

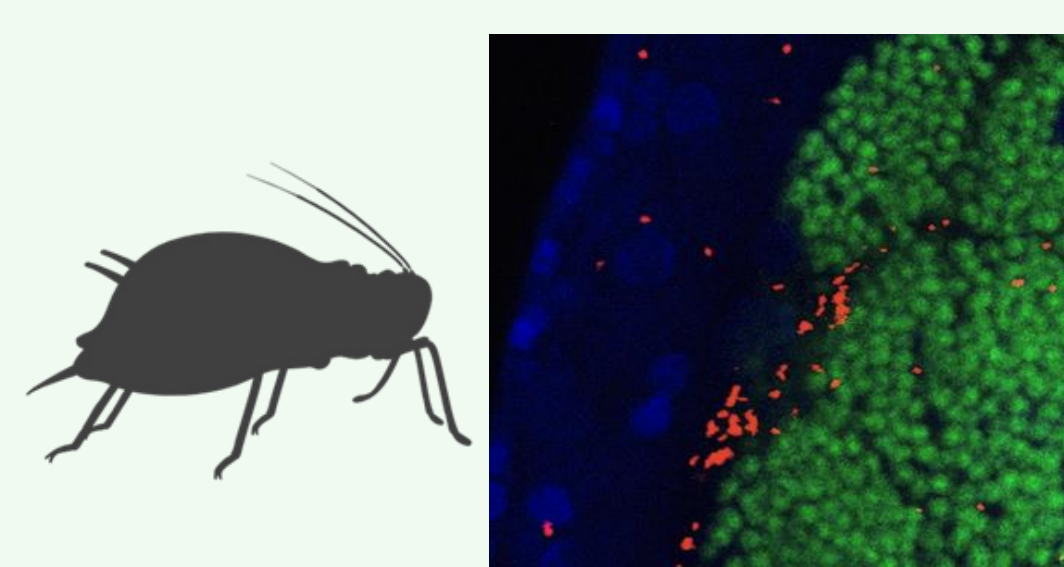
Building high-quality genomic resources for studying the evolution, functioning, and future ecological outcomes of multisymbiotic systems

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Context

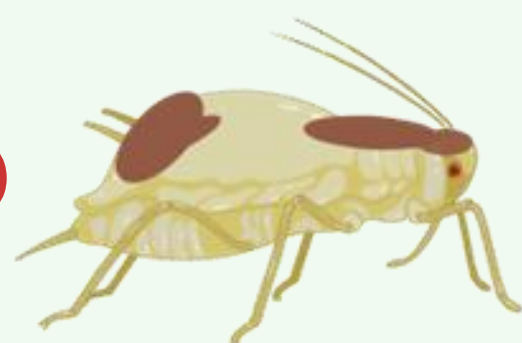
Insects, and aphids in particular, have evolved a wide range of relationships with heritable symbiotic bacteria, thereby forming complex biological systems involving intricate metabolic exchanges and other characteristics. These relationships result in specific pressures on the genome, leading to genomic reduction and evidence of horizontal gene transfer (HGT) between the host and its bacterial partners. The producing **chromosome-level host genome assemblies** has become essential for a **better understanding of the evolution and functioning of multisymbiotic systems**. Here, Pore-C method is used to investigate two symbiotic systems, allowing the production of chromosomal-scale assembly using long read sequencing.



Pentalonía nigronervosa

Buchnera aphidicola

Wolbachia pipientis (wPni)
Poorly known association,
heritable through germline



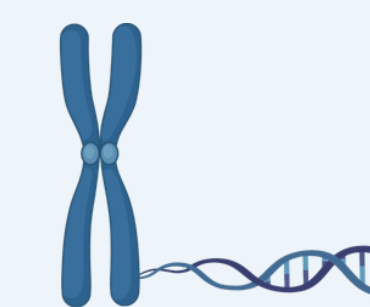
Periphyllus lyropictus

Buchnera aphidicola

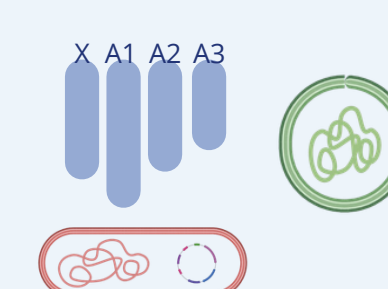
Serratia symbiotica (pSsPI-LLN)
Co-obligate but highly
invasive nutritional
symbiont, both intra
and extracellular

Why Pore-C

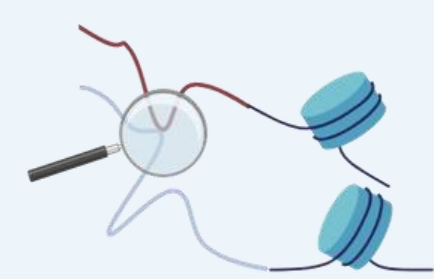
Pore-c enables multi-scale genome analysis from sequence to 3D organization in a single experiment.



Chromosome-level genome assemblies



Simultaneous resolution of host and symbiont genomes

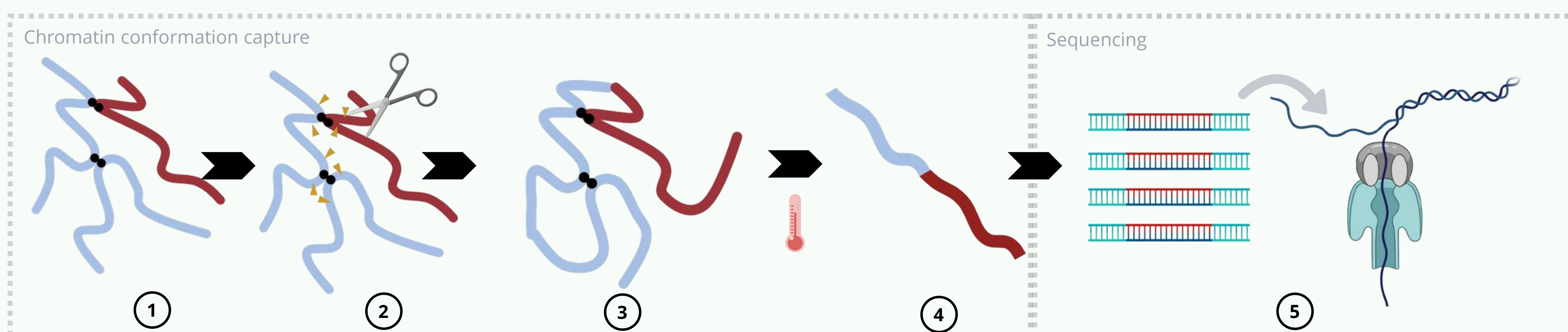


Detection of 3D genome contacts



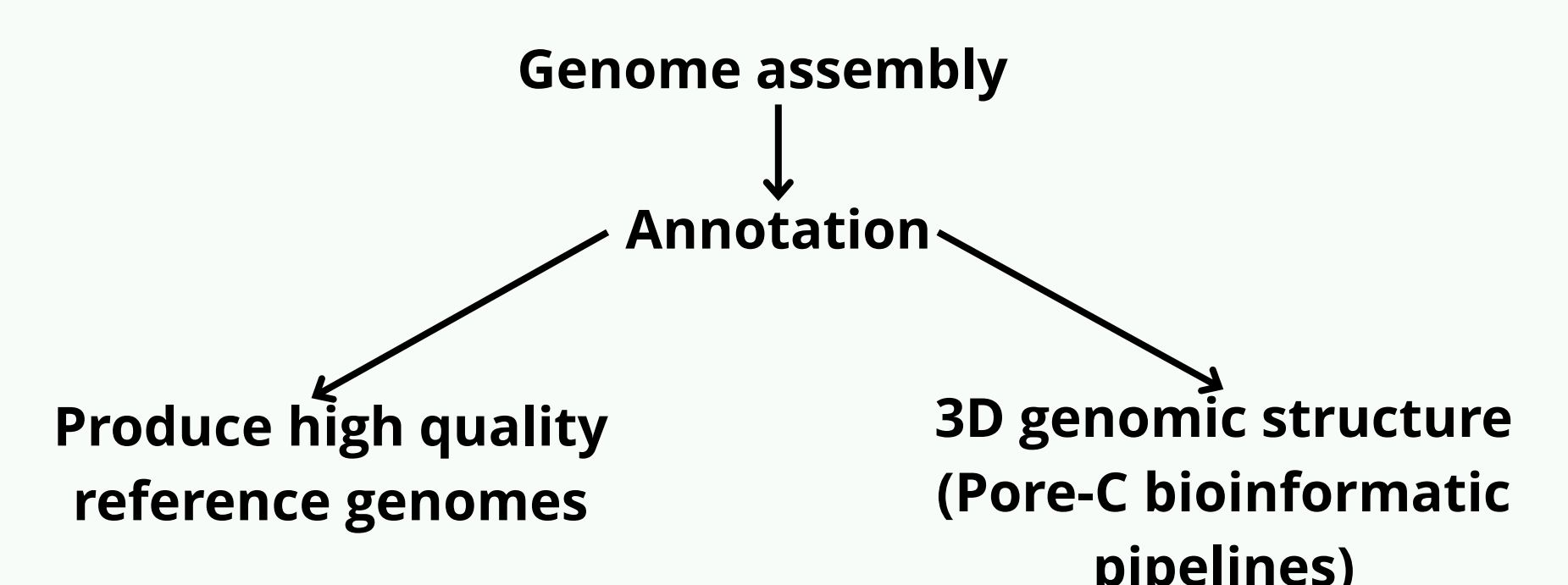
Native DNA methylation profiling

Pore-C workflow



Pore-C workflow for aphid-symbiont systems. Chromatin is crosslinked with formaldehyde to preserve in vivo DNA-DNA interactions (1), followed by restriction enzyme digestion to fragment the genome (2). Spatially proximal DNA ends are then ligated (3), generating chimeric molecules that capture higher-order chromatin contacts. Crosslinks are subsequently reversed (4), and DNA is purified prior to library preparation for long-read Oxford Nanopore sequencing (5).

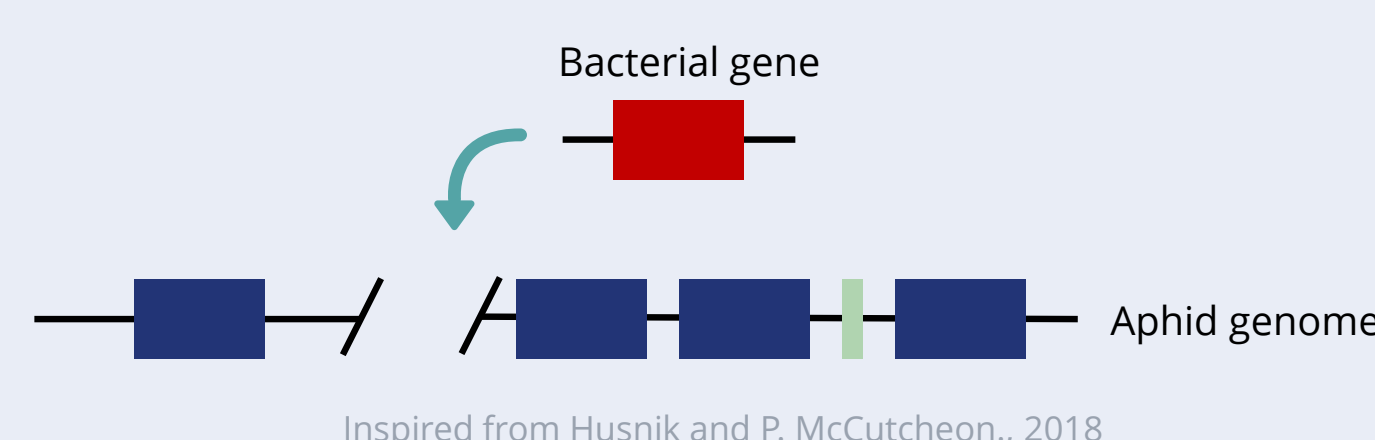
Data analysis



Research Questions

Host- symbiont gene transfer

- Are there any functional or non-functional horizontally transferred bacterial genes in these aphid genomes?
- If so, do they allow maintenance of previously lost functions, or has new functionality been gained through HGT?
- Do transferred genes show coordinated organization with symbiont functions?



Inspired from Husnik and P. McCutcheon, 2018

Symbiotic evolution



P. lyropictus system

Associated with co-obligate symbiont
Intra- & extracellular lifestyle
Intermediate “organelle-like” integration
• Evolution of endosymbionts integration



P. nigronervosa – *wPni*

Relationship still poorly understood
Investigating:
• Reproductive manipulation
• Metabolic interactions

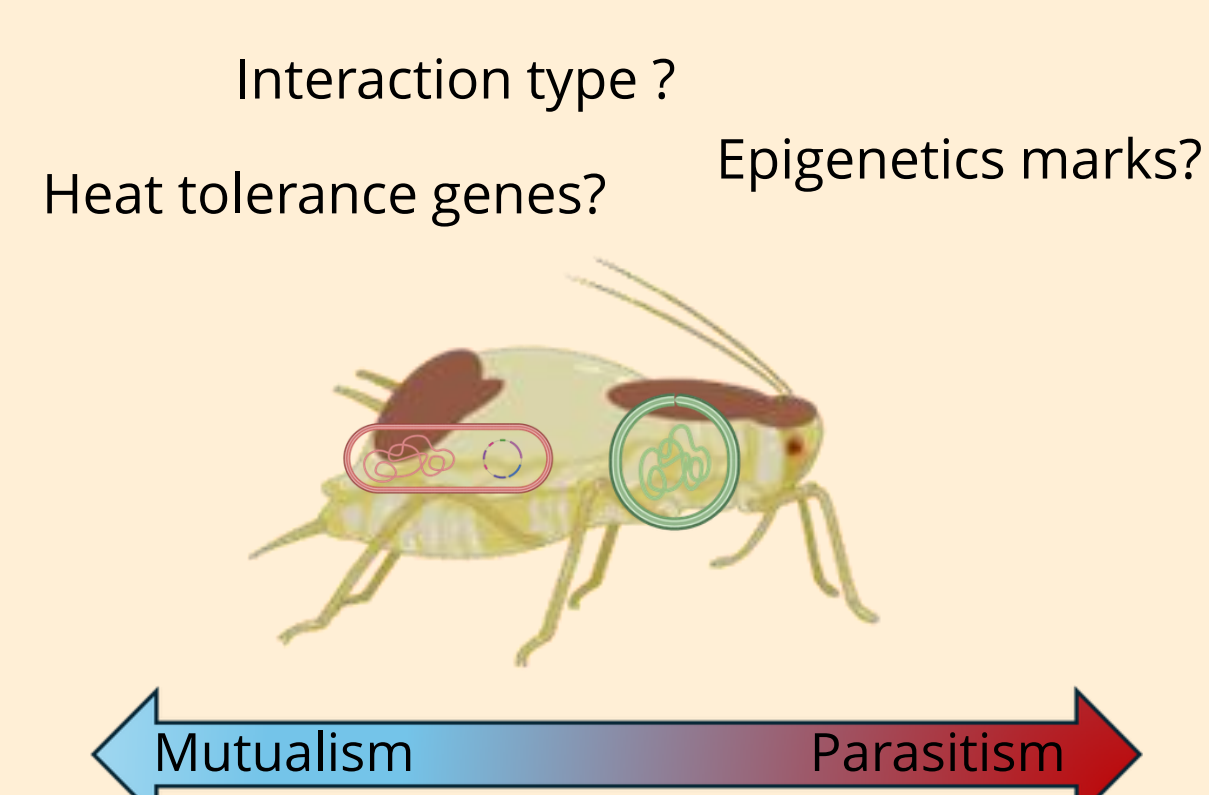
Metabolic integration

- Are metabolically linked genes spatially clustered in the genome?
- Is there structural coordination between host and symbiont genomes?

Gene A			
Gene B			
Gene C			
ABC metabolic pathway			

Symbiosis in a changing world

Aphid-bacteria symbioses are known to be **thermosensitive**, but the impact of global environmental changes such as temperature are still poorly known. High-quality genomic resources are fundamental for studying **how will these associations evolve**, and the ecological consequences for aphid populations.



Current progress

Decoding aphid symbiosis evolution...

DNA extraction ... OK
Genomes sequencing ... OK
Pore-c 3D structure ... in progress
Genome annotation ... in progress
Data analysis ... in progress



References
Husnik et al. 2018. « Functional Horizontal Gene Transfer from Bacteria to Eukaryotes ». Nature Reviews Microbiology 16 (2): 67-79. Ulahannan et al. 2019. « Nanopore Sequencing of DNA Concatemers Reveals Higher-Order Features of Chromatin Structure ». Renoz, François et al. 2022. « Compartmentalized into Bacteriocytes but Highly Invasive: the Puzzling Case of the Co-Obligate Symbiont Serratia symbiotica in the Aphid Periphyllus lyropictus ». Microbiology Spectrum 10 (3): e00457-22.

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