{rokbox title=| Distribution of predicted nitrogen-cycle functional genes and their taxonomic contributors by cluster :: Image: Authors|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-spatial-partitioning-microbial-functional-2026-mena-thumb-et-al.jpg|}images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-spatial-partitioning-microbial-functional-2026-mena-et-al.jpg{/rokbox}

Daniel Romano-Gude, Nestor Arandia-Gorostidi, **Catalina Mena**, Marc Diego-Feliu, Bella Almillategui, Anna J. Székely, Stefan Bertilsson, Andrea G. Bravo, Jesus Carrera, Cristina Romera-Castillo, Albert Folch, Jordi Garcia-Orellana, Valentí Rodellas, Clara Ruiz-González, 2026. **Spatial Partitioning of Microbial Functional Potential Suggests Complex Nitrogen Cycling in a Subterranean Estuary.** Environmental Microbiology. Volume 28. Issue 8. Aug 2026. https://doi.org/10.1111/1462-2920.70400

Abstract:Subterranean estuaries (STEs) are key bioreactors regulating the quantity and chemical composition of groundwater- derivednitrogen (N) reaching coastal ecosystems. Yet, the microbial controls on N-cycling within these groundwater–seawater mixingzones remain poorly understood. We investigated the spatio-temporal variations in microbial communities and their N-cyclingpotential within an alluvial Mediterranean STE with high N concentration. We explored changes in microbial abundance, heter-otrophic activity, taxonomic composition, and the abundance of N-cycling genes across groundwater samples collected at severaldepths and distances from the shoreline in winter and summer. Microbial abundance, activity, and diversity varied stronglyacross hydrochemical zones according to physicochemistry and aquifer depth but showed limited seasonality. Functional pre-dictions suggested a complex, spatially structured suite of N pathways encoded by diverse taxa occupying different STE zones,and quantitative-PCR revealed niche partitioning between ammonia-oxidizing archaea, prevalent in fresh-groundwater, andbacterial denitrifiers enriched in deep-saline layers. Multiple linear model predictions showed a stronger fit for $NO_2^-$ and $NH_4^+$concentrations when using microbial properties than when using environmental variables, highlighting their importance for un-derstanding N cycling in STEs. Our results suggest that the functional potential of the STE microbiome is complex and spatiallystructured across hydrochemical zones, explaining spatial variations in STE N-cycling.

Keywords:functional potential,microbial communities,nitrogen cycling,PICRUSt2,qPCR,subterranean estuary.