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Introducing *Candidatus* Bathyanammoxibiaceae, a family of bacteria with the anammox potential present in both marine and terrestrial environments

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Abstract:

Anaerobic ammonium oxidation (Anammox) bacteria are a group of extraordinary bacteria exerting a major impact on the global nitrogen cycle. Their phylogenetic breadth and diversity, however, are not well constrained. Here we describe a new, deep-branching family in the order of *Candidatus* Brocadiales, *Candidatus* Bathyanammoxibiaceae, members of which have genes encoding the key enzymes of the anammox metabolism. In marine sediment cores from the Arctic Mid-Ocean Ridge (AMOR), the presence of *Ca.* Bathyanammoxibiaceae was confined within the nitrate-ammonium transition zones with the counter gradients of nitrate and ammonium, coinciding with the predicted occurrence of the anammox process. *Ca.* Bathyanammoxibiaceae genomes encode the core genetic machinery for the anammox metabolism, including hydrazine synthase for converting nitric oxide and ammonium to hydrazine, and hydrazine dehydrogenase for hydrazine oxidation to dinitrogen gas, and hydroxylamine oxidoreductase for nitrite reduction to nitric oxide. Their occurrences assessed by genomes and 16S rRNA gene sequencing surveys indicate that they are present in both marine and terrestrial environments. By introducing the anammox potential of *Ca.* Bathyanammoxibiaceae and characterizing their ideal niche in marine sediments, our findings suggest that the diversity and abundance of anammox bacteria may be higher than previously thought, and provide important insights on cultivating them in the future to not only assess their biogeochemical impacts but also constrain the emergence and evolutionary history of this functional guild on Earth.

Keywords: anaerobic ammonium oxidation, *Candidatus*, marine sediment, nitrate-ammonium transition zone, hydrazine synthase, biogeochemical impact