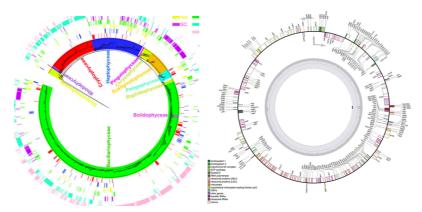
# **Reconstructing plastid evolution by metagenomics**



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 geneand 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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