Metagenomics and single-cell genomics reveal high abundance of comammox Nitrospira in a rapid gravity sand filter treating groundwater

Palomo, Alejandro; Fowler, Jane; Gülay, Arda; Rasmussen, Simon; Schramm, Andreas; Sicheritz-Pontén, Thomas; Smets, Barth F.

Publication date:
2016

Document Version
Peer reviewed version

Citation (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

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.
**Topic: Applying -omics approaches to understand microbial functioning**

Metagenomics and single-cell genomics reveal high abundance of comammox *Nitrospira* in a rapid gravity sand filter treating groundwater.


¹Department of Environmental Engineering, Technical University of Denmark, Kongens Lyngby, Denmark.

²Center for Biological Sequence Analysis, Department of Systems Biology, Technical University of Denmark, Kongens Lyngby, Denmark

³Center for Geomicrobiology, Department of Bioscience, Aarhus University, Aarhus, Denmark

The recent discovery of complete ammonia oxidizing (comammox) *Nitrospira* has revealed that the metabolic division of labor in nitrification is not obligate as was assumed during the last century. Despite the detection and enrichment of comammox *Nitrospira* from different nitrifying environments, the ecological relevance of comammox remains unknown. In this study, we analyzed the microbial communities from various locations within a groundwater-fed rapid sand filter (RSF), where *Nitrospira* were at very high relative abundances. Through metagenomics, a highly abundant composite multi-genome of *Nitrospira* genus was recovered harboring metabolic capacity for complete ammonia oxidation. We developed a cell extraction strategy that enables the disruption of *Nitrospira* cell clusters attached to the mineral coating of the sand. Individual cells were identified via fluorescent in situ hybridization (FISH) with *Nitrospira*-specific 16S rRNA probes and sorted via fluorescence-activated cell sorting (FACS). Sorted cells were screened and selected *Nitrospira* spp. were subject to whole-genome sequencing. The single cell genomes confirmed the genomic presence of a complete ammonia oxidation pathway and revealed clear taxonomic differences with the recently described comammox *Nitrospira* genomes. The high abundance of comammox *Nitrospira* spp. together with the low abundance of canonical ammonia oxidizing prokaryotes in the investigated RSF system suggests the essential role of this novel comammox *Nitrospira* in the RSFs and potentially other nitrifying environments.