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Chromatin landscaping in algae reveals novel regulation pathway for biofuels production

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Chromatin landscapping in algae reveals novel regulation pathway for biofuels production

Chlamydomonas as model for algal biofuel feedstock

Chlamydomonas reinhardtii as a reference model
- Unicellular green algae (Chlorophyta), found all over the world, in soil, fresh water, oceans
- The most widely used laboratory species is Chlamydomonas reinhardtii
- Cells can grow on a simple medium of inorganic salts, using photosynthesis to provide energy
- Reference genome available

Lack of nutrients induces lipid accumulation chlamydomonas.

Experimental Design

Microalgae potentially produces the highest oil yield with the smallest land area required.

Unique Advantages of Algae as Biofuel Feedstock
- High area productivity
- Non-seasonal, fast growing
- Minimum competition with agriculture
- Flexibility on water quality
- Renewable energy
- Recycles stationary emissions of CO2

Transcriptome

Data summary
Total 9 timepoints x 2 conditions, Total reads of >50m per lib

Chromatin Landscape

Genomic features

Histone marks indicate a promoter-centric regulation.

• H3K27me3 marks heterochromatin.

• H3K27Ac-specific marks indicates potential distal regulatory elements/ enhancers.

• Simultaneous H3K27me3 and H3K4me3 marking indicates potential bivalent domain.

ChIP-seq Data summary

Data Reproducibility

Multiple approaches targeting common differentially regulated components in nitrogen and sulfur depleted conditions.

- Simple differential modified histone marks
- Differential gene expression (targeting early response)
- Clustering (gene expression)
- Potential regulators
- Differential chromatin state (ChromHMM)

Chromatin as an epigenetic landscape tool for understanding lipid biosynthesis in algae

Discussion

Here, we report a pilot attempt to understand the regulation of algal lipid biosynthetic pathways by genome wide chromatin landscaping. Deep sequencing of transcriptome also provide supporting data to further dissect the regulatory pathways.

Computational analysis have enabled us to narrow into a smaller group of highly potential regulators. In-depth analysis is still on going to map out a potential interaction or inter-regulatory pathways. Effort to further validate these findings in the biological system is currently underway.

This approach shall provide a more feasible way of dissecting regulatory elements in algae and potentially overcome the limitation of the laborious and low-throughput mutagenesis screening approach.