A site-specific curated database for the microorganisms of activated sludge and anaerobic digesters

McIlroy, Simon Jon; Kirkegaard, Rasmus Hansen; McIlroy, Bianca; Nierychlo, Marta; Kristensen, Jannie Munk; Karst, Søren Michael; Albertsen, Mads; Nielsen, Per Halkjær

Creative Commons License
Unspecified

Publication date:
2016

Link to publication from Aalborg University

Citation for published version (APA):

General rights
Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain.
- You may freely distribute the URL identifying the publication in the public portal.

Take down policy
If you believe that this document breaches copyright please contact us at vbn@aub.aau.dk providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from vbn.aau.dk on: August 11, 2024
A site-specific curated database for the microorganisms of activated sludge and anaerobic digesters

Simon J. McIlroy, Rasmus H. Kirkegaard, Bianca McIlroy, Marta Nierychlo, Jannie M. Kristensen, Søren M. Karst, Mads Albertsen and Per H. Nielsen

Standard 16S rRNA protocols

Amplicon sequencing of the 16S rRNA gene now allows high throughput analyses and monitoring of the whole microbial communities of wastewater treatment systems.

However, meaningful cross study comparisons are hindered by the substantial influence of the selected DNA extraction method, PCR primers and reference taxonomy.

MiDAS provides protocols for DNA extraction, 16S rRNA gene amplicon library preparation and bioinformatic analysis – all optimised for application to wastewater treatment system samples.

Curated site-specific taxonomy

Reliable function prediction for phylotypes requires taxonomic assignment to the species or genus level.

Many of the abundant activated sludge and anaerobic digester organisms have no cultured representatives and are not annotated in popular public databases applied for taxonomic assignment.

i.e. the uncultured fermentative bulking filament “Ca. Promineofilum” (0092 morphotype).

MiDAS provides a site-specific taxonomic database curated for the organisms of wastewater treatment systems.

Distribution

Large scale surveys of the microbial communities of wastewater treatment systems incl. >50 full-scale systems over several years.

MiDAS includes abundance values for influent wastewater, activated sludge and anaerobic digester (AD) – identifying abundant phylotypes and giving an insight into migration. An important example being the link between foaming episodes in anaerobic digesters and migration of “Ca. Microthrix spp.” from activated sludge.

Linking identity with function

The online MiDAS field guide provides profiles for all abundant and process important phylotypes - linking their identity to current information on their morphology, physiology and distribution. This currently includes profiles for >300 bacterial and 8 archaeal genus level taxa.

MiDAS is intended as a collaborative resource for all interested in the biotechnologically important fields of wastewater treatment and biogas production.

1 McIlroy et al. (2015) MiDAS: the field guide to the microbes of activated sludge. Database. 2015, bav062.