



Exploring microbiomes in environmental biotechnological processes

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Microbiomes in different processes

Many processes in environmental biotechnology are working due to the presence of a mix of microbes, with each group playing a specific role, like being responsible for one step of a multistage conversion process. Even in industrial fermentations which have the purpose of producing biomass of one specific microorganism, an accompanying flora of other microbes is almost always present.

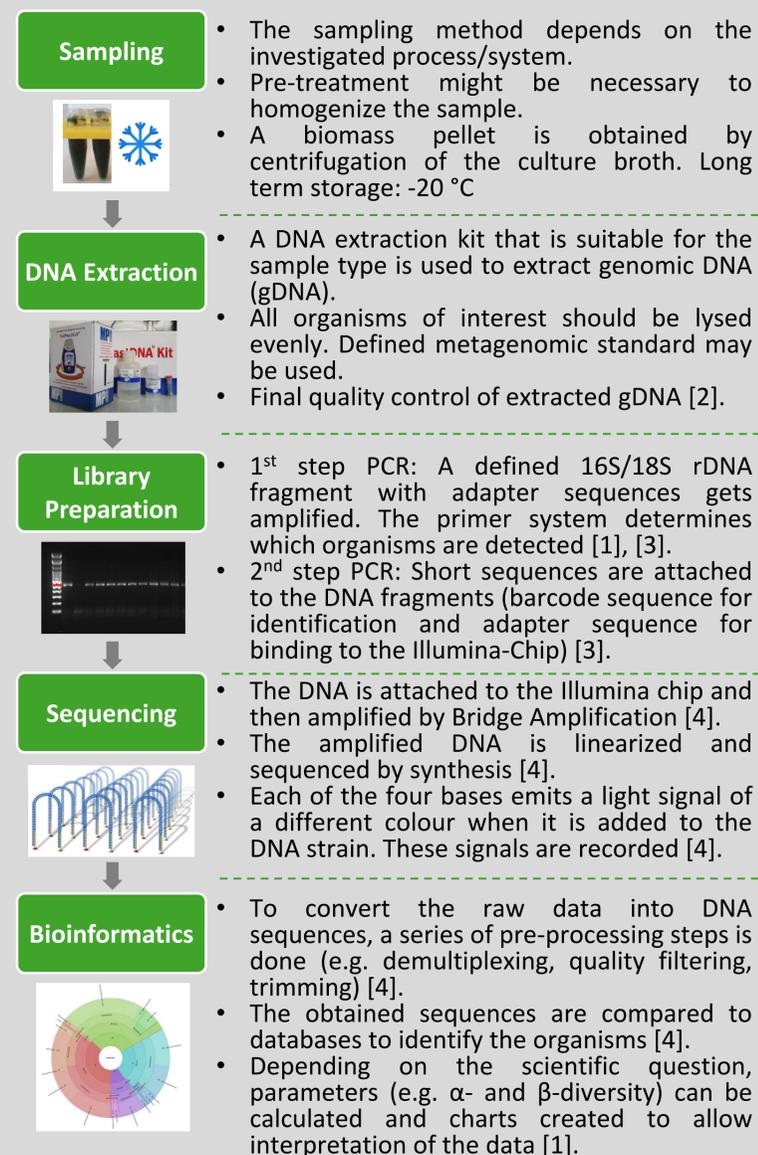
In all cases, the composition of the microbiome is important for the success of the whole process. A change in environmental conditions (e.g. temperature, pH, nutrient availability) can lead to a shift of the microbiome which affects the result of the process. Therefore, it is important to understand the dynamics of the microbial composition in an environmental biotechnological process.

Next Generation Sequencing

Using Next Generation Sequencing methods, the microbial composition of a sample can be analysed.

Depending on the purpose of the analysis, different methods can be used. Analysis of the **DNA** will reveal which organisms are present while analysis of the **RNA** will

16S/18S rDNA Amplicon metagenomics (Illumina MiSeq™)



provide information on biochemical activities that are performed [1].

Shotgun metagenomics are non-targeted and aim to sequence all genomic sequences contained in the sample. However, such an approach is costly. On the contrary, using **amplicon metagenomics**, short DNA sequences (marker genes) of a group of microbes are sequenced. The targeted sequences must be chosen carefully to capture all relevant organisms and be able to identify them. [1]

Application in environmental biotechnology

The analysis of the microbiome can be useful for all processes involving a mixed or not axenic culture. Some examples of applications in processes in environmental biotechnology that we investigate are given below.

Accompanying organisms of microalgae

- Determine the purity of microalgae production strains
- Compare the microbiome of healthy and crashed cultures to identify harmful organisms (Fig. 1)

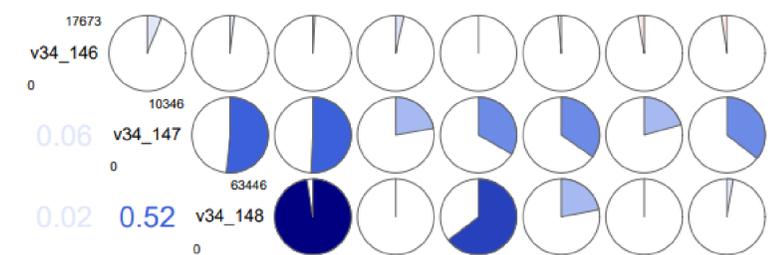


Fig. 1: Comparison of different samples (β -diversity). The darker the blue circle is, the more similar the samples are.

Microbiomes in gas fermenters, biogas plants, and during anaerobic biohydrogen production from wastewaters

- Detect prevailing microbes
- Determine functional groups of microbes by analyzing their taxonomic relationship (Fig. 2, left)
- Follow the transition of microbial mixed cultures during trials via relative abundance analysis (Fig. 2, right)

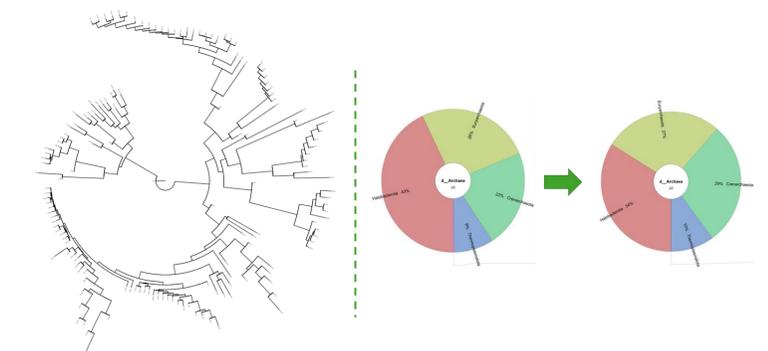


Fig. 2: Left: Taxonomic tree for the analysis of relationships of detected organisms. Right: Change of microbial consortium after adaption to a new substrate.

References

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