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## Motivation

Flocculation has been widely employed in water and wastewater treatment to facilitate water-solids separation. The process requires the use of flocculants that are able to form strong flocs. Currently, the flocculant market is dominated by fossil-based organic flocculants that are poorly biodegradable and potentially toxic. This explains why natural flocculants have emerged as an alternative, environmentally friendly solution since they are non toxic, biodegradable, and have high flocculation performance [1].

## Technological challenge

Microbial extracellular polymeric substances (EPS) have been explored as promising natural flocculants due to their physicochemical properties [2].

EPS are microbial secretions and may either be produced by pure or mixed cultures [3]. In this context, combination of a non-sterile mixed-culture approach with the use of low-cost feedstocks emerges as cost-effective strategy to produce natural flocculants (Fig. 1).

## Research goals

The objective of this research project is to utilize organic waste(water) streams as organic substrate to produce microbial EPS by employing a mixed microbial culture approach, followed by investigating the potential of the produced EPS as natural flocculants. This is accompanied by several challenges and research questions including:

- What is the response of the microbial community to the use of varied organic substrates?
- Can EPS production be maintained when fed with different substrates and what are the effects of it on the EPS composition in terms of protein, carbohydrate, and other biopolymers?
- Which factors determine the competition between production of EPS and internal storage products (e.g PHA)?
- Can the mixed-culture EPS be employed as natural flocculants and if necessary, how can the flocculation efficiency be improved?

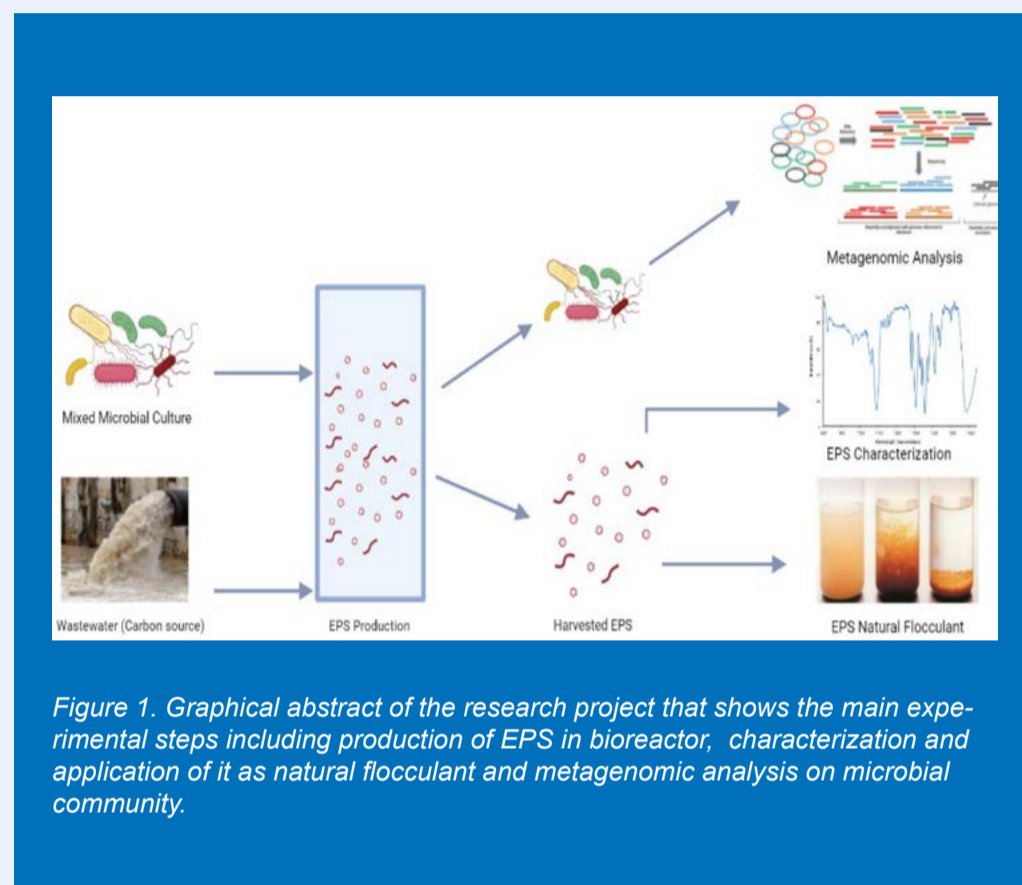


Figure 1. Graphical abstract of the research project that shows the main experimental steps including production of EPS in bioreactor, characterization and application of it as natural flocculant and metagenomic analysis on microbial community.

## References

- [1] Ajao, V., Bruning, H., Rijnaarts, H., Temmink, H., Chemical Engineering Journal (2018), 622-632.
- [2] Ajao, V., Fokkink, R., Leermakers, F., Bruning, H., Rijnaarts, H., Temmink, H., Journal of Colloid and Interface Science(2021), 533-544.
- [3] Nacher-Pellicer, C., Domingo-Felez, C., Mutlu, G., Smets, B., Water Research (2013), 5564-5574.