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Genomic investigation of the filamentous foam forming Candidatus 'Microthrix parvicella' isolated from activated sludge

Mcllroy, Simon Jon; Seviour, Robert; Rossetti, Simona; Tandoi, Valter; Kristiansen, Rikke; Nielsen, Jeppe Lund; Petrovski, Steve; Nielsen, Per Halkjær

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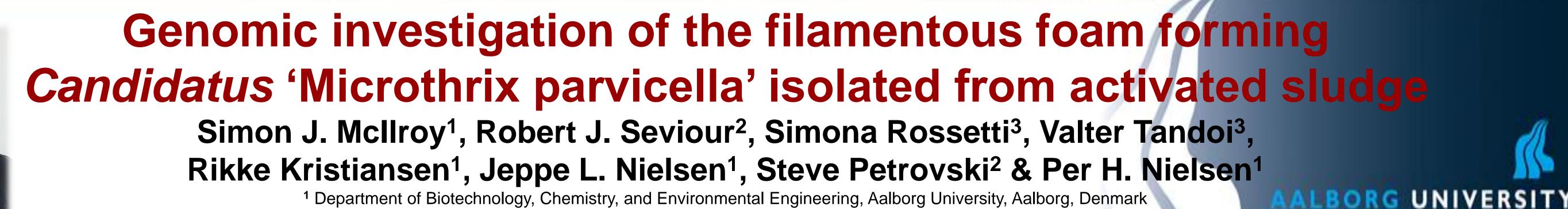
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¹ Department of Biotechnology, Chemistry, and Environmental Engineering, Aalborg University, Aalborg, Denmark ² Biotechnology Research Centre, La Trobe University, Bendigo, Vic 3552, Australia ³ Water Research Institute, CNR, Via Reno 1, 00198 Rome, Italy

Introduction

Candidatus 'Microthrix parvicella' (henceforth referred to as '*Microthrix*') is a Gram positive, filamentous member of the *Actinobacteria* (**Fig. 1**). It is observed in activated sludge wastewater treatment plants where it is often associated with the poor sludge separation problems known as 'bulking' and 'foaming' (**Fig. 2**).

Despite the importance of '*Microthrix*' 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 future control strategies.

Candidatus'Microthrix parvicella' st. RN1, X93044 Candidatus'Microthrix parvicella' st. DAN1-3, X82546 Candidatus'Microthrix parvicella' st. Ben43, X89774 Candidatus'Microthrix parvicella' st. EU18, DQ147280

Summary of metabolic model

Based on the annotation of key pathways the main features of the proposed metabolic model for '*Microthrix*' in activated sludge is summarised as follows (**Fig. 3**).

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Anaerobic conditions:

- Uptake and storage of lipids as intracellular triacylglycerols (TAGs).
- Hydrolysis of polyphosphate provides energy for carbon uptake and storage.

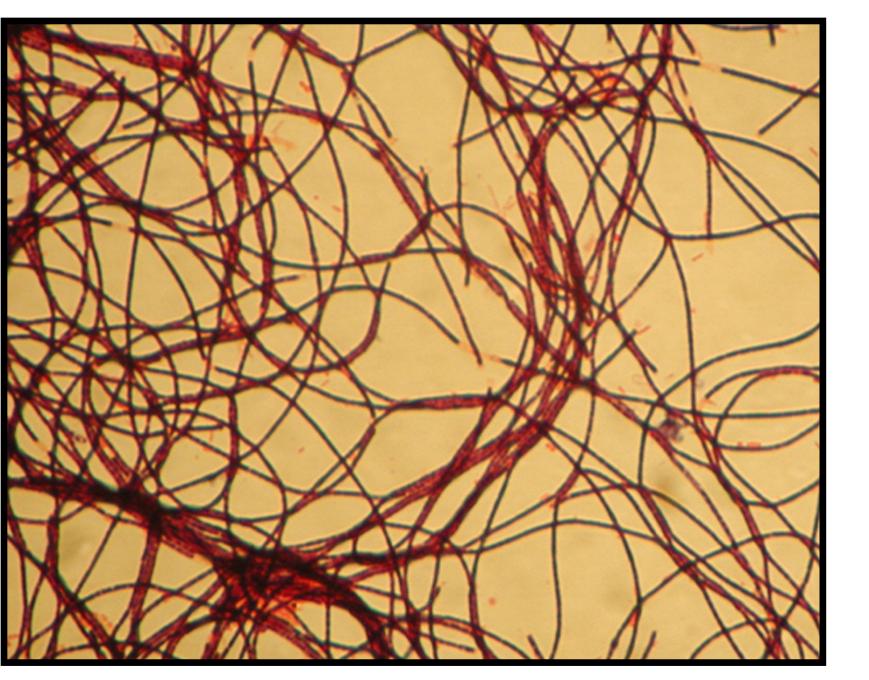
Aim

To develop a putative metabolic model to explain the success of '*Microthrix*' under the dynamic conditions of activated sludge treatment (**Fig. 3**).

Approach

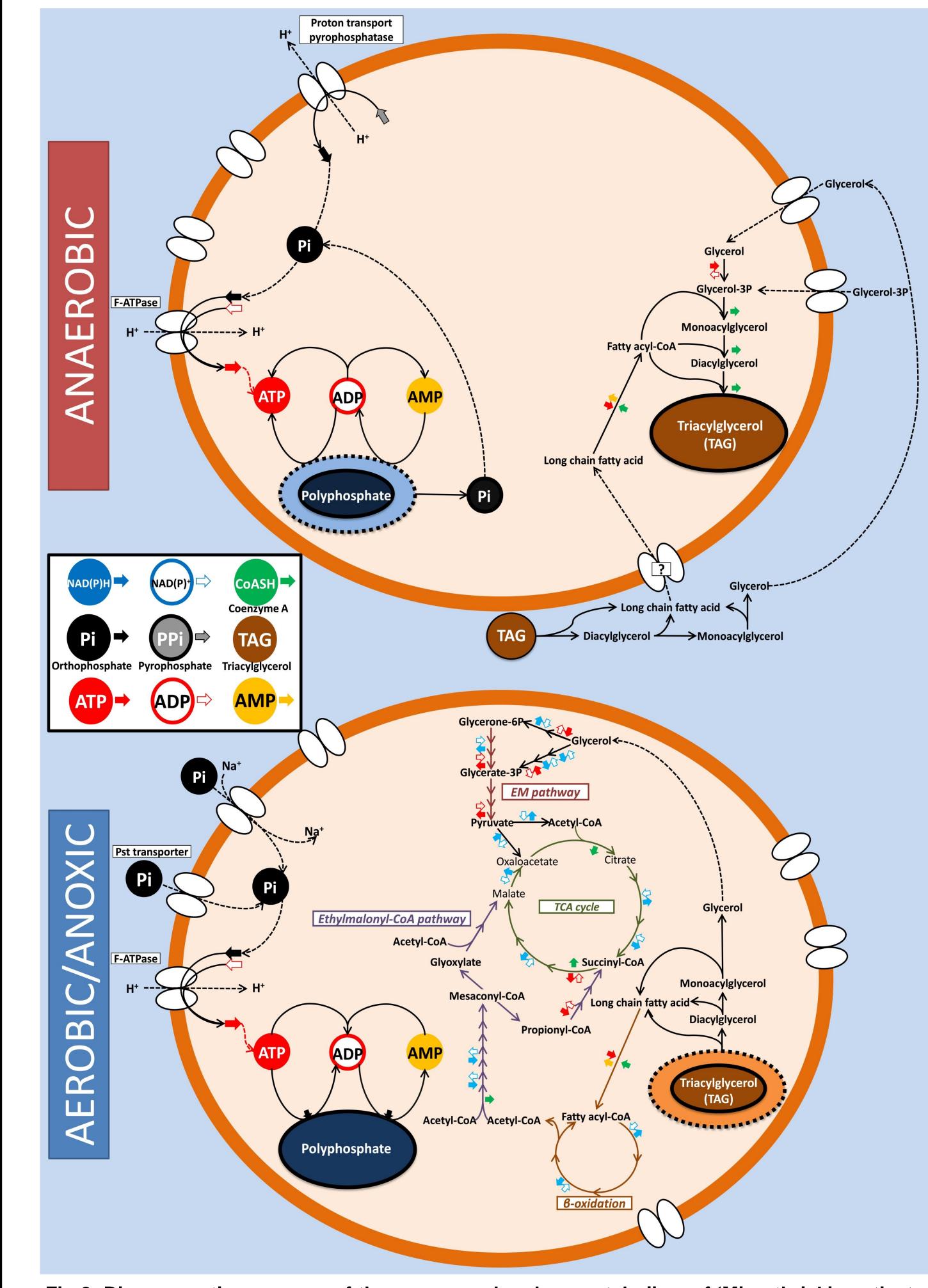
 An almost complete genome Of '*Microthrix*' strain RN1 (Fig. 1) Candidatus Microthrix parvicella' st. EU18, DQ147280 Candidatus Microthrix calida' st. TNO1-1, DQ147281 Acidimicrobium ferrooxidans, U75647 Ferrimicrobium acidiphilum, AF251436 Ferrithrix thermotolerans, AY140237 Iamia majanohamensis, AB360448 Ilumatobacter fluminis, AB360343 Dietzia maris, X79290 Tsukamurella spumae, Z37150 Mycobacterium phlei, AF480603 Gordonia amarae, X80635 Millisia brevis, AY534742 Nocardia asteroides, X806606 Rhodococcus erythropolis, X81929 Tetrasphaera jenkinsii, DQ007321 Trichococcus flocculiformis, AJ306611

Fig 1. 16S rRNA gene ML phylogenetic tree of '*Microthrix*' isolates and selected related sequences.



Aerobic/anoxic conditions:

- Stored TAGs are utilised via the β-oxidation pathway, ethylmalonyl-CoA pathway and TCA cycle providing energy and carbon for growth and cell maintenance.
- Phosphate is taken up and stored as polyphosphate.



was obtained using the 454 sequencing method.

Fig 2. Gram stain micrograph of the biomass from an activated sludge plant dominated with '*Microthrix*'.

 Annotations were made with the MaGe platform (Genoscope) for the key metabolic pathways, entailing the carbon, nitrogen and phosphorus metabolism.

Summary of key pathways

Pathway	Present in genome?	
Central carbon metabolism		
Oxidative TCA cycle	Yes	
Reductive TCA cycle	No	
Glyoxylate shunt	No	
Ethylmalonyl-CoA	Yes	
Glycolysis EM	Yes	
Glycolysis ED	No	
Gluconeogenisis	Yes	
Fermentation	No	
Storage polymers		

Fig 3. Diagrammatic summary of the energy and carbon metabolism of 'Microthrix' in activated sludge wastewater treatment systems.

Polyhydroxyalkanoate synthesis	No
Glycogen synthesis	No
Polyphosphate synthesis	Yes
Triacylglycerol synthesis	Yes
Denitrification	
Nitrate (NO ₃ ⁻) \rightarrow Nitrite (NO ₂ ⁻)	Yes
Nitrite $(NO_2^-) \rightarrow Nitric oxide (NO)$	Yes
Nitric oxide (NO) \rightarrow Nitrogen (N ₂)	No

Table 1. Summary of selected pathways in the 'Microthrix' genome.

Closing remarks

- As indicated by *in situ* data the '*Microthrix*' genome indicates that it is a lipid specialist.
- The annotated genome provides the foundation for -omic based methods such as transcriptomic and proteomic studies that will validate this model and provide further insight into its *in situ* physiology.
- The annotation analysis of the '*Microthix*' genome is an ongoing project.



