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Genomic investigation of the lipid accumulating filamentous bacterium *Candidatus* ‘*Microthrix parvicella*’



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Introduction

Candidatus ‘*Microthrix parvicella*’ is a Gram positive, filamentous member of the *Actinobacteria* (Fig. 1). It is observed in activated sludge wastewater treatment plants (WWTP) where it is often associated with the poor sludge separation problems known as ‘bulking’ and ‘foaming’.

Despite the importance of ‘*M. parvicella*’ little is known about its physiology and why it thrives in these treatment plants; an improved understanding is likely to provide the key to improving control strategies.

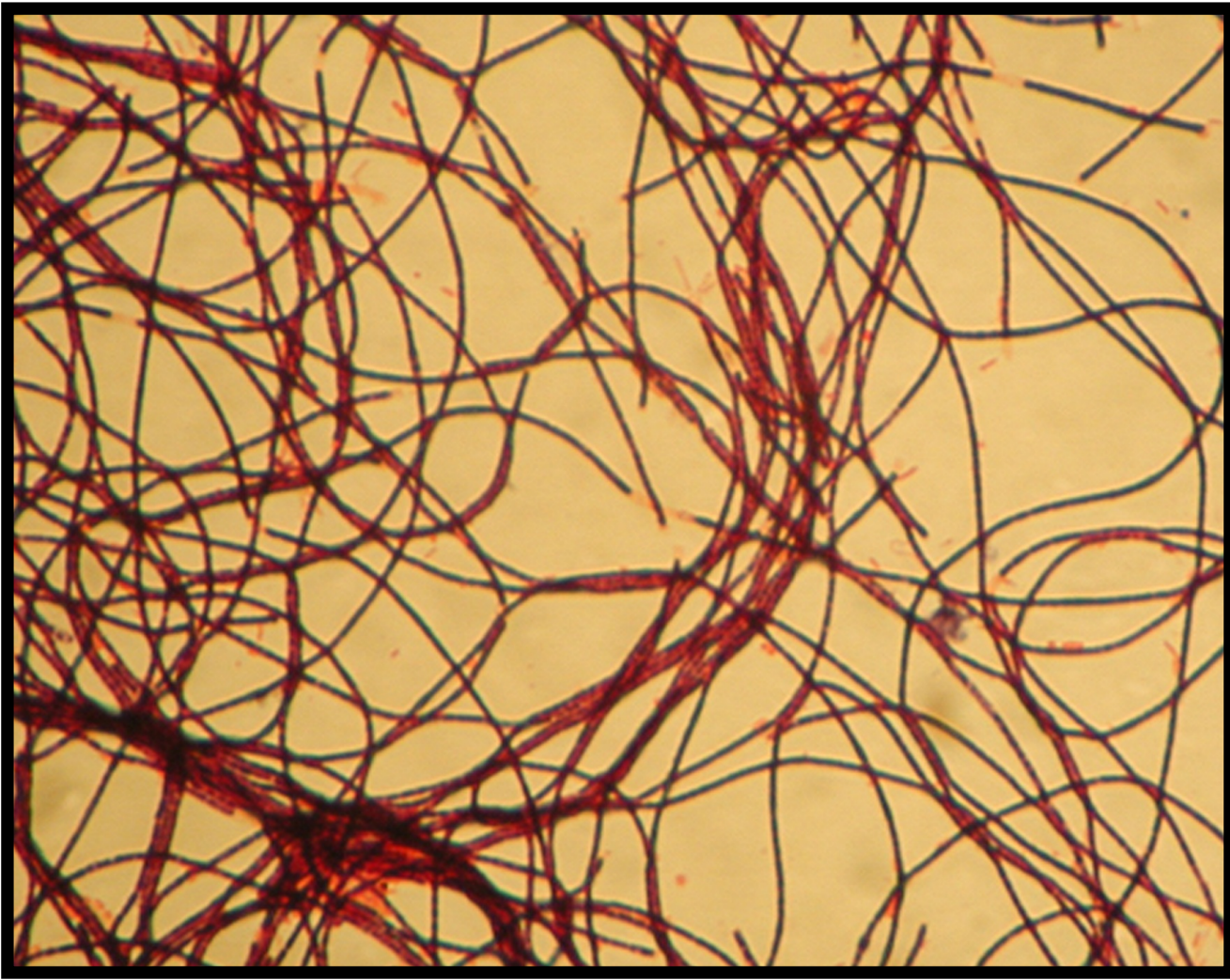


Fig 1. Micrograph of Gram stained biomass from a WWTP dominated with ‘*M. parvicella*’.

Aims & Approach

- The aims were to develop a putative metabolic model for ‘*M. parvicella*’ in activated sludge treatment plants (Fig. 3) and to make genomic comparisons between pure culture isolates and *in situ* strains.
- To achieve these aims we sequenced and annotated ‘*M. parvicella*’ strain RN1 and compared the genome with strains present in two metagenomes from full scale WWTPs.

Genetic diversity

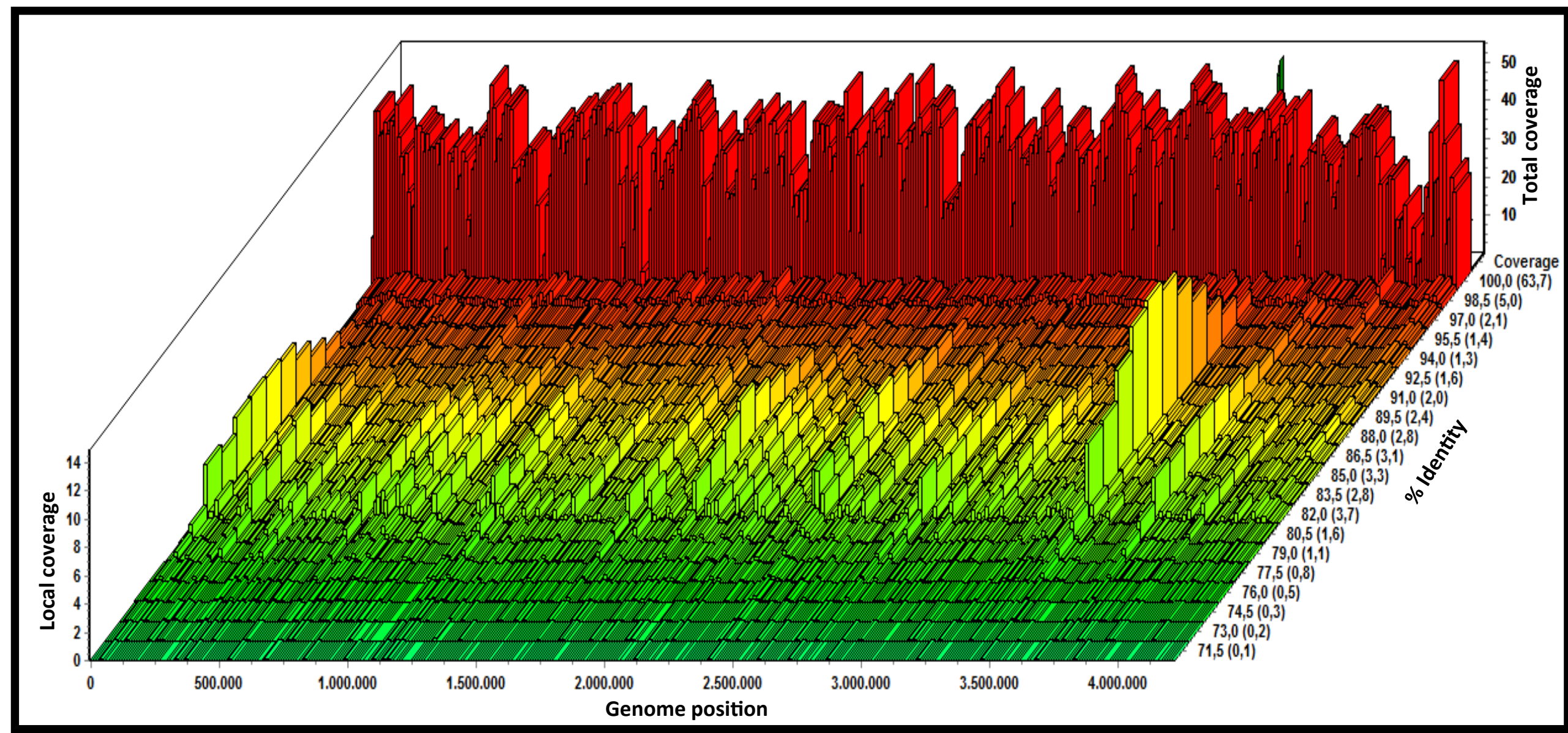


Fig 2. Graphical overview of the mapping of the short metagenome reads from the Aalborg West EBPR WWTP to the genome of ‘*M. parvicella*’ as a function of percent identity of each read.

- RN1 is remarkably similar to *in situ* strains (Fig. 2).
- Identifiable genetic differences between strains are mainly associated with mobile genetic elements and exopolysaccharide synthesis.
- Other differences include genes involved in fructose metabolism and mercury resistance.

Metabolic model

Anaerobic conditions:

Utilisation of polyphosphate, trehalose and long chain fatty acids may provide energy and reducing equivalents for lipid uptake and storage as triacylglycerols (TAGs).

Aerobic/anoxic conditions:

Stored TAGs are utilised providing energy and carbon for growth and cell maintenance.

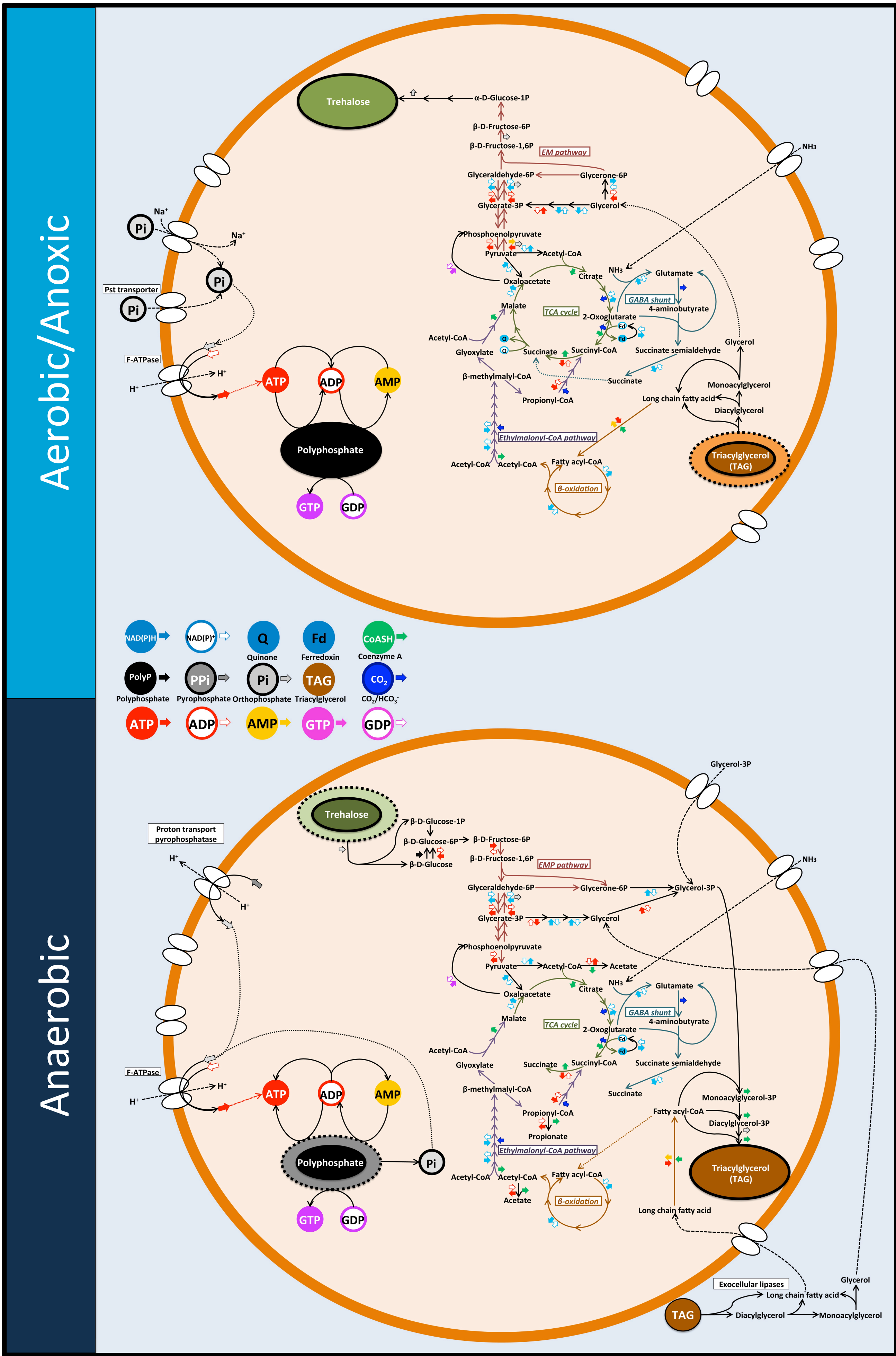


Fig 3. Overview of the energy and carbon metabolism of ‘*M. parvicella*’ in activated sludge WWTPs.

Closing remarks

The annotated genome provides the foundation for future studies, such as transcriptomics and proteomics, that will validate the proposed model and provide further insight into the *in situ* physiology of ‘*M. parvicella*’. Such advances in our understanding will likely lead to improved control strategies for this problematic organism.