Comparative genomics sheds light on niche differentiation and the evolutionary history of comammox Nitrospira

The description of comammox Nitrospira spp., performing complete ammonia-to-nitrate oxidation, and their co-occurrence with canonical β-proteobacterial ammonia oxidizing bacteria (β-AOB) in the environment, calls into question the metabolic potential of comammox Nitrospira and the evolutionary history of their ammonia oxidation pathway. We report four new comammox Nitrospira genomes, constituting two novel species, and the first comparative genomic analysis on comammox Nitrospira. Unlike canonical Nitrospira, comammox Nitrospira genomes lack genes for assimilatory nitrite reduction, suggesting that they have lost the potential to use external nitrite nitrogen sources. By contrast, compared to canonical Nitrospira, comammox Nitrospira harbor a higher diversity of urea transporters and copper homeostasis genes and lack cyanate hydratase genes. Additionally, the two comammox clades differ in their ammonium uptake systems. Contrary to β-AOB, comammox Nitrospira genomes have single copies of the two central ammonia oxidation pathway operons. Similar to ammonia oxidizing archaea and some oligotrophic AOB strains, they lack genes involved in nitric oxide reduction. Furthermore, comammox Nitrospira genomes encode genes that might allow efficient growth at low oxygen concentrations. Regarding the evolutionary history of comammox Nitrospira, our analyses indicate that several genes belonging to the ammonia oxidation pathway could have been laterally transferred from β-AOB to comammox Nitrospira. We postulate that the absence of comammox genes in other subgroup II Nitrospira genomes is the result of subsequent loss.

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