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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.

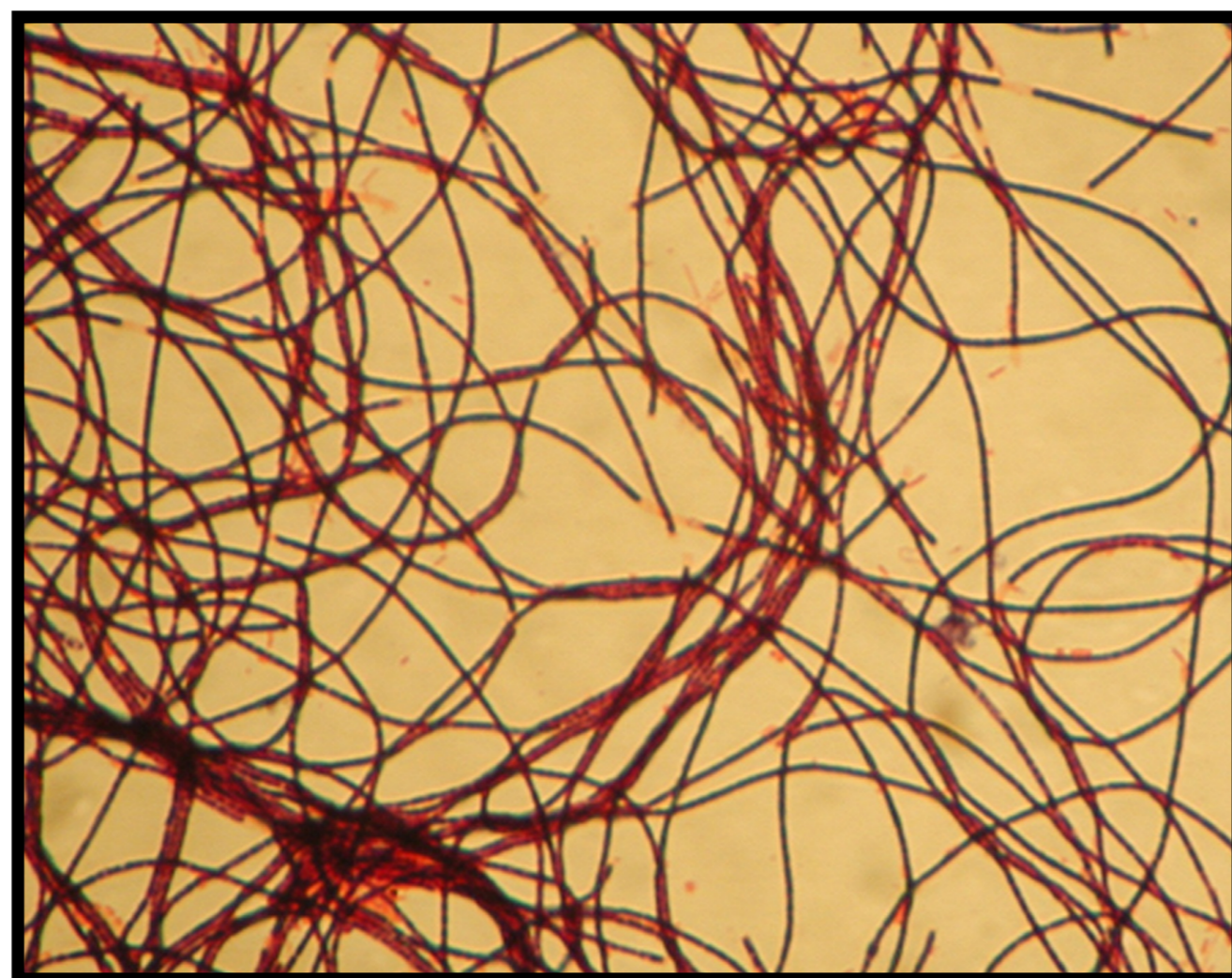


Fig 1. Micrograph of Gram stained biomass from a WWTP dominated with '*M. parvicella*'.

## 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

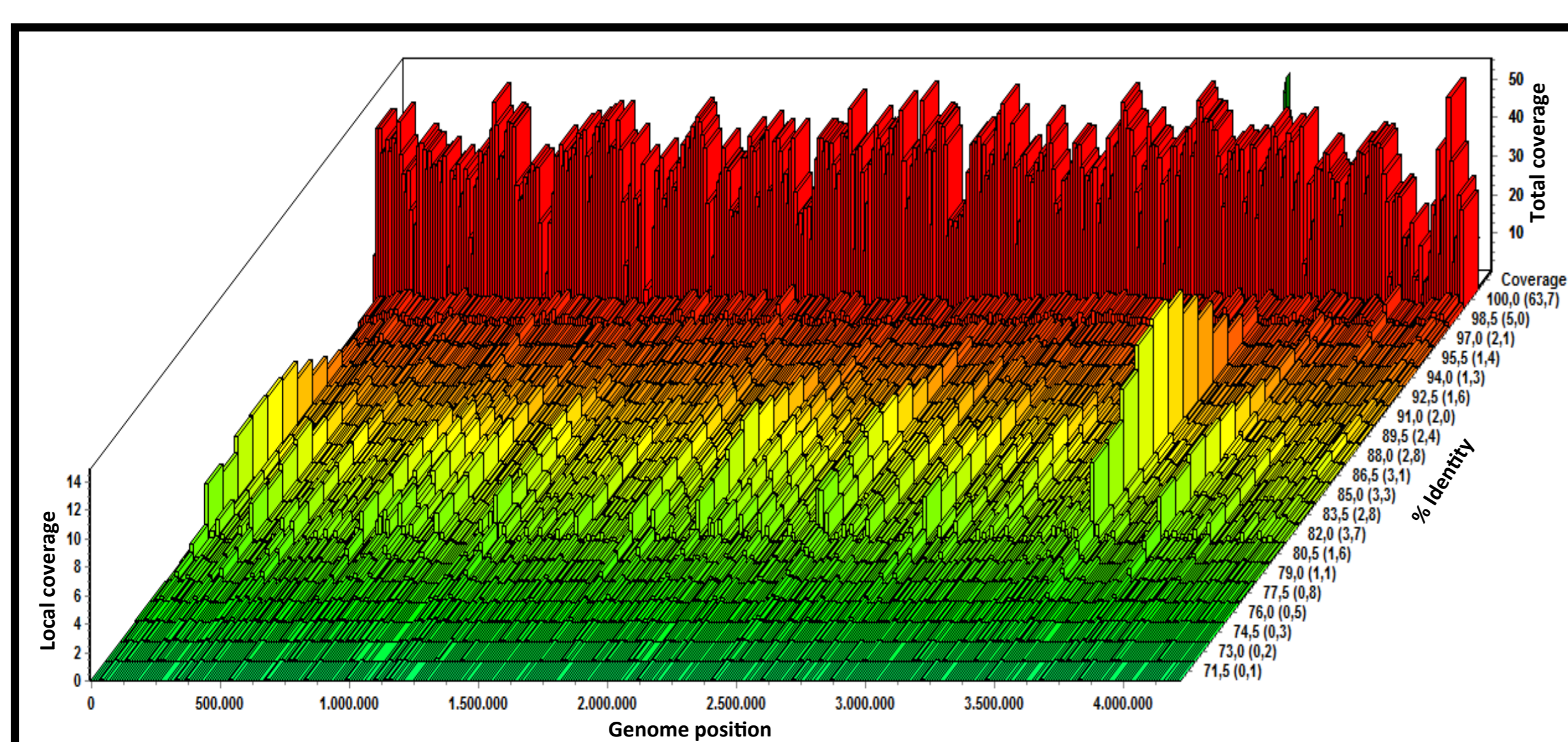


Fig 2. Graphical overview of the mapping of the short metagenome reads from the Aalborg West EBPR WWTP to the genome of '*M. parvicella*' as a function of percent identity of each read.

- 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.

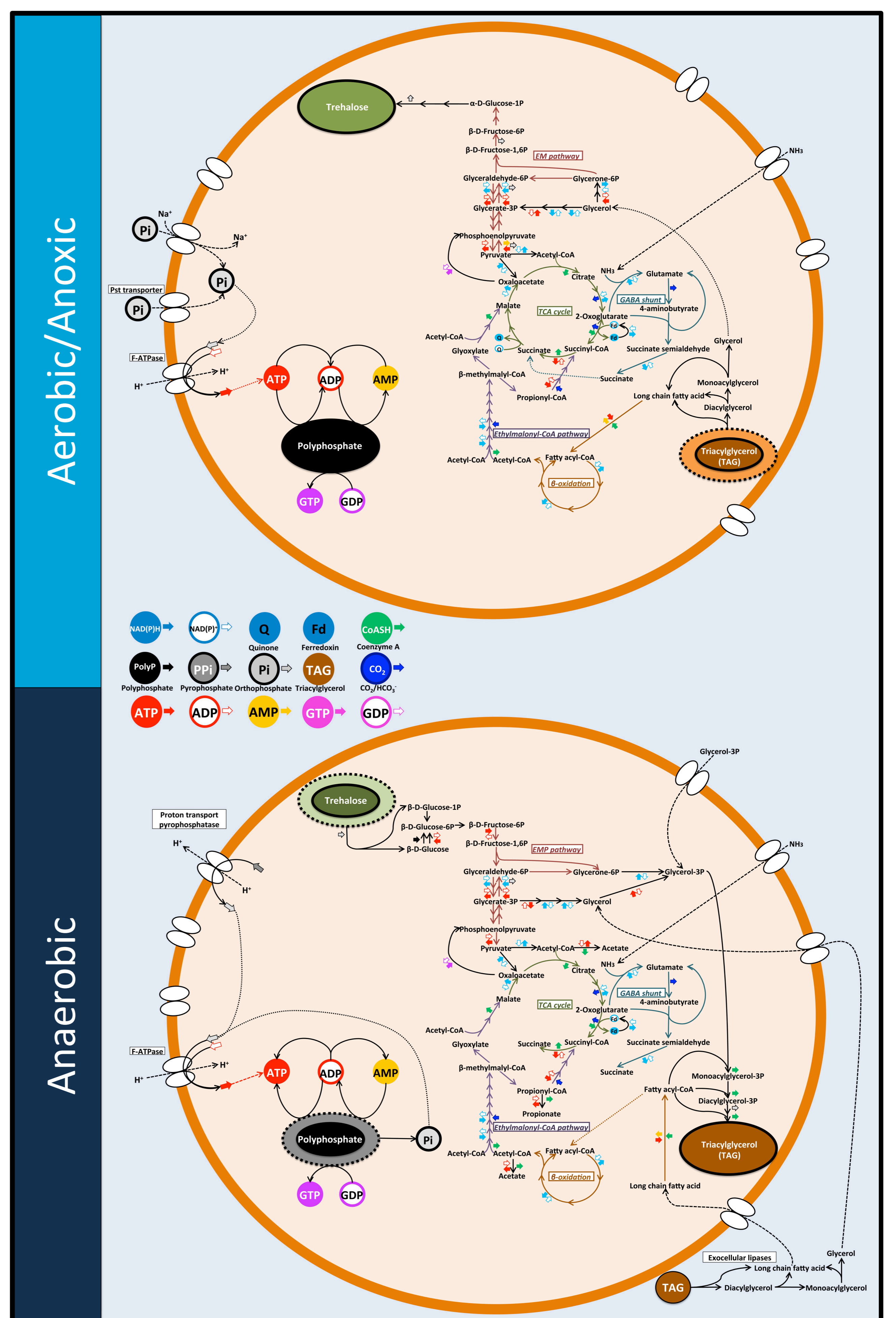


Fig 3. Overview of the energy and carbon metabolism of '*M. parvicella*' in activated sludge WWTPs.

## 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.