

Symbiont maintenance and host control in Acantharea-*Phaeocystis* photosymbioses revealed through single-holobiont transcriptomics



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Background

Photosymbioses are important to primary production in low-nutrient regions^{1,2} and are opportunities to study the early stages of plastid acquisition³. Although traditionally assumed mutualistic—with hosts benefiting from organic carbon fixed by symbionts and symbionts benefiting from nutrients supplied by hosts—it is now doubted whether many photosymbioses, including among acantharians, are truly mutualisms⁴.

Acantharians are the most abundant photosymbiotic Rhizaria in oligotrophic surface waters, where they create localized productivity hot spots². Acantharians maintain *Phaeocystis* (Haptophyta) symbionts without systematically digesting them⁵, but symbionts undergo a dramatic phenotypic transformation, including increased cell size and chloroplast proliferation⁶. However, it is unclear how acantharians manage symbiont populations or whether symbionts benefit from the relationship.

Aims

Determine molecular mechanisms involved in nutrient transfer and symbiont population control in Acantharea-*Phaeocystis* symbioses by comparing gene expression in symbiotic and free-living cells of two *Phaeocystis* species.

Methods

Sequenced single holobiont transcriptomes for 16 individual acantharians with diverse symbiont communities.

Assessment of reference transcriptome completeness

Sequenced transcriptomes from three biological replicates each for two symbiont species, *P. cordata* and *P. jahnii*.

Performed differential expression testing (DESeq2) for free-living replicates compared to holobiont replicates.

Performed GO term and KEGG pathway enrichment testing with differentially expressed gene sets.

Results

P. cordata

GO terms enriched among genes **upregulated** in symbiosis

GO terms enriched among genes **downregulated** in symbiosis

P. jahnii

GO terms enriched among genes **upregulated** in symbiosis

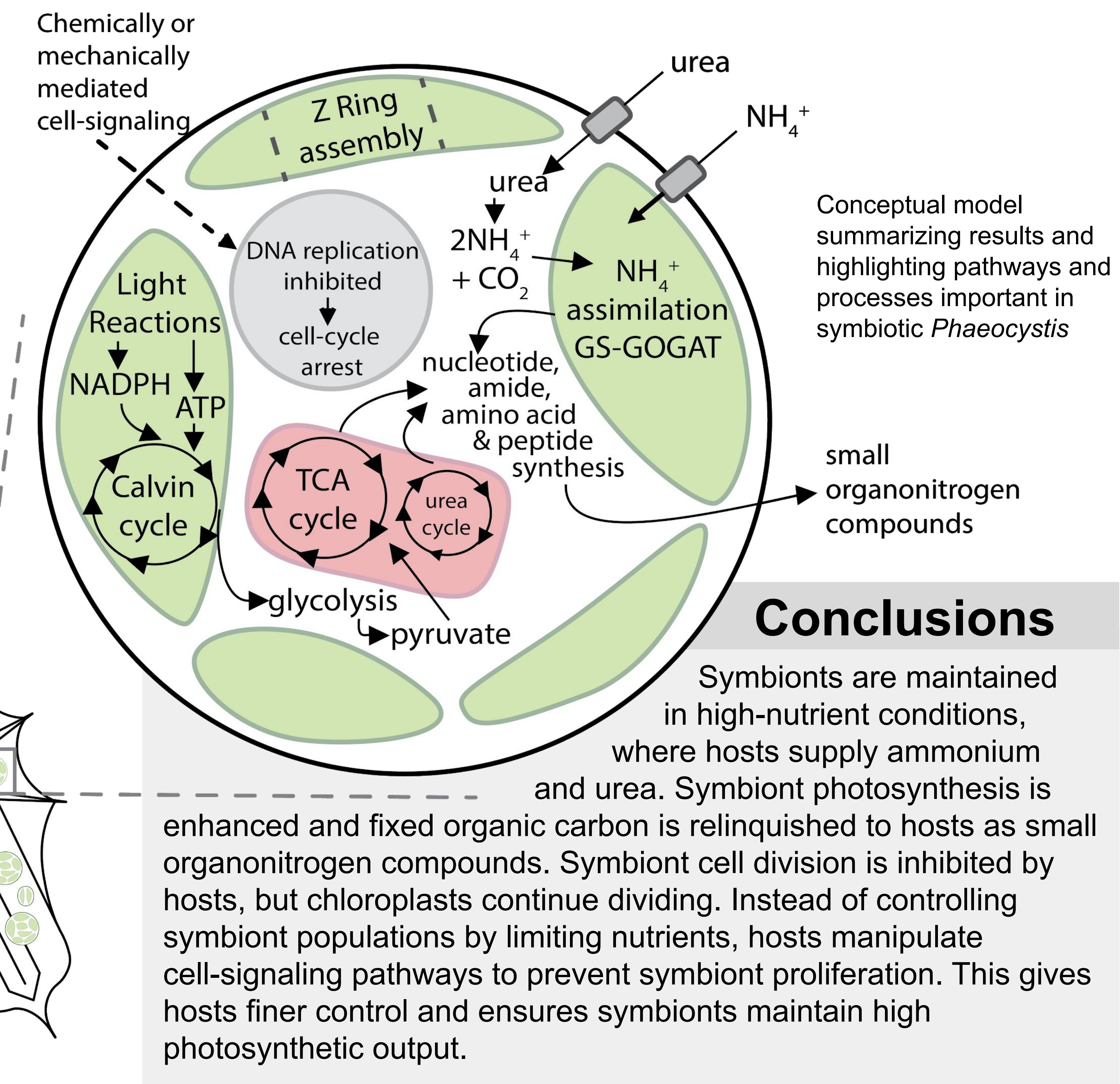
GO terms enriched among genes **downregulated** in symbiosis

Photosynthesis GO terms are enriched among genes upregulated in symbiosis for both species. Biosynthesis of storage carbohydrates and lipids is downregulated.

DNA replication GO terms are enriched among downregulated genes in both species, as are DNA replication and cell-cycle KEGG pathways. Genes in the Mitogen Activated Protein Kinase (MAPK) pathway that influence cell proliferation are downregulated in symbiosis.

Nuclear encoded chloroplast division genes are expressed at similar levels in symbiotic and free-living cells in both species.

Neither species expressed genes associated with P or N limitation in symbiosis. Urea and ammonium transporter genes and ammonium assimilation genes are expressed in symbiosis.



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