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Characterization of the gene content of Coxiella *burnetii* from different lineages in Europe

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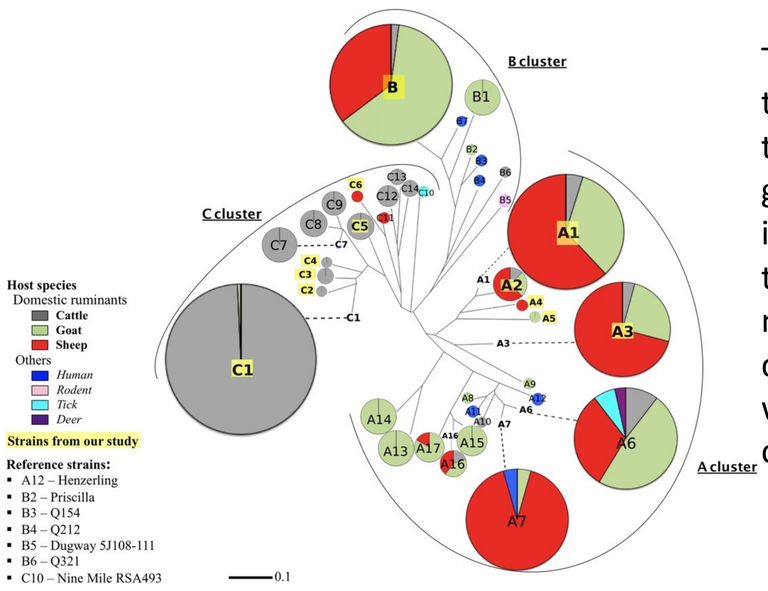
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Context and objectives

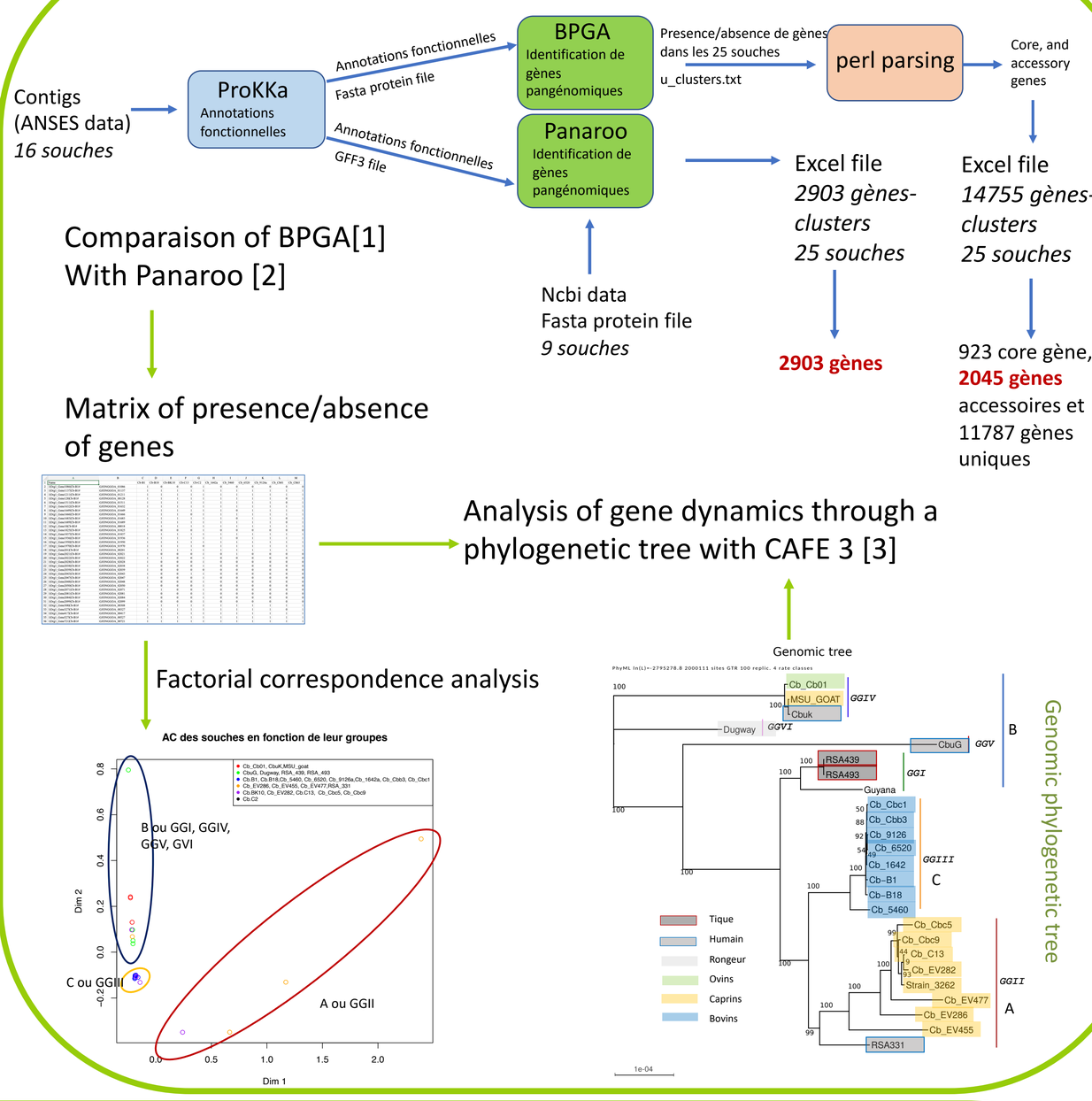
Coxiella *burnetii* is the bacterium responsible for Q fever in humans. It causes fevers, headache, endocarditis, obstetrical complications, hepatitis, pneumonia, endovascular infections. C. *burnetii*, whose main reservoirs are ruminants, is resistant to heat, UV radiation and conventional disinfectants. In these ruminants, it is excreted mainly through the vagina, through the faeces and through the milk.
It is thus found in dust, which is the main route of contamination in humans and ruminants.

In Europe, host specificity has been demonstrated [4]. We hypothesize that differences in host spectrum could have a genetic basis.



The aim of the study is therefore to understand the evolution of *C. burnetii* genomic diversity, by identifying and analyzing the specific genes of the main lineages and by describing the dynamics which lead to the distribution of the genes.

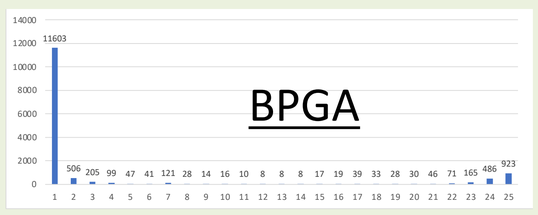
Methods

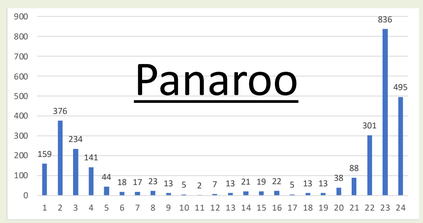


Results

Comparison of BPGA with Panaroo

BPGA: many noises (unique genes)
Panaroo: Expected outcomes

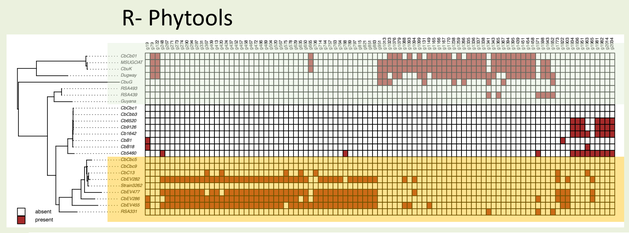




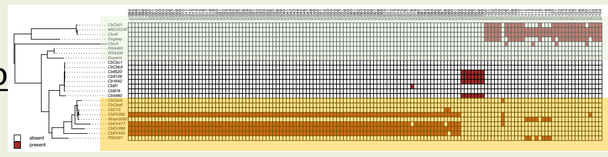
Panaroo's presence/absence matrix

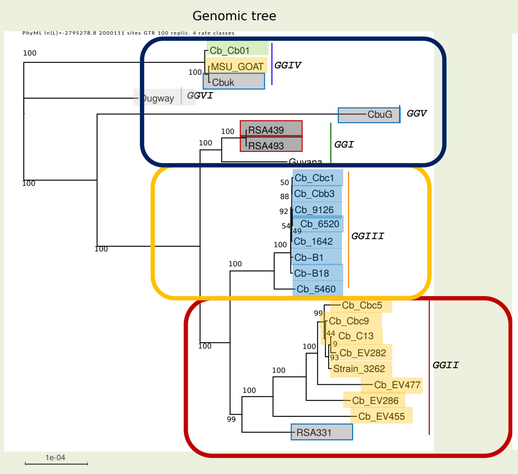
R- Phytools

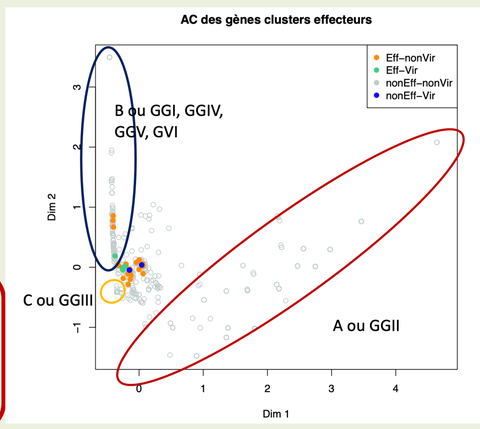
BPGA



Panaroo

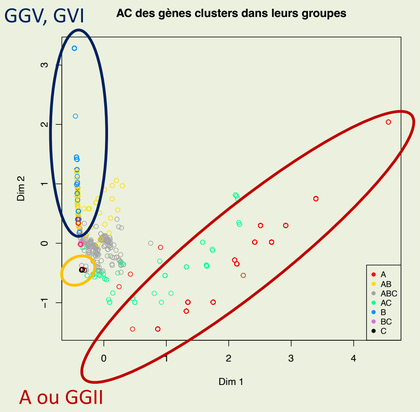




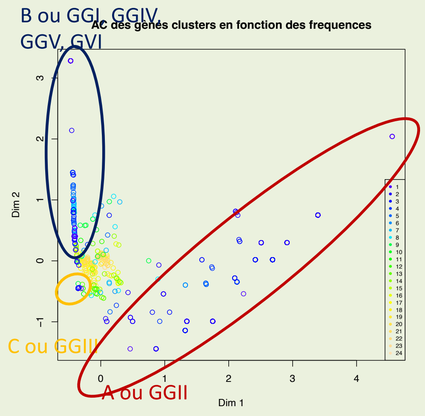


We clearly find our groups, A, B and C [4]

B ou GGI, GGIV, GGV, GVI



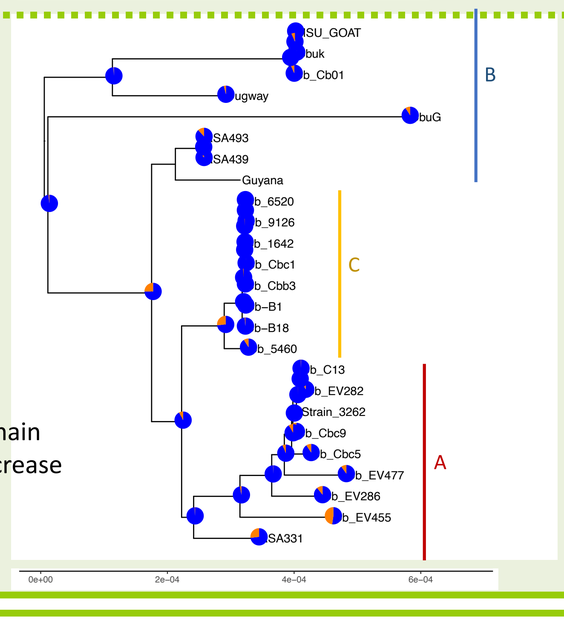
B ou GGI, GGIV, GGV, GVI



✓ Group C genes are also very homogeneous but present in most strains.
✓ Those of the A lineage are delineated and present in very few strains.
✓ Group B genes are also well delineated.

Factorial correspondence analysis

CAFE 3



Genes remain
Genes decrease

- group C gene content is highly homogenous.
- Throughout evolution, there were two main period of gene loss that influenced the genomic composition of *C. burnetii* : one that impacted lineages A and C and a related group including american isolates, and another impacting lineage C only.

Conclusion

Some genes are very specific to lineages and constitute a first set of candidate for host specificity.

Also, a gene dynamic is at the origin of gene losses on the internal nodes of the tree (nodes at the origin of large groups), influencing an absence of genes in the lineages.

Perspectives

Further analyzes are needed to clearly identify the host-specific polymorphisms.

The analysis of synonymous and non-synonymous substitution rates in C. *burnetii* strains could give complementary information in the impact of selective pressures associated with host-range in *C. burnetii*.

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