

Use of low-coverage whole genomes (LC-WG) to improve the phylogenetic backbone of Bruchinae

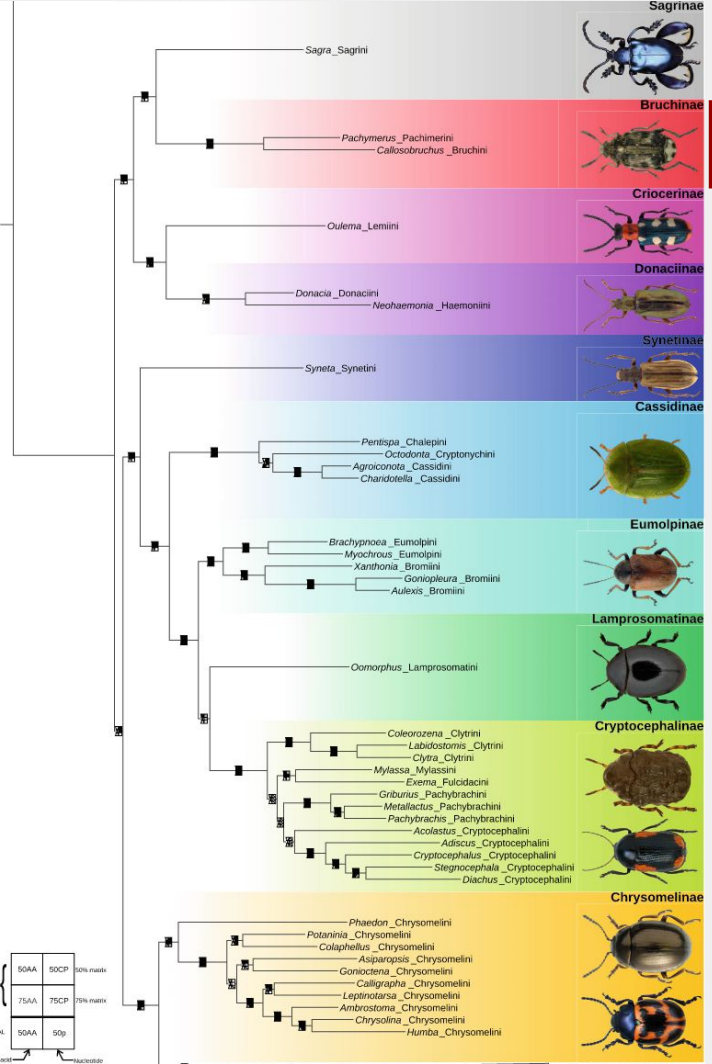
Master 2 internship

supervised by **Gaël Kergoat** and **Anne-Laure Clamens**

Roland GODON



Chrysomelidae



Sagrinae

Bruchinae

Bruchinae

Criocerinae



Donaciinae



Synetinae



Cassidinae



Eumolpinae



Lamprosomatinae



Cryptocephalinae



Chrysomelinae



[See Galerucinae Figure 3]

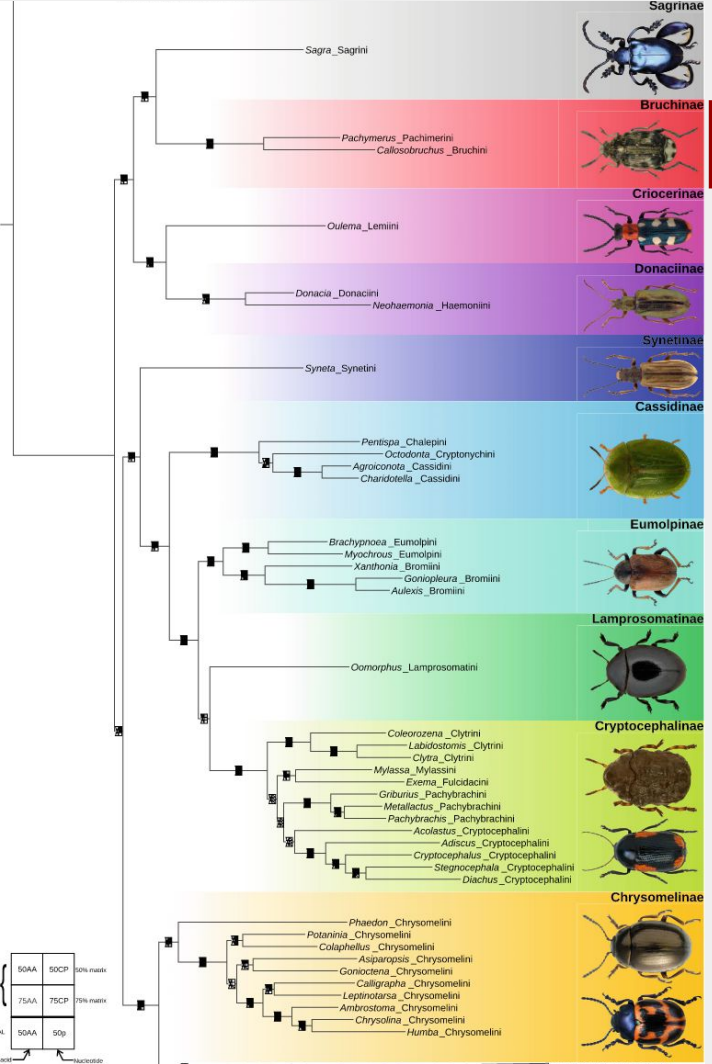
Chrysomelidae

Sagrinae

Bruchinae

Bruchinae : seed beetles

Sagrinae : frog-legged beetles



[See Galerucinae Figure 3]

Study focused on 3 groups:

radiation in Palearctic + Bruchini + Fabaceae



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(1) *Bruchus*



Bruchus affinis

Fabeae



Study focused on 3 groups:

radiation in Palearctic + Bruchini + Fabaceae

(1) *Bruchus*



Bruchus affinis

(2) Cisti groupe (*Bruchidius*)



Bruchidius biguttatus



Fabeae



IRLC



Loteae



Cistaceae

Study focused on 3 groups:

radiation in Palearctic + Bruchini + Fabaceae

(1) **Bruchus**



Bruchus affinis

Fabeae

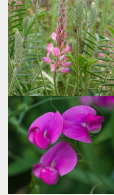


(2) **Cisti groupe (*Bruchidius*)**



Bruchidius biguttatus

IRLC



Loteae



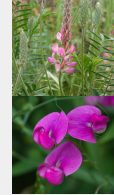
Cistaceae

(3) ***Bruchidius* groupe**



Bruchidius seminarius

IRLC



Loteae



Genisteae



Geranium



Eryngium

Questions and hypotheses:

Classic questions:

Is the appearance of these groups synchronous with the appearance of their hosts?

dated phylogeny



Questions and hypotheses:

Classic questions:

Is the appearance of these groups synchronous with the appearance of their hosts?



Specific questions:

Interaction between groups ? What is the impact on host register evolution?

2 datasets:

Dataset “sanger”:

Séquences : 4 mitogène: 16S, 12S, CytB, CO1

6 Nuclear gene: 28S(3), H3, EF1A

Spécimens: 222

Espèces: \approx 80



2 datasets:

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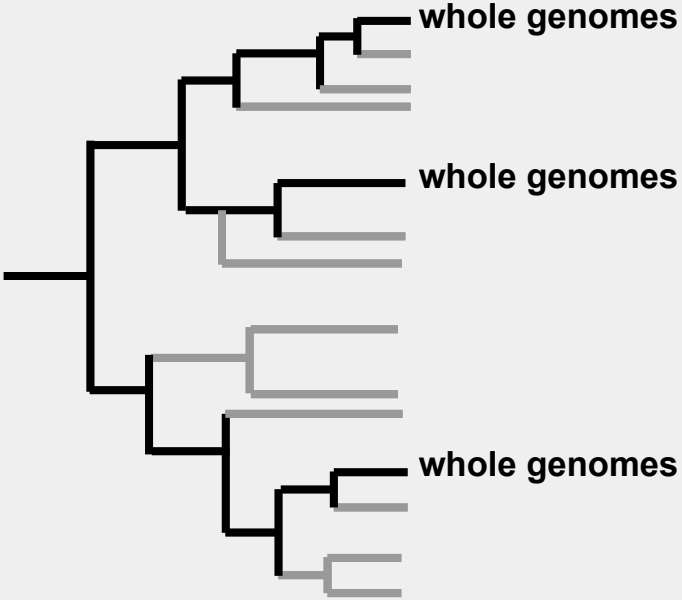
Spécimens: 222
Espèces: ≈ 80



Dataset “illumina”: whole genomes (LC-WG)

Séquences : mitogénome 16 genes
X Nuclear gene

Spécimens: 50
Espèces: ≈ 50



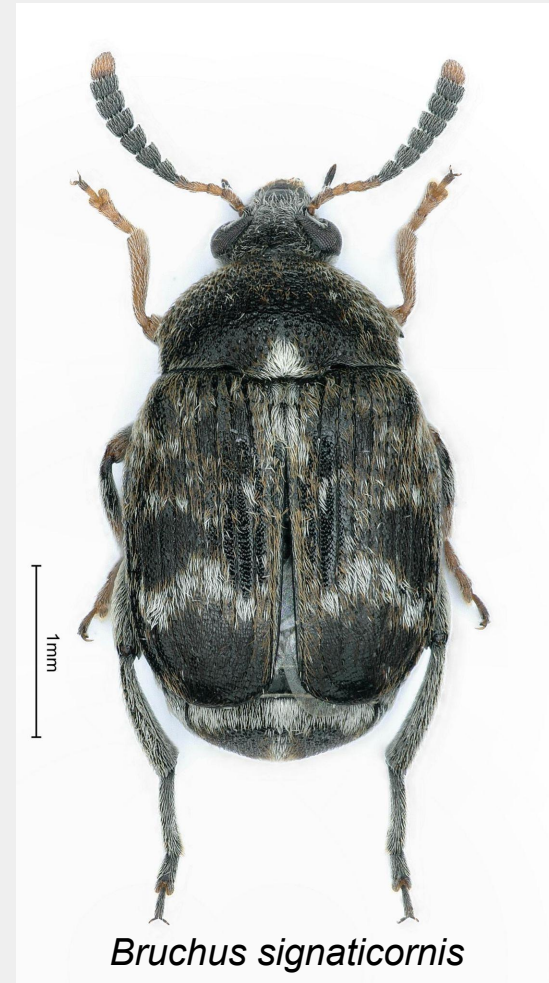
How can we recover the best possible phylogenetic information from low-coverage WG sequences?

Difficult extraction:

Non-destructive

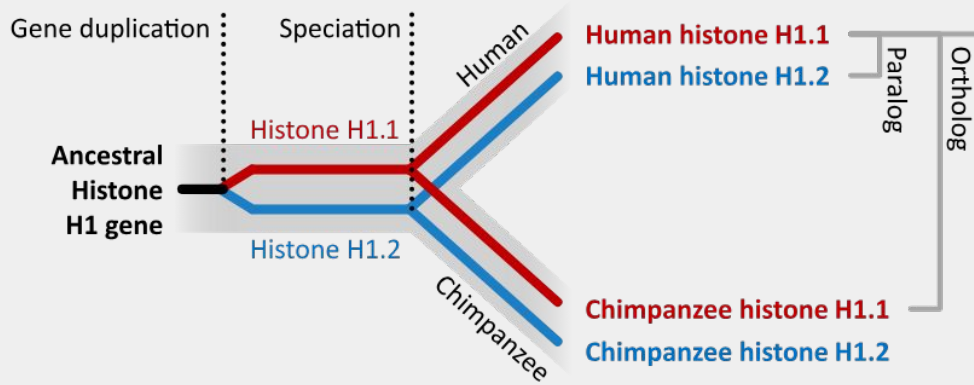
Old specimens,

Small insects



How can we recover the best possible phylogenetic information from low-coverage WG sequences?

which genes to choose?



How to identify the **orthologs**? → orthologs database



Petit ver de farine
(*Tribolium castaneum*)



Scolyte du pin ponderosa
(*Dendroctonus ponderosae*)

Search for better references:



Bruche du haricot
(*Acanthoscelides obtectus*)



Bruche du niébé
(*Callosobruchus maculatus*)



Orthologous genes?



Bruche du haricot azuki
(*Callosobruchus chinensis*)



Bruche du lablab
(*Callosobruchus analis*)



1

1

1

1

2

2

2

2

3

3

3

3

4

4

4

4

genes



genes



Pairwised orthologs





genes



Pairwised orthologs



Orthologs + paralogs

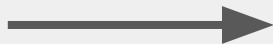
Hierarchical Orthologs Groups (HOGs)
(orthology graphs)



1 Clique



genes



Pairwised orthologs



Orthologs + paralogs

Hierarchical Orthologs Groups (HOGs)
 (orthology graphs)



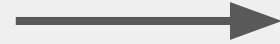
1 Clique



2 Cliques = 2
 paralogues



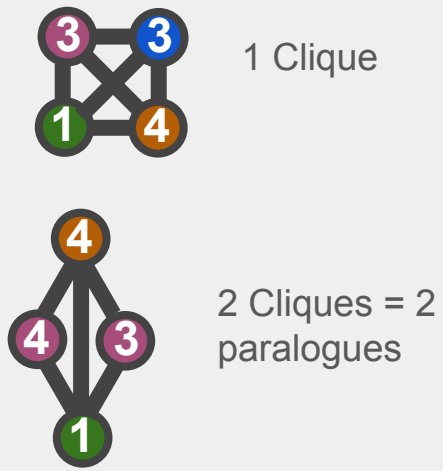
genes



Pairwised orthologs



Orthologs + paralogs
Hierarchical Orthologs Groups (HOGs)
(orthology graphs)



37,000 orthologous genes

Read2Tree (Dylus et al 2024)

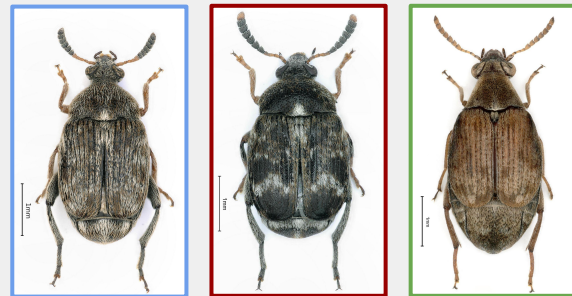


1 ortholog gene

Read2Tree (Dylus et al 2024)



1 ortholog gene

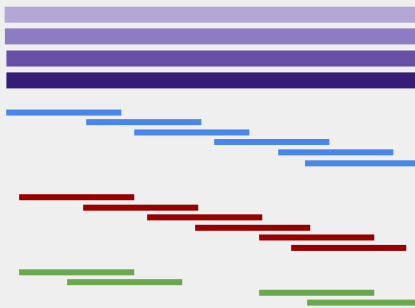


Raw reads

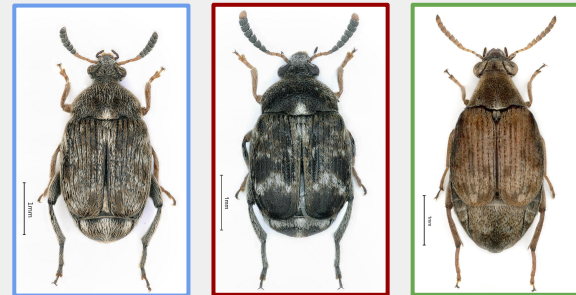
Read2Tree (Dylus et al 2024)



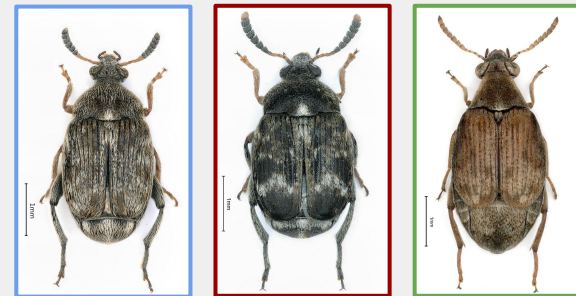
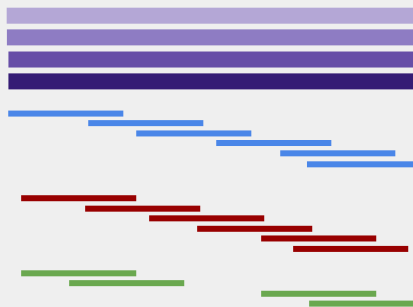
1 ortholog gene



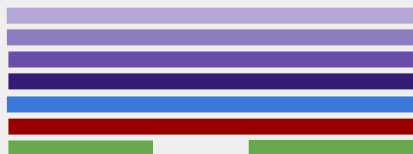
Raw reads



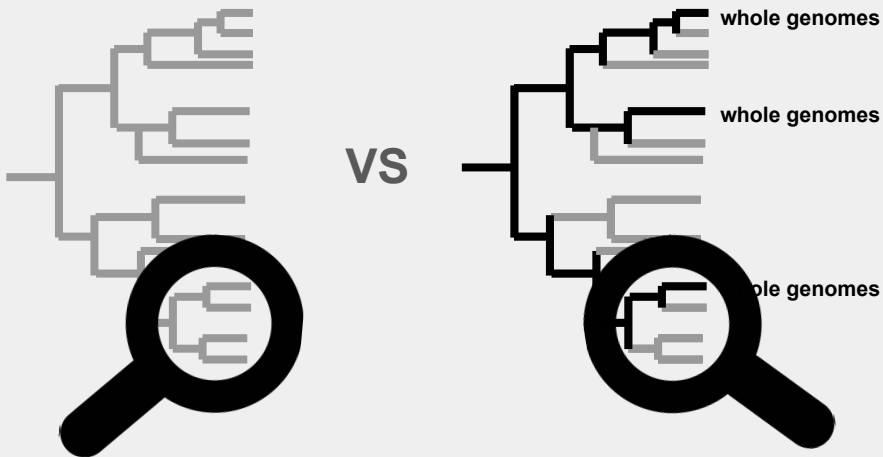
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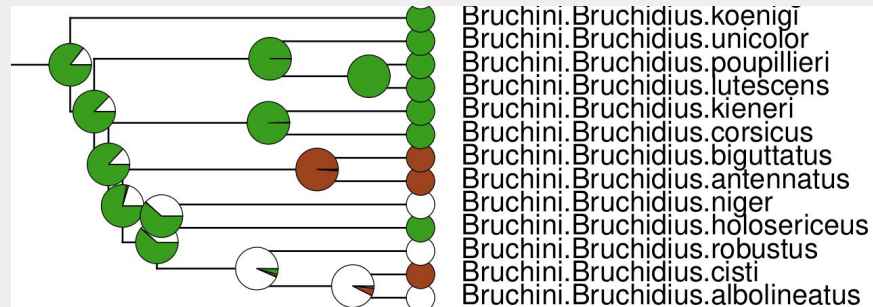
Multi alignent



What is the impact of whole genome addition?



Cisti groupe (*Bruchidius*)



Fabaceae

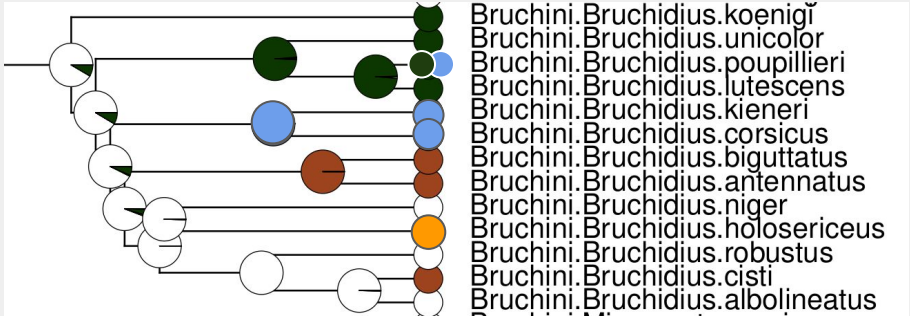
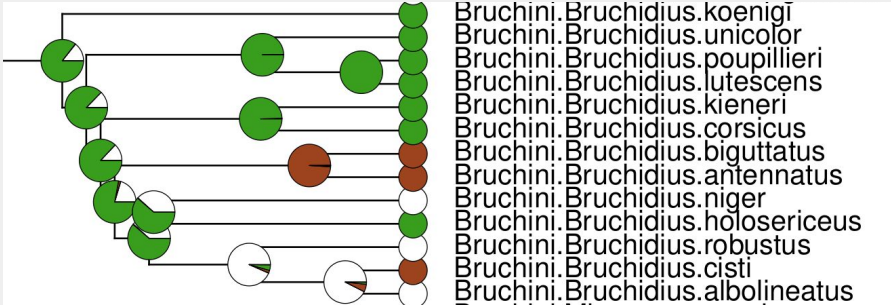


Cistaceae



What's next?

increasing taxonomic precision



Fabaceae

Cistaceae

Hedysareae

Loteae

Trifolieae



Merci pour votre attention !

Miam !

