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## The New MiDAS Field Guide: Comprehensive Online Ecosystem-specific Database of Microorganisms in Wastewater Treatment Systems

Nierychlo, Marta Anna; Xu, Yijuan; David Green, Nick; Andersen, Kasper Skytte; Dueholm, Morten Simonsen; Nielsen, Per Halkjær

*Publication date:*  
2019

[Link to publication from Aalborg University](#)

### *Citation for published version (APA):*

Nierychlo, M. A., Xu, Y., David Green, N., Andersen, K. S., Dueholm, M. S., & Nielsen, P. H. (2019). *The New MiDAS Field Guide: Comprehensive Online Ecosystem-specific Database of Microorganisms in Wastewater Treatment Systems*. Poster presented at 8th IWA Microbial Ecology and Water Engineering Specialist Conference, Hiroshima, Japan.

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# The new **MiDAS Field Guide**: comprehensive online **ecosystem-** **specific database** of microorganisms in wastewater treatment systems



**Marta Nierychlo**, Yijuan Xu, Nick Green, Kasper S. Andersen, Morten Dueholm, Per H. Nielsen  
Center for Microbial Communities, Department of Chemistry and Biosciences, Aalborg University, Denmark

## MiDAS3 taxonomy

### Browse taxonomy

Search by name  
Tetrasphaera

There are 6 matches for the term "Tetrasphaera"

- Kingdom: Bacteria
- Phylum: Acidobacteria
- Class: Actinobacteria
- Order: Actinomycetales
- Order: Corynebacteriales
- Order: Frankiales
- Order: Kineosporiales
- Class: Micrococcales
- Order: Beutenbergiaceae
- Order: Bogoriellaceae
- Order: Cellulomonadaceae
- Order: Demequinaceae
- Order: Dermatophilaceae
- Order: Intrasporangiaceae
- Genus: **Tetrasphaera**

Species list:

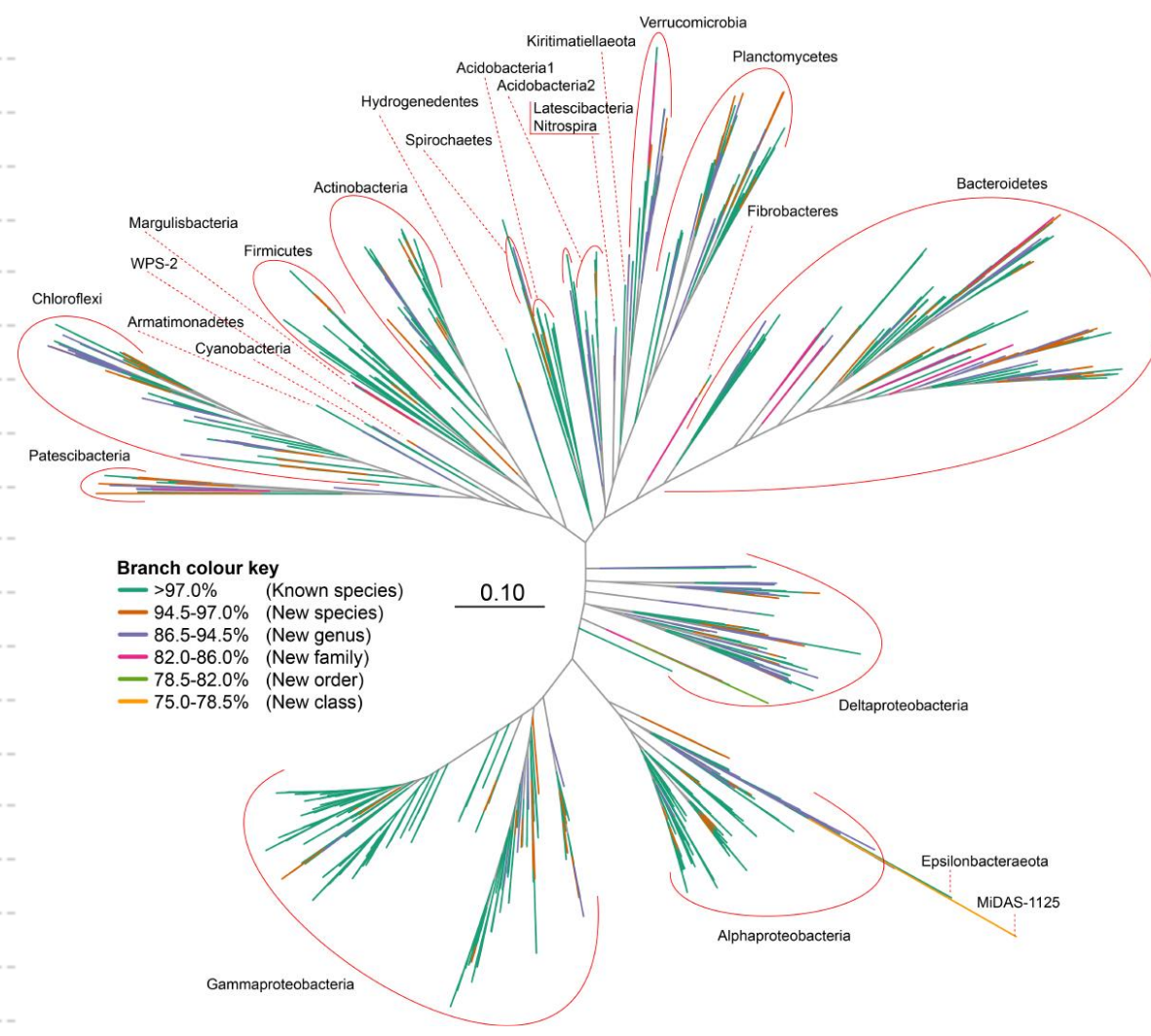
- midas\_s\_5
- midas\_s\_45
- midas\_s\_220
- midas\_s\_299
- midas\_s\_328
- midas\_s\_469
- midas\_s\_1378
- midas\_s\_7982
- Tetrasphaera elongata*
- midas\_s\_544
- midas\_s\_1404
- Tetrasphaera jenkinsii*
- Tetrasphaera vanveanii*
- midas\_s\_4011
- midas\_s\_5540
- midas\_s\_5776
- Tetrasphaera australiensis*
- midas\_s\_6115
- Tetrasphaera japonica*

Reference database (full-length sequences) is based on extensive study of Danish BNR plants and anaerobic digesters (Dueholm et al., 2019)

Browse Taxonomy function contains all microbes found in the ecosystem:

**1809 genera**  
**4245 species**

Functional information provided for 220 (and counting!) abundant and/or important microbes in the ecosystem

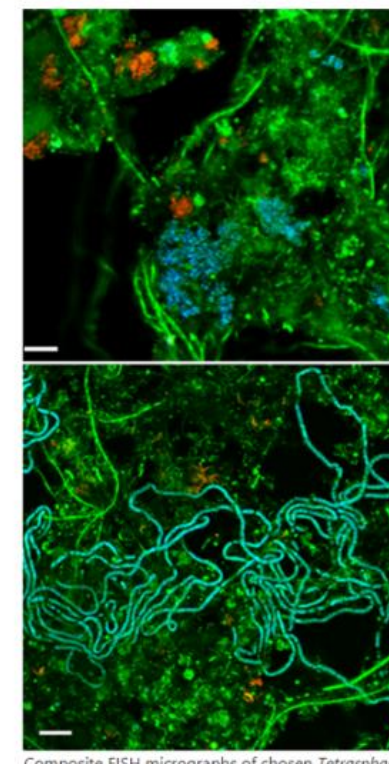


## Linking identity with function

### Genus: *Tetrasphaera*

Alternative names: n/a  
Source: Published  
NCBI Taxonomy ID: 99479  
Genome: Yes 1 NCBI  
16S rRNA Gene Copy Number: 1-2  
MiDAS 3.5 Taxonomy

- Kingdom: Bacteria
- Phylum: Actinobacteria
- Class: Actinobacteria
- Order: Micrococcales
- Family: Intrasporangiaceae
- Genus: *Tetrasphaera*



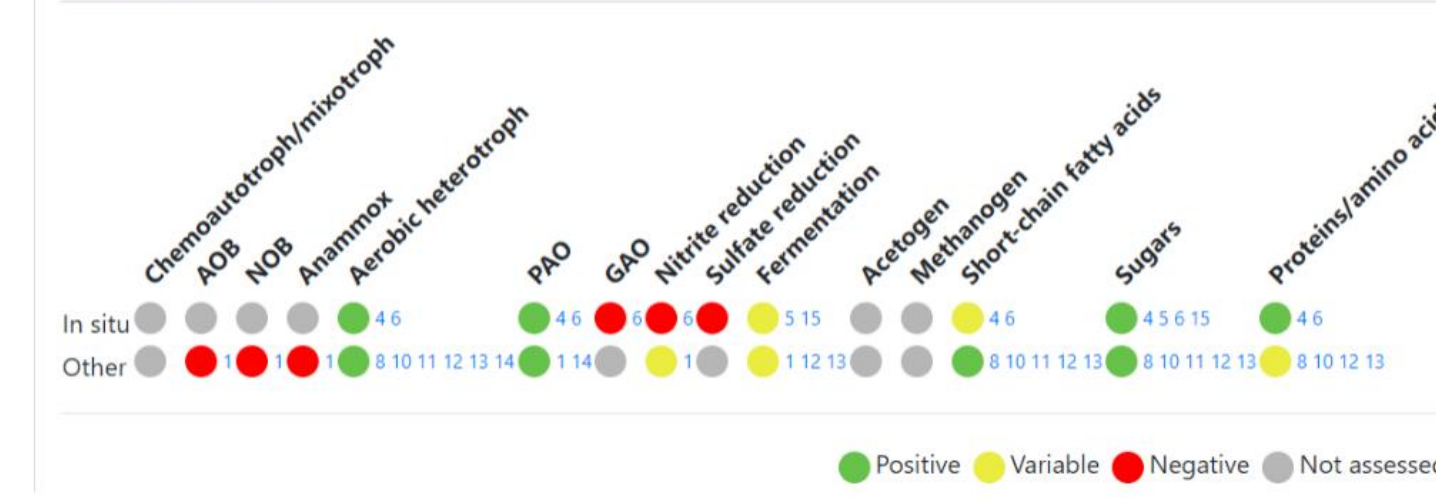
### Description

*Tetrasphaera* is the most abundant PAO in Danish WWTPs<sup>1</sup>. Members of *Tetrasphaera* have been identified as PAOs, reported to cycle polyphosphate, but without PHA or glycogen accumulation. Instead, they seem to mainly utilize sugars and amino acids through a fermentative metabolism, where polyphosphate supplements anaerobic energy requirements<sup>1,14</sup>. Some may also be involved in denitrification<sup>1</sup>. Interestingly, *T. elongata* can accumulate assimilated carbon and metabolites intracellularly (at approx. 4 mM) under anaerobic conditions for later use when oxygen becomes available<sup>1</sup>. Thus, members of the genus in activated sludge may utilize several physiological strategies. *T. jenkinsii*, *T. vanveanii* and *T. veronensis*, previously belonging to Eikelboom "Nostocoida limicola II", can form filaments<sup>14</sup>, but rarely cause foaming or bulking problems. Species *midas\_s\_328* was also identified to possess filamentous morphology and was found among the top-10 most abundant *Tetrasphaera* species in activated sludge<sup>2</sup>.

### FISH probes

Tetra183 together with Tetra617 (Tetra-mix) is a genus-level probe targeting all abundant species. Previously designed probes (designed against partial sequences<sup>3</sup>) have much lower coverage of the genus, therefore it is recommended to use the new probes<sup>3</sup>. Species-level probes are available<sup>3</sup>.

### Metabolism



## Distribution information



Abundance information is based on long-term 16S rRNA amplicon sequencing surveys of >20 Danish full-scale BNR plants for activated sludge and >20 anaerobic digesters; and on 3 months-long survey of 14 Danish full-scale BNR plants for influent wastewater.

**BLAST function** makes it possible to search DNA sequences against the MiDAS3 taxonomic database directly on the website and find the best matches using the BLAST search algorithm (Altschul et al., 1990)

## BLAST function

### Blast with the MiDAS 3.6 taxonomy

1. Enter your sequence in the sequence boxes below
2. If you have an identifier, put it in the query label box above the sequence, or use the pre-filled default value.
3. You can add more queries (up to the max) by clicking "Add another query", repeat steps 1 and 2.
4. Click "Submit queries", and view your results

If you have more queries than the maximum allowed then click "Reset queries" and start again.

There is a maximum of 3 sequences allowed per submission.

### Blast queries

NR\_024735.1

TTCCGSSGCTTETACACAGCCGCCCTCAAGTCCAGAAAGTCCGTAACACCCGAAAGCGGTGGCCCAACC  
CTTGTGCGGSSAGCCGCTCAAGGTGGAGCTGCGGATTTGGACT

+ Add another query Submit queries Reset queries

### Results

Query label: NR\_024735.1

Species: *Tetrasphaera elongata* : Percent ident: 99.792%; E value: 0.0; Length: 1443; Mismatch: 2  
Genus: *Tetrasphaera* View in Field Guide  
K: Bacteria | P: Actinobacteria | C: Actinobacteria | O: Micrococcales | F: Intrasporangiaceae

Species: *midas\_s\_5776* : Percent ident: 98.201%; E value: 0.0; Length: 1445; Mismatch: 22  
Genus: *Tetrasphaera* View in Field Guide  
K: Bacteria | P: Actinobacteria | C: Actinobacteria | O: Micrococcales | F: Intrasporangiaceae

Species: *midas\_s\_299* : Percent ident: 98.201%; E value: 0.0; Length: 1445; Mismatch: 23 View in Field Guide  
Genus: *Tetrasphaera* View in Field Guide  
K: Bacteria | P: Actinobacteria | C: Actinobacteria | O: Micrococcales | F: Intrasporangiaceae

Species: *midas\_s\_5* : Percent ident: 97.852%; E value: 0.0; Length: 1443; Mismatch: 30 View in Field Guide  
Genus: *Tetrasphaera* View in Field Guide  
K: Bacteria | P: Actinobacteria | C: Actinobacteria | O: Micrococcales | F: Intrasporangiaceae

MiDAS Field Guide is a central online repository for current knowledge of microbes in activated sludge and anaerobic digesters

Searchable database of referenced information

Collaborative platform - all working in the field are invited to contribute

Species-level identities available

Provisional (*midas\_*) names, act as unique identifiers → common vocabulary for the identity across independent studies

BLAST against MiDAS3 directly on the website!

Global survey of WWTPs is ongoing. MiDAS4 (containing sequences from >600 WWTPs across the world) will be released in 2020

References:  
Dueholm, M.S., Andersen, K.S., Petriglieri, F., Mcllroy, S.J., Nierychlo, M., Petersen, J.F., Kristensen, J.M., Yashiro, E., Karst, S.M., Albertsen, M., Nielsen, P.H., 2019. Comprehensive ecosystem-specific 16S rRNA gene databases with automated taxonomy assignment (AutoTax) provide species-level resolution in microbial ecology. BioRxiv.  
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Altschul, S.F., Gish, W., Miller, W., Myers, E.W., Lipman, D.J., 1990. Basic local alignment search tool. Journal of Molecular Biology 215, 403–410.



@MartaNierychlo  
mni@bio.aau.dk



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