S1 Supplementary Methods

**Modelling of oxygen consumption rates.** Density was calculated using the data processing program SeaSoft (Sea-Bird Electronics). The stability of the water column was expressed using the Brunt-Väisälä frequency \( N \), defined as:

\[
N^2 = \frac{g}{\rho} \frac{\partial \rho}{\partial z}
\]

where \( \rho \) is the water density, \( g \) is the gravitational acceleration and \( z \) is the water depth. The density gradient was calculated over 3-6 m bins. The turbulent diffusivity \( Ez \) was calculated according to Gregg et al. [1] from the Brunt-Väisälä-Frequency and the dissipation rate of turbulent kinetic energy \( \varepsilon \):

\[
Ez = \frac{\gamma \varepsilon}{N^2}
\]

A mixing coefficient \( \gamma \) of 0.2 was applied. We used a mean \( \varepsilon \) of 1.85 \( \times 10^{-9} \) W kg\(^{-1}\). This value was measured by Gregg et al. [1] for the open ocean thermocline and was applied in several rate diffusion models [2] [3]. Concentration gradients for O\(_2\) were calculated over 2-6 m bins. Oxygen fluxes at respective depths were calculated according to Fick’s law:

\[
J = -Ez \frac{\partial C}{\partial z}
\]

O\(_2\) consumption was determined from O\(_2\) flux gradients, calculated over 1-4 m bins:

\[
R = \frac{\partial J}{\partial z}
\]
**Processing of Peruvian OMZ metagenome data.** A total of 1,204,437 raw reads were obtained for the metagenome samples from the Peruvian OMZ. Raw reads were clustered using Cd-hit [4] with a sequence identity threshold of 98% and a word length of 8. The ribosomal-gene cluster representative sequences were identified by BLASTn searches [5] against the SILVA database [6] (bit score cut off: 86). Of all sequences, 0.24% were of ribosomal gene origin and subsequently separated from non-ribosomal-gene cluster representative sequences using MEGAN [7]. The latter were compared against the non-redundant NCBI database using BLASTx (bit score cut off: 35) and scanned with profile hidden Markov models of the ModEnzA Enzyme Commission groups [8]. Of all non-ribosomal-gene sequences, 69.6% were identified as protein-coding; the remainder could not be assigned. Sequences, cluster sizes and cluster identification numbers as well as results from the BLAST searches and EC scans were added to a MySQL database for analysis [9,10]. For the functional (cytochrome oxidase type) and taxonomic assignment of the cluster representatives the top hit of each BLAST search was used.

**Aggregate-size-dependent respiration rates.** Diffusion-limited aerobic respiration (R) below a threshold O\(_2\) concentration was estimated by rearranging the analytical solution for solute transport and reaction in a sphere [11]:

\[
R = R_0 - R_0 \left( 1 - \frac{6 \times C \times D_{\text{agg}}}{R_0 \times r_0^2} \right)^\frac{3}{2}
\]

Here, \(R_0\) is the non-limited O\(_2\) consumption rate, \(C\) is the ambient O\(_2\) concentration, \(D_{\text{agg}}\) is the diffusion coefficient inside the aggregate (1.3 \(\times\) \(10^{-9}\) m\(^2\) s\(^{-1}\)), and \(r_0\) is the aggregate diameter. For simplicity, the diffusive boundary layer around the aggregate was neglected and zero-order O\(_2\) consumption was assumed. An empirically
A determined relationship between aggregate diameter (in mm) and respiration rate (in nmol h⁻¹) in the Mauritanian upwelling region [12], with $R_0 = 1.8 \, d^{1.8}$, was used to calculate $O_2$ consumption as a function of $O_2$ concentration for particles of 0.01 - 10 mm in diameter. To account for the somewhat lower incubation temperatures in our study ($\Delta O_2 \approx 5 \, ^\circ C$, Supplementary Table 1 and 2), $O_2$ consumption rates were corrected using a temperature coefficient ($Q_{10}$) of 2 [13].

**Stoichiometries used to calculate NH$_4^+$ budgets for the upper Namibian and Peruvian OMZs:**

**Aerobic remineralization:**

$$(CH_2O)_{106}(NH_3)_{16}H_3PO_4 + 106 \, O_2 + 16 \, H^+$$

$\rightarrow 106 \, CO_2 + 16 \, NH_4^+ + 106 \, H_2O + H_3PO_4$

**Nitrification:**

$NH_4^+$ oxidation: $NH_3 + 1.5 \, O_2 \rightarrow NO_2^- + H^+ + H_2O$

$NO_2^-$ oxidation: $NO_2^- + 0.5 \, O_2 \rightarrow NO_3^-$

$NO_3^-$ reduction to $NO_2^-$: $$(CH_2O)_{106}(NH_3)_{16}H_3PO_4 + 212 \, NO_3^- + 16 \, H^+$$

$\rightarrow 106 \, CO_2 + 16 \, NH_4^+ + 212 \, NO_2^- + 106 \, H_2O + H_3PO_4$

**DNRA:**

$$(CH_2O)_{106}(NH_3)_{16}H_3PO_4 + 53 \, NO_3^- + 122 \, H^+$$

$\rightarrow 106 \, CO_2 + 69 \, NH_4^+ + 53 \, H_2O + H_3PO_4$

**Anammox:**

$$NH_4^+ + NO_2^- \rightarrow N_2 + 2 \, H_2O$$
References


