

Evolution of nutritional endosymbiont in Cinara genus

Rouil Jeff

Encadrants : Jouselin Emmanuelle
and Alejandro Manzano Marin

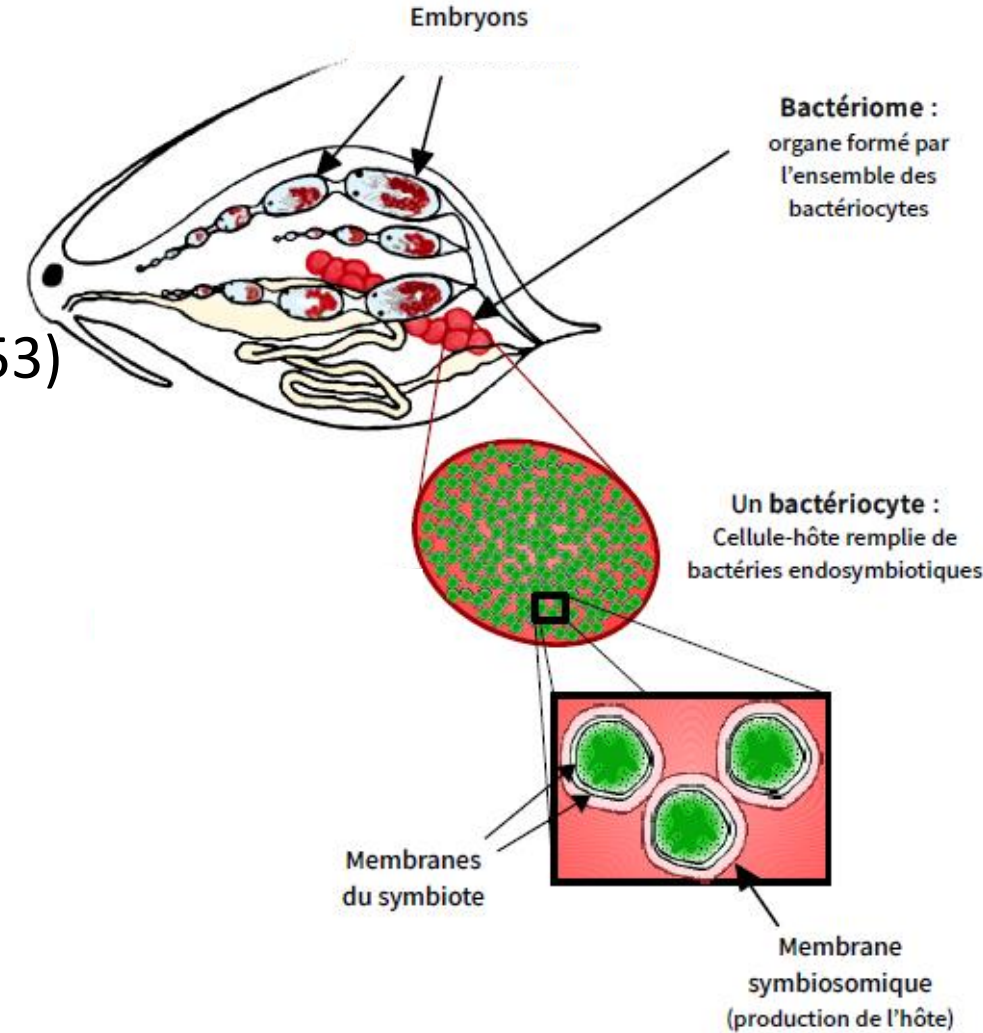
Context : Bacterial endosymbiosis

- Found in almost all insect orders
- Nutrition, protection, others...
- Colonization of new ecological niches
- Diversification of living organisms



Context : Aphids

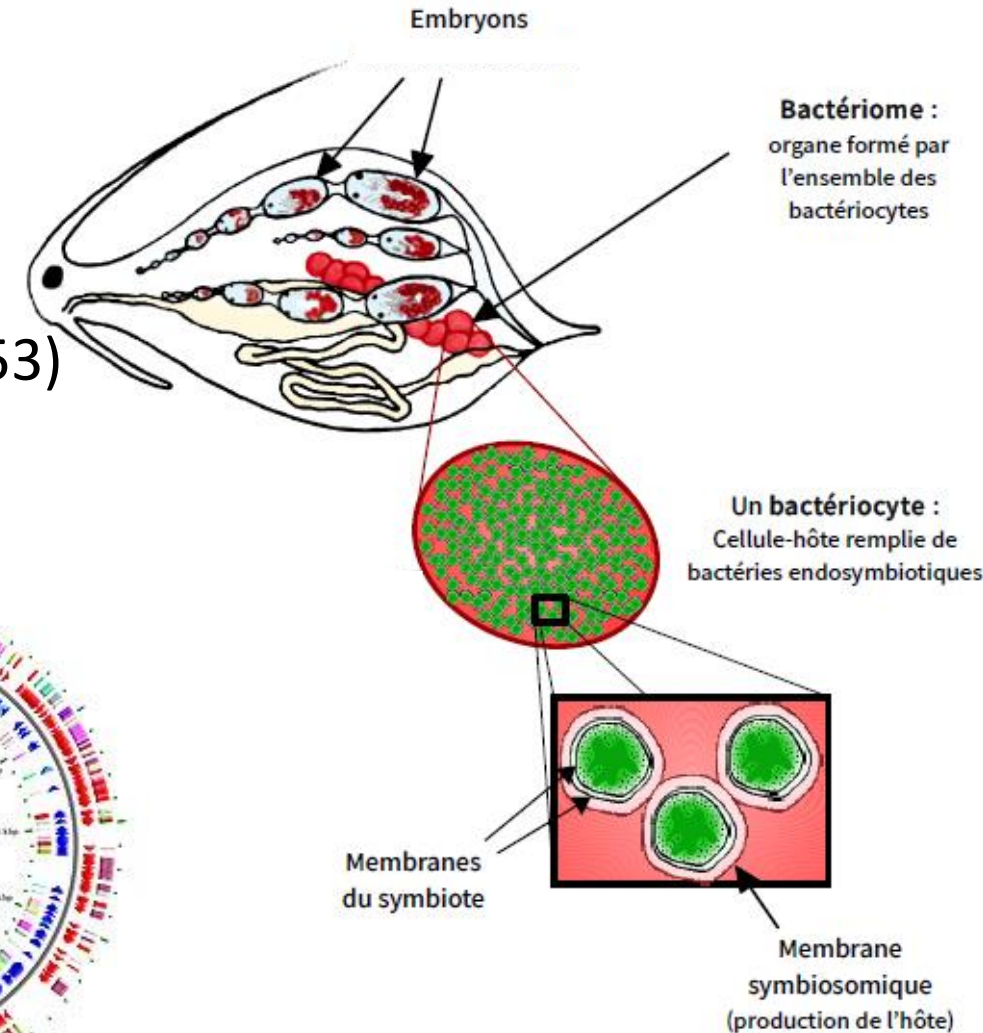
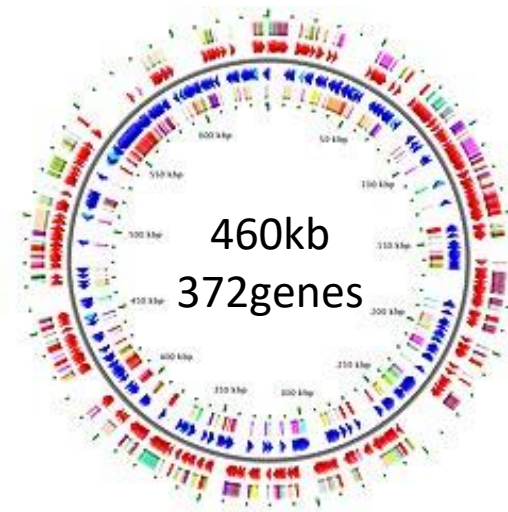
- Feed on phloem
- *Buchnera aphidicola* primary symbiont (Buchner 1953)
- Supplements AA and vitamins (Douglas 1998)



Context : Aphids

- Feed on phloem
- *Buchnera aphidicola* primary symbiont (Buchner 1953)
- Supplements AA and vitamins (Douglas 1998)

- Obligate endosymbiont
- Specific characteristics
 - Genome reduction
 - Loss of gene associated with « free living »
 - Complementary metabolic function to the host

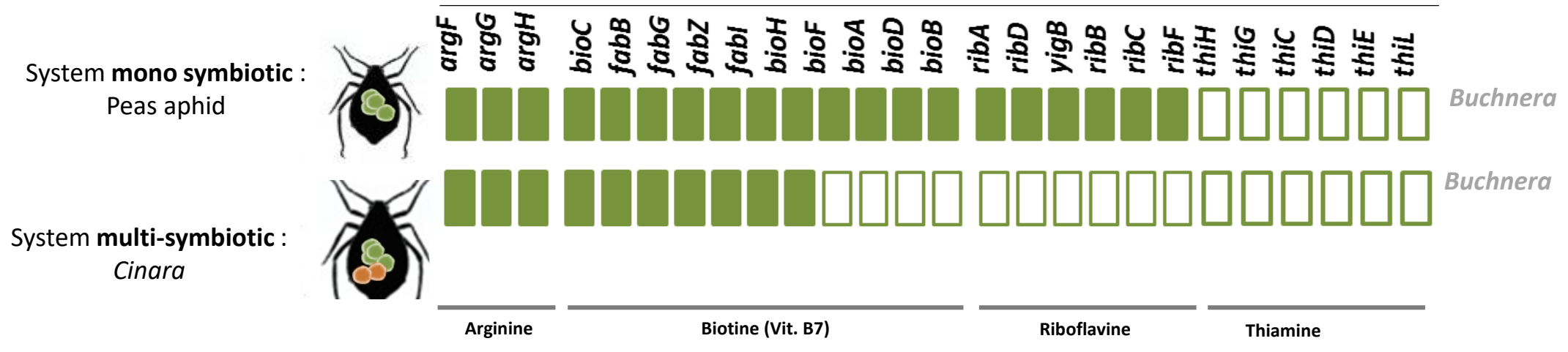


Context : *Cinara* spp



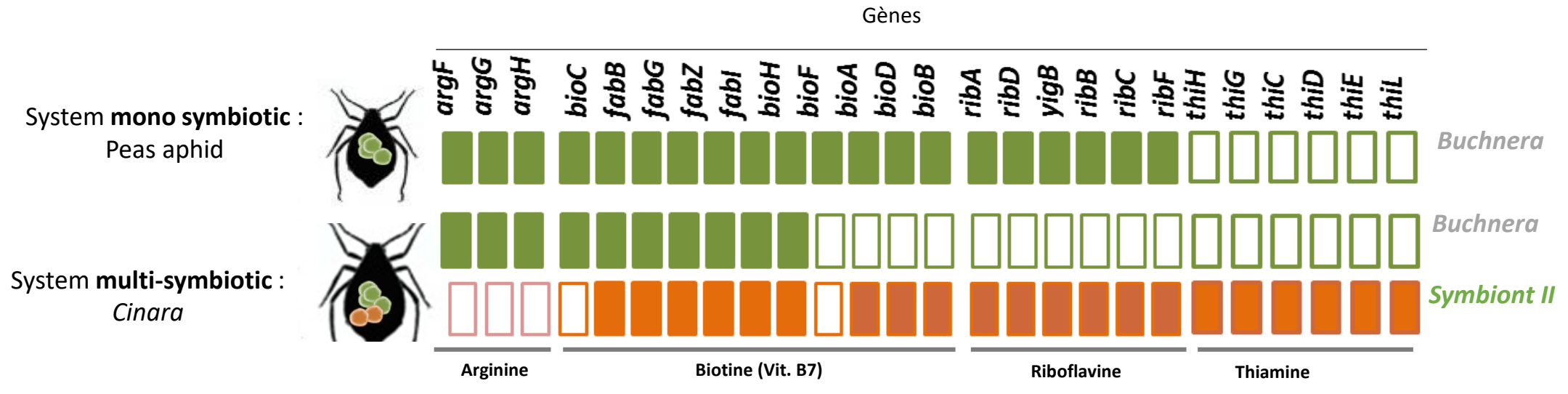
- 248 species feeding on conifers (Meseguer et al 2015,2017)
- 2 obligate symbionts : *Buchnera* and a « co-symbiont »

Gènes



Context : *Cinara* spp

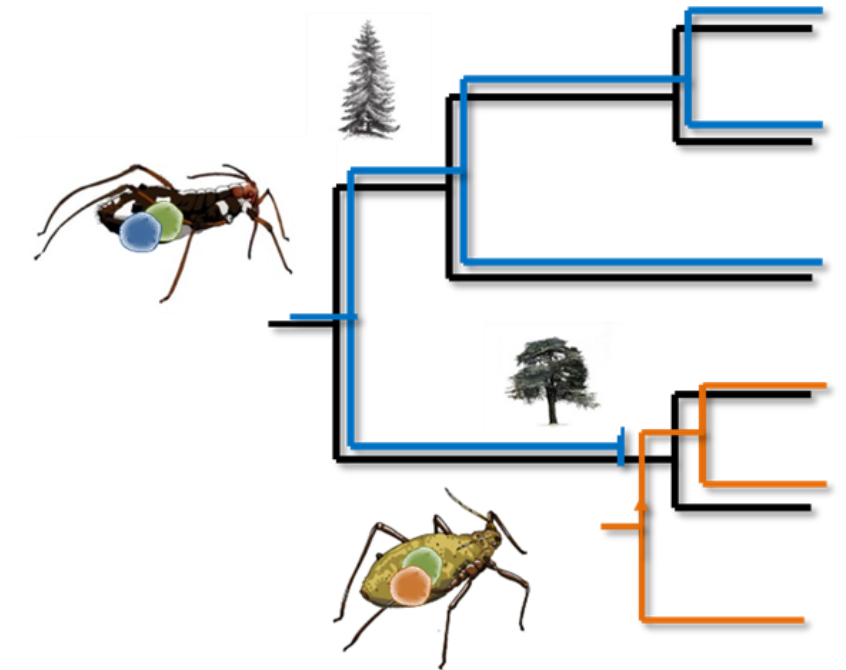
→ 2 obligate symbionts : *Buchnera* and a « co-symbiont »



- Understand the evolution of this obligatory tripartite symbioses :

➔ Reconstruction of the co-evolutionary history of *Cinara* and their symbionts (especially *Serratia symbiotica*)

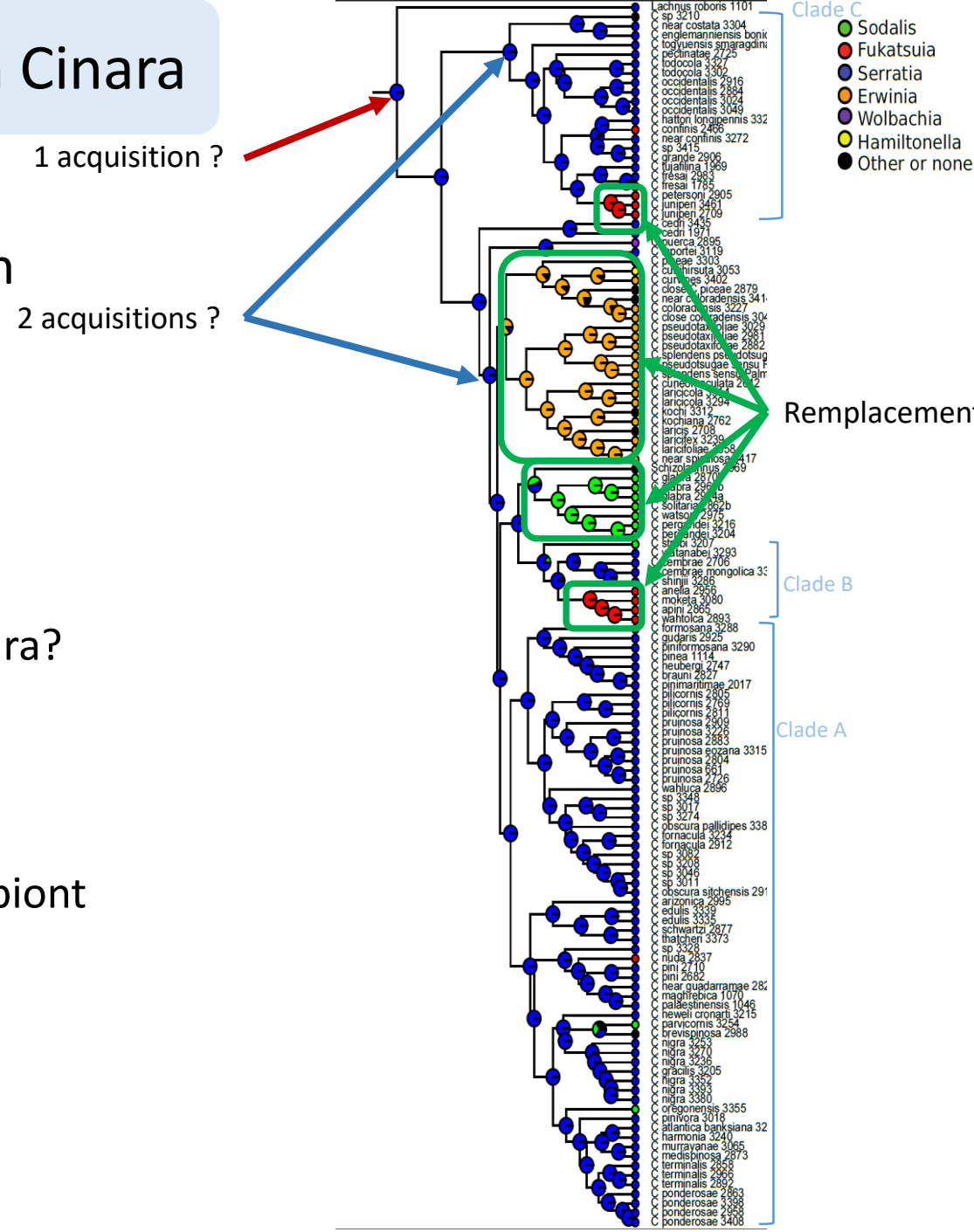
- Co-speciation event
- Symbiont gene content
- Partnership consequence on symbiont genomes



Evolutionary history of secondary symbionts in *Cinara*


Meseguer et al 2017 : symbiont/host association in *Cinara* phylogeny


- ➔ Serratia evolutionary history :
 - ➔ How many Serratia acquisitions/replacements in *Cinara*?
 - ➔ Do these symbionts bring new functions ?
 - ➔ Consequences of tri-partite association on endosymbiont genome evolution ?




Data set



 **Buchnera**
44 genomes

 **Serratia**
31 genomes

 Aphids/host
42 mitogenomes

Search for **orthologous genes**

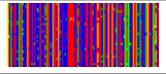
Prodigal + OrthoMCL Mitosweb

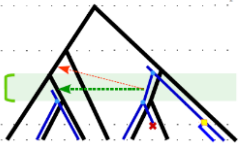
248 CDS

184 CDS

13 genes

Alignments, concatenation and **phylogenetic reconstructions**

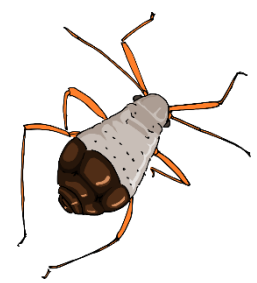
 *Iqtree*
phylobayes *Iqtree*
phylobayes *Partitionfinder*
MrBayes

 Reconciliation analysis
Maximum parsimony : Mowgli

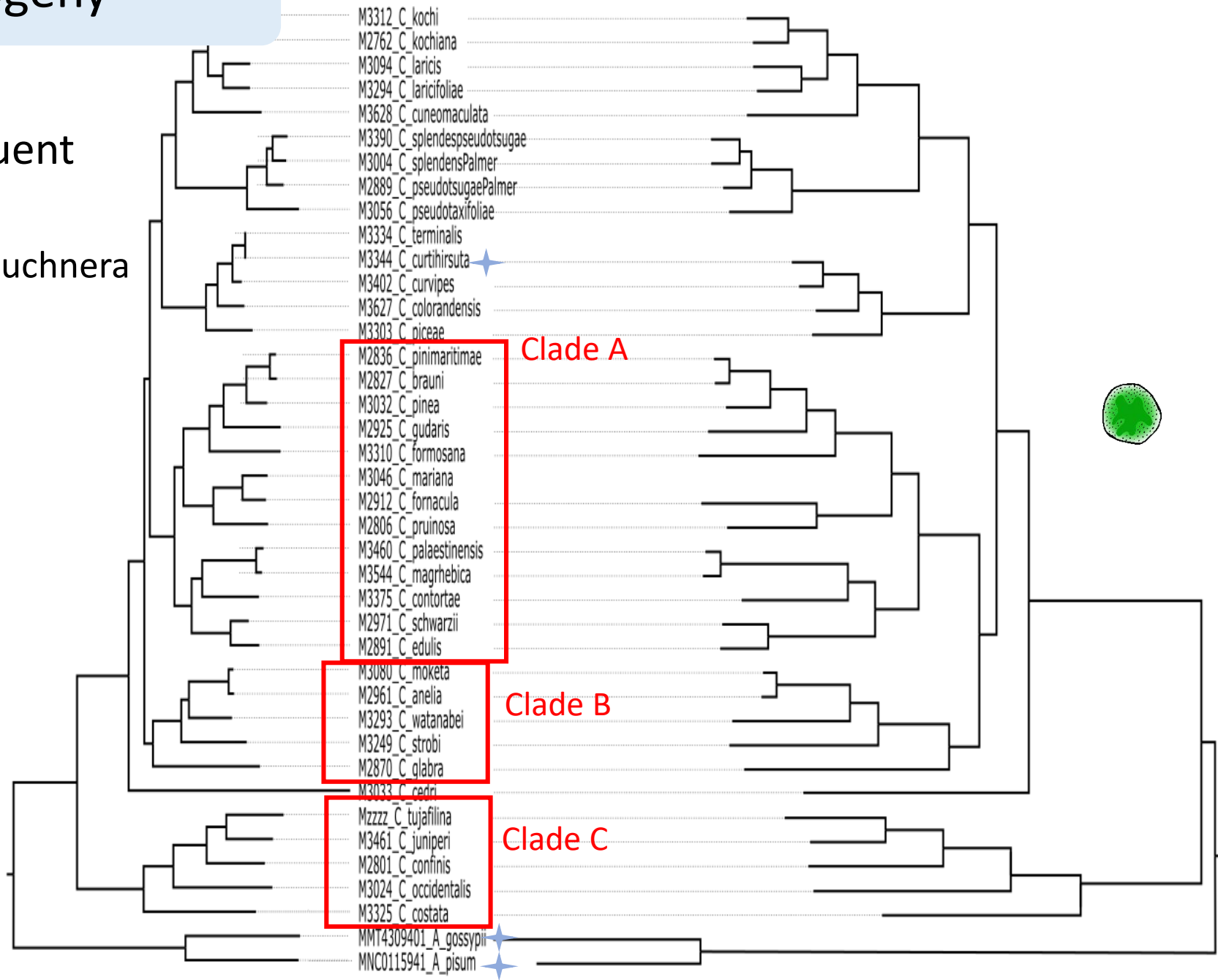
Cinara and Buchnera phylogeny

→ Cinara/Buchnera congruent phylogeny :

Perfect cospeciation between Buchnera and Cinara (*as expected*)

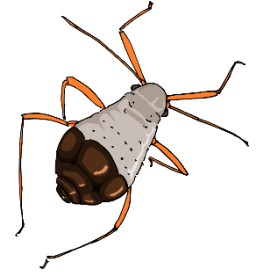


★ facultative serratia

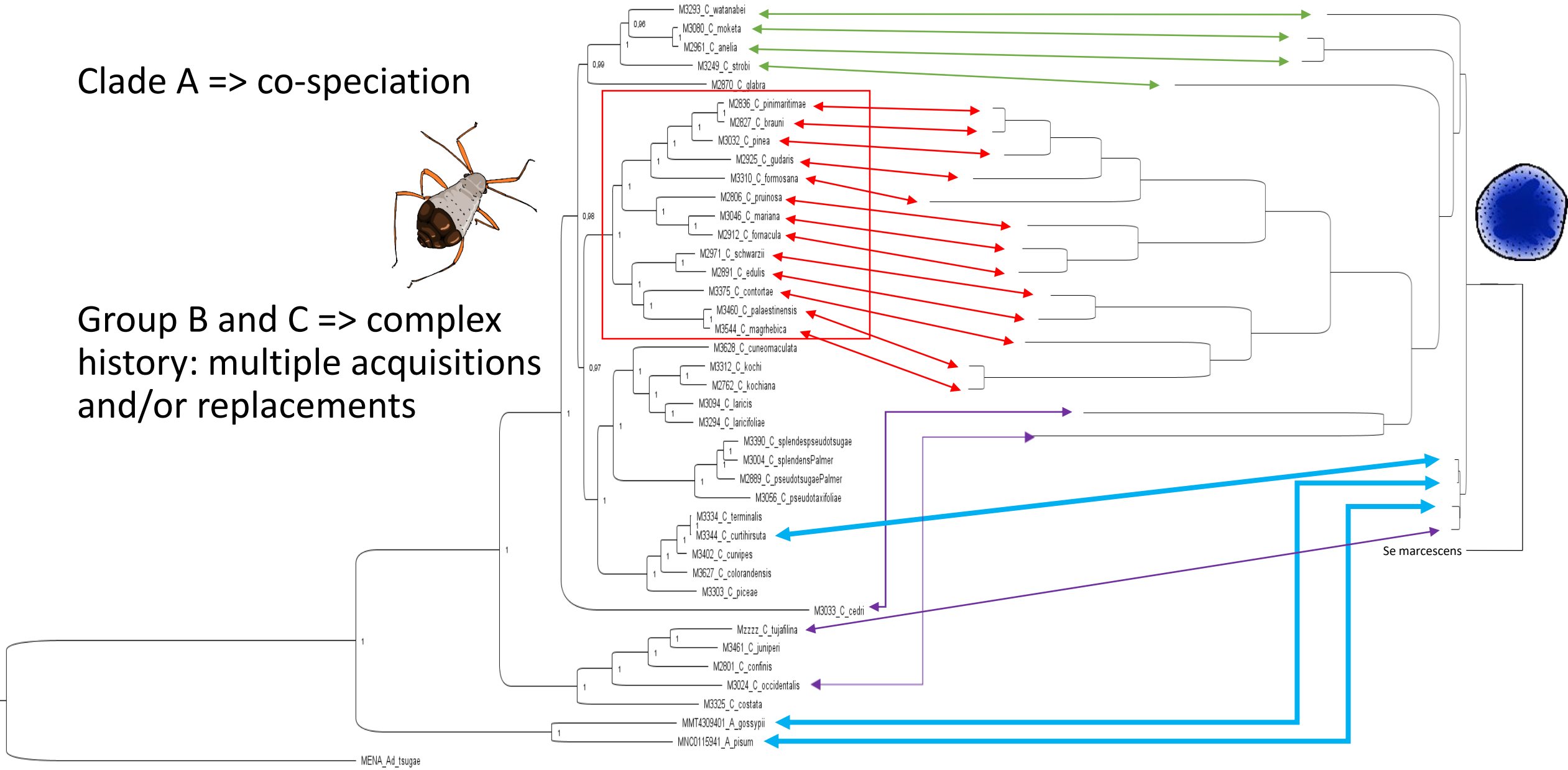


Co-speciation between *Cinara* and *Serratia* ?

Clade A => co-speciation

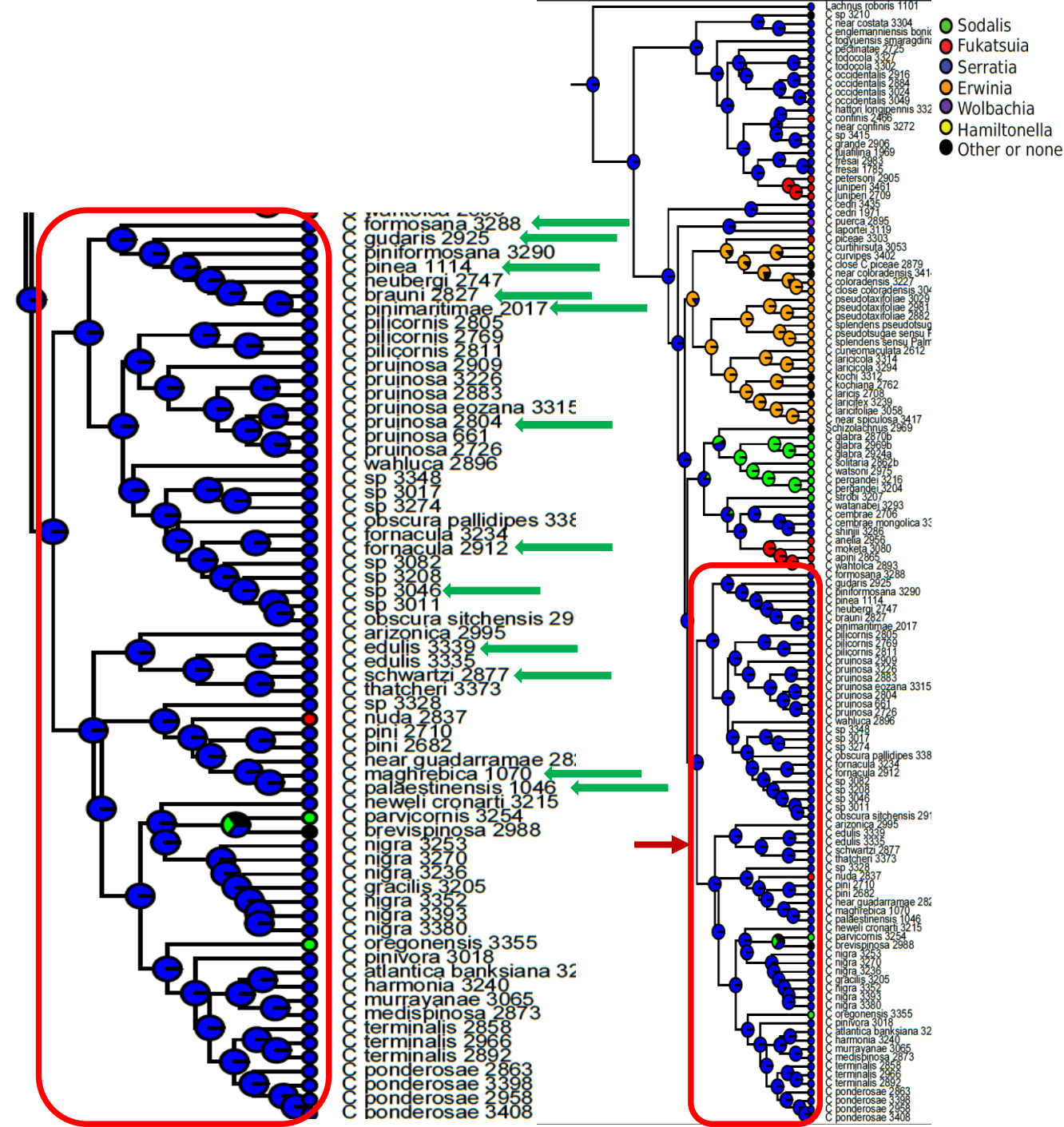


Group B and C => complex history: multiple acquisitions and/or replacements



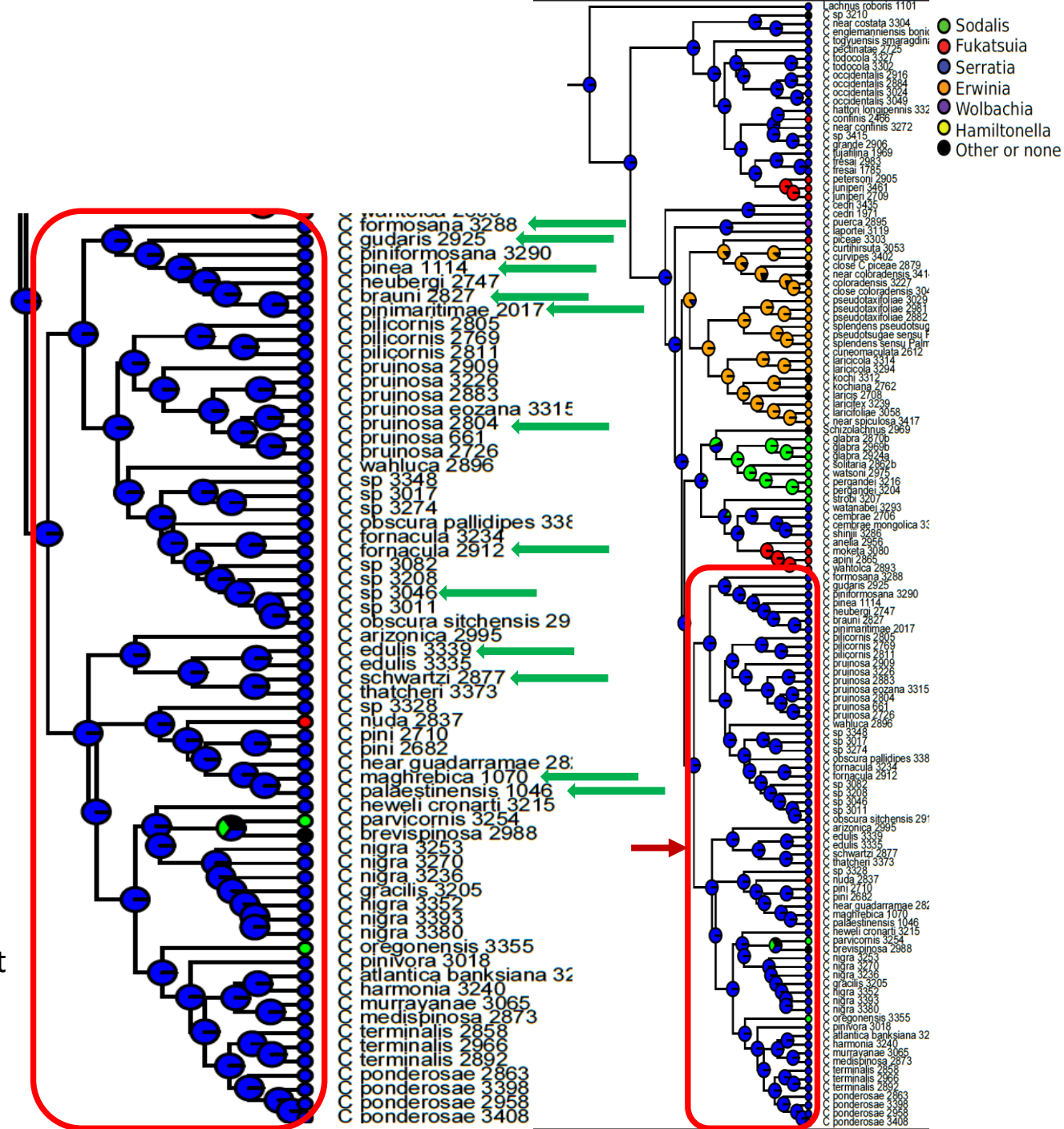
The case of clade A

- ➔ Monophyletic
- ➔ Associated with *Serratia*
- ➔ 13 species whose symbionts were sequenced
- ➔ Cospeciation between *Serratia*/Buchnera/aphids

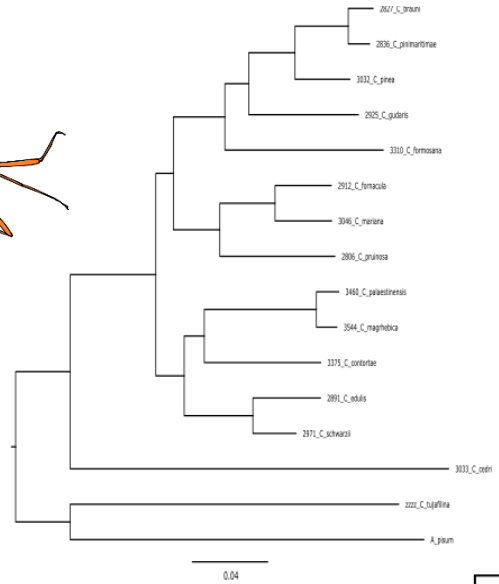
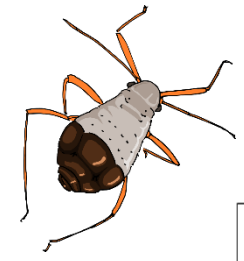


The case of clade A

- ➔ Monophyletic
 - ➔ Associated with Serratia
 - ➔ 13 species whose symbionts were sequenced
 - ➔ Cospeciation between Serratia/Buchnera/aphids
-
- ➔ Does Serratia and Buchnera evolve at the same pace ?
 - ➔ Which consequences has this long-term association on Serratia and Buchnera genome evolution ?
- (loss of genes, genomic characteristic, relaxation on redundant genes...)

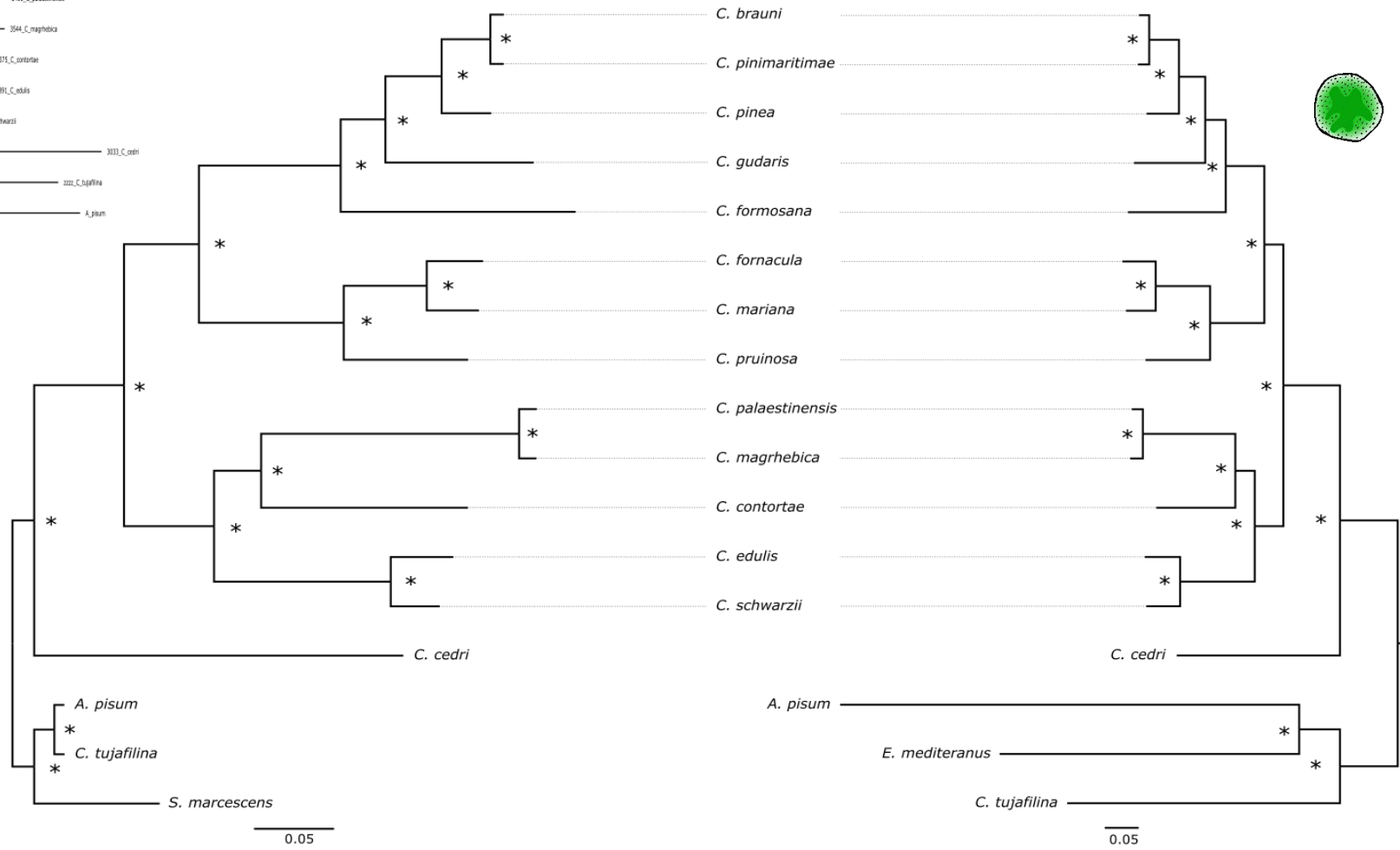
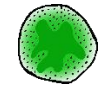


Co-speciation tripartite in Clade A



Serratia

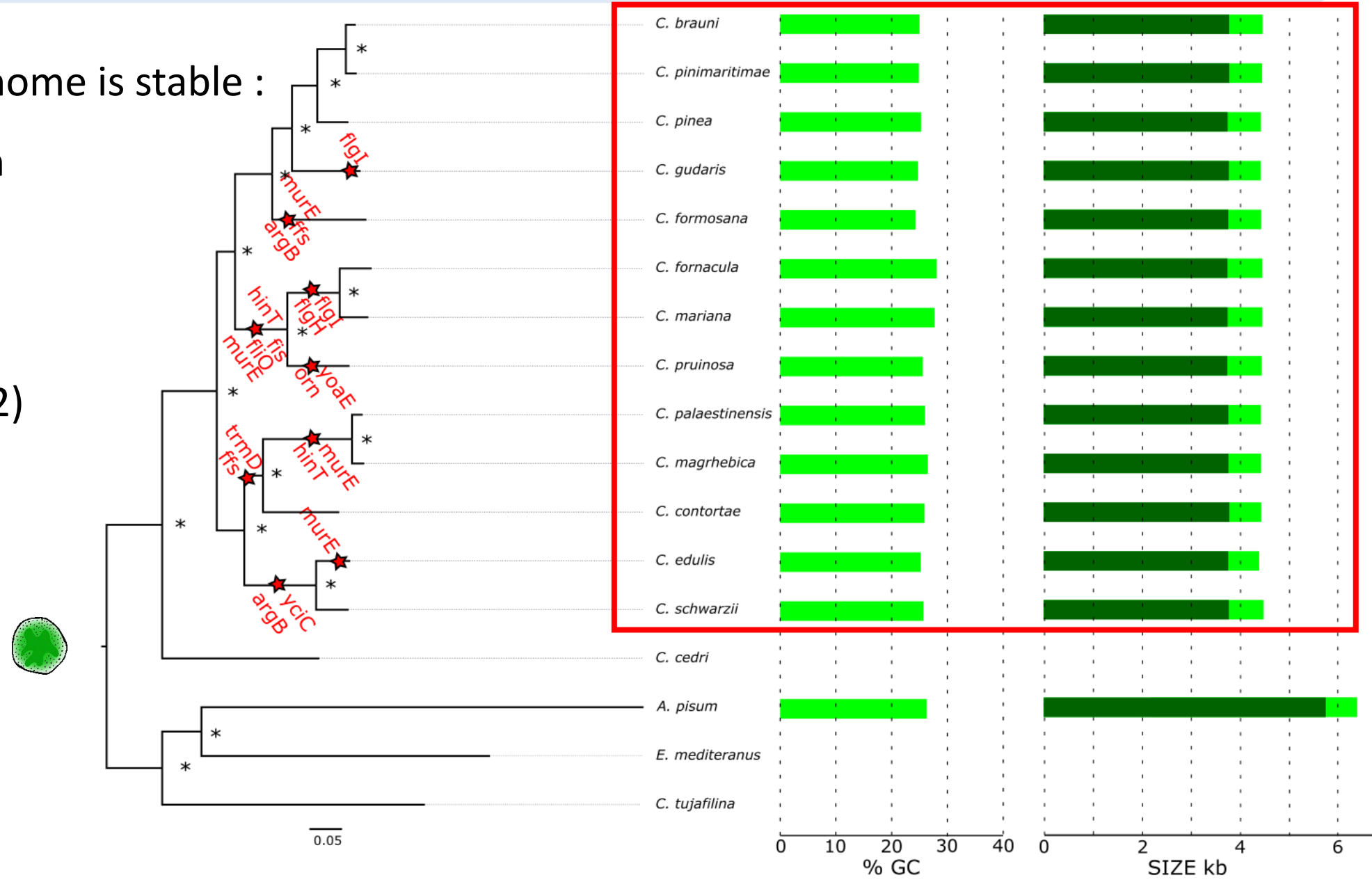
Buchnera



Which consequence does Serratia have on Buchnera genomic characteristic ?

➔ Buchnera Genome is stable :

- Coding proportion
- GC%
- Size
- Gene content (372)



Which consequence does obligate symbiotic life have on *Serratia* genomic characteristic ?

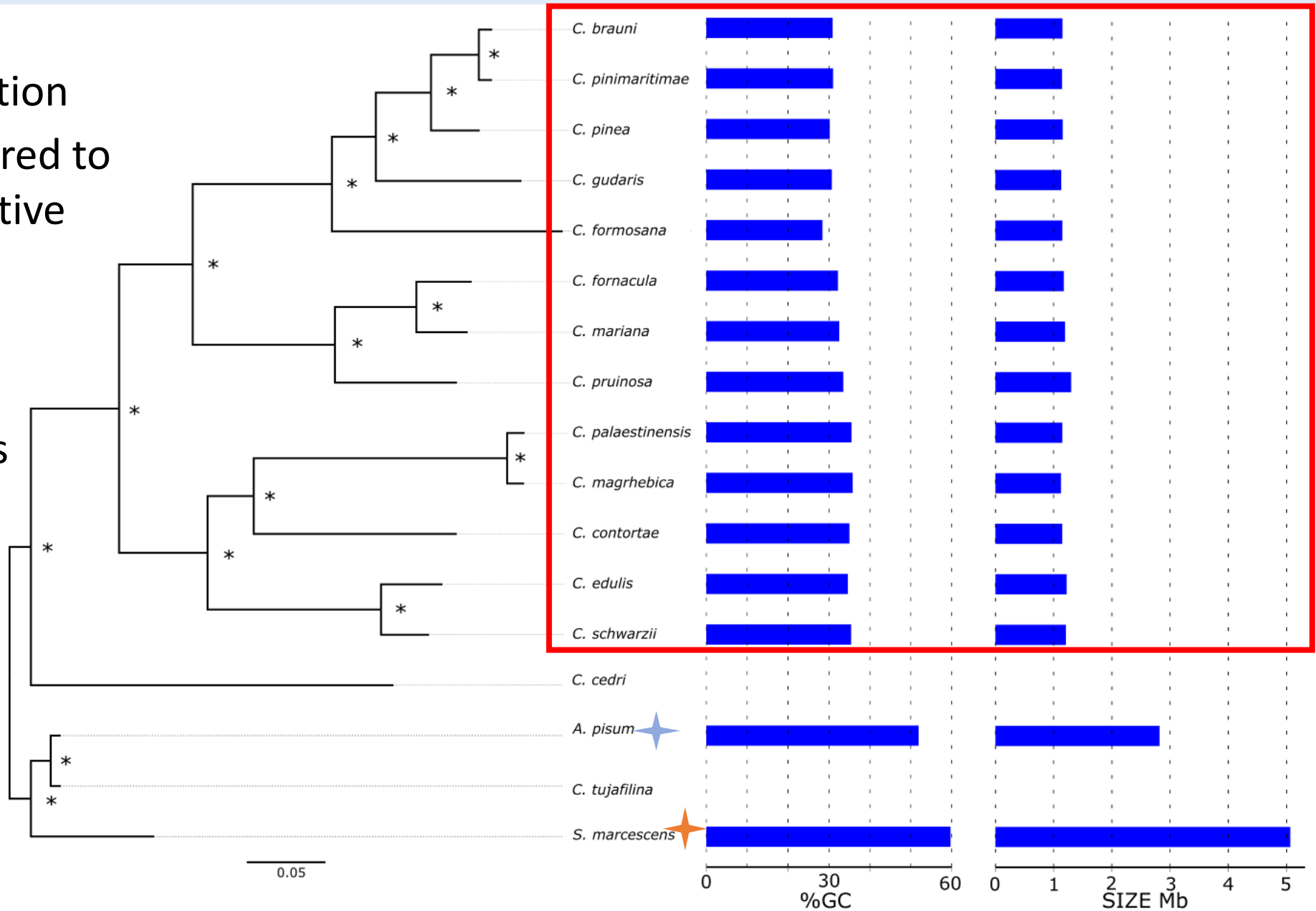
→ Genome degradation

- GC%: very low compared to free living and facultative
- Size: half the size

→ Same characteristic as *Buchnera* genomes

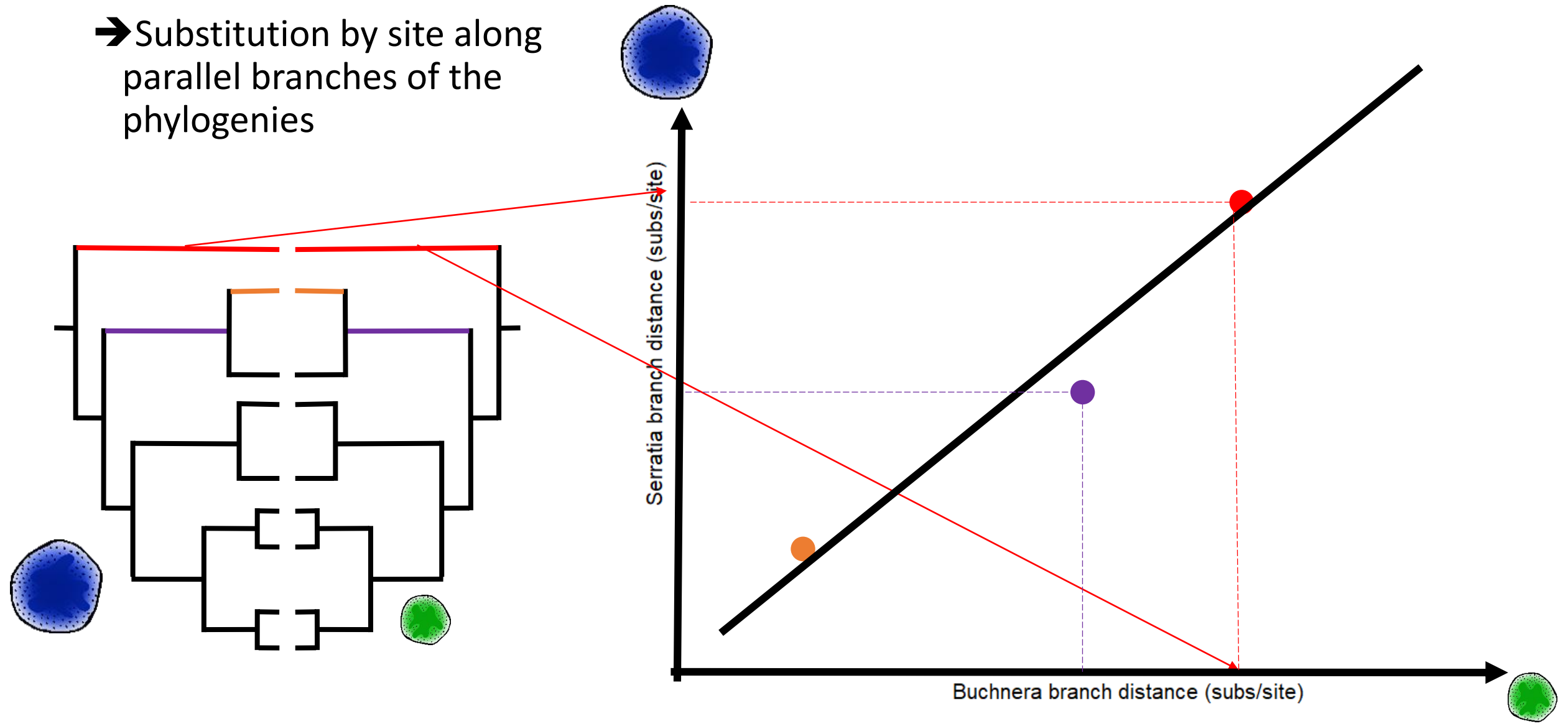


- ★ facultative *serratia*
- ★ Free living *serratia*



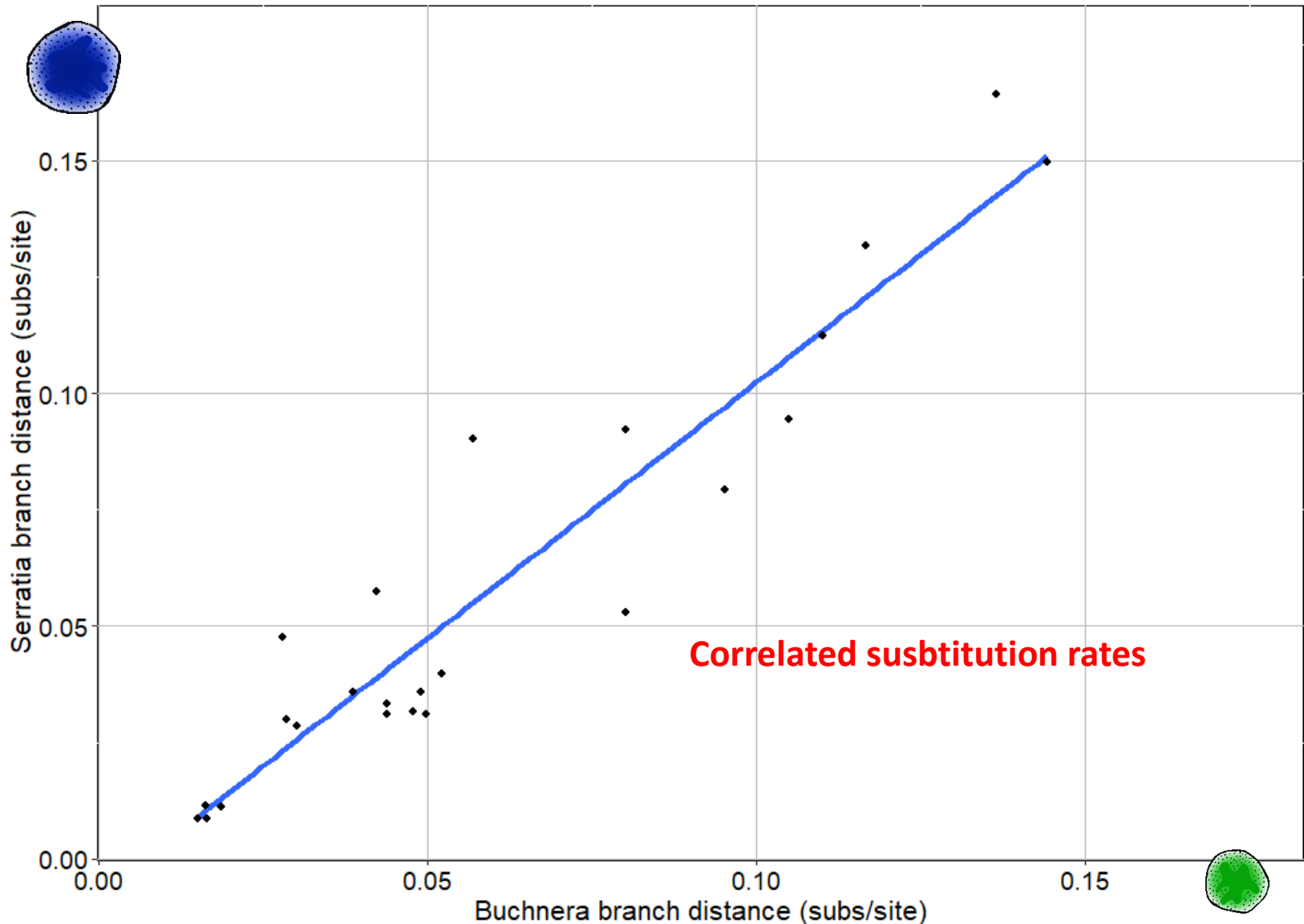
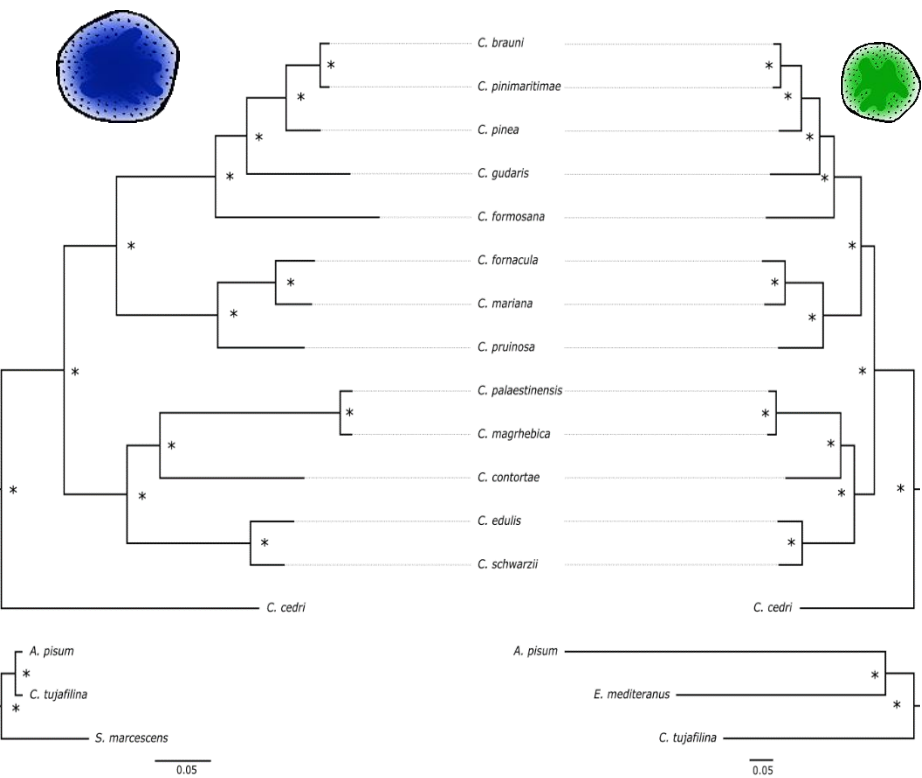
Do Serratia and Buchnera evolve at the same pace ?

→ Substitution by site along parallel branches of the phylogenies



Do Serratia and Buchnera evolve at the same pace ?

➔ Substitutions by site along parallel branches of the phylogenies

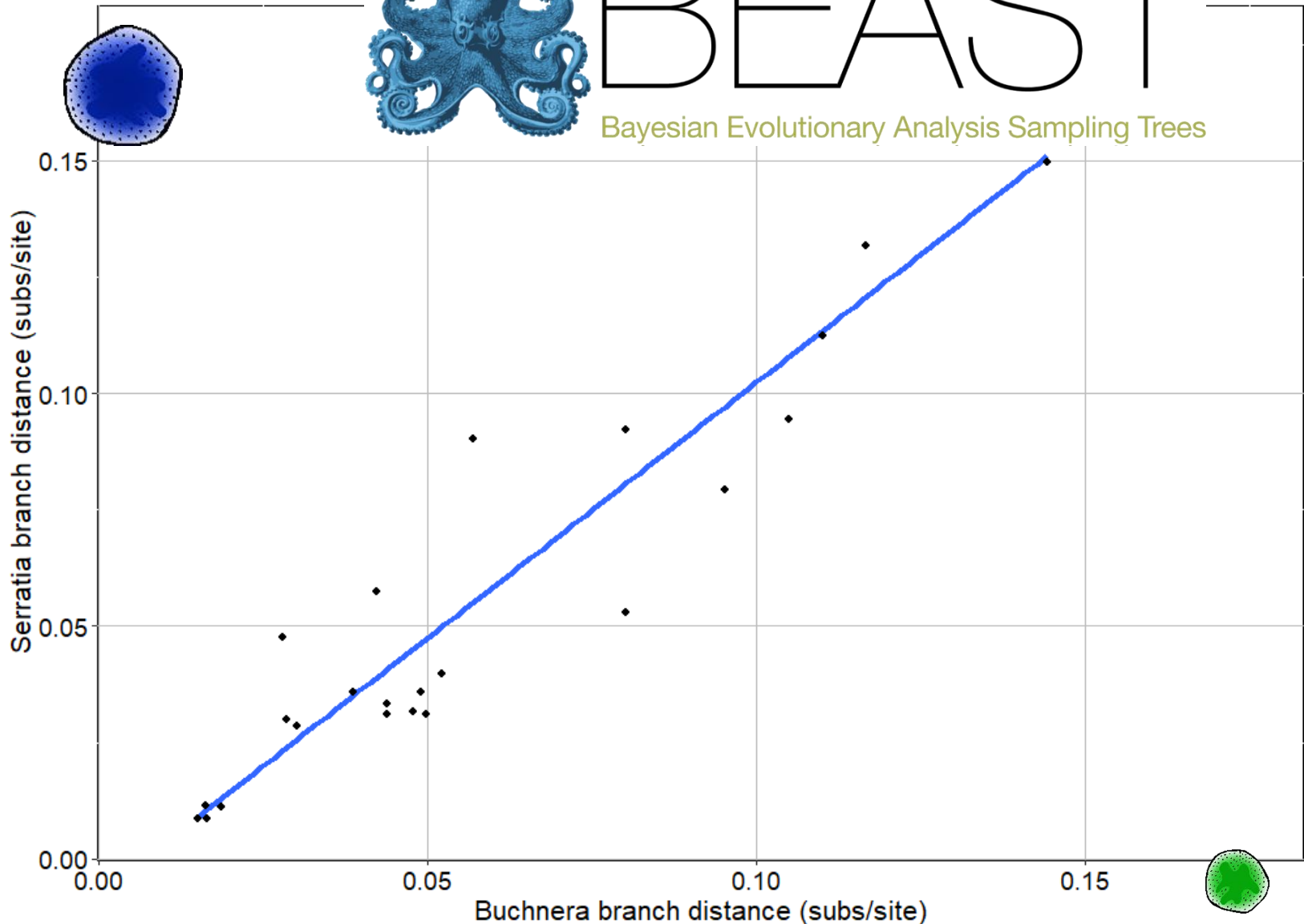
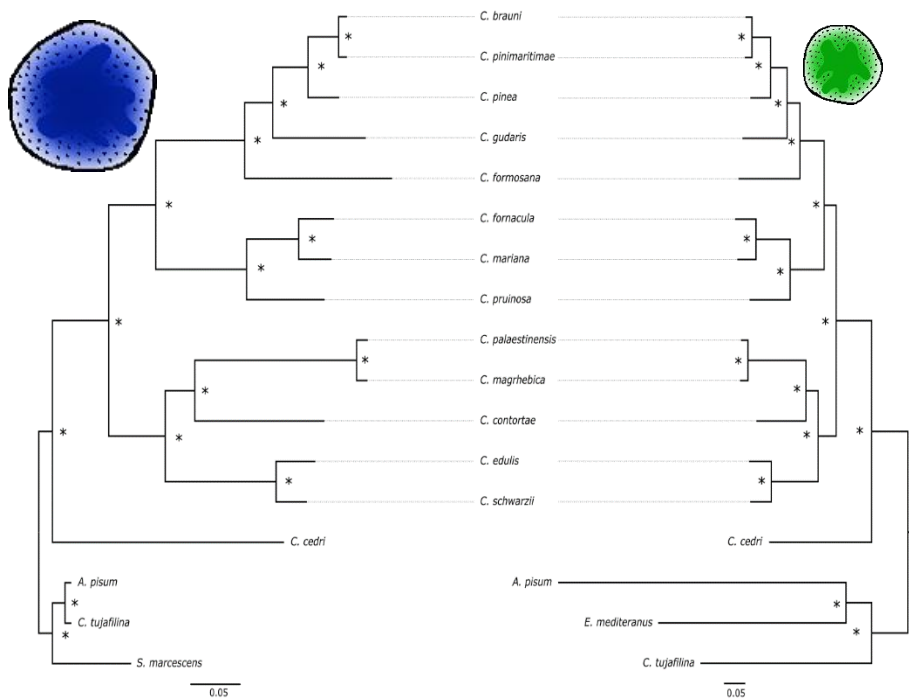


Do Serratia and Buchnera evolve at the same pace ?



BEAST

Bayesian Evolutionary Analysis Sampling Trees



Does the presence of *Serratia* change selective pressures on *Buchnera* genome ?



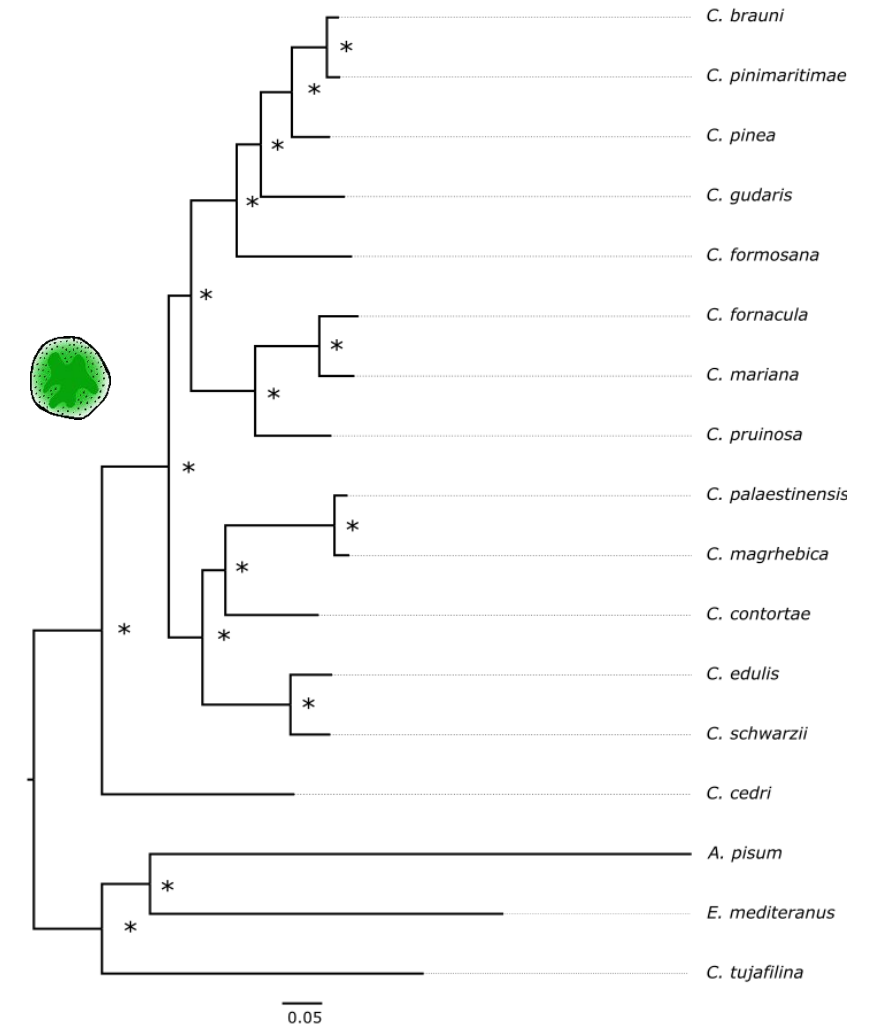
We could expect redundant genes to be under relaxed selective pressures

→ Selection test with Busted

- Gene under positive selection :

→ *Buchnera* : 0/218 genes tested

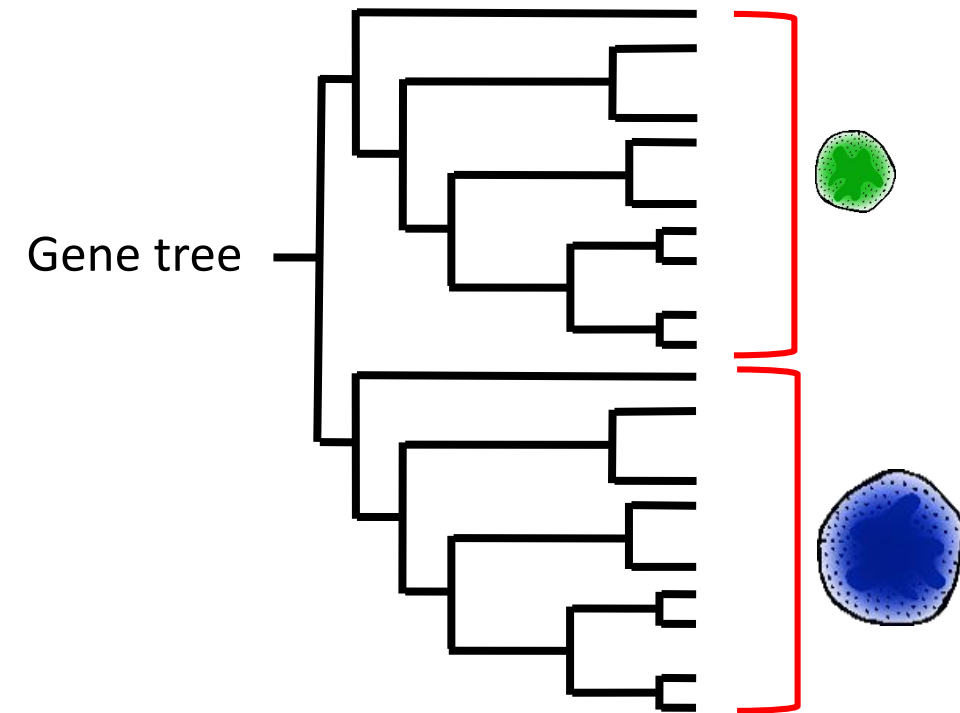
→ *Serratia* : in progress



Does the presence of *Serratia* change selective pressures on *Buchnera* genome ?

→ Relaxed Selection test (with relax)

→ shared genes between *Serratia* and *Buchnera*

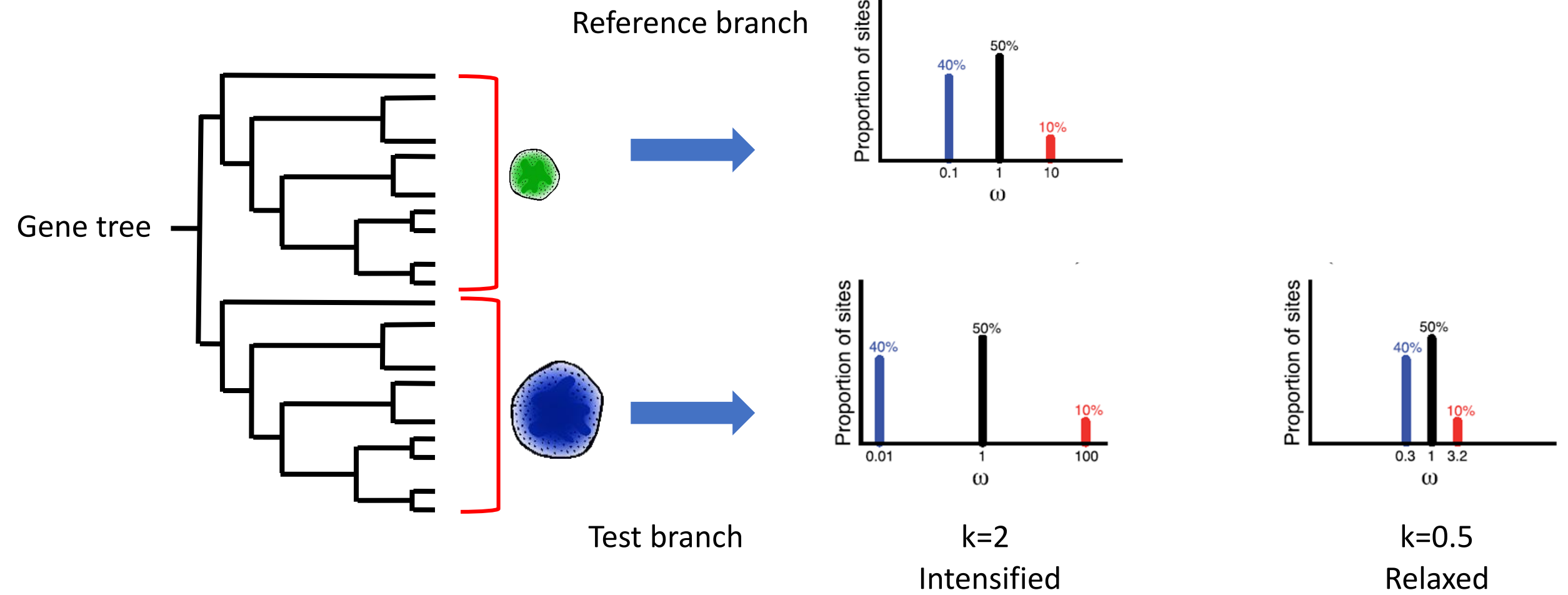


Does the presence of *Serratia* change selective pressures on *Buchnera* genome ?

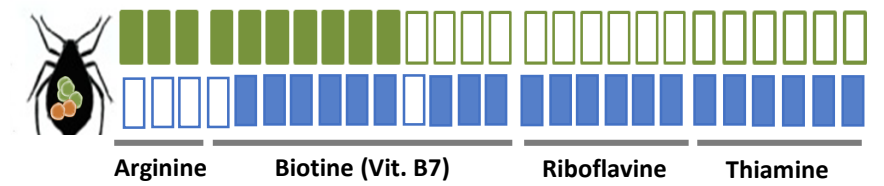
RELAX: Detecting Relaxed Selection in a Phylogenetic Framework

Joel O. Wertheim,^{*1} Ben Murrell,¹ Martin D. Smith,² Sergei L. Kosakovsky Pond,¹ and Konrad Scheffler^{*1,3}

→ Relaxed Selection test with relax

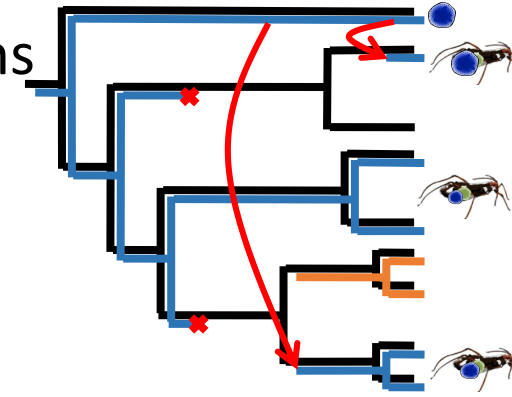


Conclusion



→ Unstable relationship with cosymbiont: multiple acquisitions of *Serratia* throughout *Cinara*'s phylogeny

→ But co-speciation in one Clade



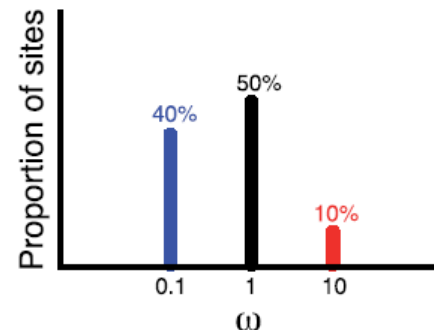
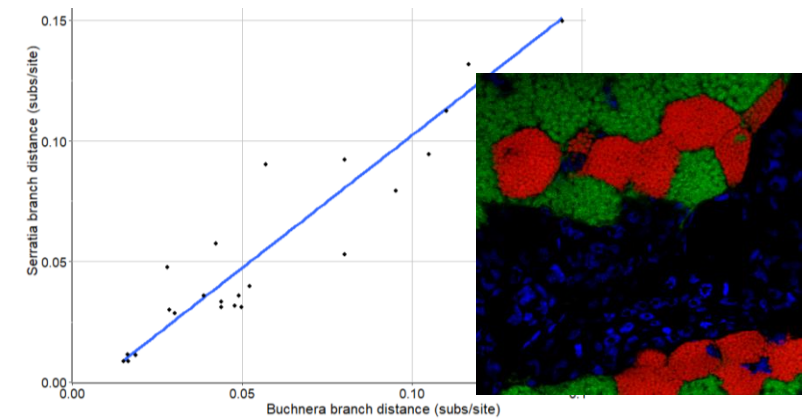
Consequences of coevolution between co-symbionts

→ Genome reduction and losses of genes for both symbionts

→ Symbiont genomes evolve at the same pace (same demographic event?..)

→ Gene selection...

→ Relaxed selection on redondant genes ?



Thank you



Alejandro Manzano-
Marin



Valerie Barbe
Céline Orvain
Corinne Cruaud



dome
— DIVISION OF —
MICROBIAL ECOLOGY

INRAE