GEORG-AUGUST-UNIVERSITÄT GÖTTINGEN IN PUBLICA COMMODA SEIT 1737

MAX-PLANCK-INSTITUT FÜR MULTIDISZIPLINÄRE NATURWISSENSCHAFTEN

Evolutionary Genomics: Consequences of Biodiverse Reproductive Systems (EvoReSt)

EvoReSt

C1

Leveraging Hi-C to map regulatory chromosomal 3D architectures

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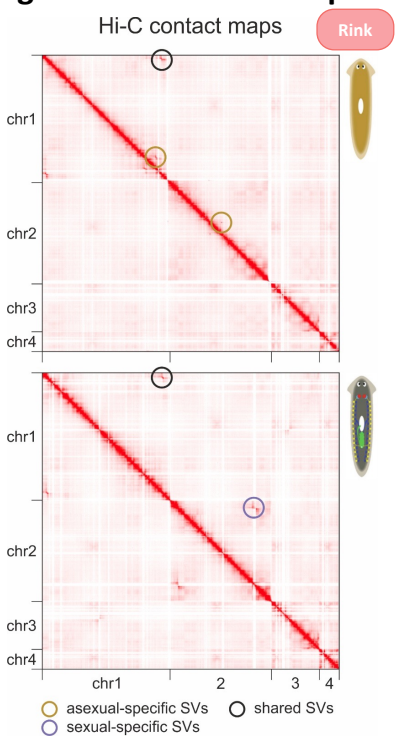
State of the art

- Linear genomic information cannot explain the regulatory complexity of living cells, and 3D genomics approaches have come to bridge this gap.
- 3D genomics data can be leveraged to build cell type-specific chromosomal scaffolds and uncover regulatory landscapes in a single experiment.
- In combination with long-read sequencing data, Hi-C data now overcome challenges by repetitive, poor-built genome drafts and address ploidy changes.

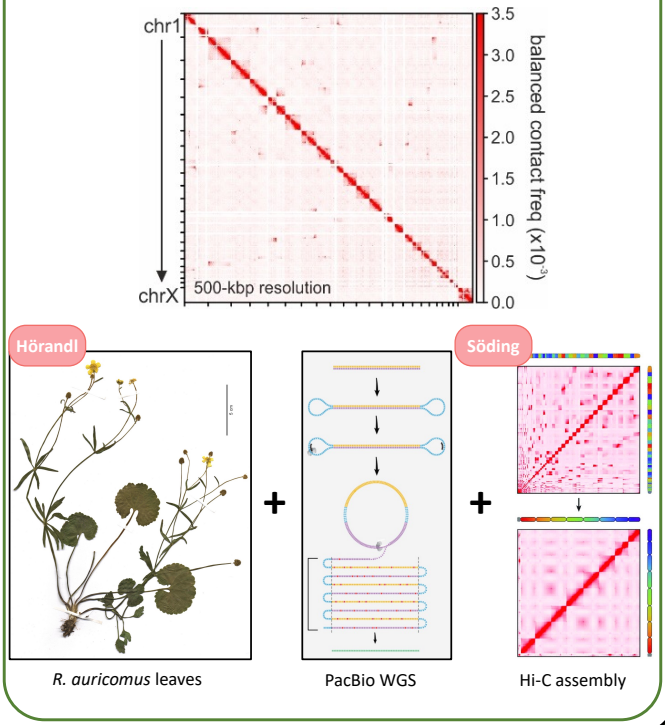
Objectives

- Exploit 3D genomics to investigate how changes in spatial genome architecture differentiate sexually- from asexually-reproducing *S. mediterranea* strains.
- Produce an *in silico* framework for accurate haplotype assembly and ploidy deconvolution in new model organisms (e.g., *R. auricomus*).

PhD 1 - Regulatory genome architectures underlying sexual vs asexual reproduction



PhD 2 - Leveraging Hi-C data for genome assembly and haplotype deconvolution



References

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