

{rokbox title=|Schematic representation of the workflow :: Image: Authors|
thumb=|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-decoupling-respiration-marine-prokaryoplankton-munson-et-al-2022-thumb.jpg|}images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-decoupling-respiration-marine-prokaryoplankton-munson-et-al-2022.jpg{/rokbox}

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[Decoupling of respiration rates and abundance in marine prokaryoplankton.](https://doi.org/10.1038/s41586-022-05505-3)

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Abstract: The ocean–atmosphere exchange of CO₂ largely depends on the balance between marine microbial photosynthesis and respiration. Despite vast taxonomic and metabolic diversity among marine planktonic bacteria and archaea (prokaryoplankton), their respiration usually is measured in bulk and treated as a ‘black box’ in global biogeochemical models⁴; this limits the mechanistic understanding of the global carbon cycle. Here, using a technology for integrated phenotype analyses and genomic sequencing of individual microbial cells, we show that cell-specific respiration rates differ by more than 1,000× among prokaryoplankton genera. The majority of respiration was found to be performed by minority members of prokaryoplankton (including the Roseobacter cluster), whereas cells of the most prevalent lineages (including Pelagibacter and SAR86) had extremely low respiration rates. The decoupling of respiration rates from abundance among lineages, elevated counts of proteorhodopsin transcripts in Pelagibacter and SAR86 cells and elevated respiration of SAR86 at night indicate that proteorhodopsin-based phototrophy probably constitutes an important source of energy to prokaryoplankton and may increase growth efficiency. These findings suggest that the dependence of prokaryoplankton on respiration and remineralization of phytoplankton-derived organic carbon into CO₂ for its energy demands and growth may be lower than commonly assumed and variable among lineages.

Keywords: