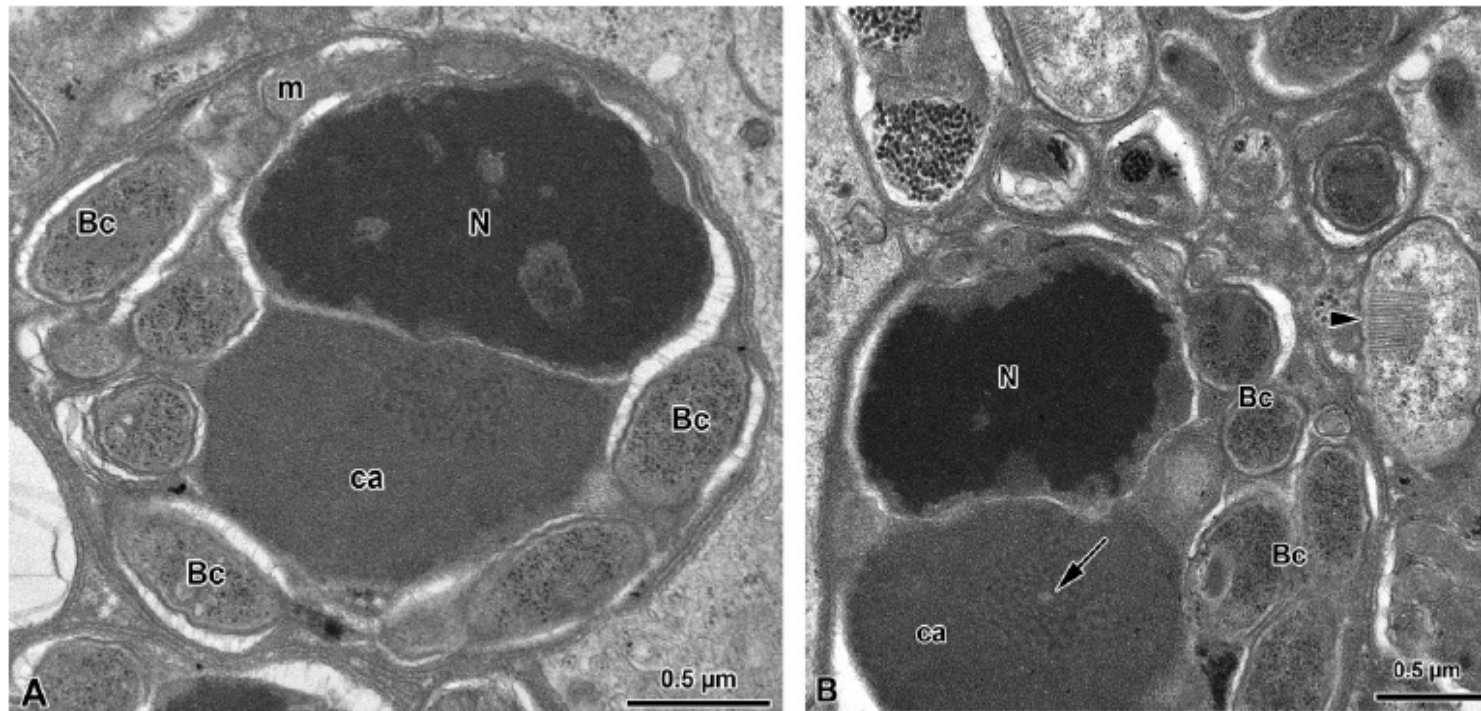


Fig. 3. (A–B) Cross sections through the aflagellate sperm cells of *A. muscorum* at the end of the reproductive process. Note some mitochondria and the numerous bacteria (Bc) in the narrow space between the nucleus (N) and the centriole adjunct material (ca); a bacterium provided with the characteristic microtubule-like complex (MLC) (arrowhead). Centriole: arrow.

Phylogenomic Evidence for the Presence of a Flagellum and *cbb*₃ Oxidase in the Free-Living Mitochondrial Ancestor

Davide Sasseria,^{†1} Nathan Lo,^{†2} Sara Epis,¹ Giuseppe D'Auria,³ Matteo Montagna,¹ Francesco Comandatore,¹ David Horner,⁴ Juli Peretó,^{3,5,6} Alberto Maria Luciano,⁷ Federica Franciosi,⁷ Emanuele Ferri,⁸ Elena Crotti,⁹ Chiara Bazzocchi,¹ Daniele Daffonchio,⁹ Luciano Sacchi,¹⁰ Andres Moya,^{3,5,11} Amparo Latorre,^{3,5,11} and Claudio Bandi^{1*}

Mol. Biol. Evol. 28(12):3285–3296. 2011

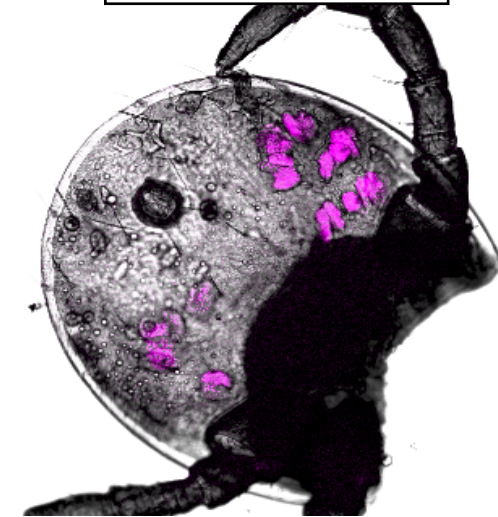
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PLOS ONE

Evolution of Mitochondria Reconstructed from the Energy Metabolism of Living Bacteria

Mauro Degli Esposti^{1*}, Bessem Chouaia², Francesco Comandatore³, Elena Crotti², Davide Sasseria^{3#a}, Patricia Marie-Jeanne Lievens^{1#b}, Daniele Daffonchio², Claudio Bandi³

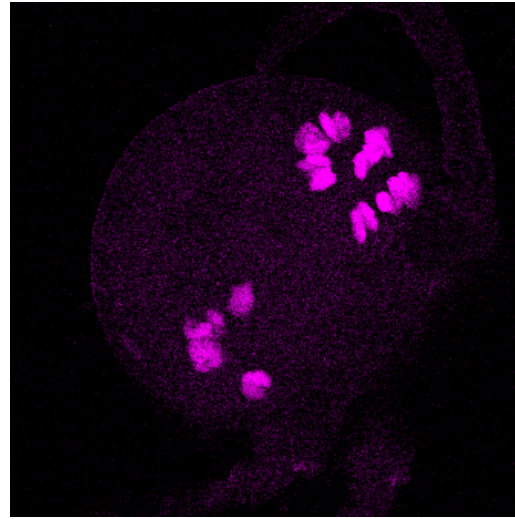
¹ Italian Institute of Technology, Genoa, Italy, ² Department of Food, Environmental and Evolutionary Sciences, University of Milan, Milan, Italy, ³ Dipartimento di Scienze Veterinarie e Sanità Pubblica, University of Milan, Milan, Italy



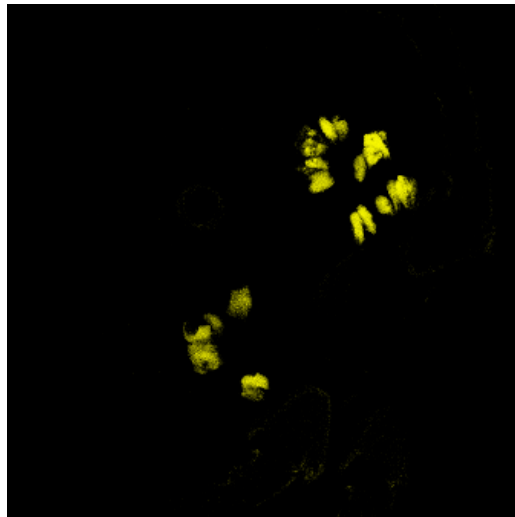
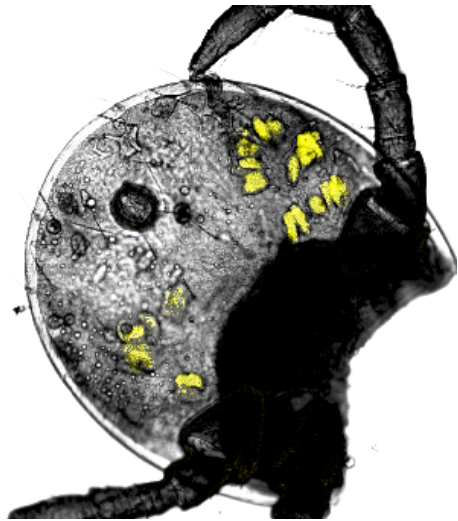
S. Epis et al. / Ticks and Tick-borne Diseases 4 (2013) 39–45

Localization of the bacterial symbiont *Candidatus Midichloria mitochondrii* within the hard tick *Ixodes ricinus* by whole-mount FISH staining

Sara Epis^{a,d}, Mauro Mandrioli^b, Marco Genchi^c, Matteo Montagna^a, Luciano Sacchi^c, Dario Pistone^a, Davide Sasseria^{a,*}



Cy3 probe
mitochondria



Cy5 probe
Midichloria

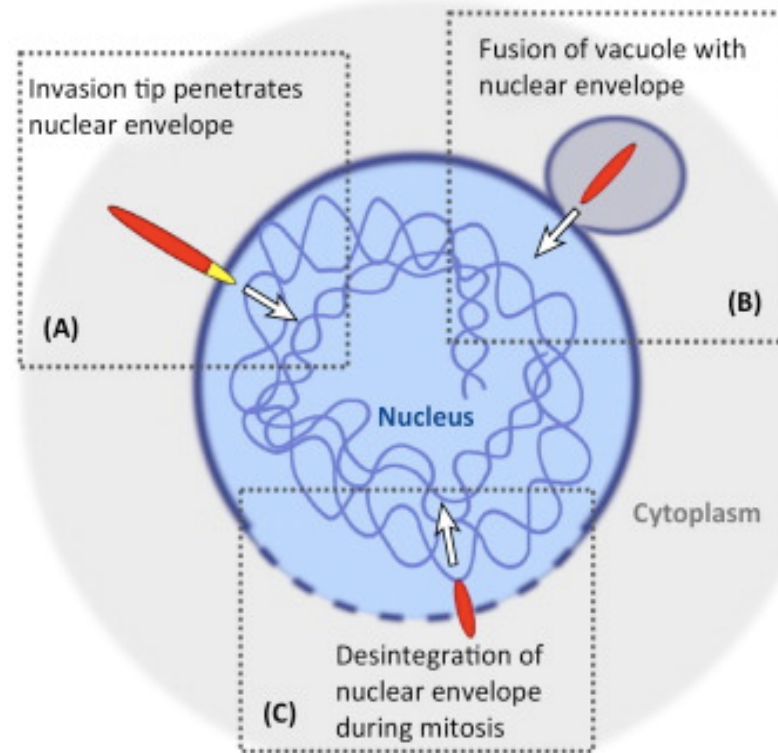
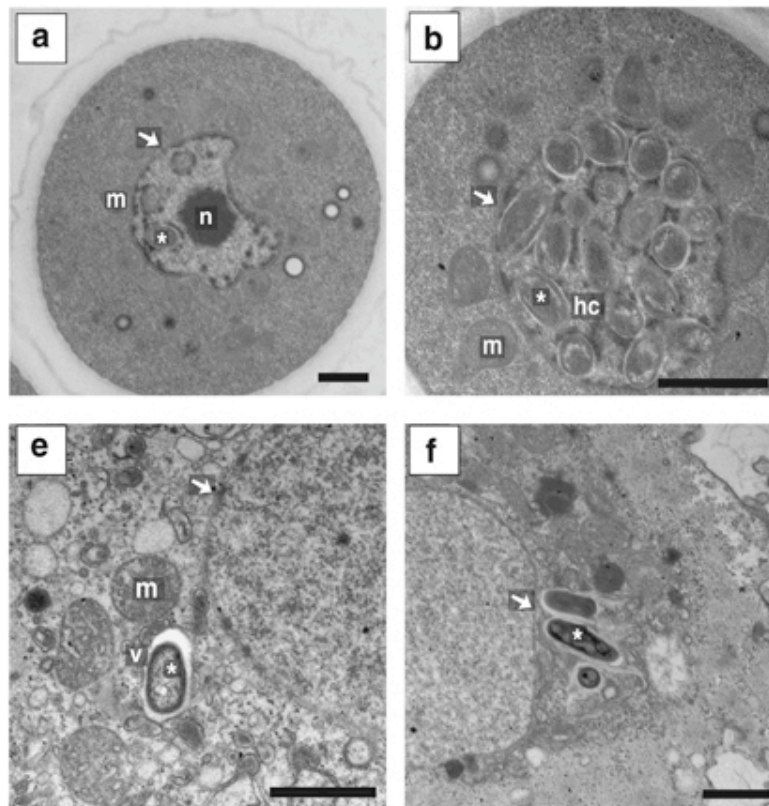
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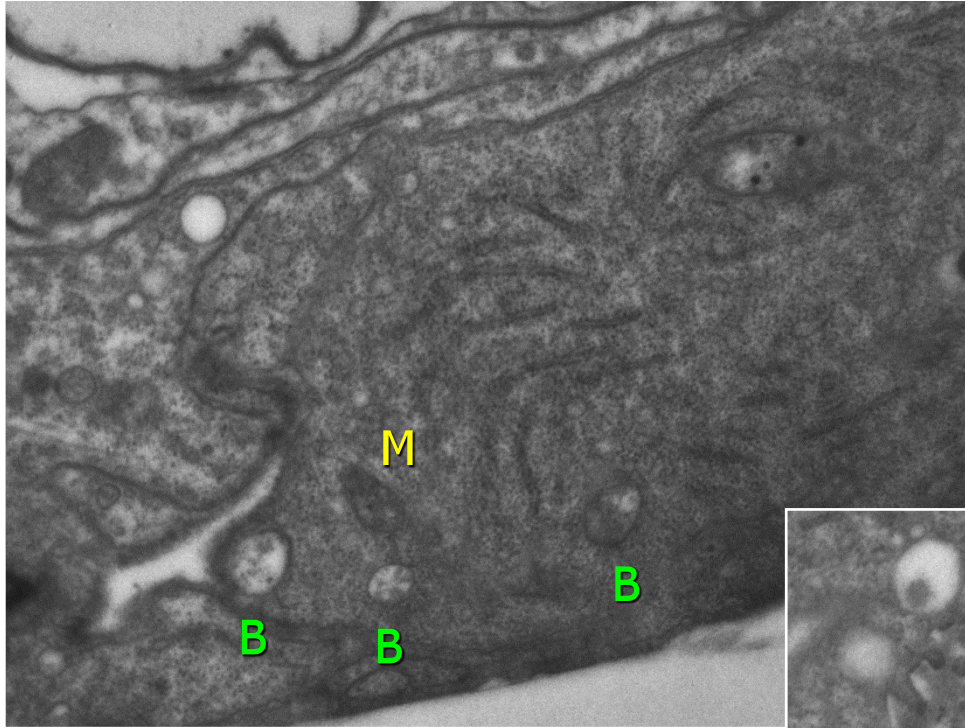
Life in an unusual intracellular niche: a bacterial symbiont infecting the nucleus of amoebae

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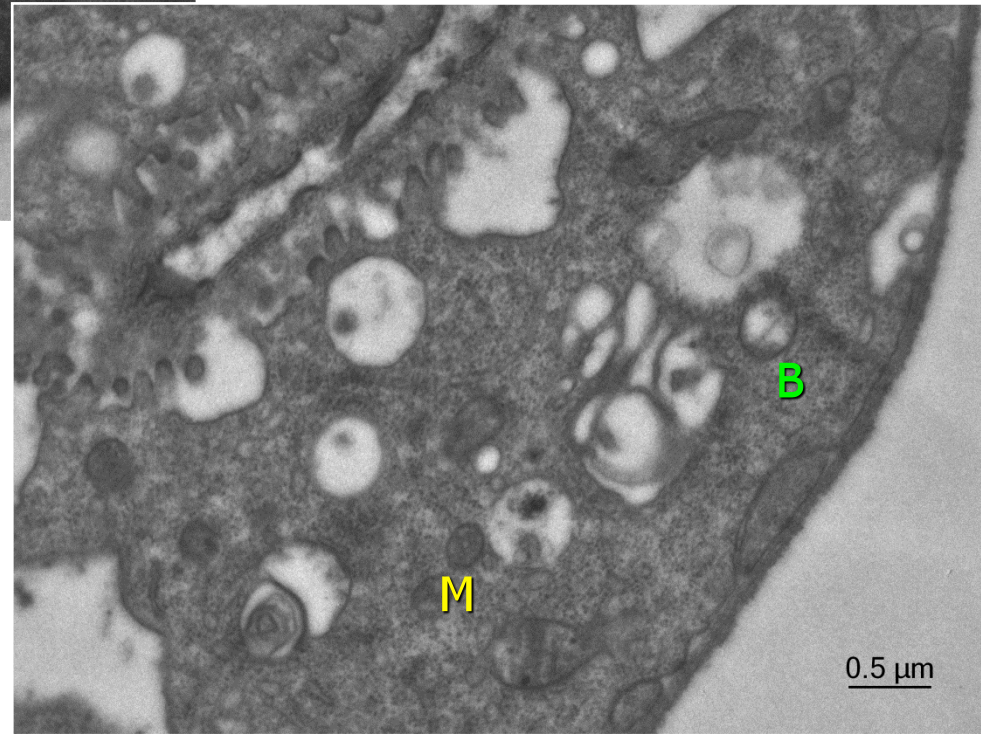
Frederik Schulz¹, Ilias Lagkouravdos¹, Florian Wascher¹, Karin Aistleitner¹,
Rok Kostanjšek² and Matthias Horn¹



Candidatus Nucleicultrix amoebiphila in *Acanthamoeba castellanii*



?



Bacterial endosymbionts in animals

Nancy A Moran* and Paul Baumann†

Molecular phylogenetic studies reveal that many endosymbioses between bacteria and invertebrate hosts result from ancient infections followed by strict vertical transmission within host lineages. Endosymbionts display a distinctive constellation of genetic properties including AT-biased base composition, accelerated sequence evolution, and, at least sometimes, small genome size; these features suggest increased genetic drift. Molecular genetic characterization also has revealed adaptive, host-beneficial traits such as amplification of genes underlying nutrient provision.

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Current Opinion in Microbiology 2000, 3:270–275

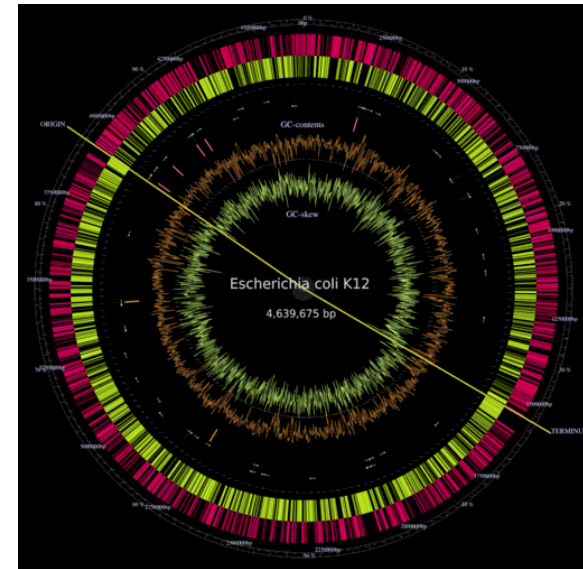


Table 1. Genomic features of primary bacteriocyte endosymbionts of insects

	<i>Blochmannia floridanus</i>	<i>Blochmannia pennsylvanicus</i>	<i>Wigglesworthia glossinidius</i>	<i>Buchnera aphidicola</i> Aps	<i>Buchnera aphidicola</i> BCc	<i>Buchnera aphidicola</i> Bp	<i>Buchnera aphidicola</i> Sg
Phylum	<i>γ-Proteobacteria</i>	<i>γ-Proteobacteria</i>	<i>γ-Proteobacteria</i>	<i>γ-Proteobacteria</i>	<i>γ-Proteobacteria</i>	<i>γ-Proteobacteria</i>	<i>γ-Proteobacteria</i>
Host	<i>Camponotus floridanus</i>	<i>Camponotus pennsylvanicus</i>	<i>Glossina morsitans</i>	<i>Acyrtosiphon pisum</i>	<i>Cinara cedri</i>	<i>Baizongia pistacea</i>	<i>Schizaphis graminum</i>
Genome size (bp)	705,557	791,654	697,724	640,681	422,434	615,980	641,454
GC content (%)	27.4	29.6	22.5	26.2	20.1	25.3	25.3
Plasmids (total size in bp)	0	0	1 (5280)	2 (11,434)	1 (6054)	1 (2399)	2 (11,547)
Predicted protein coding sequences (number on plasmids)	583	610	617 (6)	562 (9)	357 (5)	504 (3)	550 (9)
rRNAs	3	3	6	3	3	3	3
tRNAs	37	39	34	32	31	32	32
Small RNA genes	2	2	2	2	2	2	2
Pseudogenes	4	4	14	13	3	9	33
ORF average length (bp)	1006	995	990	990	994	990	983
Host nutrition	Omnivorous	Omnivorous	Blood	Phloem	Phloem	Phloem	Phloem
Reference	Gil et al. (2003)	Degnan et al. (2005)	Akman et al. (2002)	Shigenobu et al. (2000)	Perez-Brocal et al. (2006)	van Ham et al. (2003)	Tamas et al. (2002)

Horizontal transfer of genes in bacteria

Paul H. Roy

Symbiont Genes in Host Genomes: Fragments with a Future?

Mark Blaxter^{1,*}

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DOI 10.1016/j.chom.2007.09.008

While lateral transfer is the rule in the evolutionary history of bacterial and archaeal genes, events of transfer from prokaryotes to eukaryotes are rare. Germline-transmitted animal symbionts, such as *Wolbachia pipientis*, are well placed to participate in such transfers. In a recent issue of *Science*, Dunning Hotopp et al. identified instances of transfer of *Wolbachia* DNA to host genomes. It is unknown whether these transfers represent innovation in animal evolution.

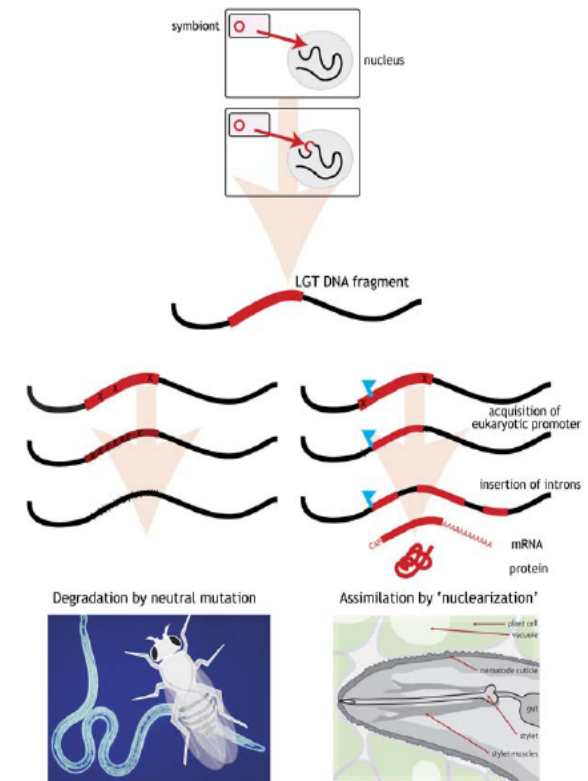
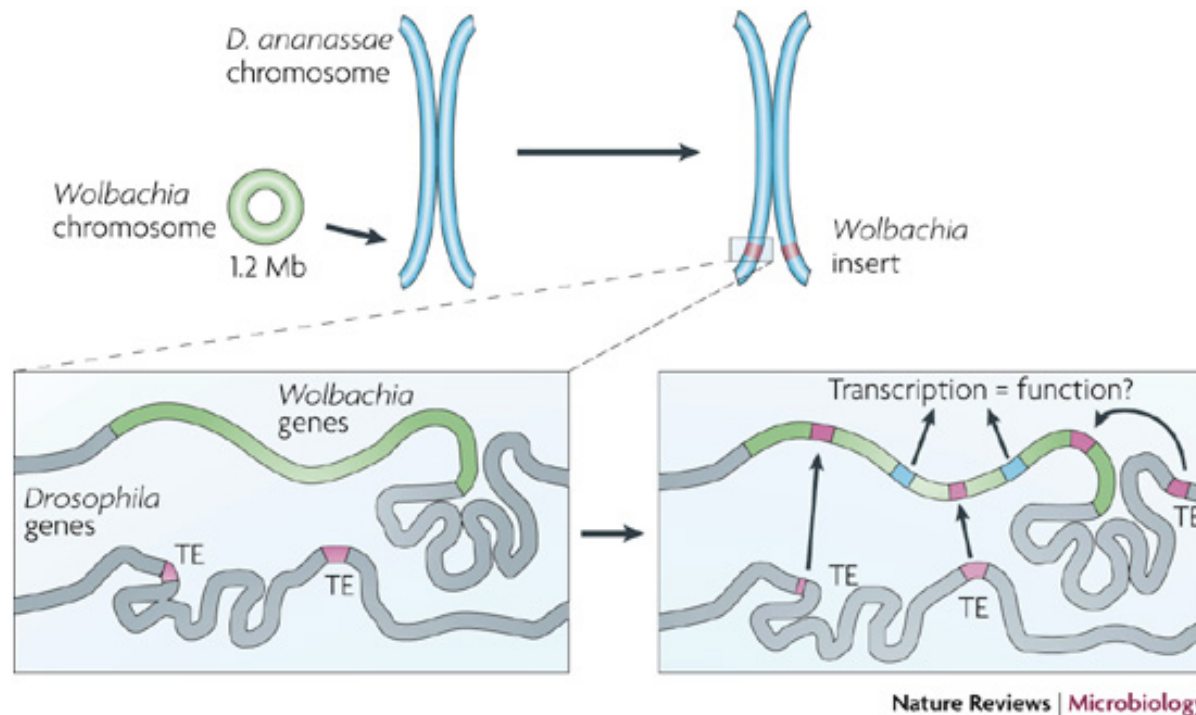


Figure 1. The Fate of Laterally Transferred Genes

A DNA fragment laterally transferred from an intracellular germline symbiont to the nucleus of an eukaryotic cell (top) can either be degraded by neutral mutation, and play no significant part in the evolution of the eukaryotic host genome (left), or become integrated into the host genome and provide a novel function (right) by acquiring eukaryotic promoter elements and RNA processing signals. The *Wolbachia* insertions thus far described fit the left-hand model, while the rhizosphere bacterial genes acquired by plant parasitic nematodes fit the right-hand model. The images below represent *Drosophila melanogaster*, the filarial nematode *Brugia malayi*, and a cartoon of a transmission electron micrograph of a *Meloidogyne* sp. nematode within a root showing the feeding stylet (in the center) used to penetrate cell walls with the aid of laterally transferred gene products.

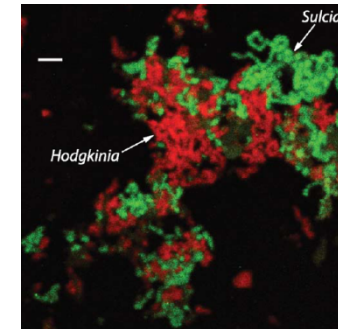


Almost the entire *Wolbachia* genome (green) has been transferred into the second chromosome of *Drosophila ananassae* (blue). Following this lateral gene transfer, *Drosophila ananassae* transposable elements (TEs) have become inserted within *Wolbachia* genes. At least 28 *Wolbachia* genes are transcribed from within the *D. ananassae* genome, although the functional significance of this is unknown.

Origin of an Alternative Genetic Code in the Extremely Small and GC-Rich Genome of a Bacterial Symbiont

John P. McCutcheon^{1,2*}, Bradon R. McDonald², Nancy A. Moran²

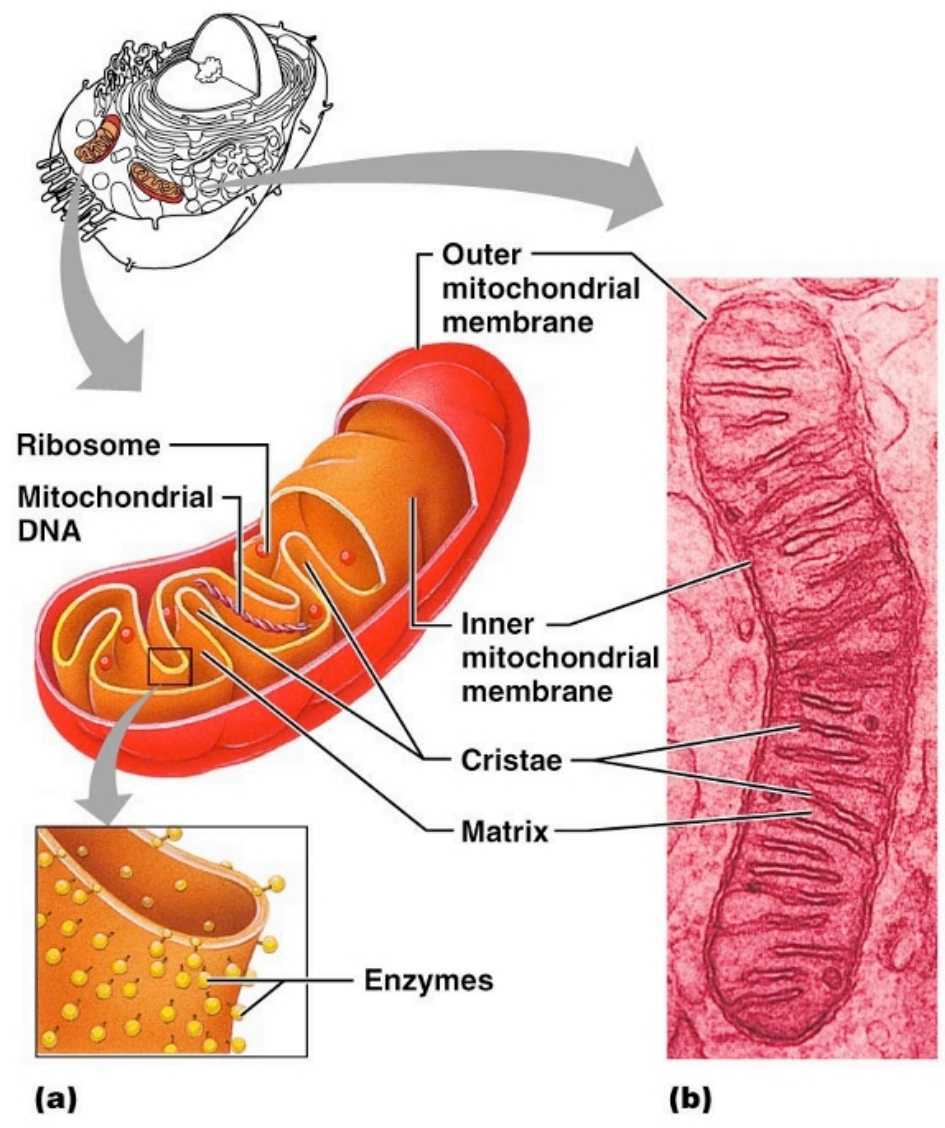
¹Center for Insect Science, University of Arizona, Tucson, Arizona, United States of America, ²Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, Arizona, United States of America

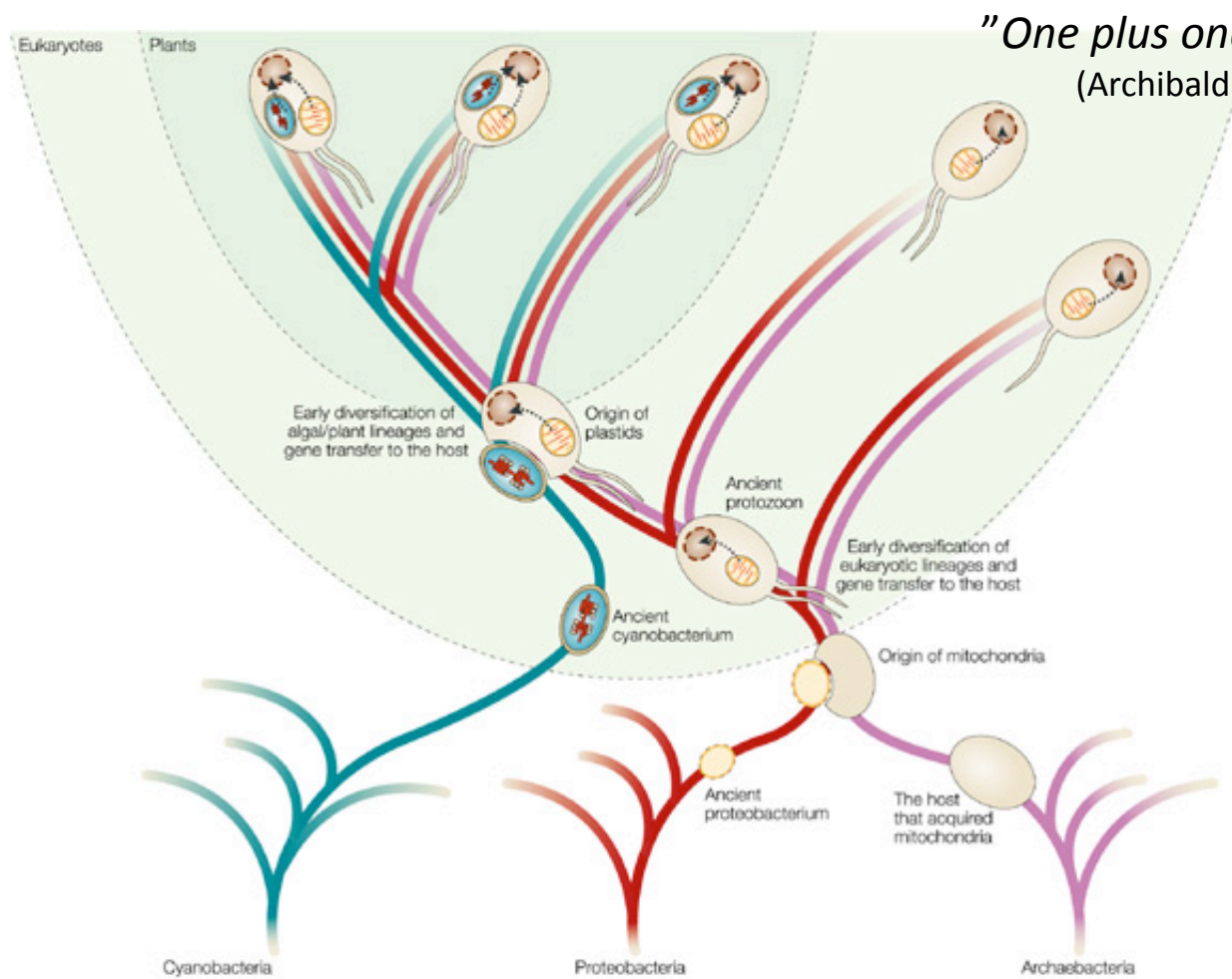


UGA stop codon to Tryptophan (StopRTrp) recoding in the α -proteobacterial symbiont *Candidatus Hodgkinia cicadicola* from the cicada *Diceroprocta semicincta*



	tRNA-Trp anticodon	release factors	UGA encodes
initial state	CCA	RF1 RF2	STOP
1 mutation of tRNA-Trp gene			
some readthrough of UGA	*CCA	RF1 RF2	STOP Trp
2 loss of Release Factor 2 (RF2)			
only UAA and UAG read as stop	*CCA	RF1	Trp
3 mutation of tRNA-Trp anticodon			
UGA, UGG both read by wobble rules	UCA	RF1	Trp
4 genomic codon adaptation			
new UAA and UAG stops generated; some UGG codons changed to UGA	UCA	RF1	Trp

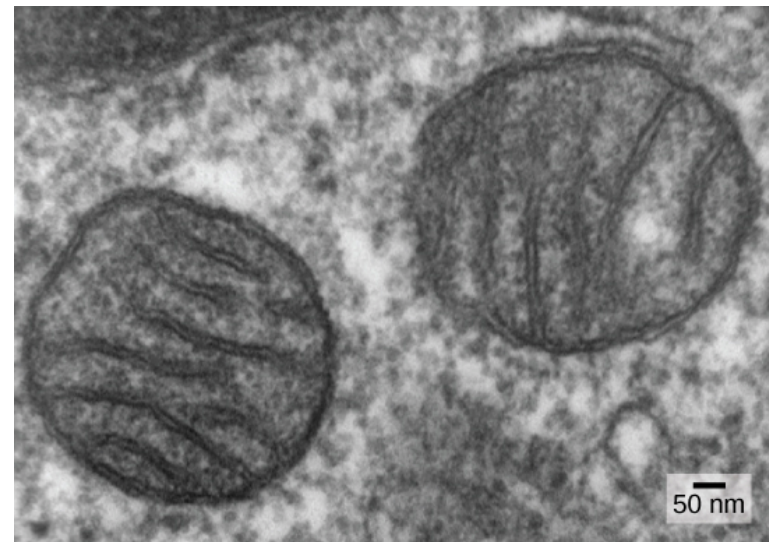
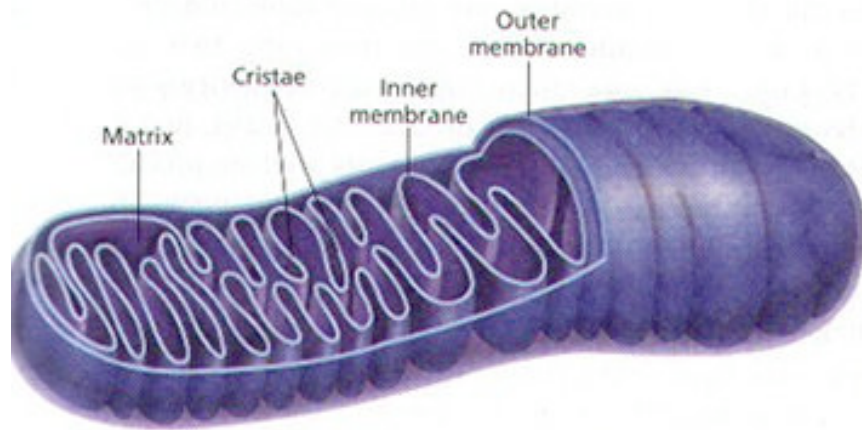
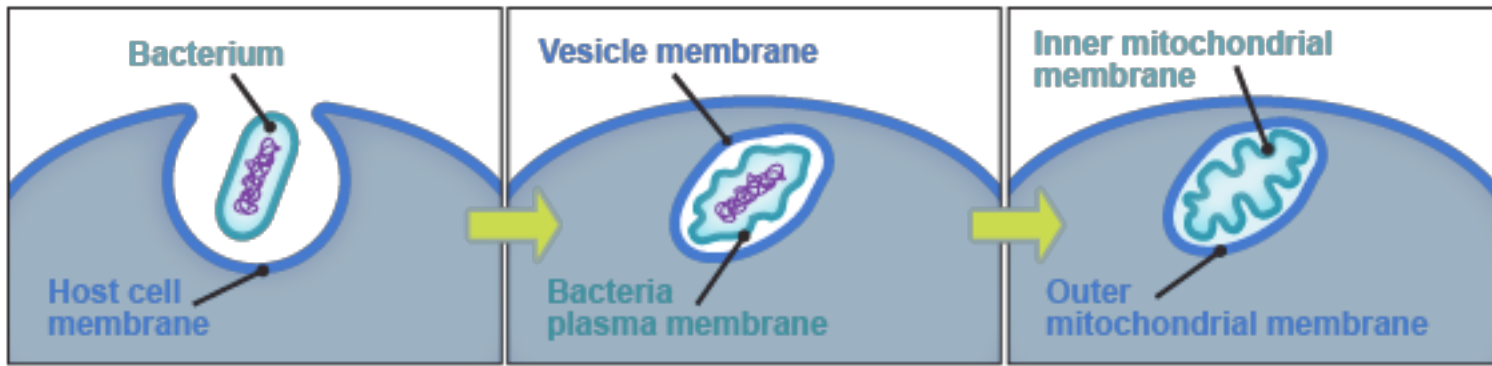


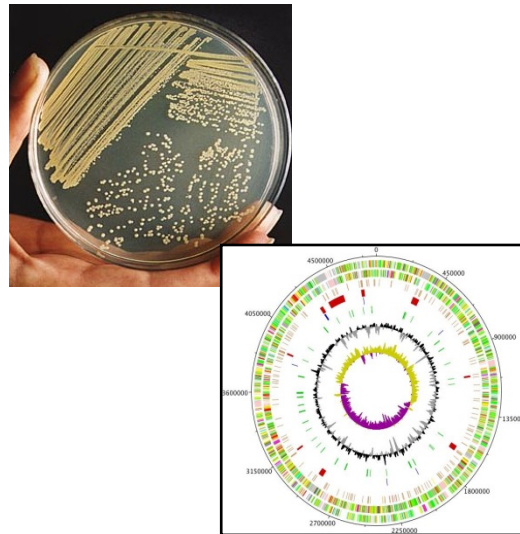
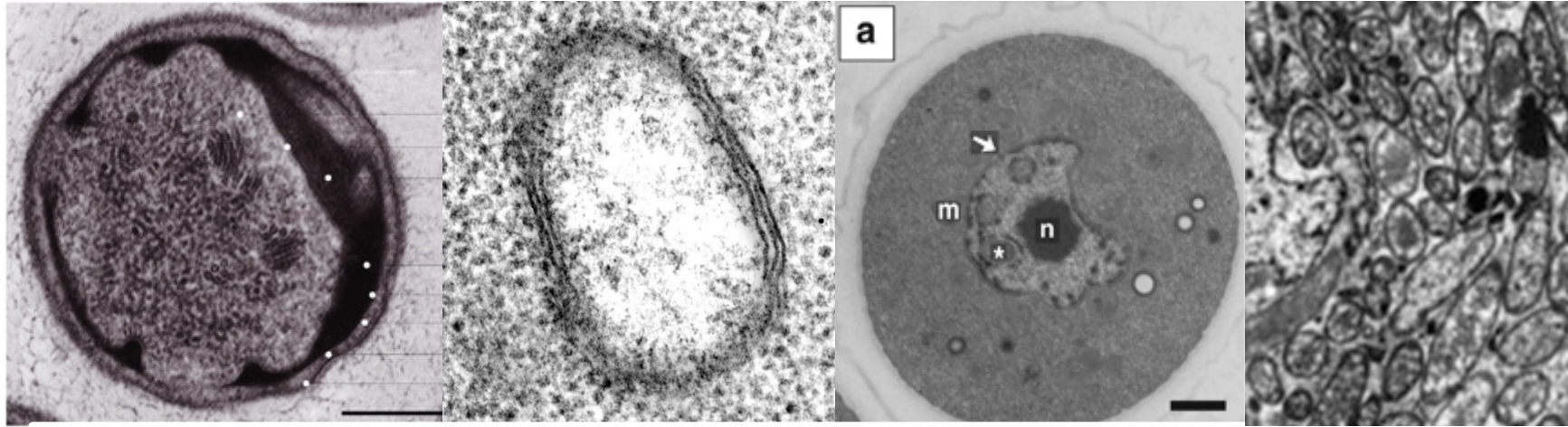


"One plus one equals one"
 (Archibald JM, 2014)

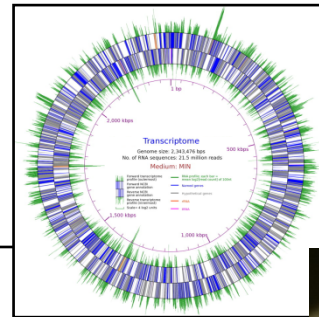
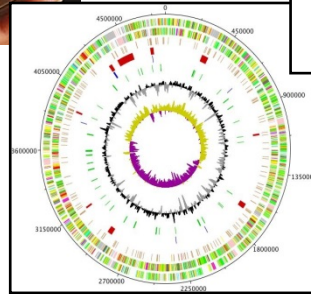
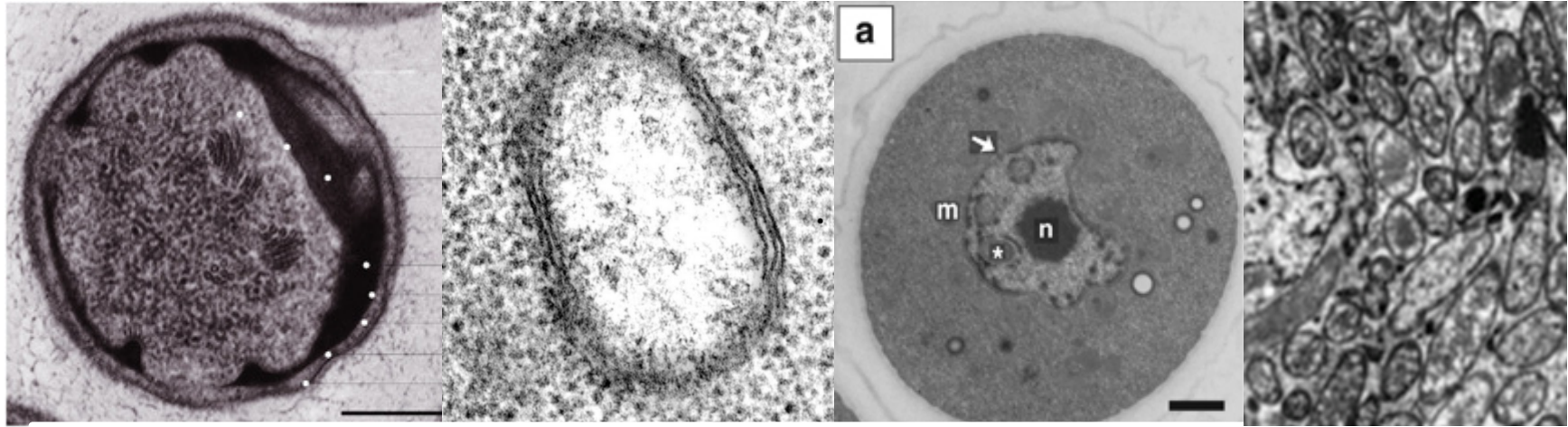
Nature Reviews | Genetics

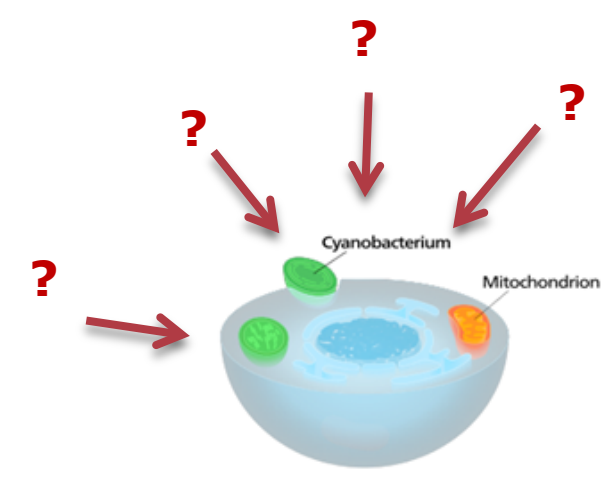
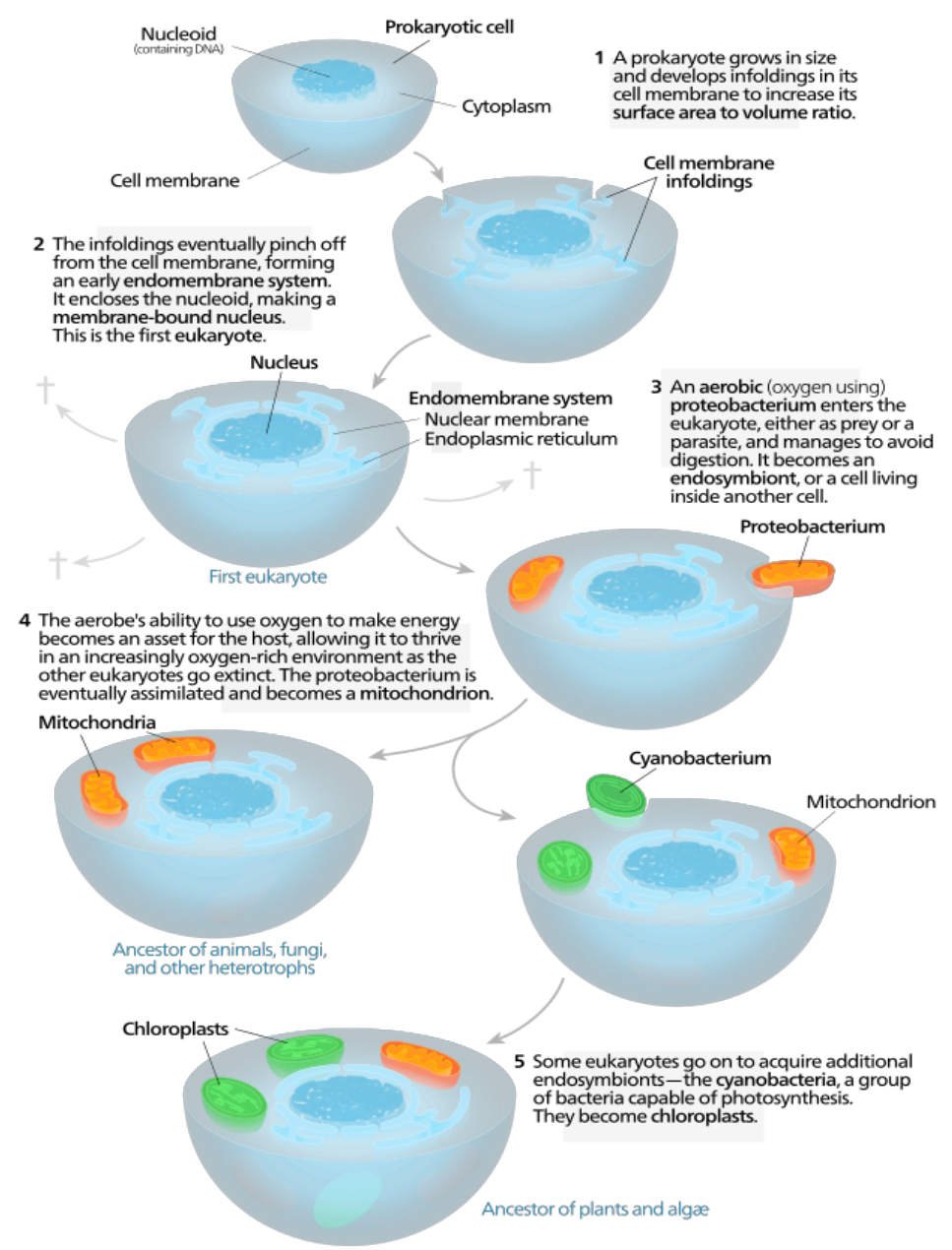
Timmis, J. N. et al. Endosymbiotic gene transfer: organelle genomes forge eukaryotic chromosomes. Nature Reviews Genetics 5, 123–135 (2004).





Epis S, Luciano AM, Franciosi F, Bazzocchi C, Crotti E, Pistone D, Bandi C, Sasser D (2010) A novel method for the isolation of DNA from intracellular bacteria, suitable for genomic studies. *Annals of Microbiology*. 60:455-460





The Major Antigenic Membrane Protein of “*Candidatus* Phytoplasma asteris” Selectively Interacts with ATP Synthase and Actin of Leafhopper Vectors

Luciana Galetto¹, Domenico Bosco², Raffaella Balestrini³, Andrea Genre⁴, Jacqueline Fletcher⁵, Cristina Marzachi^{1*}

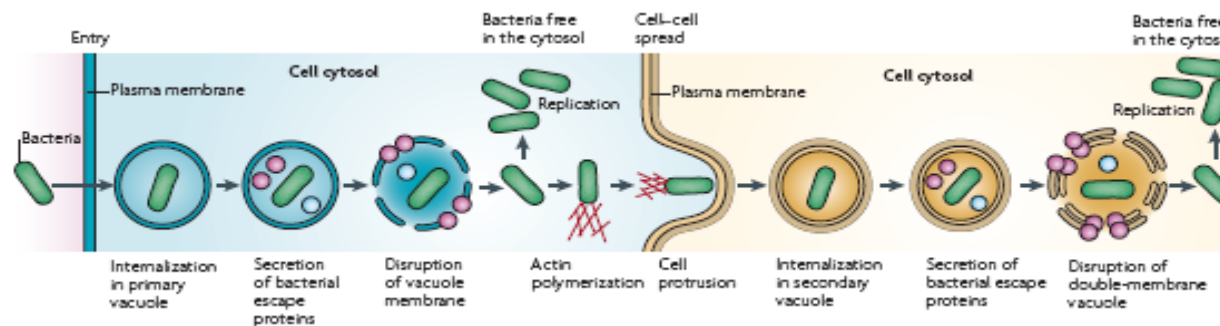
Life on the inside: the intracellular lifestyle of cytosolic bacteria

Katrina Ray^{*}, Benoit Marteyn^{*†}, Philippe J. Sansonetti[†] and Christoph M. Tang^{*}

Abstract | Bacterial pathogens exploit a huge range of niches within their hosts. Many pathogens can invade non-phagocytic cells and survive within a membrane-bound compartment. However, only a small number of bacteria, including *Listeria monocytogenes*, *Shigella flexneri*, *Burkholderia pseudomallei*, *Francisella tularensis* and *Rickettsia* spp., can gain access to and proliferate within the host cell cytosol. Here, we discuss the mechanisms by which these cytosolic pathogens escape into the cytosol, obtain nutrients to replicate and subvert host immune responses.

NATURE REVIEWS | MICROBIOLOGY

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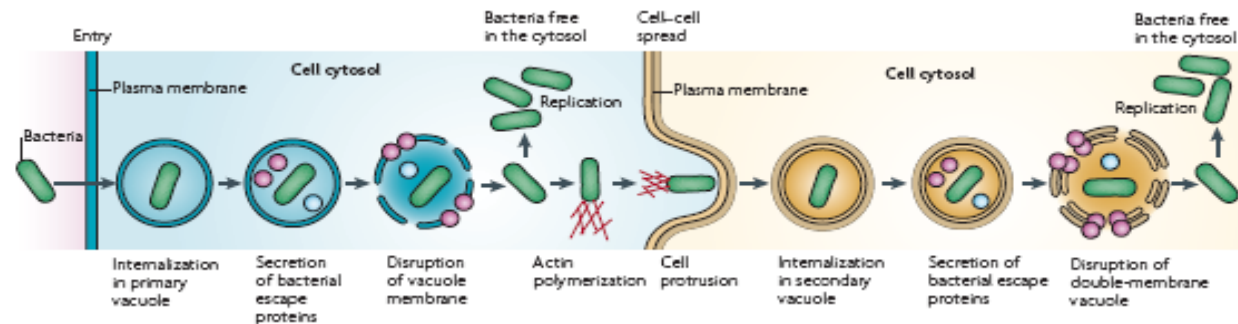
Considering that bacteria frequently hijack the host endocytic and secretory pathway...

Invasion between prokaryotes and the origin of eukaryotes

*Yaacov Davidov and Edouard Jurkevitch**

Department of Plant Pathology and Microbiology, The Hebrew University of Jerusalem, Rehovot, Israel

BioEssays 31:748–757, © 2009 Wiley Periodicals, Inc.



Unravelling the *Wolbachia* evolutionary role: the reprogramming of the host genomic imprinting

Ilaria Negri^{1,*}, Antonella Franchini², Elena Gonella¹, Daniele Daffonchio³, Peter John Mazzoglio¹, Mauro Mandrioli² and Alberto Alma^{1,*}

¹*Di.Va.P.R.A.—Entomology and Zoology Applied to the Environment, University of Turin, Via Leonardo da Vinci 44, 10095 Grugliasco (Turin), Italy*

²*Department of Animal Biology, University of Modena, via Campi 213/D, 41100 Modena, Italy*

³*Di.S.T.A.M., University of Milan, Via Celoria 2, 20133 Milan, Italy*

Environmental factors can induce significant epigenetic changes that may also be inherited by future generations. The maternally inherited symbiont of arthropods *Wolbachia pipientis* is an excellent candidate as an 'environmental' factor promoting trans-generational epigenetic changes: by establishing intimate relationships with germ line cells, epigenetic effects of *Wolbachia* symbiosis would be manifested as a 'maternal effect', in which infection of the mother modulates the offspring phenotype. In the leafhopper *Zyginidia pullula*, *Wolbachia* feminizes genetic males, leaving them as intersexes. With the exception of male chitinous structures that are present in the last abdominal segment, feminized males display phenotypic features that are typical of females. These include ovaries that range from a typical histological architecture to an altered structure. Methylation-sensitive random amplification of polymorphic DNA profiles show that they possess a female genomic imprint. On the other hand, some rare feminized males bear testes instead of ovaries. These specimens possess a *Wolbachia* density approximately four orders of magnitude lower than feminized males with ovaries and maintain a male genome—methylation pattern. Our results indicate that *Wolbachia* infection disrupts male imprinting, which dramatically influences the expression of genes involved in sex differentiation and development, and the alteration occurs only if *Wolbachia* exceeds a density threshold. Thus, a new *Wolbachia*'s role as an environmental evolutionary force, inducing epigenetic trans-generational changes, should now be considered.

Transposable element proliferation as a possible side effect of endosymbiont manipulations

Ken Kraaijeveld^{1,*} and Jens Bast²

Mobile Genetic Elements 25, 253–256; September/October 2012; © 2012 Landes Bioscience

PeerJ

The relative importance of DNA methylation and *Dnmt2*-mediated epigenetic regulation on *Wolbachia* densities and cytoplasmic incompatibility

Daniel P. LePage¹, Kristin K. Jernigan^{1,2} and Seth R. Bordenstein^{1,3}

LePage et al. (2014), PeerJ, DOI 10.7717/peerj.678



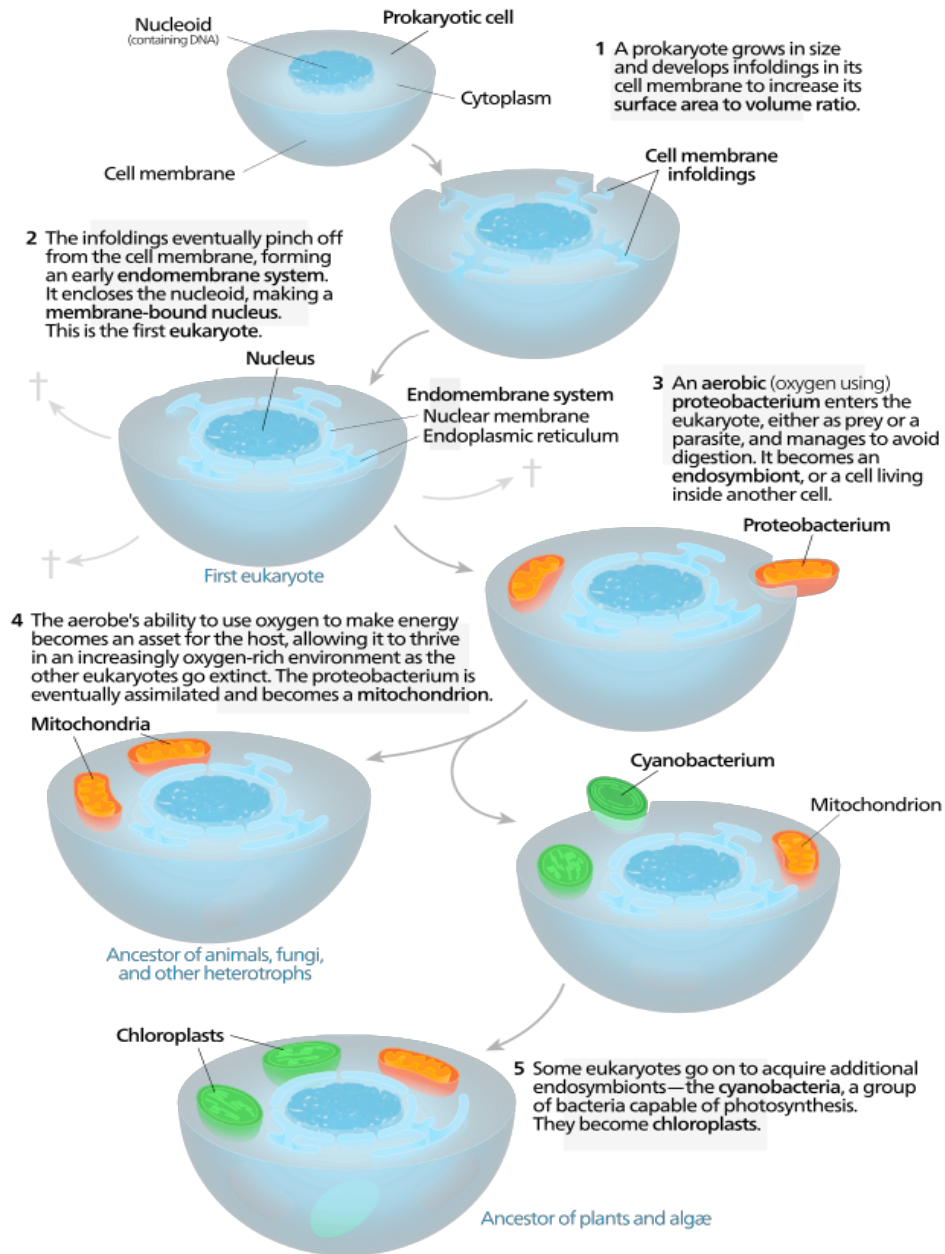
“If you could rewind the tape of life, erasing what actually happened and let it run again, you'd get a different set of ten each time”.



«*In perspective, our work provides new means for selecting bacterial organisms that are most suitable for **experimentally reevolving proto-mitochondria with mitochondria-depleted eukaryotic cells***». (Degli Esposti et al. 2014)



**Thank you for your
attention!**



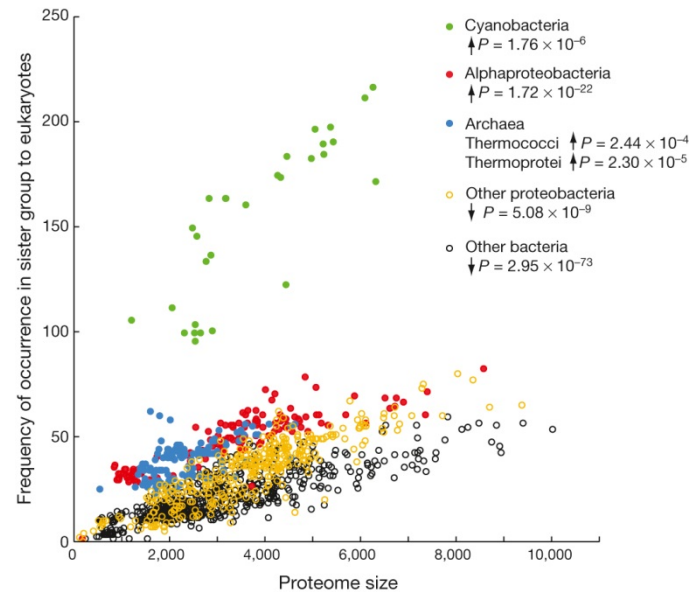
"One plus one equals one"
 (Archibald JM, 2014)

Endosymbiotic origin and differential loss of eukaryotic genes

nature

Chuan Ku¹, Shijulal Nelson-Sathi¹, Mayo Roettger¹, Filipa L. Sousa¹, Peter J. Lockhart², David Bryant³, Einat Hazkani-Covo⁴, James O. McInerney^{5,6}, Giddy Landan⁷ & William F. Martin^{1,8}

27 AUGUST 2015 | VOL 524 | NATURE | .



The cyanobacterial signal for plastids, the alphaproteobacterial signal for mitochondria, and the archaeal signal for the host bear out the predictions of endosymbiotic theory. But beyond those three signals, no significant contributions are detected from other prokaryotes that are discussed in various formulations of endosymbiotic theory

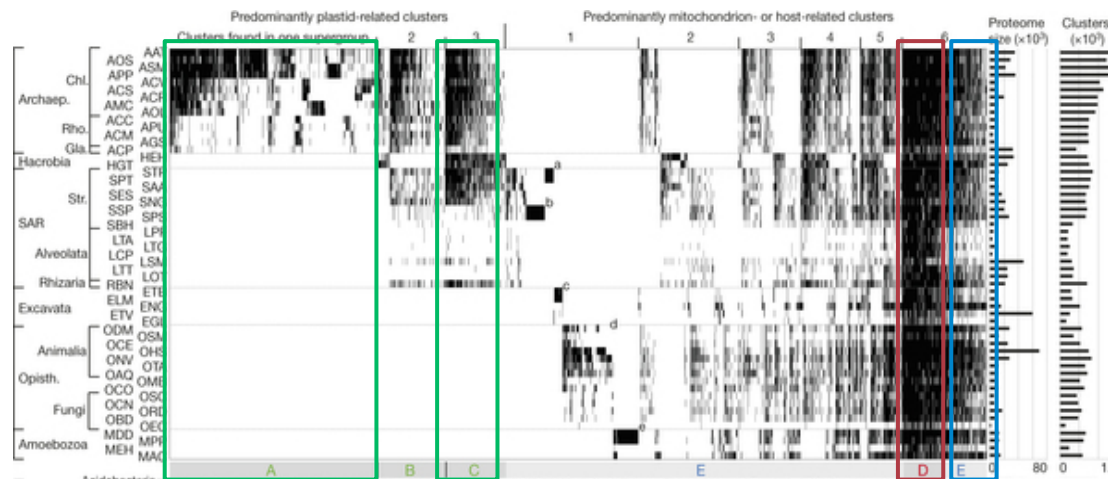
Endosymbiotic origin and differential loss of eukaryotic genes

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27 AUGUST 2015 | VOL 524 | NATURE | .

"We clustered 956,053 protein sequences from 55 eukaryotes from six supergroups and 6,103,025 sequences from prokaryotes (5,793,897 from 1,847 bacteria and 309,128 from 134 archaea)"



Blocks A and C are densely distributed in cyanobacteria in accordance to the endosymbiotic theory
Block E encompasses genes present in the eukaryotic common ancestor
Block D mitochondrion gain

