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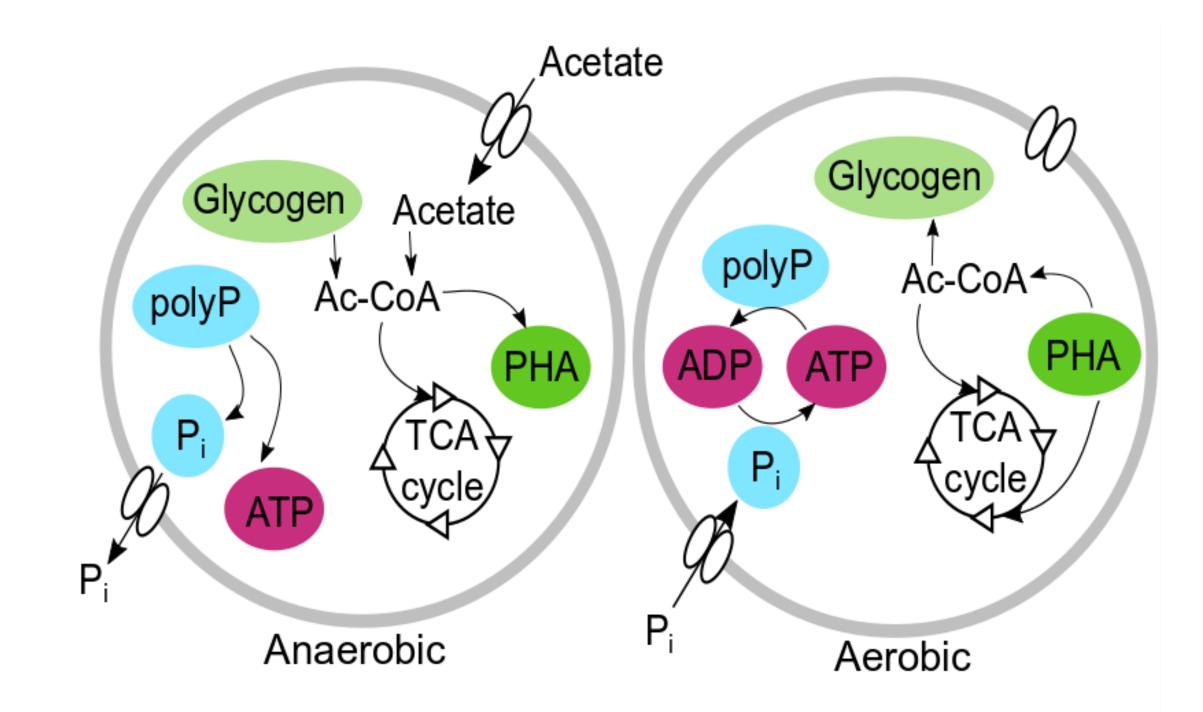
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Mapping of Several Putative Polyphosphate-Accumulating Organisms

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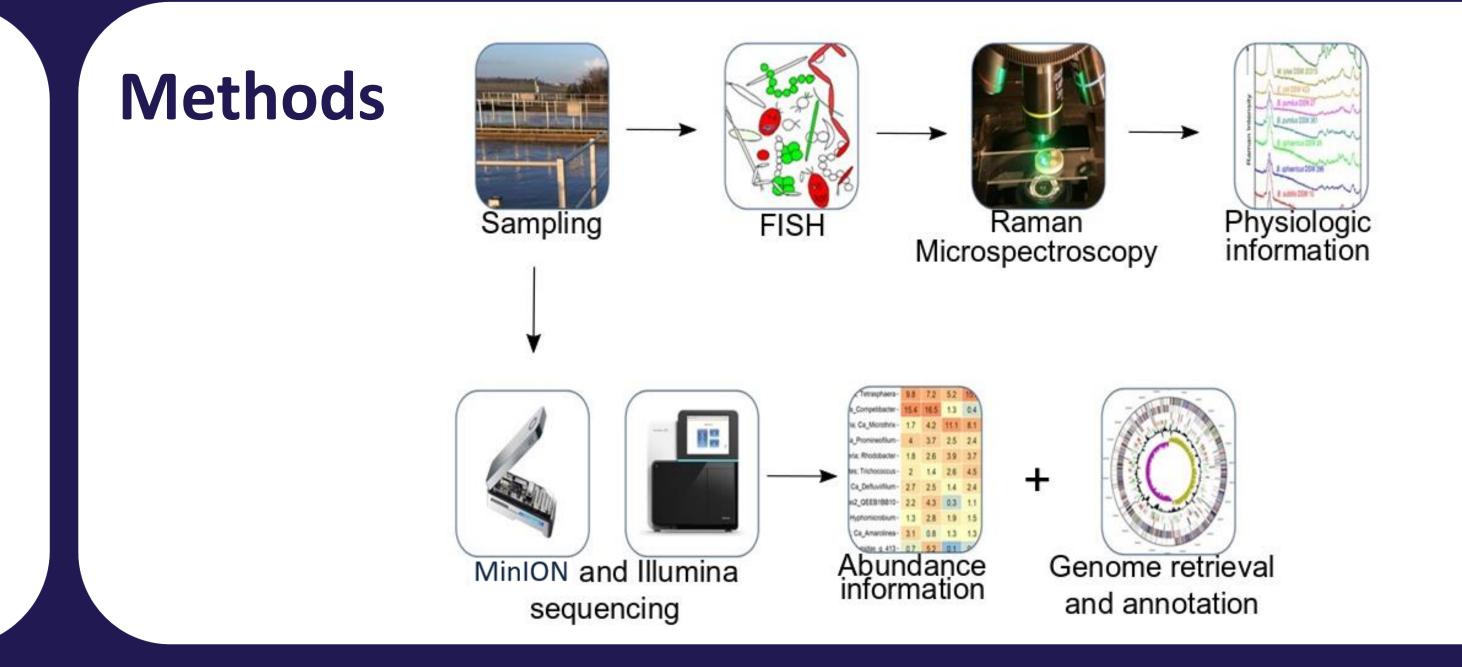
Background

Phosphate (P) is a vital but limited resource in nature, so recycling it will become important to support the increasing demand. By utilizing the Enhanced Biological Phosphorus Removal (EBPR) process in wastewater treatment plants, recycling of P from the wastewater is one way to combat this challenge. The EBPR process is controlled by polyphosphate-accumulating organisms (PAOs), such as Candidatus Accumulibacter, Tetrasphaera, and Dechloromonas, but all are not known. They store phosphate intracellularly for further removal and recovery due to alternating anaerobic and aerobic conditions.



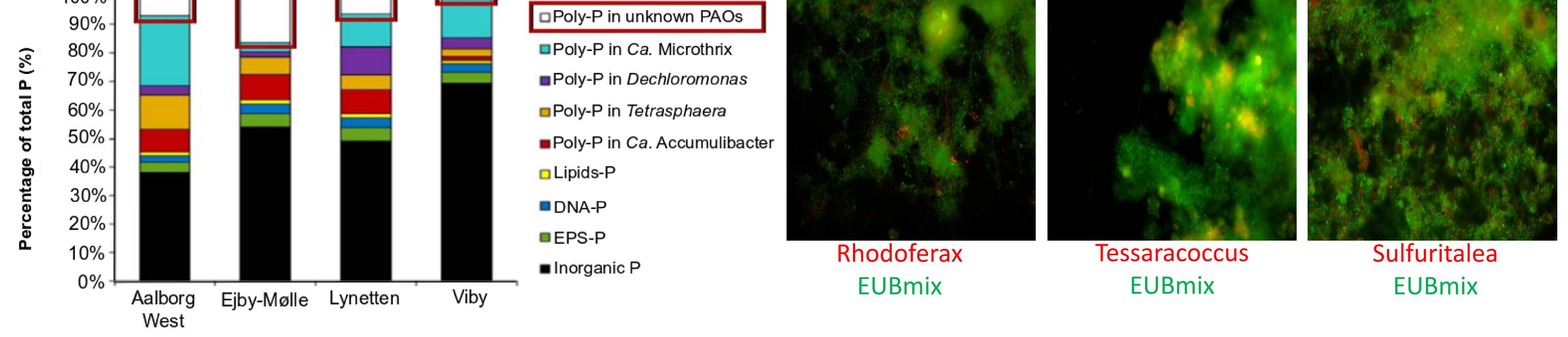
Aim

 Investigate whether the putative PAOs *Rhodoferax, Tessaracoccus, and Sulfuritalea* are in fact PAOs
 Determine their metabolic potential using metagenomics
 Define the levels and dynamics of important storage polymers by FISH-Raman microspectroscopy



Results

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- Recent P mass balance showed that we are still missing some PAOs
- The putative PAOs were abundant in varying degree in DK wastewater treatment plants

Proteobacteria; Rhodoferax -	0.9	0.9	0.6	1	0	1.1	1.9	0.8	1.6	0.7	1.2	0.2	1.3	0.9	0.8	0.6	0.1	1.5	0.7	1.5	0.5	2.1	0.8	2	0.9	2	1.8	1	0.9	0.9	1.2	1.1	1.5	1.2	0.9	0.9	2.1	1.8	0.5
Proteobacteria; Sulfuritalea -	1.3	0.9	0.4	0.7	0	1.7	0.8	1.1	1.6	1.4	0.3	0.2	1	0.6	1.1	0.2	o	0.2	0.2	0.7	1.3	1.4	0.4	0.3	0.2	0.9	1.2	0.8	1.5	0.7	1.1	0.4	1	0.7	1.3	0.2	1	0.7	0.2
Actinobacteria; Tessaracoccus -	0.1	0.3	0.3	0.5	0	0.4	0.5	0.1	0.1	0.5	0.8	2.2	0.5	0.2	0.2	0.3	0.1	0.7	0.6	0.3	0.1	0.2	2.6	0.7	0.6	0.4	0.6	0.4	0.2	0.2	0.3	0.6	0.1	0.5	0.5	0.5	0.5	0.7	0.1

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Conclusion

Genus- or species specific FISH probes were designed. Intracellular storage polymers of the FISH-defined cells were investigated with Raman microspectroscopy and all showed potential for poly-P storage, but not necessarily with the classic PAO metabolism. The ecophysiology was supported by annotating their metabolic pathways with the use of high-quality metagenome assembled genomes.





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