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

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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 microalgal cultivations can provide long-term stability but might harbor microbial species harmful for human health. Understanding the interaction can help developing gentle downstream protocols remediating harmful microbial species within microalgal cultivations for recovering edible, safe, and nutritious biomass.

2 Method overview

- Cultivation
  - *Chlorella vulgaris*
  - Cultivation in shaking incubator/μ-gravity reactor.
- Isolation
  - 1. Isolation of cultivable strains
  - 2. DNA isolation whole microbiota
- Characterization
  - 1. Characterization of pure strains
  - 2. Illumina (MiSeq) based 16S rRNA high throughput sequencing

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

3 Results and discussion

4 Conclusion

The research project established a base for the development of gentle microalgal 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

5 References