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The unaccounted yet abundant nitrous oxide-reducing microbial community: a potential nitrous oxide sink

C.M. Jones*¹, D.R.H. Graf¹, D. Bru², L. Philippot², S. Hallin¹

¹*Swedish University of Agricultural Sciences, Sweden,* ²*INRA, UMR Agroecologie, Dijon, France*

Nitrous oxide (N₂O) is a major radiative forcing and stratospheric ozone-depleting gas emitted from terrestrial and aquatic ecosystems. It can be transformed to nitrogen gas (N₂) by bacteria and archaea harboring the N₂O reductase (N₂OR), which is the only known N₂O sink in the biosphere. Despite its crucial role in mitigating N₂O emissions, knowledge of the N₂OR in the environment remains limited. Here, we report a comprehensive phylogenetic analysis of the nosZ gene coding the N₂OR in genomes retrieved from public databases. The resulting phylogeny revealed two distinct clades of nosZ, with one unaccounted for in studies investigating N₂O-reducing communities. Examination of N₂OR structural elements not considered in the phylogeny revealed that the two clades differ in their signal peptides, indicating differences in the translocation pathway of the N₂OR across the membrane. Sequencing of environmental clones of the previously undetected nosZ lineage in various environments showed that it is widespread and diverse. Using quantitative PCR, we demonstrate that this clade was most often at least as abundant as the other, thereby more than doubling the known extent of the overall N₂O-reducing community in the environment. Furthermore, we observed that the relative abundance of nosZ from either clade varied among habitat types and environmental conditions. Our results indicate a physiological dichotomy in the diversity of N₂O-reducing microorganisms, which might be of importance for understanding the relationship between the diversity of N₂O-reducing microorganisms and N₂O reduction in different ecosystems.

Keywords: Nitrous oxide reductase, amplicon sequencing, phylogeny, soil