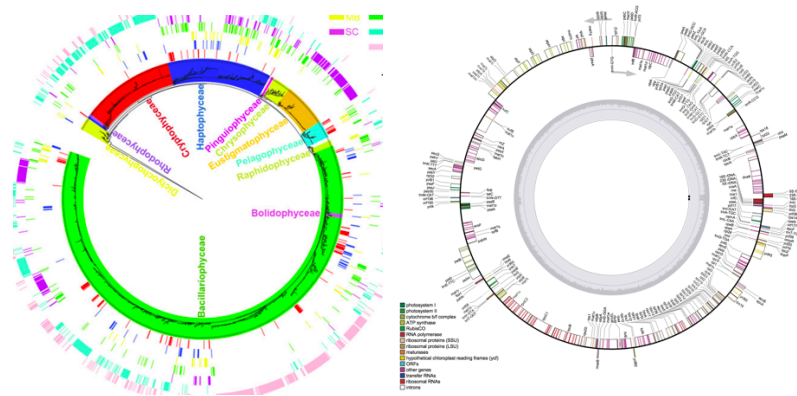


Reconstructing plastid evolution by metagenomics



Oxygenic photosynthesis converts light into energy, an essential process for life. The origin of photosynthetic organelles, *i.e.* plastids (or chloroplasts), was a landmark event in the history of eukaryotes, launching an astonishing diversification of micro- and macroscopic algae and land plants. Although the endosymbiotic theory explains well the origin of plastids from cyanobacteria, the subsequent evolution of plastids within eukaryotes is complex and controversial. A growing body of evidence suggests that plastids have experienced a convoluted evolution, moving laterally across eukaryotes by several rounds of complex endosymbioses. The result is an unresolved web of related endosymbiotic and unrelated host lineages. A major current limitation to our understanding of plastid evolution is that plastid genomes are available for only a tiny fraction of the algal diversity, mostly corresponding to described species. Here, we propose to overcome this limitation by building a gene- and taxon-rich plastid phylogeny using environmental plastid genomes reconstructed from metagenomes.

Goals

- Gather available metagenomic datasets from various sources
- Screen metagenomic datasets for plastid sequences
- Reconstruct novel, near-full plastid genomes from existing metagenomes
- Build the most complete plastid genome phylogeny using reference genomes and the novel metagenomes

Data provided

Data available on major databases, *e.g.* TARA, EBI, JGI, MG-RAST.

Methods

Database mining, phylogenetics, metagenomics, metagenomic binning, phylogenomics.

Requirements

Motivation, curiosity, and wits indispensable. Experience in **bioinformatics and programming** necessary. Knowledge of **molecular evolution** highly desired.

Useful information

- Start date: as soon as agreed upon
- This project will be co-supervised by:
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