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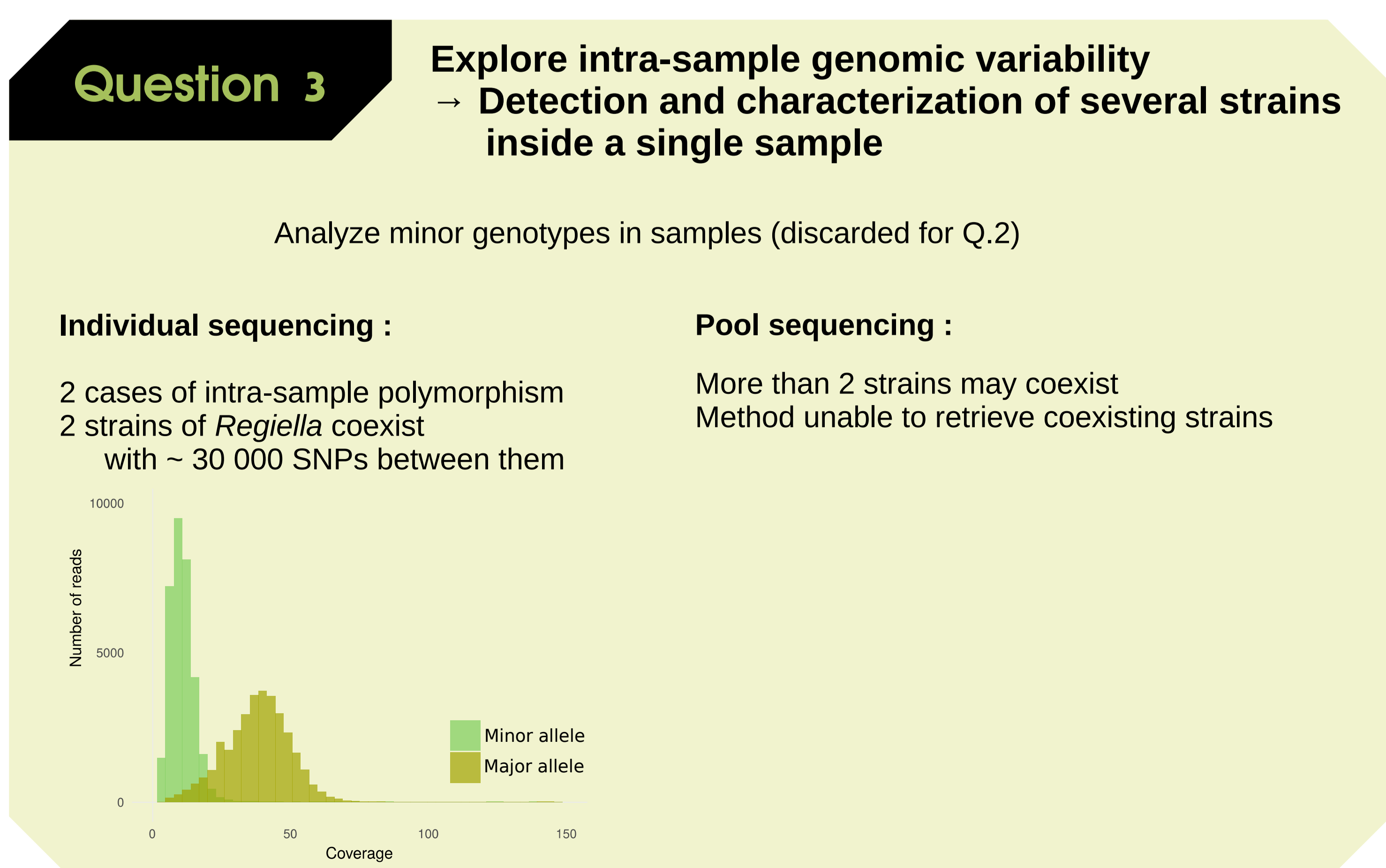
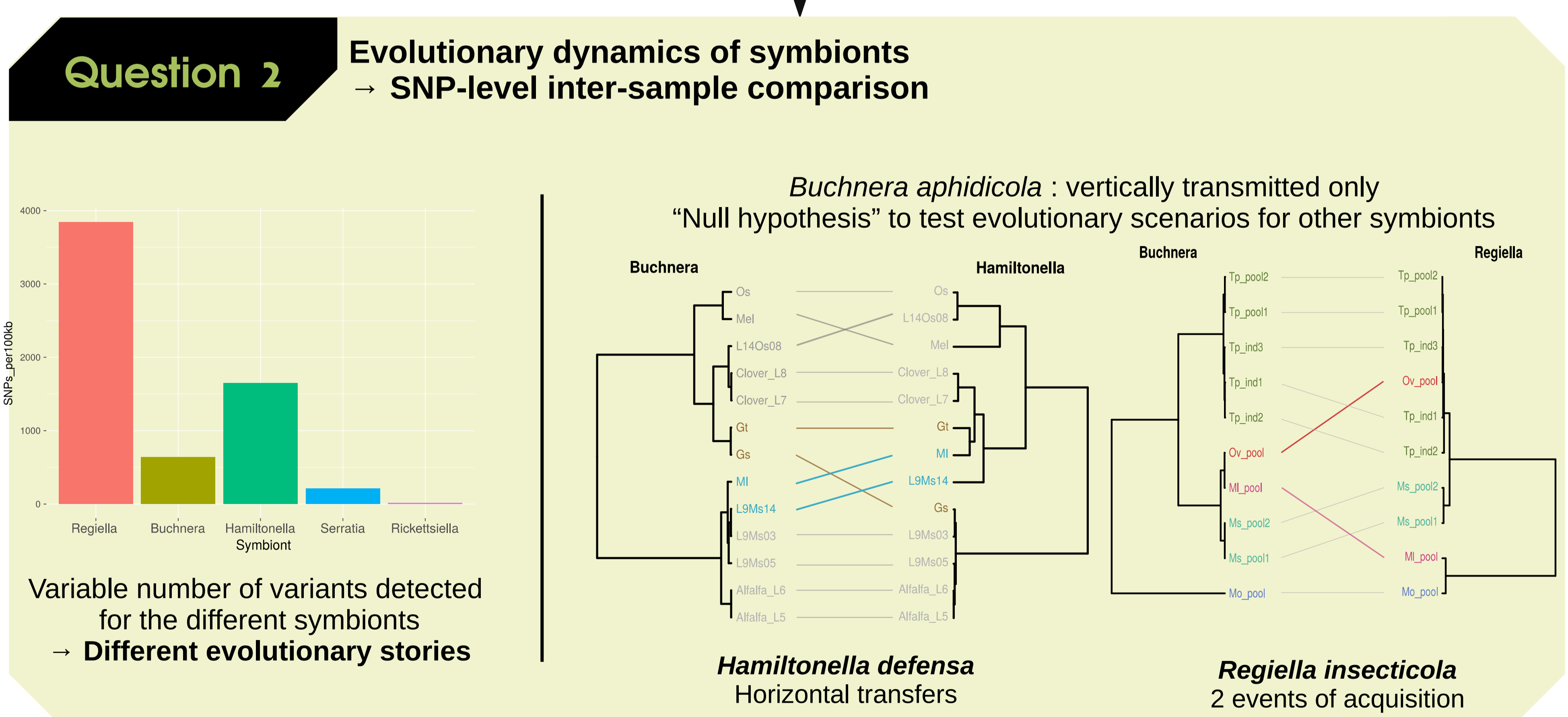
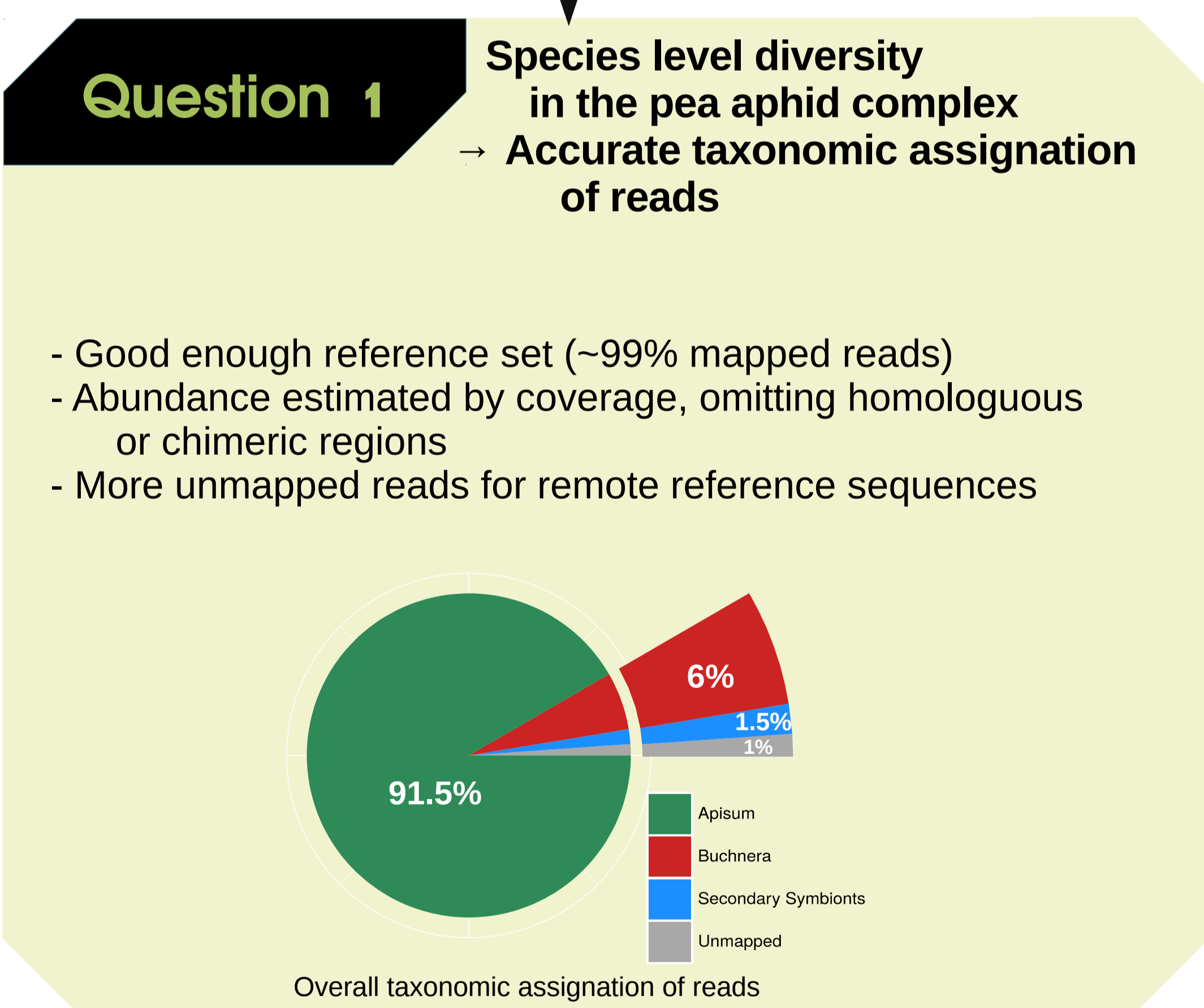
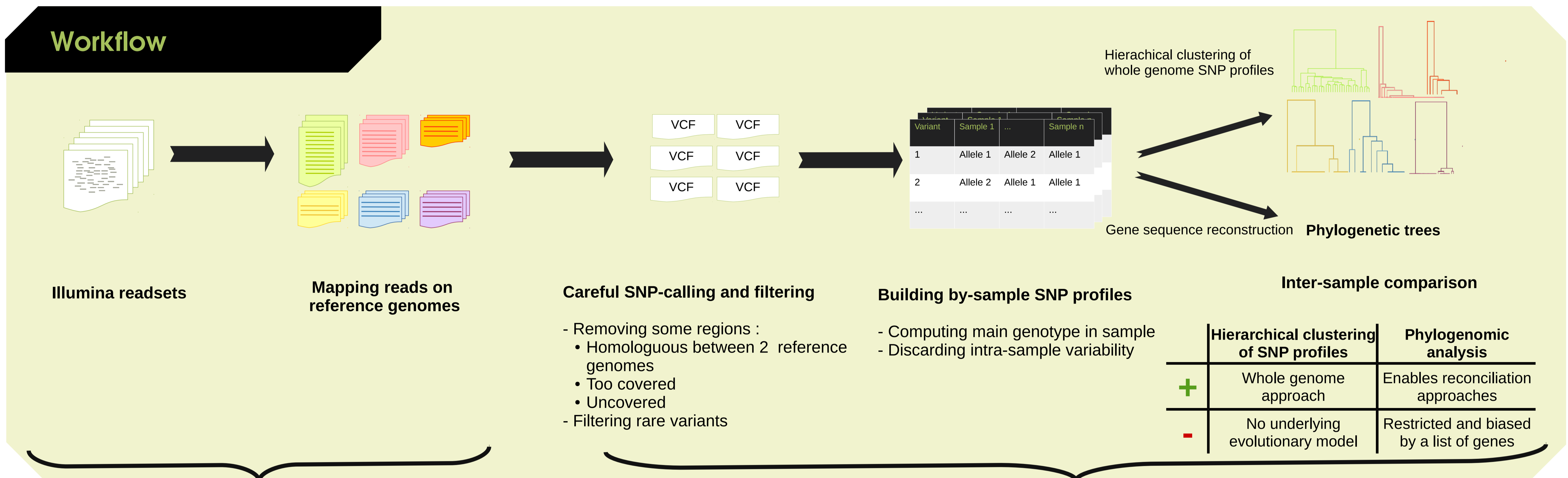
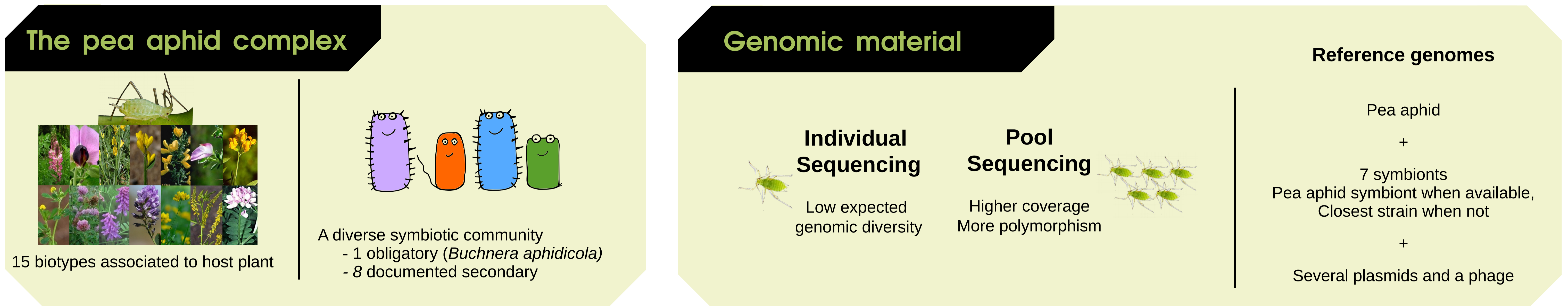
Multi-scale characterization of symbiont diversity in the pea aphid complex through metagenomic approaches



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In a nutshell : exploit multi-sample metagenomic datasets to explore finely the pea aphid microbial community



Conclusions

Simple bacterial community finely explained by analysis of multi-sample metagenomic data

- Reference mapping able to capture the most of the diversity for this model
- SNP-calling to sketch evolutionary stories of secondary symbionts
- Able to exploit intra-sample polymorphism in some cases

Limits and todo-list

- Statistical testing of evolutionary scenarios from phylogenetic trees
- What about the 1% of unmapped? Large variant detection and reference free methods