

# Evolutionary Genomics of *Buchnera aphidicola*

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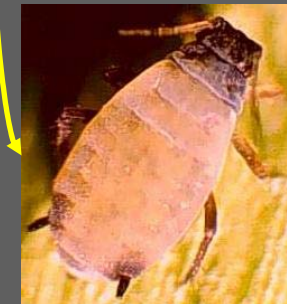
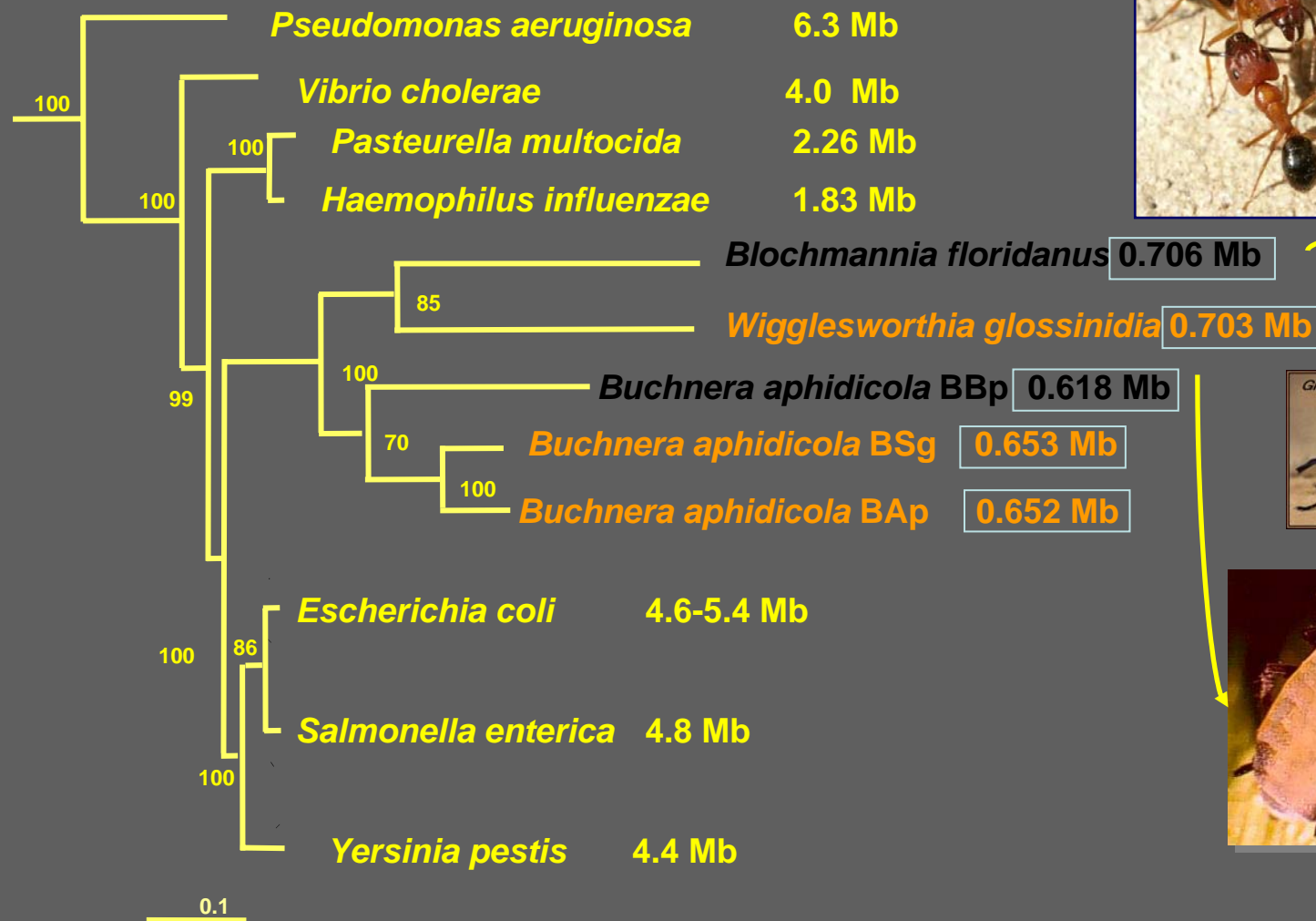
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# Topics

- Genome reduction in endosymbiotic bacteria from insects
- Evolutionary genomics of *Buchnera aphidicola*
- Current genome projects on endosymbiotic bacteria

# Phylogeny of $\gamma$ -Proteobacteria



# Comparative genomics of reduced genomes



Carpenter ant:  
Omnivore



Tsetse fly:  
Blood



Aphid:  
Plant-sap

# Carpenter ant (*Camponotus floridanus*)

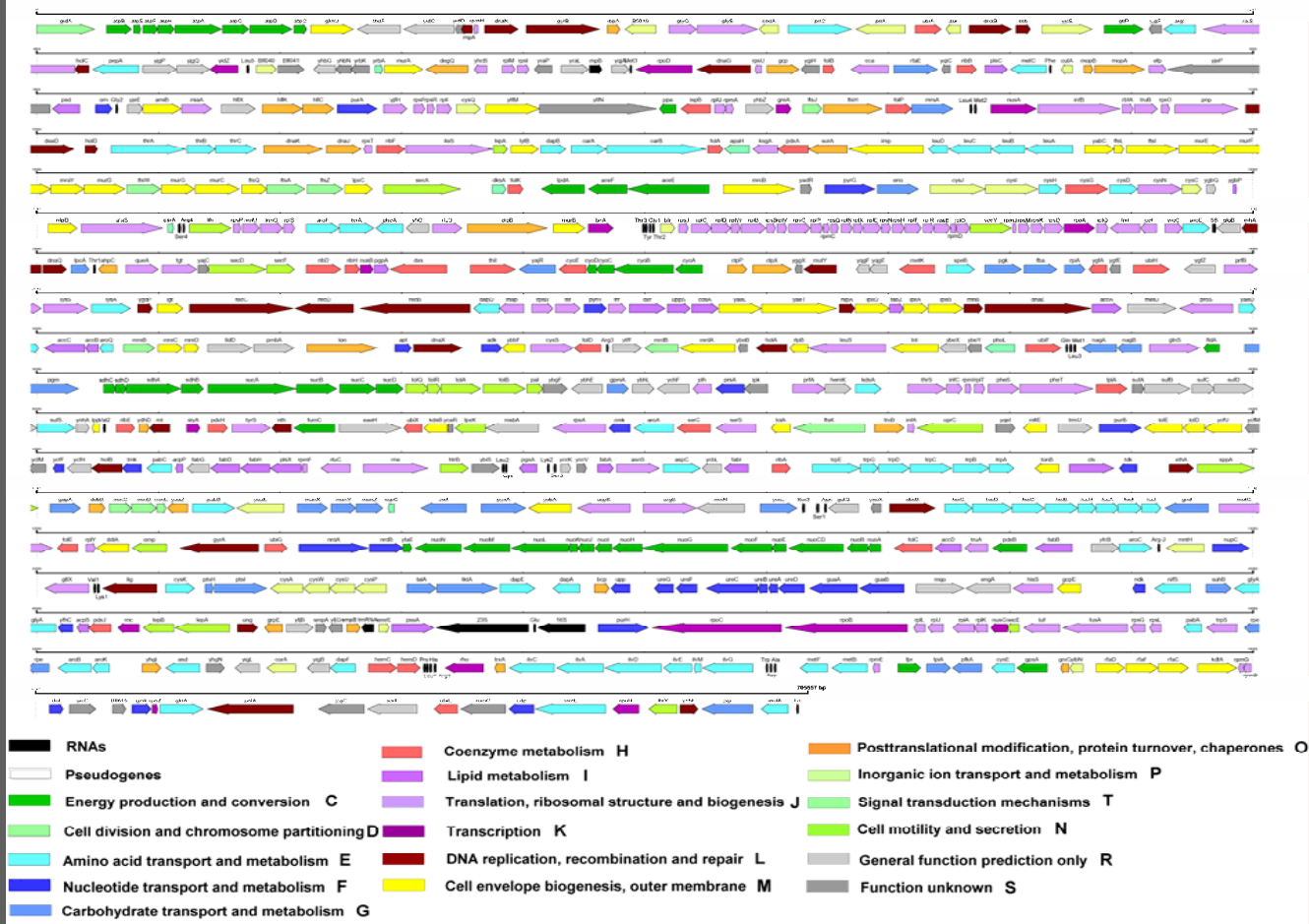


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# B. floridanus genome map

## Blochmannia genome



# Some other features associated with genome reduction

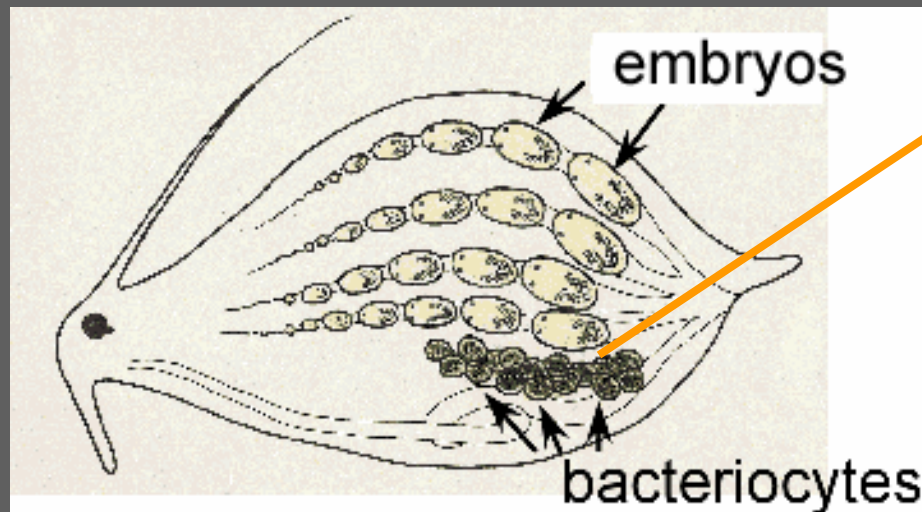
- High A+T content.
- Loss of codon bias.
- Bias in amino acid composition.
- Increment of the number of non-synonymous substitutions.
- Accelerated evolutionary rate.
- Plasmid-mediated gene amplification.
- Some genes are positively selected.

# Three basic features on aphid endosymbiosis

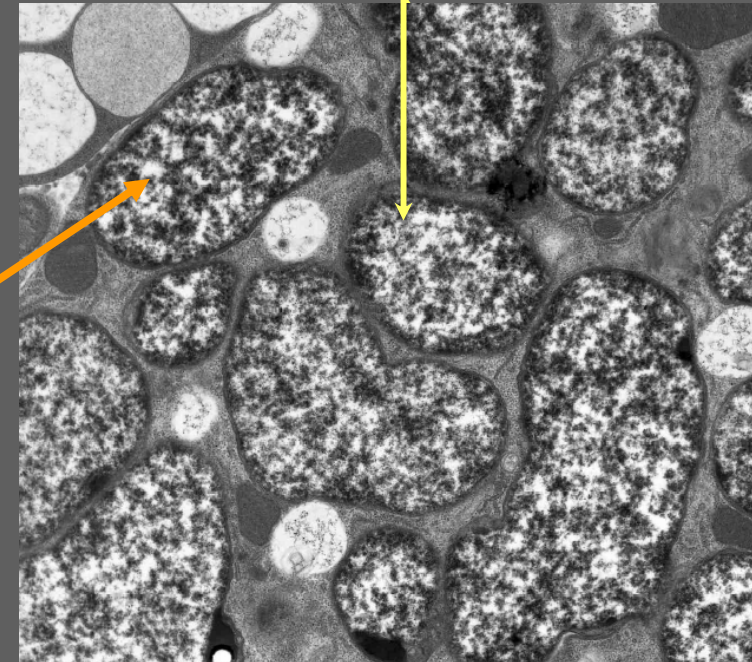
1. Aphids (Homoptera, Aphididae) are plant phloem-feeding insects that harbor the  $\gamma$ -proteobacteria *Buchnera aphidicola* as a primary endosymbiont
2. *B. aphidicola* provides the host with the nutrients (mainly amino-acids) that are in short supply in its strict phloem diet
3. During the symbiotic process *B. aphidicola* has suffered drastic changes, specially genome size reduction

# Aphids have an endosymbiotic association with *B. aphidicola*

CROSS SECTION  
OF AN APHID



*Buchnera aphidicola*



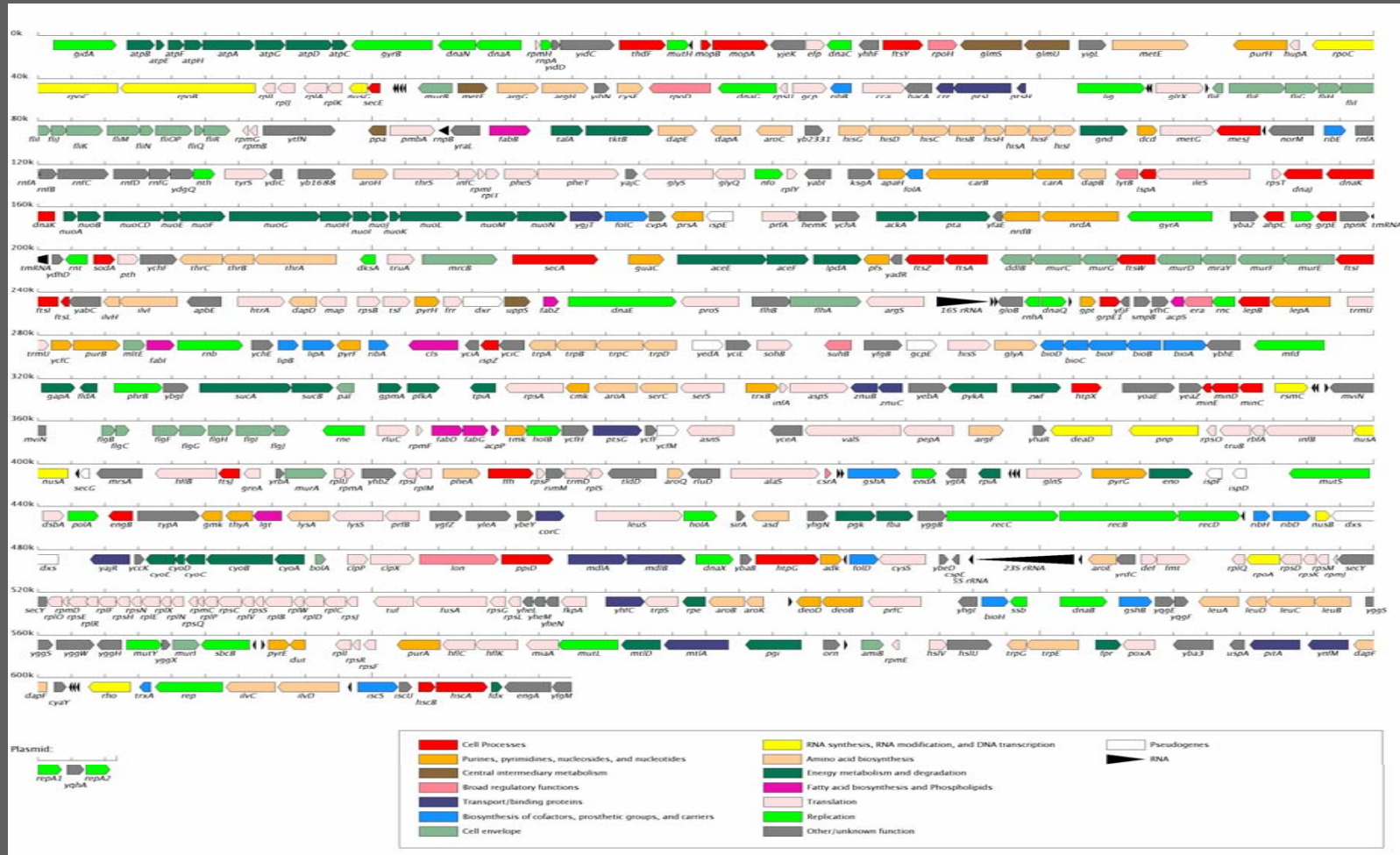
# Aphid (*Baizongia pistaciae*)



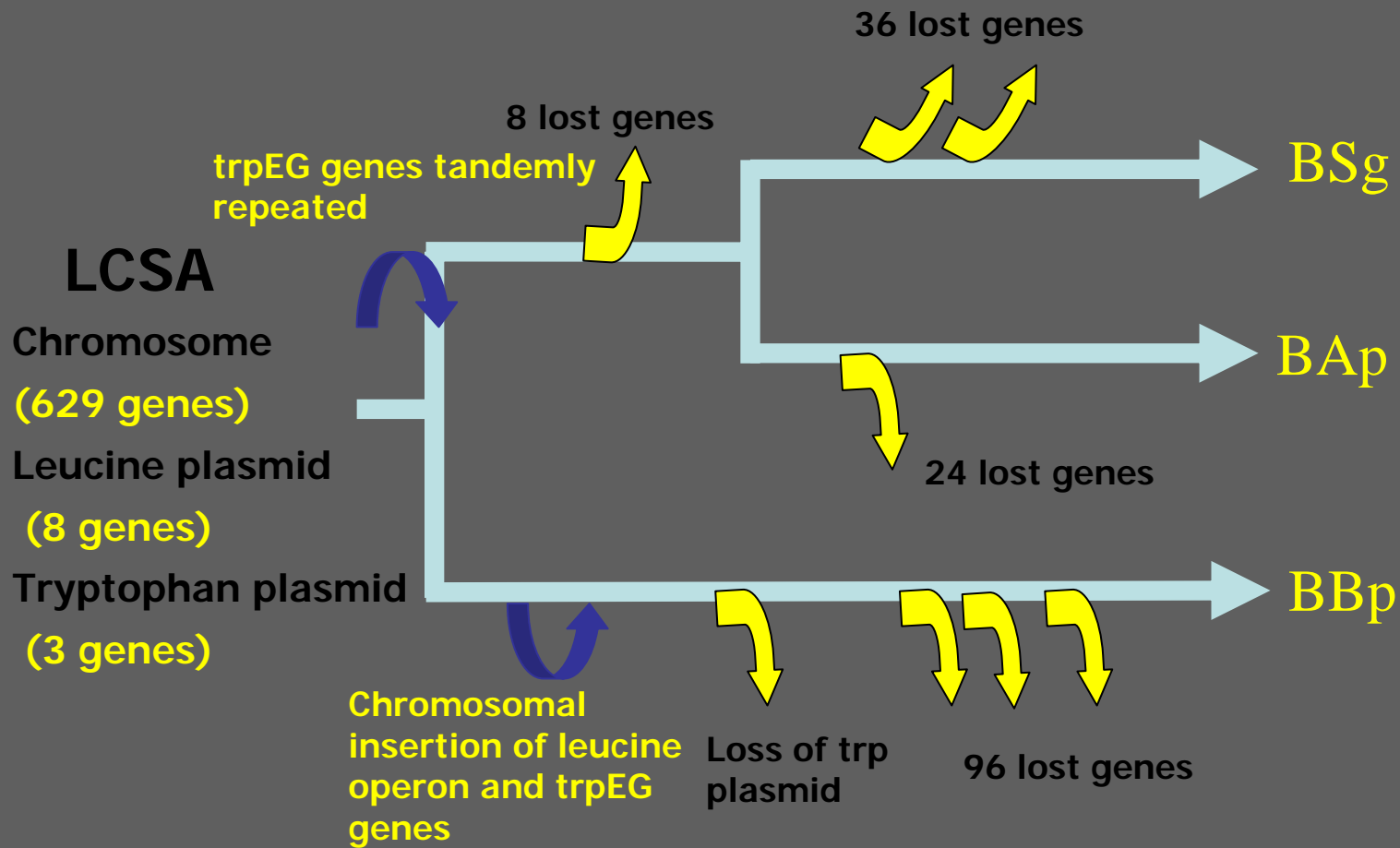
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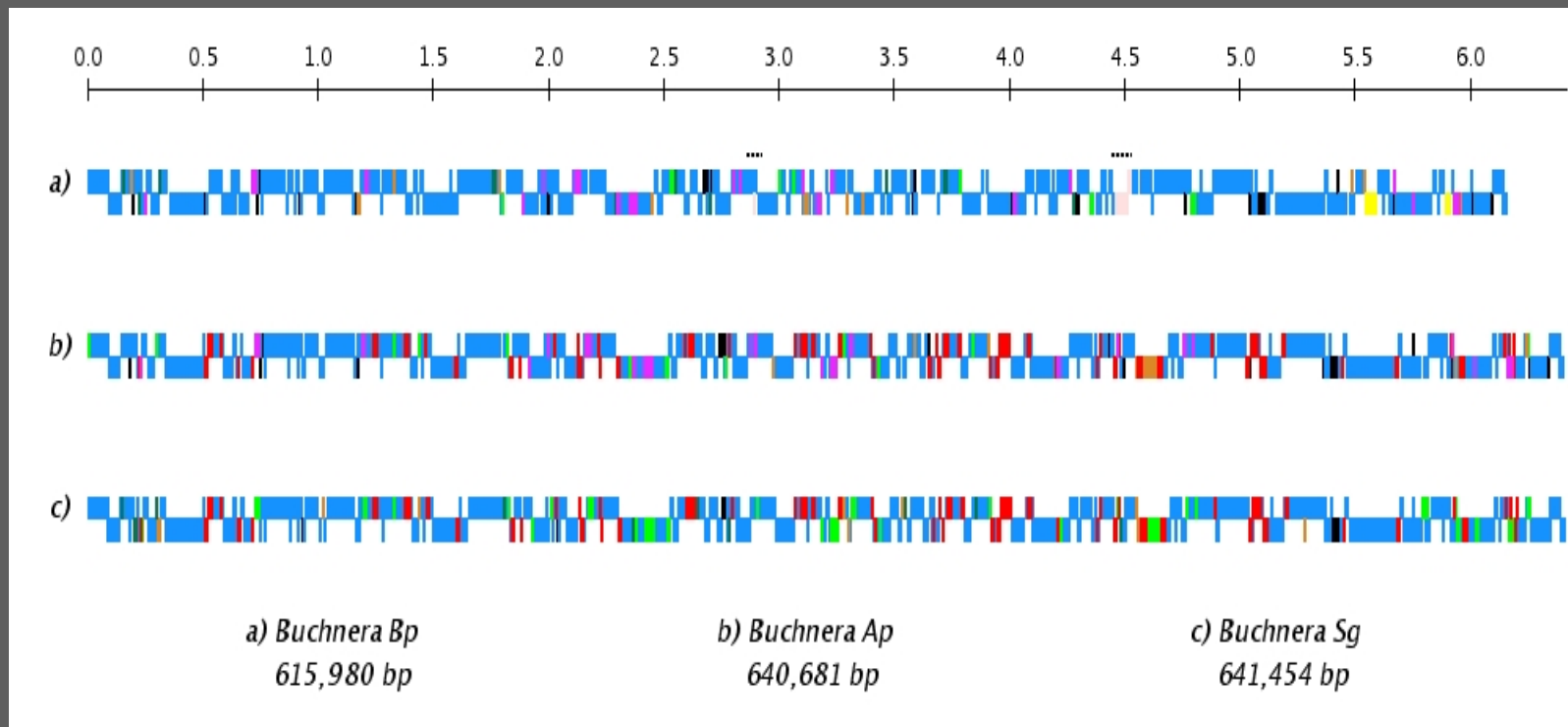
# *B. aphidicola* BPI genome map



# Evolution of *B. aphidicola* genome content

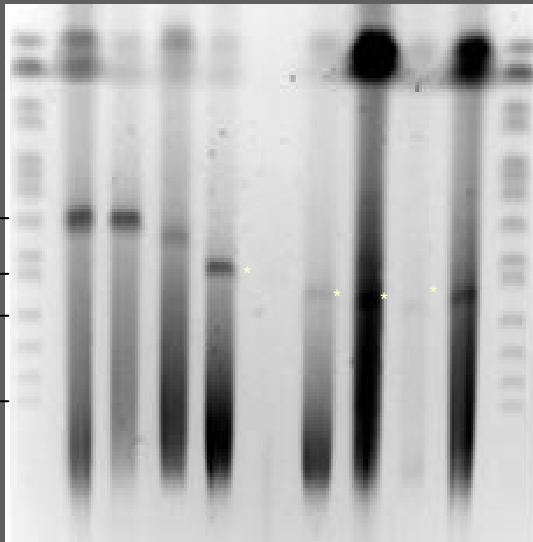


# Genome comparison of the three *B. aphidicola* genome maps



# The genome of *B. aphidicola* from several aphid subfamilies is still undergoing a reductive process

Y 1 2 3 4 5 6 7 8 9 Y



**PFGE**

Aphid Species	Genome Size (Kb)	Aphid Subfamily
1. <i>Acyrtosiphum pisum</i>	670	Aphidinae
2. <i>Macrosiphum rosae</i>	670	Aphidinae
3. <i>Baizongia pistaceae</i>	640	Pemphiginae
4. <i>Tetraneura caerulescens</i>	565	Pemphiginae
5. <i>Thelaxes suberi</i>	550	Thelaxinae
6. <i>Chaitophorus populeti</i>	520	Chaitophorinae
7. <i>Cinari cedri</i>	450	Lachninae
8. <i>Cinara cupressi</i>	475	Lacninae
9. <i>Cinara tujaefilina</i>	475	Lachninae

# *Cinara cedri*



*Buchnera aphidicola*: 416 kb

The smallest described genome

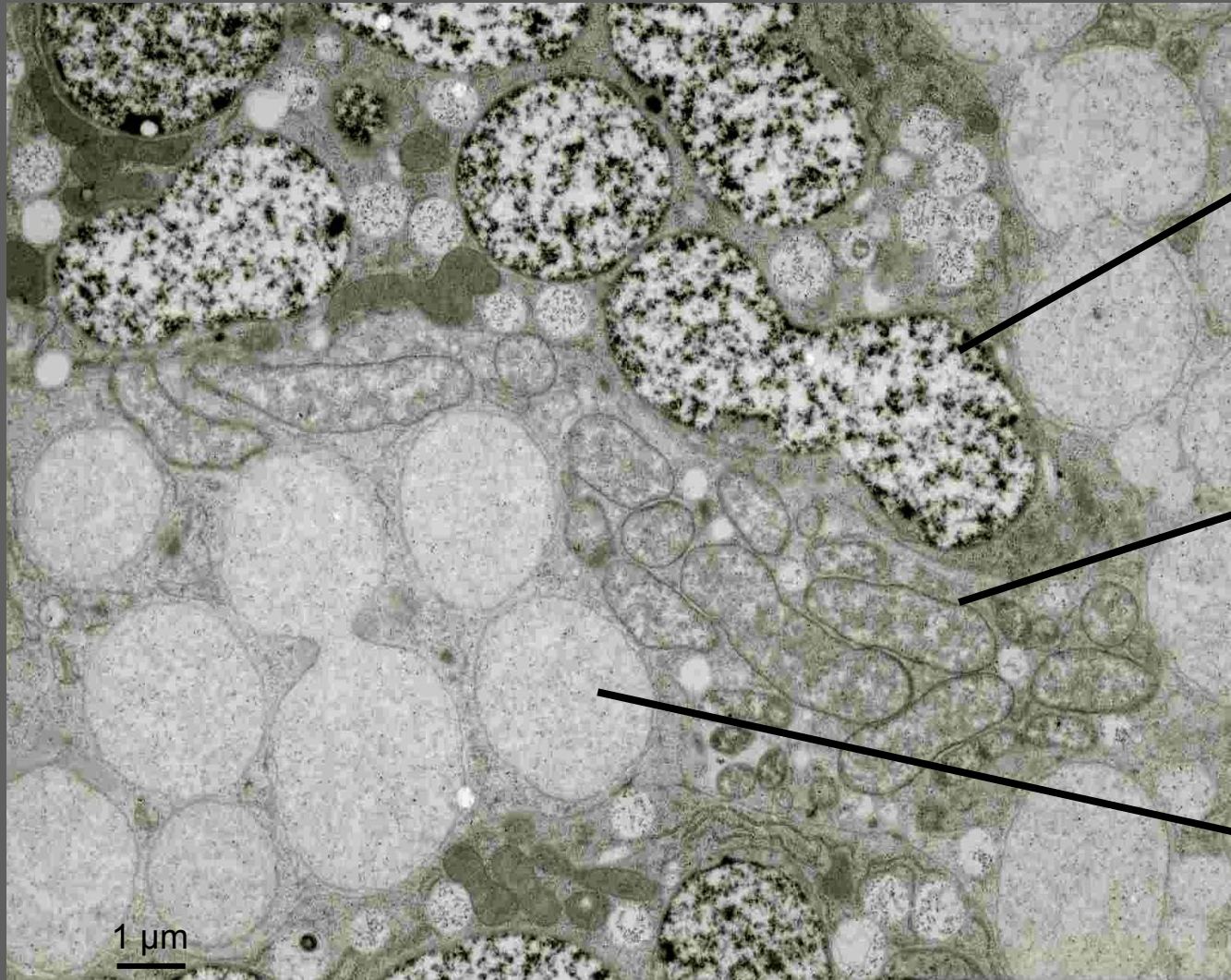
Sequencing: done

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Wed 26 May 15:03:59 2005: Database information  
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Database size	8000
Max reading length	30000
No. Readings	4715
No. Contigs	2
No. Annotations	7282
No. Templates	6377
No. Clones	1
No. Vectors	1
Total contig length	422441
Average length	106497.8
Total characters in readings	1661945.0
Average reading characters per consensus character	3.90
Average used length of reading	351.51
Current maximum consensus length	477689

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# Symbionts of *C. cedri*



*B. aphidicola*

Wolbachia

R-type  
or PASS

# Ongoing genome projects on endosymbiotic bacteria

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# SOPE: Primary endosymbiont of the weevil *Syptophilus oryzae*



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# Flavobacteria from cockroaches



*Blatta orientalis*



*Blatella germanica*



*Periplaneta americana*

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