GEORG-AUGUST-UNIVERSITÄT GÖTTINGEN IN PUBLICA COMMODA SEIT 1737

MAX-PLANCK-INSTITUT FÜR MULTIDISZIPLINÄRE NATURWISSENSCHAFTEN

Evolutionary Genomics: Consequences of Biodiverse Reproductive Systems (EvoReSt)

EvoReSt

B4

Evolutionary consequences of inheritance-coupled symbiont transmission

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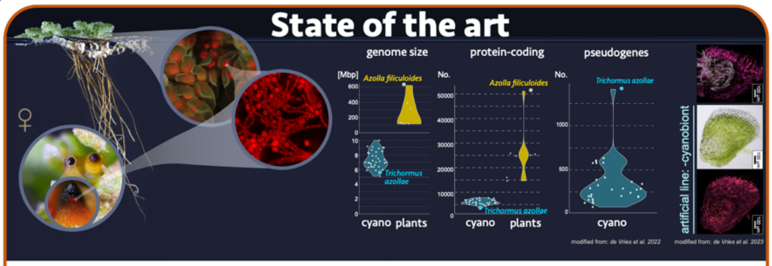
State of the art



- *Azolla* reproduces asexually & sexually
- only land plant that vertically inherits cyanobacterial symbiont (cyanobiont)
- co-evolution between host & cyanobiont observed
- cyanobiont genome has high pseudogene content

Objectives

- **How is coordination of reproduction & transmission regulated?**

WP1: identification of molecular transmission network & conservation

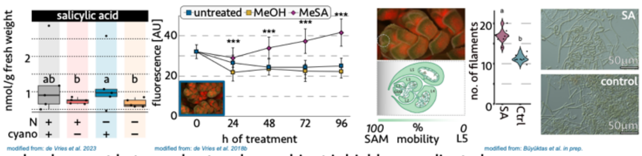
- **How is this linked to co-evolution & maintenance of the symbiosis?**

WP2: determine evolutionary forces that shape the transmission network

WP3: identify mechanisms that act on the cyanobiont genome that contribute to co-evolution

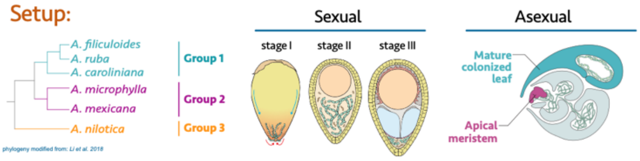
PhD 1 - Evolution of reproductive coordination in Azolla

WP1: identification of the molecular transmission network



- development between host and cyanobiont is highly co-ordinated
- we identified salicylic acid as a first molecular candidate in host-symbiont communication
- Question: Does a conserved core transcriptional transmission network exist that allows for a co-ordinated reproductive development of host and cyanobiont?

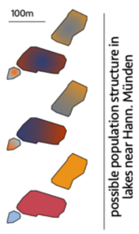
Setup:



▶ Dual-RNA Seq

WP2: determine evolutionary forces that shape the host transmission network

- Azolla induces the sexual cycle on average once a year upon crowding
- communication may have to remain dynamic, but at the same time cannot allow for relaxed constraints
- Question: What is the evolutionary history of the transmission network?



▶ Illumina DNASeq

(i) 20 subsections across 3 lake populations

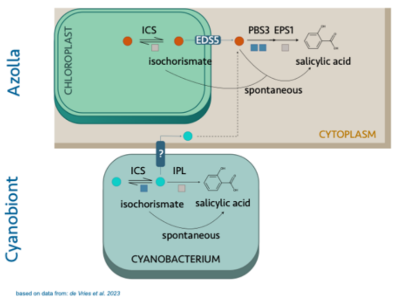
(ii) several different populations

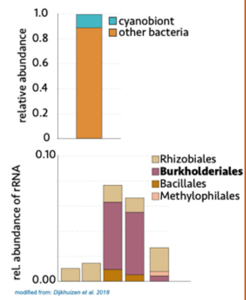
Collaboration: EH (population structure), JS (dn/ds incl. epistasis)

PhD 2 - Evolutionary dynamics shaping Azolla-cyanobiont co-evolution

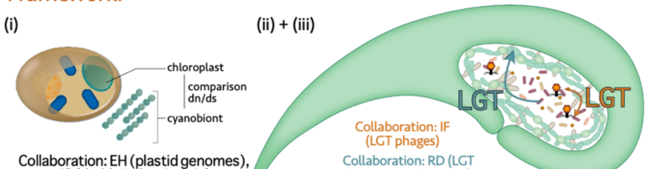
WP3: determinne whether evolutionary dynamics of the cyanobiont genome contriubte to co-evolution

- cyanobacterial symbioses have an associated microbiome
- Azolla's cyanobiont is not alone in the cavity & bacterial consortium is likely co-inherited
- the cyanobiont genome is highly reduced, but checkered, collaborative pathways between cyanobiont and host may exist
- Question: What factors drive the evolution of the symbiotic transmission network?





Framework:



Collaboration: EH (plastid genomes), JS (dn/ds incl. epistasis)

Collaboration: IF (LGT phages)

Collaboration: RD (LGT between prokaryotes)

- uses public data from Azolla species (+chloroplast&cyanpbiont), and metagenomes from cavity & data from WP1 & 2

References

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3. Li F.-W. et al. 2018. Fern genomes elucidate land plant evolution and cyanobacterial symbioses. Nature Plants.4: 460-472.
4. de Vries S. et al. 2022. Evolutionary genomic insights into cyanobacterial symbioses in plants. Quant. Plant Biol. 3:e16.
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RTG 2984/1