Metagenomics study of Enhanced Biological Phosphorus Removal (EBPR)

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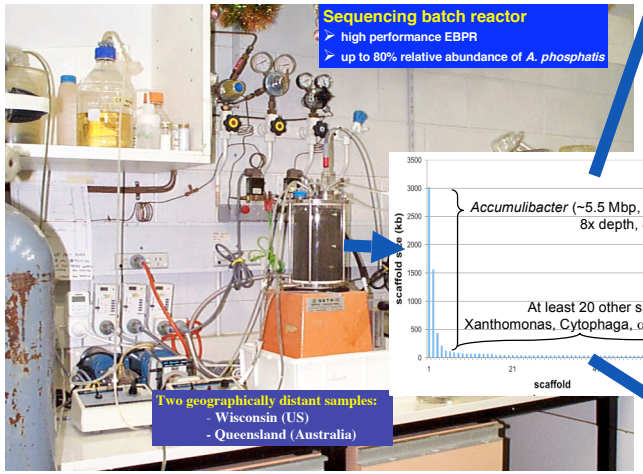
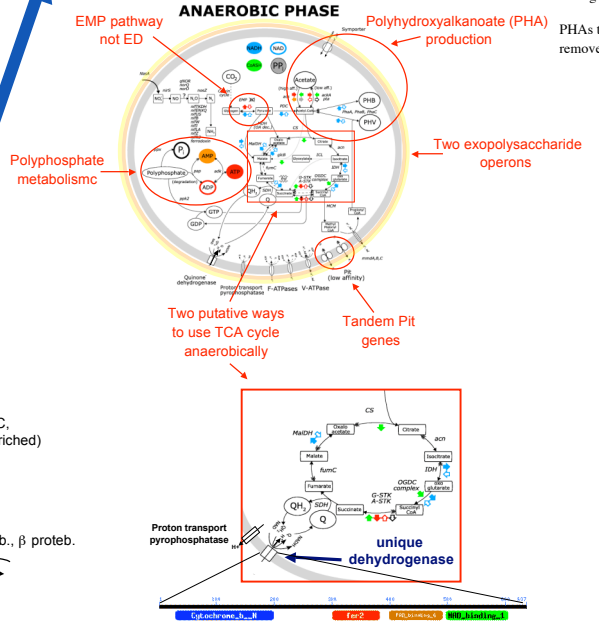
What is EBPR?

- Enhanced Biological Phosphorus Removal (EBPR) is a **bacterially mediated** process to achieve low levels of phosphorus (P) in treated wastewater.
- EBPR is **cheaper** and has a **lesser environmental impact** than the alternative process, chemical removal.
- Although the main phosphorus removing agent has been identified (*Accumulibacter phosphatis*), EBPR **genetic and biochemical details were unknown** until now.



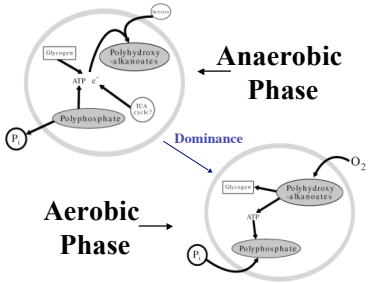
Accumulibacter phosphatis genome

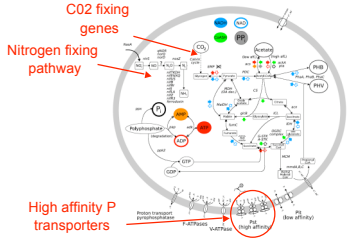
Full gene complement for EBPR metabolism.



A unique dehydrogenase putatively functioning in reverse enable anaerobic use of TCA cycle. This provides extra reducing power (NADH) that confers a competitive edge in storing acetate in the form of PHAs.

A.phosphatis likely achieves dominance by storing most acetate in the wastewater during the anaerobic phase. In the aerobic phase it uses stored acetate in the form of PHAs to restore glycogen and polyphosphate levels; in doing so phosphate is removed from water:

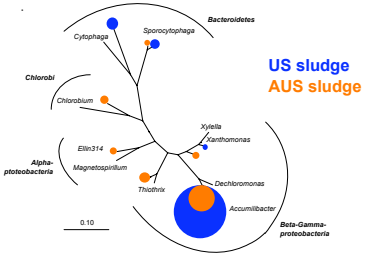




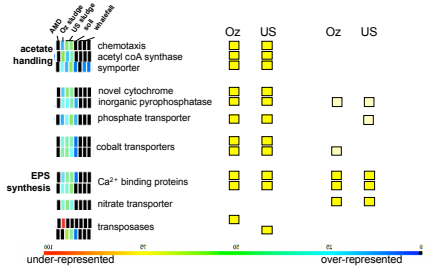
Presence of gene complement necessary for C, N, P limited habitats (which wastewater is not) suggests that the population is being replenished from outside.

Community analysis

Community composition based on 16S rRNA genes from assembled metagenomic data. Circle size approximately corresponds to population abundance. The species flanking *A. phosphatis* are highly variable between the two sludges.



Environmental Gene Tag (EGT) analysis groups genes in families and counts relative number of genes from a given family in each environment. Highly represented families indicate gene complements advantageous in a given environment.



The availability of an almost complete genome for the main agent of EBPR, in principle, allows detailed insights into the pathways necessary for EBPR, the genetic reasons underlying the dominance of *A. phosphatis* and the requisites for its cultivation, the latter being a requirement for metabolic engineering. The present study illustrates that metagenomics provides detailed, often novel, insights into even well-studied communities and accelerates understanding of complex biological systems.

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