



High Throughput Sequencing Based Analysis Of *Chlorella vulgaris* Associated Microbial Diversity

Conference Poster

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Publication date:

2018-05-17

Permanent link:

<https://doi.org/10.3929/ethz-b-000310060>

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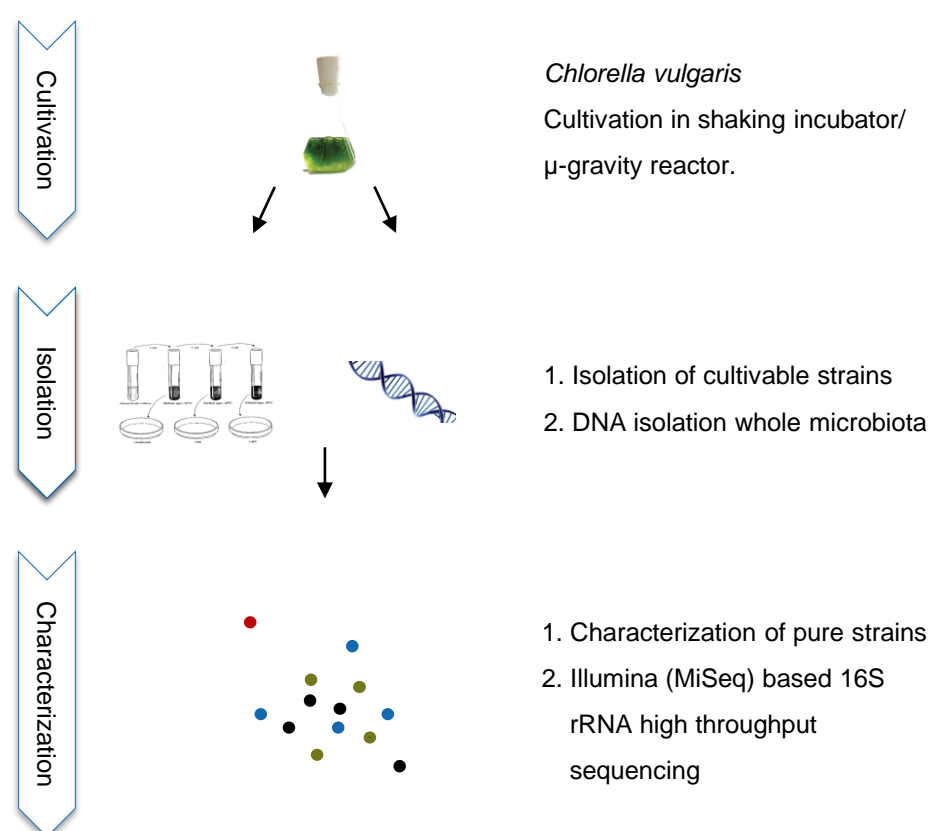
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1 Introduction

Future midterm manned spaceflight and surface exploratory missions to Moon and Mars require the development of life support systems (LSS) including biotechnological subsystems. Microalgae, such as *Chlorella vulgaris*, could be an integral part. Due to their photoautotrophic growth, high biomass yield, and nutritional value they can contribute to creating closed ecosystems by recycling waste into oxygen, water and edible biomass. Non-axenic microalgae cultivations can provide long-term stability but might harbour microbial species harmful for human health. Understanding the interaction can help developing gentle downstream protocols remediating harmful microbial species within microalgae cultivations for recovering edible, safe, and nutritious biomass..

2 Method overview



4 Conclusion

The research project established a base for the development of gentle microalgae downstream processes.

- Identification of a core microbiome for further inactivation studies

Bacteria may be considered beneficial counterparts of microalgae.

- Potential for innovating upstream processes towards microbiome tailoring

3 Results and discussion

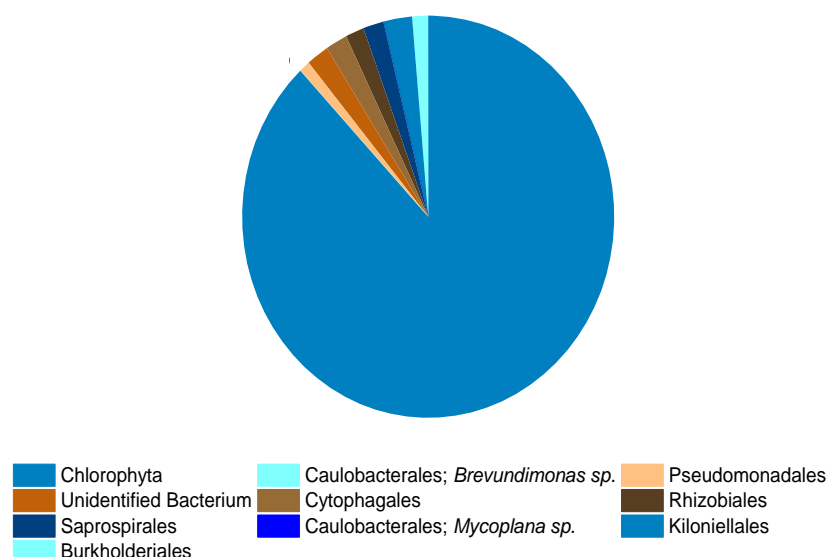


Fig. 1: Microbial community structure of non-axenic *Chlorella vulgaris* SAG 211-12 samples after 4 weeks cultivation in a shaking incubator. Analysis was based on high throughput sequencing of the 16S rRNA using the Illumina (MiSeq) platform.

- Shaking incubator:

Identification of 8 operational taxonomic units (OTUs) including *Pseudomonadales*, *Cytophagales*, *Rhizobiales*, *Saprospirales*, *Burkholderiales*, *Kiloniellales* and *Chlorella vulgaris* (Fig. 1).

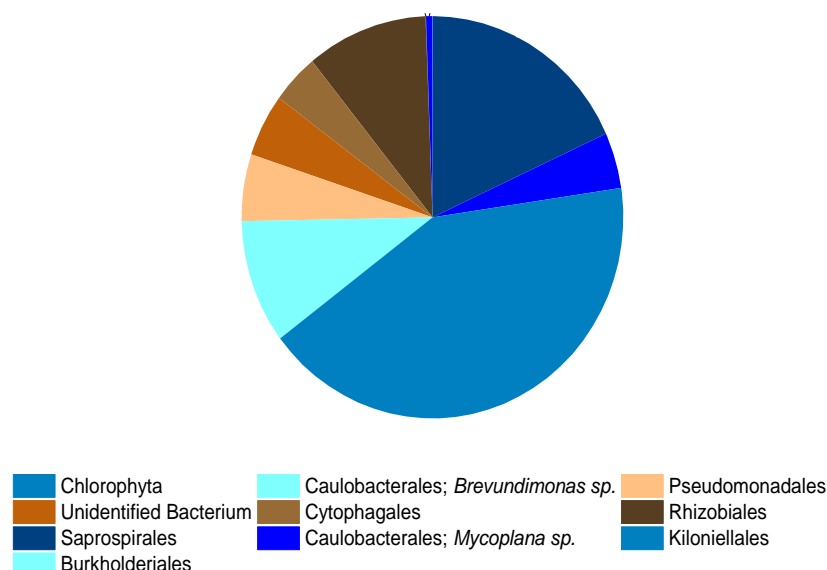


Fig. 2: Microbial community structure of non-axenic *Chlorella vulgaris* SAG 211-12 samples in a μ -gravity reactor. Analysis was based on high throughput sequencing of the 16S rRNA using the Illumina (MiSeq) platform.

- μ -gravity reactor:

2 additional OTUs of order *Caulobacteriales*, identified (Fig. 2).

- No human pathogens
- Similar microbial community pattern, but differing abundances of OTUs
- Culturing conditions can favour *Chlorella vulgaris* abundancies

5 References

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2. Melorose, J., Perroy, R. & Careas, S. World Population Prospects: The 2015 Revision, Key Findings and Advance Tables. Working Paper No. ESA/P/WP.241. United Nations, Dep. Econ. Soc. Aff. Popul. Div. 1, 1–59 (2015).