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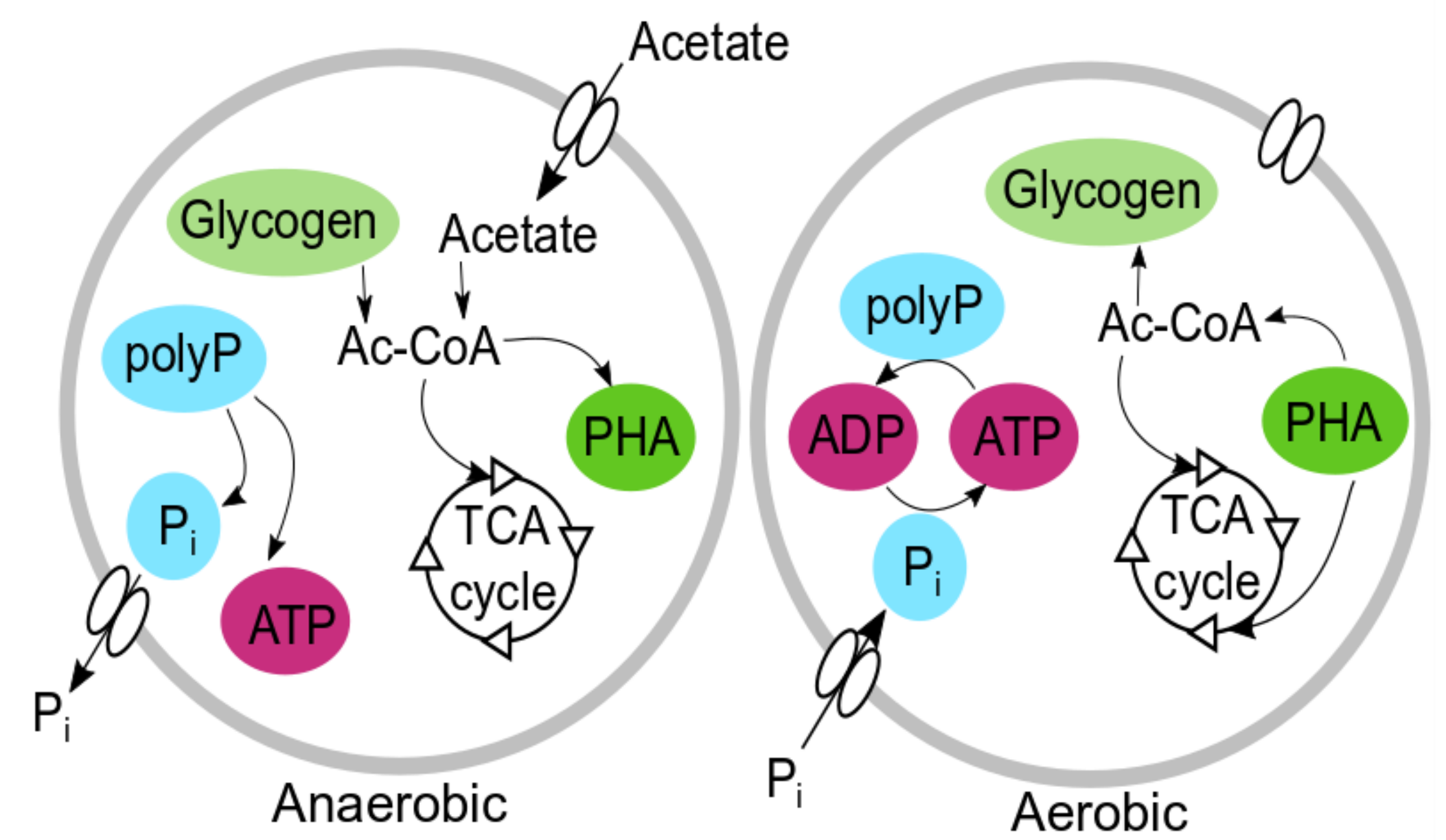
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Mapping of Several Putative Polyphosphate-Accumulating Organisms

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Background

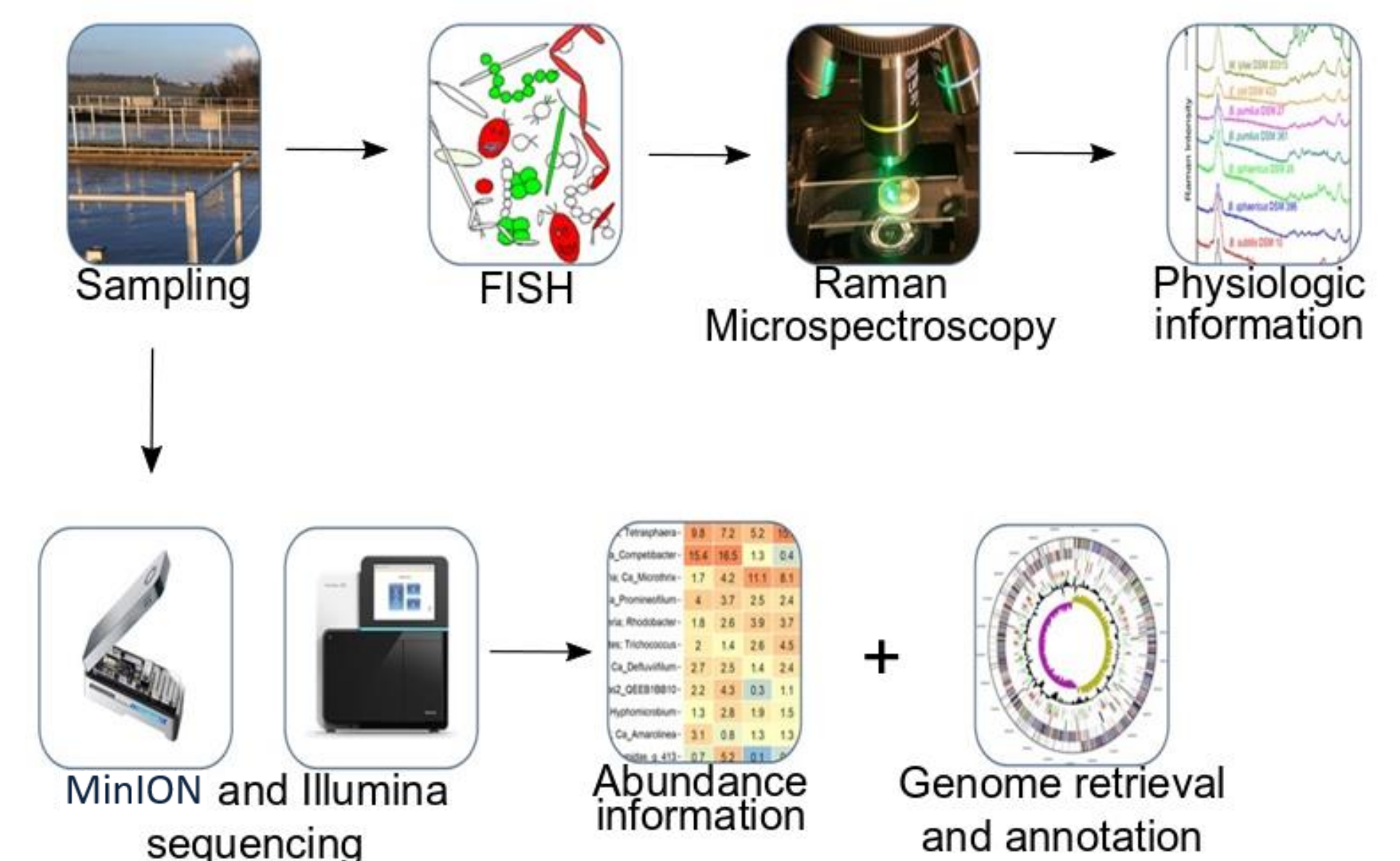
Phosphate (P) is a vital but limited resource in nature, so recycling it will become important to support the increasing demand. By utilizing the **Enhanced Biological Phosphorus Removal (EBPR)** process in wastewater treatment plants, recycling of P from the wastewater is one way to combat this challenge. 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**.



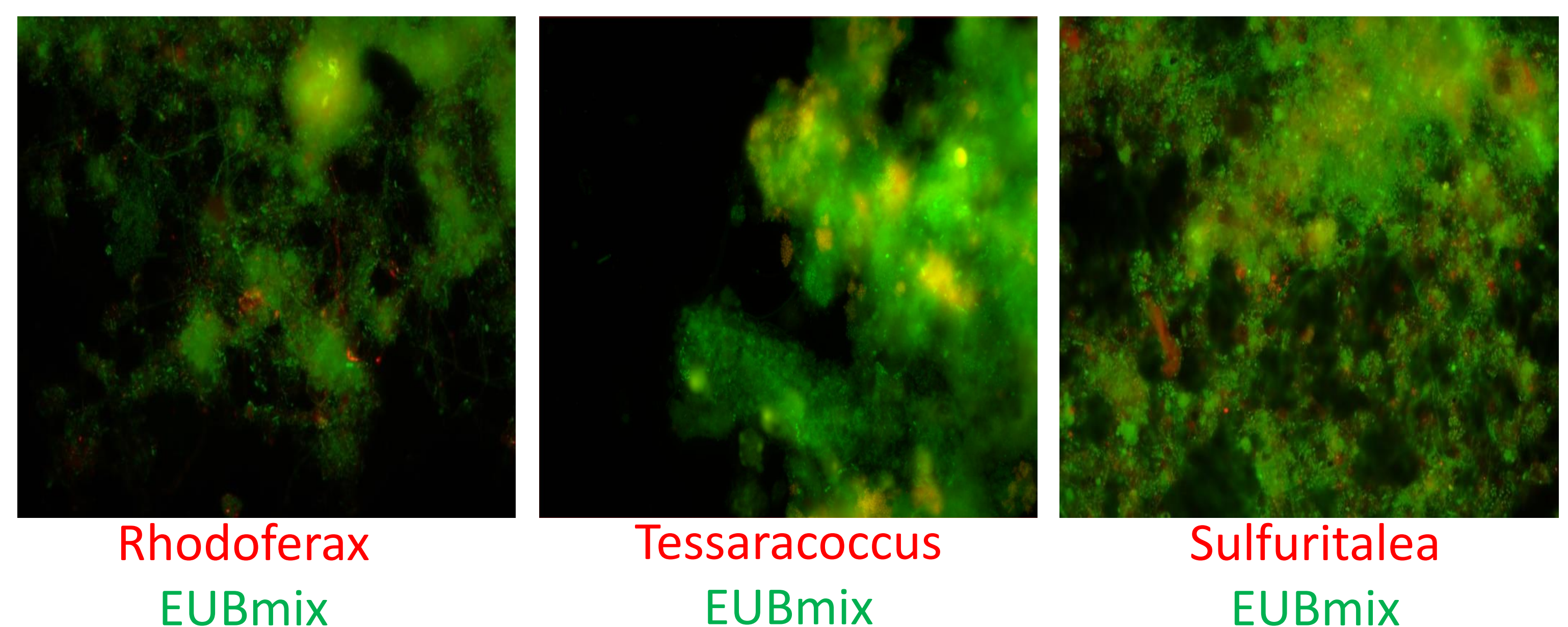
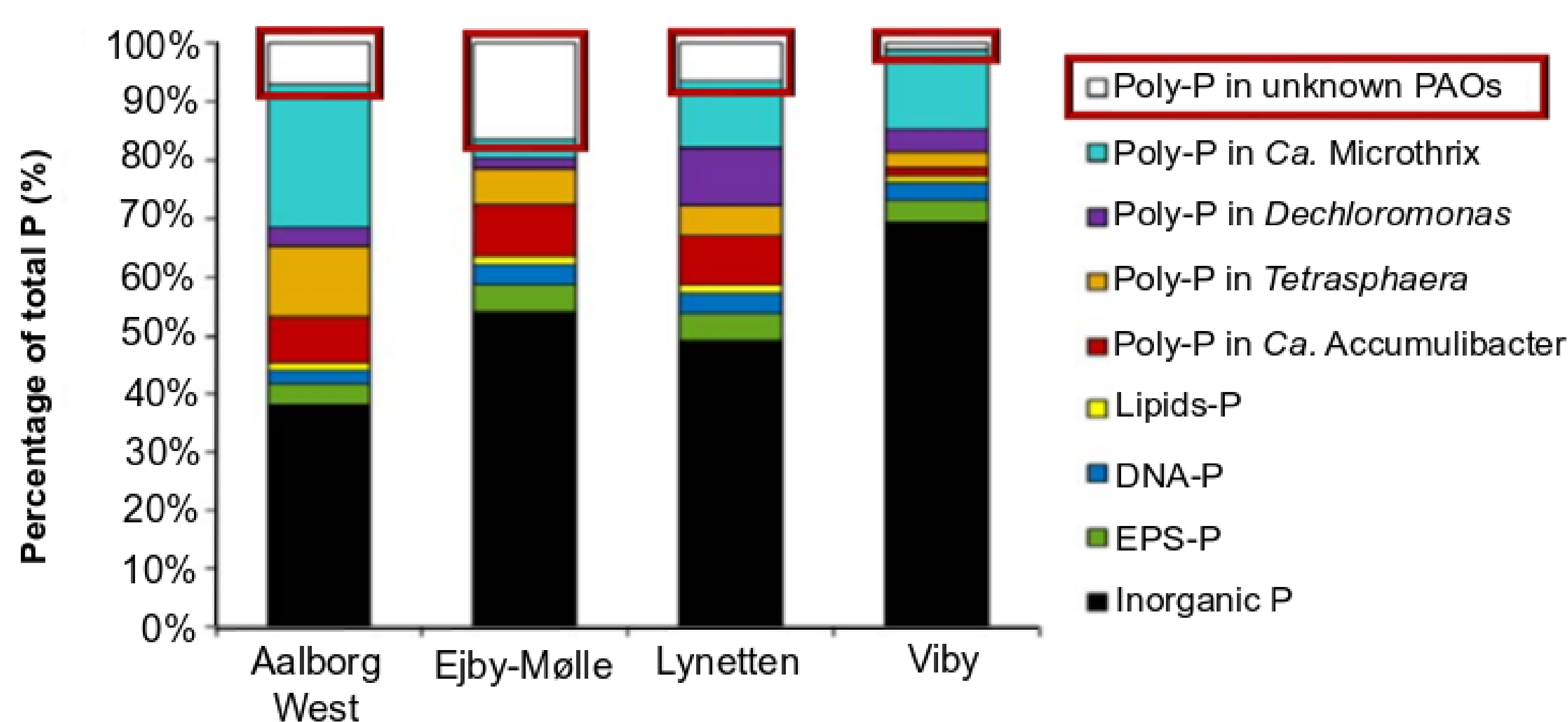
Aim

- Investigate whether the putative PAOs *Rhodofex*, *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

Methods



Results



- 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; Rhodofex	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	0	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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