

# How nutrients are removed in oxygen-depleted regions of the ocean

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In the course of global climate change, scientists are observing the increase of low-oxygen areas in the ocean, also termed oxygen minimum zones (OMZs). Large-scale OMZs exist, for example, in the Pacific off the coast of South America or in the Indian Ocean. Since little to no oxygen is present in these regions—depending on the depth of the water—organisms whose metabolisms are independent of oxygen have a distinct advantage. These organisms include some representatives of the foraminifera: unicellular, shell-forming microorganisms, which have a

nucleus and thus belong to the eukaryotes. Their lifestyle involves a particular metabolic pathway termed anaerobic respiration. In the absence of oxygen, they convert nitrate present in the water into molecular nitrogen.

This process is called denitrification and it plays a central role in the global recycling of nitrogen – an essential element for the life processes of all organisms – in the ocean. In marine areas with a particularly low oxygen content, foraminifera are highly abundant. There, they metabolise nitrate on a large scale and thus remove it from the global nutrient cycle. In this way, foraminifera make a significant contribution to the removal of nutrients in the OMZs. A research team from the Institute of General Microbiology at Kiel University (CAU), the Collaborative Research Center 754 (SFB 754) "Climate-Biogeochemistry Interactions in the Tropical Ocean" at the GEOMAR Helmholtz Centre for Ocean Research Kiel, and the Kiel Evolution Center (KEC) have now succeeded in describing the previously unknown denitrification process in foraminifera.

The researchers were able to demonstrate that *Globobulimina turgida* and the related species *Globobulimina auriculata* possess a unique, eukaryotic [metabolic pathway](#) for denitrification. On August 2, 2018, the research team published a characterisation of the required genetic attributes of these [foraminifera species](#) for the first time in the renowned scientific journal *Current Biology*.

The research team collected sediment samples in the Gullmar Fjord in southern Sweden. Due to its special shape and the associated water stratification, the fjord experiences a seasonal deoxygenation similar to the large oceanic OMZs. In the fjord, foraminifera live in the top few centimetres of the seabed. The researchers were able to observe the microorganisms in laboratory, using a specially-developed infrastructure: "In order to investigate the foraminifera in detail and because they are

specialised for their particular environmental conditions, we had to artificially simulate the natural oxygen conditions at a depth of around 120 meters," emphasised Dr. Alexandra-Sophie Roy from the Genomic Microbiology working group at the CAU. Together with her colleague Dr. Christian Wöhle, she is lead author of the newly published study conducted in the framework of the SFB 754.

The researchers examined the entire set of genetic information of the foraminifera for clues about whether they are capable of denitrification independently, or whether [symbiotic bacteria](#) are responsible. It is already known that bacteria and fungi can perform denitrification, and therefore have suitable genetic attributes. The researchers were thus searching the genome of the foraminifera for specific genes already known in bacteria and fungi. "We discovered three protein-coding genes, which definitely do not come from symbiotic bacteria," said Wöhle. Although we have not found all of the genes involved in nitrate conversion, the newly discovered genetic information is part of the foraminifera's own genome. Their metabolism definitely distinguishes these marine microorganisms from all other eukaryotic organisms, underlined Roy and Wöhle.

This result is also supported by the ecological success of foraminifera in oxygen-depleted marine environment. Investigations of the OMZ off the Peruvian coast, for example, have shown that the microorganisms there play a key role in the nitrate cycle, and are found in high abundance of more than 500 individuals per cubic centimetre of sediment. It is speculated that foraminifera could achieved this dominance by evolutionarily acquiring the ability to perform complete denitrification. A participation of symbiotic bacteria in the nitrate reduction can be excluded in Globobulimina species studied here, because the abundance of symbiotic bacteria is too low to explain the phenomenon. Therefore, the eukaryotic microorganisms must be able to independently perform denitrification. In further research, the scientists aim to identify the

missing denitrification genes in Globobulimina. They also want to clarify whether the findings obtained regarding certain species in a specific marine area are also applicable to other foraminifera from OMZs in general.

"A better understanding of how the genetic basis of denitrification evolved in different organisms provides us with an important piece of the puzzle, and one step further towards a bigger picture of the biogeochemical cycles in the ocean," said Professor Tal Dagan, co-author of the study and head of the Genomic Microbiology research group at the CAU. Based on the evolution of the genes involved, we could better determine the geological origin of this nutrient cycle, and the extent of the role played by individual organisms, continued Dagan.

"In the context of global environmental change, a more accurate understanding of the conversion and distribution of elementary substances in the ocean is becoming increasingly important. With the new results, we make a contribution to better understanding the influence of climate change on the oxygen content-dependent nutrient cycles in the ocean," added Dr. Joachim Schönfeld from the SFB 754, who is also involved in the study. So, for example, in the future, researchers could better estimate how changed environmental conditions will affect the nutrient supply, and thus the nutritional relationships between different creatures in the ocean.

**More information:** Christian Woehle et al. A Novel Eukaryotic Denitrification Pathway in Foraminifera, *Current Biology* (2018). [DOI: 10.1016/j.cub.2018.06.027](https://doi.org/10.1016/j.cub.2018.06.027)

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