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Genomic and ecological variation in comammox Nitrospira populations

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Introduction and Objectives
- Complete ammonia oxidizing (comammox) bacteria belong to Nitrospira, an extremely diverse genus of nitrite oxidizing bacteria.
- Described comammox Nitrospira genomes belong to Nitrospira lineage II, and comprise two clades (clade A and B) based on the phylogeny of their ammonia monooxygenases.
- Nitrospira spp. are widespread in both natural and engineered ecosystems where nitrogen cycling occurs; multiple species frequently coexist.
- However, the forces driving differentiation and diversification in Nitrospira populations remain poorly understood.
- The purpose of this study was to investigate the distribution of comammox and other Nitrospira spp. across different environments and geographical locations.

Approach
- 55 different metagenome-assembled genomes (MAG) of Nitrospira were retrieved from 13 Danish groundwater-fed rapid sand filters and multiple publicly available metagenomes by combining different binning tools (MetaBAT3, MaxBin2 and CONCOCT3) followed by binning refinement (Binning refiner5, DAS Tool6 and metaWRAP7) and dereplication (dRep8).
- These Nitrospira MAGs together with 37 published Nitrospira genomes were clustered (genomes with ANI > 95% were classified as member of same species) to create a database of Nitrospira species.
- The abundance of each Nitrospira species across 1000 metagenomes was assessed using MIDAS9.
- Distribution patterns of Nitrospira genomes across the metagenomes was visualized through principal component analysis (PCA).

Global distribution of Nitrospira spp.

More Nitrospira genomes were detected in metagenomes from DWTP (drinking water treatment plant) and freshwater samples compared to soil and WWTP (wastewater treatment plant) samples. Only DWTP metagenomes contained multiple abundant Nitrospira genomes (coverage > 5).

Genomic and diversity patterns of Nitrospira spp.

Comammox Nitrospira Clade A genomes (purple and pink) form two different clusters: CladeA1 genomes (purple) co-occur with non-comammox Nitrospira lineage I genomes and are present in WWTP samples; CladeA2 genomes (pink) are present in DWTP, groundwater and freshwater samples.

Conclusions
- Nitrospira genomes were detected in metagenomes from very different environments and geographical locations; a higher abundance was observed in DWTP metagenomes.
- Environment more than geography separates different Nitrospira spp.: WWTP metagenomes separate strongly from DWTP metagenomes based on presence and type of Nitrospira genomes.
- Nitrospira spp. affiliated to the same lineage or clade inhabit similar environments.
- Environmental partitioning within the comammox Clade A was detected. A similar separation was observed based on the phylogeny of hydroxylamine oxidoreductase subunit A amino acid sequences.

References: