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Bacterial oxygen production in the dark

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INTRODUCTION

In dim anoxic waters of stratified lakes where oxygen-respiring organisms normally cannot survive, a tiny aerobic eukaryote nevertheless makes a living. This heterotrophic ciliate, Histiobalantium natans, can survive without external oxygen because it sequesters chloroplasts from ingested Euglenoid flagellates (Phacus suecicus). The chloroplasts, kept active in the ciliate and surrounded by the mitochondria, photosynthesize and produce oxygen that allows the host to thrive in deep waters of stratified lakes, where it avoids metazoan predation and competition with other aerobic ciliates (Esteban et al., 2009). This is just one example of nature’s many twists that allow organisms to take a specific niche: If an essential compound is not available, make it yourself by inventing a variation on a general mechanism.

For a long time, photosynthesis was the only biological process known to produce oxygen. Cyanobacteria, green plants, and algae use light energy to split water (\(E^0 = +0.82 \text{ V}\)) via photosystem II. The electrons obtained serve NADPH and ATP generation for carbon dioxide fixation; oxygen is a by-product of this metabolism. This pathway evolved at least 2.7 billion years ago (Canfield, 2005), and, after the vast pools of reduced compounds on early earth were exhausted, oxygen started to accumulate in the atmosphere around 2.45 billion years ago (Holland, 2006). As a consequence, organisms evolved numerous mechanisms to cope with and/or exploit its strong oxidative properties. To prevent oxidative damage by reactive oxygen species (ROS) like superoxide (\(O_2^−\)), hydrogen peroxide (\(H_2O_2\)), or the most damaging of all, the hydroxyl radical (\(OH^−\)), detoxification systems, which often result in the regeneration of oxygen (e.g., by catalase or superoxide dismutase) evolved. These reactions have been studied and reviewed in detail elsewhere (Apel and Hirt, 2004; Murphy, 2009) and are beyond the scope of this article.

On the other hand, a large number of extant organisms are completely dependent on oxygen as the terminal electron acceptor for the respiration of (per)chlorate, nitrate, and nitrite, respectively. In this perspective, we review knowledge about intra-aerobic pathways, their potential presence in other organisms, and identify candidate enzymes related to quinol-dependent NO reductases (qNORs) that might be involved in the formation of oxygen.

Keywords: oxygen production, nitric oxide, nitric oxide reductase, chlorate reduction, chlorite dismutase, Candidatus Methylobomirabilis oxyfera, strain HDN1

Nitric oxide (NO) and nitrous oxide (\(N_2O\)) are among nature’s most powerful electron acceptors. In recent years it became clear that microorganisms can take advantage of the oxidizing power of these compounds to degrade aliphatic and aromatic hydrocarbons. For two unrelated bacterial species, the “NC10” phylum bacterium “Candidatus Methylobomirabilis oxyfera” and the \(\gamma\)-proteobacterial strain HDN1 it has been suggested that under anaerobic conditions with nitrate and/or nitrite, monooxygenases are used for methane and hexadecane oxidation, respectively. No degradation was observed with nitrous oxide only. Similarly, “aerobic” pathways for hydrocarbon degradation are employed by (per)chlorate-reducing bacteria, which are known to produce oxygen from chlorite (\(ClO_2^−\)). In the anaerobic methanotroph \(M.\ oxyfera\), which lacks identifiable enzymes for nitrogen formation, substrate activation in the presence of nitrite was directly associated with both oxygen and nitrogen formation. These findings strongly argue for the role of NO, or an oxygen species derived from it, in the activation reaction of methane. Although oxygen generation elegantly explains the utilization of “aerobic” pathways under anaerobic conditions, the underlying mechanism is still elusive. In this perspective, we review the current knowledge about intra-aerobic pathways, their potential presence in other organisms, and identify candidate enzymes related to quinol-dependent NO reductases (qNORs) that might be involved in the formation of oxygen.

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**OXYGEN PRODUCTION IN CHLORATE-REDUCING BACTERIA**

The first group of organic chemotrophs identified were perchlorate and chlorate respiring bacteria (Riddik et al., 1996; van Ginkel et al., 1996). These organisms reduce perchlorate (ClO₄⁻) and/or chlorate (ClO₃⁻) to chloride (ClO₂⁻). Rather than being further reduced to hypochlorite (ClO₂⁻), chlorite is converted into chloride (Cl⁻) and O₂. Perchlorate occurs naturally, but rarely in the environment, with significant concentrations only found in the Chilean salpeter deposits (Beckurts, 1886; Ericksen, 1983). In an extremely arid climate (Rajagopalan et al., 2006; Xu et al., 2003), an initial surprise was the widespread occurrence of perchlorate reduction among microorganisms and in different ecosystems, much broader than could be expected from the known natural sources and the short timeframe of anthropogenic contamination (Coates et al., 1999).

Perchlorate is continuously generated in trace amounts in the atmosphere. Accumulation to measurable amounts, however, only occurs where deposition is high, but leaching and microbial reduction is low: in an extremely arid climate (Rajagopalan et al., 2006; Xu et al., 2003). An initial surprise was the widespread occurrence of perchlorate reduction among microorganisms and in different ecosystems, much broader than could be expected from the known natural sources and the short timeframe of anthropogenic contamination (Coates et al., 1999).

In past decades, anthropogenic contamination from either the use of Chile salpeter as fertilizers, or from chemical waste (e.g., solid rocket fuel spills and explosives) has been a concern and incentive for research on microbial (per)chlorate reduction (Mottet, 2003; Kostant et al., 2010).

**PERCHLORATE RESPIRATION IN PRINCIPAL ONLY Requires Two Enzymes**

At first, (per)chlorate reductase, a molybdo-hyster-containing respiratory reductase, catalyzes the reduction of perchlorate to chloride and chlorate to chlorite. Then, chlorite is converted into a single energetic reaction into chloride and oxygen (Eq. 1; van Ginkel et al., 1996).

This is a net disproportionation or dismutase reaction in which the chloride atom becomes reduced and oxygen oxidized.

\[
\text{ClO}_3^− \rightarrow \text{Cl}^- + O_2 (\Delta G = −100 \text{ kJ mol}^{-1} O_2) \]

The reaction is catalyzed at a high rate and with extraordinary specificity by chlorite dismutases (Cld, EC 1.13.11.49), members of the CDE superfamily of heme enzymes (Gohlich et al., 2011). This homohexameric or homopentameric heme b enzyme was first purified in the nineties from the β-proteobacterium *Azospira oxyrea* (then called strain GR-1, van Ginkel et al., 1996). The enzyme is now well characterized by the resolution of the atomic structures from several species (de Geus et al., 2009; Mehboob et al., 2009b; Gohlich et al., 2010; Kostant et al., 2010; Mlynek et al., 2011). Detailed kinetic analysis established that oxygen is not derived from water, but from chlorite itself (Lee et al., 2008; Streit and DuBois, 2008). Catalysis proceeds via an oxoferryl species and a ClO₂⁻ anion, indicating that, after initial binding to the catalytic heme b, chlorite is first cleaved, after which both oxygen atoms recombine, yielding chloride and oxygen. Most chlorate-reducing organisms found thus far are facultative aerobes that, in absence of extracellular oxygen use the chloride-derived oxygen for aerobic respiration, analogous to the use of chloroacetate by *H. natans* in the introduction.

What else to do with oxygen produced by chlorite dismutases? Surprisingly, functional chlorite dismutases have also been found in Bacteria and Archaea that cannot grow with chlorate as electron acceptor, e.g., in the nitrite-oxidizing genera *Nitrosipira* (Maihner et al., 2008) and *Nitroburzer* (Mlynek et al., 2011). In the latter species, Cld is significantly smaller and present as a homodimer. The role of Cld in these organisms, however, is unclear. They possibly confer insensitivity to chloride, coupled with the advantage of producing oxygen for nitrite oxidation in microoxic niches. In the archaeon *Halofexis volcani*, chlorite dismutase is hypothesized to produce oxygen for a monoxygenase encoded in the same operon, that is involved in the biosynthesis of an antibiotic (Bah-Diniz et al., 2006).

In *Pseudomonas chloritidismutans*, oxygen likely does not only act as an electron acceptor in respiration, but is also used for alkaline activation by a monoxygenase-mediated reaction (Mehboob et al., 2009a). *P. chloritidismutans* is capable of respiring carbon substrates like fatty acids or alcohols with oxygen, chlorate, and nitrate, but growth on alkanes is not observed with nitrate as electron acceptor. This suggests that oxygen, provided externally or from chlorate reduction, is required for the initial activation of the alkane, a hydroxylation to the corresponding alcohol (Heider, 2007).

The β-proteobacterium *Dechloromonas aromatica* strain RCB can degrade benzene aerobically and anaerobically with chlorate and nitrate (Coates et al., 2001). However, signature genes of anaerobic hydrocarbon activation (Heider, 2007), like the glycol-radical enzyme benzyl-succinate synthase cluster, are missing. In contrast, the genome of strain RCB only encodes genes for the aerobic activation of aromatic compounds, including several monooxygenases (Salinero et al., 2009).

Physiological experiments under nitrate-reducing conditions strongly suggest the involvement of a hydroxyl radical-mediated activation leading to phenol as primary intermediate (Chakraborty and Coates, 2005). It is quite unlikely that the very substrate-specific Cld can catalyze O₂ production from nitrogen oxide intermediates. This possibility has been negatively tested for NO with the recombinant Cld of *Nitrosipira defluviit* (Maihner et al., 2008), which was also found to be inhibited by NO (179 μM; F. Maihner and K. Ettwig, unpublished results). The open question is: Can the oxidative power for the attack on benzene come from oxygen, also under denitrifying conditions (Weink et al., 2010)?

**OXYGEN PRODUCTION FROM NITROGEN OXIDES?**

The idea that oxygen may be an intermediate of denitrifying, anaerobic bacteria emerged when the genome of the anaerobic methane-oxidizing bacterium *Candidatus Methylocamthiobacter oxyfera* was assembled from enrichment culture metagenomes.

These freshwater enrichment cultures (Raghoebariing et al., 2006; Ettwig et al., 2009) couple complete methane oxidation with CO₂ as the end product to the reduction of nitrate (NO₃⁻) to dinitrogen (N₂) according to Eq. 2.

\[
3 \text{CH}_4 + 8 \text{NO}_3^- + 8 \text{H}^+ \rightarrow 3 \text{CO}_2 + 4 \text{N}_2 + 10 \text{H}_2\text{O} (\Delta G = −928 \text{ kJ mol}^{-1} \text{CH}_4) 
\]

Methane has the second highest activation energy (after benzene) of all organic compounds. One of the prime questions was how it could be enzymatically activated under anaerobic
conditions. Generally, two enzymatic activation mechanisms were already known: Aerobic methane-oxidizing bacteria (MOB) employ a monooxygenase reaction yielding methanol as the first intermediate (Hakemian and Rosenzweig, 2007; Turotienko and Murrell, 2008). Anaerobic methanotrophic archaea (ANME), that couple methane oxidation to sulfate reduction (most likely in association with sulfate-reducing bacteria) reverse the last step of methanogenesis catalyzed by methyl-coenzyme M reductase (Knittel and Boetius, 2009; Scheller et al., 2010).

Prominent reductases (qNORs) including the potential NO dismutases (HCO) superfamily, with a focus on quinol-dependent nitric oxide reductase; nor, nitric oxide reductase; nos, nitrous oxide reductase; nod, nitrous oxide (N2O), and eventually dinitrogen gas (N2) by means of aerobic handling (Ettwig et al., 2009), but highly sensitive to acetylene (total inhibition at 10 μM; Ettwig et al., 2010), a known inhibitor of pMMO (Prior and Dalton, 1985). Besides methane, the M. oxyfera enrichment culture also oxidized other short-chain alkanes (ethane, propane, butane), a well-known activity of pMMO (Leadbetter and Foster, 1980; Hazeu and de Bruyn, 1980). Finally, using the oxidation of propylene as a proxy for pMMO activity (Prior and Dalton, 1985), comparable rates were obtained for oxygen and nitrite as electron acceptors (Ettwig et al., 2010).

Also the analysis of the denitrification pathway caused surprise. In all microbial species studied so far, denitrification proceeds in a step-wise fashion, comprising the subsequent reduction of nitrate (NO\textsubscript{3}\textsuperscript{−}) to nitrite (NO\textsubscript{2}−), nitric oxide (NO), nitrous oxide (N2O), and eventually dinitrogen gas (N2) by dedicated reductases (Figure 1A; Zumft, 1997; Einsle and Kroneck, 2004; Tavares et al., 2006). The last step, nitrous oxide reduction, is not always present, leaving the potent greenhouse gas N2O as the end product (Stein, 2011). Thus, a second startling finding was the apparent lack of an identifiable nitrous oxide homologous to benzyl- or alkyl-succinate synthase (Thauer and Shima, 2008). Whereas no homologues of the two last mentioned signature genes for anaerobic methane and hydrocarbon degradation could be identified in the genome, surprisingly the entire pathway of aerobic methane oxidation, starting with particulate methane monooxygenase (pMMO), was present, and prominently transcribed and expressed (Ettwig et al., 2010), Luesken et al., 2012. This was consistent with several experimental findings: The M. oxyfera enrichment culture was not sensitive to aerobic handling (Ettwig et al., 2009), but highly sensitive to acetylene (total inhibition at 10 μM; Ettwig et al., 2010), a known inhibitor of pMMO (Prior and Dalton, 1985). Besides methane, the M. oxyfera enrichment culture also oxidized other short-chain alkanes (ethane, propane, butane), a well-known activity of pMMO (Leadbetter and Foster, 1980; Hazeu and de Bruyn, 1980). Finally, using the oxidation of propylene as a proxy for pMMO activity (Prior and Dalton, 1985), comparable rates were obtained for oxygen and nitrite as electron acceptors (Ettwig et al., 2010). Also the analysis of the denitrification pathway caused surprise. In all microbial species studied so far, denitrification proceeds in a step-wise fashion, comprising the subsequent reduction of nitrate (NO\textsubscript{3}\textsuperscript{−}) to nitrite (NO\textsubscript{2}−), nitric oxide (NO), nitrous oxide (N2O), and eventually dinitrogen gas (N2) by dedicated reductases (Figure 1A; Zumft, 1997; Einsle and Kroneck, 2004; Tavares et al., 2006). The last step, nitrous oxide reduction, is not always present, leaving the potent greenhouse gas N2O as the end product (Stein, 2011). Thus, a second startling finding was the apparent lack of an identifiable nitrous oxide

### References


**Figure 1**

**Pathways of canonical denitrification (A) and proposed N2 and O2 production by NO dismutation (B).** ntr, nitrate reductase; nir, nitrite reductase; nor, nitric oxide reductase; nos, nitrous oxide reductase; nod, nitrous oxide (N2O), and eventually dinitrogen gas (N2) by means of aerobic handling (Ettwig et al., 2009), but highly sensitive to acetylene (total inhibition at 10 μM; Ettwig et al., 2010), a known inhibitor of pMMO (Prior and Dalton, 1985). Besides methane, the M. oxyfera enrichment culture also oxidized other short-chain alkanes (ethane, propane, butane), a well-known activity of pMMO (Leadbetter and Foster, 1980; Hazeu and de Bruyn, 1980). Finally, using the oxidation of propylene as a proxy for pMMO activity (Prior and Dalton, 1985), comparable rates were obtained for oxygen and nitrite as electron acceptors (Ettwig et al., 2010). Also the analysis of the denitrification pathway caused surprise. In all microbial species studied so far, denitrification proceeds in a step-wise fashion, comprising the subsequent reduction of nitrate (NO\textsubscript{3}\textsuperscript{−}) to nitrite (NO\textsubscript{2}−), nitric oxide (NO), nitrous oxide (N2O), and eventually dinitrogen gas (N2) by dedicated reductases (Figure 1A; Zumft, 1997; Einsle and Kroneck, 2004; Tavares et al., 2006). The last step, nitrous oxide reduction, is not always present, leaving the potent greenhouse gas N2O as the end product (Stein, 2011). Thus, a second startling finding was the apparent lack of an identifiable nitrous oxide homologous to benzyl- or alkyl-succinate synthase (Thauer and Shima, 2008). Where
enzyme, NO dismutase (NOD). Again, such disproportionation of NO into N₂ and O₂ (Eq. 3), analogously to the chlorite dismutase reaction and to be catalyzed by a novel proportionation of eight NO molecules would give four oxygen molecules only three of which are consumed in the activation of methane. Residual O₂ appears to be respired by one of the terminal oxidases found in the *M. oxyfera* genome (Wu et al., 2011). Obviously, the most interesting question now is the identity of the enzyme that catalyzes oxygen and nitrogen formation from NO.

The intermediary role for oxygen in the activation of recalci-trant compounds during denitrification may not be limited to *M. oxyfera*. The facultatively denitrifying γ-proteobacterium *Cu. stearothermophilus* strain HN2N grows on a wide variety of substrates, including C6- to C20-alkanes (Ehrenreich et al., 2000; Zedelius et al., 2010). Growth on hexadecane was observed with oxygen, nitrate, or nitrite as electron acceptors, but not with N₂O. In contrast, N₂O did serve as a substrate for growth on the corresponding easier-to-degrade C16-alcohol and fatty acid, which do not require oxidative activation (Zedelius et al., 2010). Like *M. oxyfera*, the HN2N genome did not contain recognizable genes for the glycyl-radical-catalyzed activation of alkanes, such as alkylsuccinate synthase. Instead, two or possibly three monoxygenases were encoded in the genome. These findings suggest that the activation of the alkane substrate in *M. oxyfera* and HN2N take place by a similar mechanism involving oxygen, formed from nitrate or nitrite (Figure 1B).
FIGURE 4 | Quinol-binding and catalytic sites in the qNOR structure of Geobacillus stearothermophilus (3AYG, Matsumoto et al., 2012; left), and amino acid sequence comparison of these sites in qNORs and putative NODs (right). Sequence accession numbers and alignment are as indicated in Figure 2. Numbering above the alignment refers to the first amino acid and corresponds to the residue numbers of G. stearothermophilus. Specific changes in otherwise strongly conserved residues are highlighted. (A) Quinol binding site with a bound quinol analog, 2-heptyl hydroxyquinoline N-oxide (green molecular surface). His328 and Asp746 form hydrogen bonds with the quinol moiety and the large hydrophobic residues interact with the hydrophobic tail. (B) View of the catalytic site from the plane of the heme b. The Zn b is indicated in green and two water molecules in the coordination sphere of the Zn b are indicated as small red spheres.

The different NOR types are distinguished on the basis of the electron carrier that supplies nitric oxide reduction with reductant. Best characterized are cNORs which contain an additional cytochrome c subunit for this purpose, and qNORs which use reduced quinone (quinol) as the electron donor. Of both enzymes, atomic structures have been resolved recently (Hino et al., 2010; Matsumoto et al., 2012).

As mentioned above, the M. oxyfera genome contained three qNOR paralogs (EC 1.7.5.2, DAMO_1889, DAMO_2434, and DAMO_2437), in stark contrast to the lack of appreciable N2O production during nitrite-dependent methane oxidation (Raghoebarsing et al., 2006; Ettwig et al., 2008, 2009, 2010). DAMO_1889 was expressed in only low amounts, but the two highly similar DAMO_2434 and DAMO_2437 (84% aa identity) were among the most abundant gene products, both at the transcriptional and protein level (Ettwig et al., 2010). Detailed sequence analysis revealed that DAMO_1889 shared all important features with known qNORs, while DAMO_2434 and DAMO_2437 displayed important differences, which will be discussed in detail below. Strikingly, the unusual characteristics were consistently found in two other protein sequences available in GenBank, putative qNORs from the hexadecane-oxidizing γ-proteobacterial strain H4N1 (Zedelius et al., 2010) and from Muricauda rustringensis, a Flavobacterium...
that had been isolated with peptone as a carbon source from a hexadecane-oxidizing, denitrifying enrichment culture (Bruns et al., 2001). A species of the same genus, M. aquanovorans, was recently shown to degrade hexadecane and poly cyclic aromatic hydrocarbons aerobically (Jiménez et al., 2011). Although the three organisms are only distantly related, their unusual qNOR-like genes form one separate cluster within the qNORs (Figure 2). A similar qNOR, however, is absent from the genome of the benzene-oxidizing D. aromatica strain RCB.

CHARACTERISTICS OF THE PUTATIVE NO DISMUTASES

The overall atomic structure of qNOR strongly resembles the one of qNORs and other HCOs (Hino et al., 2010; Matsumoto et al., 2012). The enzyme is composed of a membrane-spanning region with 13 trans-membrane helices (TMHs) that enclose the heme \( h \), heme \( b_2 \), and Fe(II) moieties, which are coordinated by the conserved histidine sextet. In the qNOR structure, the latter position is occupied by a (redox-insensitive) zinc atom, which most likely is a crystallization artifact (Figure 3). A particular property of qNOR is the presence of an additional \( 14(\beta) \) N-terminal TMH that is followed by a long hydrophilic stretch of amino acids. This sequence folds at the periplasmic site as a cysteine domain like in qNOR, although a heme \( c \) itself is absent. Instead, the heme \( c \) position is filled by a number of voluminous aromatic amino acids. Two hydrophobic channels are observed in the structure that run parallel to the membrane and connect the hydrophobic membrane interior with the active site. These channels might function in substrate (NO) import and product (N\(_2\)O) export. Two more features distinguish qNOR from qNOR: (1) the presence of a quinol-binding site (Figure 4A) and of a water-filled channel that likely plays a role in the supply of protons for NO reduction (Fig. 4; Matsumoto et al., 2012; Shiro et al., 2012). The channel leads from the bottom of the enzyme in the cytoplasm up to the catalytic site.

The sequence comparison of the M. oxyfera and the other unusual qNORs establish both similarities and significant differences with respect to canonical qNORs. In DAMO\(_{2434}\), all characteristics are conserved, suggesting the protein to be a genuine qNOR. Also in DAMO\(_{2434}\), DAMO\(_{2437}\), and their relatives the overall folding is apparently maintained with respect to the one of qNORs, as is inferred from sequence comparison and structural modeling using qNOR of Geobacillus stearothermophilus (PDB 3AYF and 3AYG) as the template (not shown). The arrangement of the 14 TMHs, the hydrophilic domain devoid of heme \( c \), all histidines except one, both putative substrate channels and a portion of the amino acids related with the H\(^+\) channel are conserved. This suggests that DAMO\(_{2434}\) and its relatives, hereafter referred to as putative NOD, bind the electron-transferring heme \( h \), the catalytic heme \( b_2 \), and non-heme iron (or another catalytic metal). However, in the NODs one of the coordinating histidines is consistently replaced by an asparagine (Figure 4B). Similarly, a glutamate in close vicinity to the catalytic center, which has been implied with catalysis (Thornycroft et al., 2007; Flock et al., 2009; Hino et al., 2012; Shiro et al., 2012) is substituted by a glutamine residue. Also the amino acids lining the proposed H\(^+\) channel in qNOR have undergone several substitutions in the putative NODs. Most importantly, the unusual qNORs lack a proper quinol-binding site. Conserved residues that are assumed to constitute the quinol-binding site in qNORs are substituted for amino acids that are unlikely to provide a suitable site for quinol binding in the putative NODs (Figure 4A). In summary, the latter apparently are unable of accepting external electrons, they have a different catalytic site and might be impeded in H\(^+\) uptake from outside the protein. Obviously, these properties compromise a role as nitric oxide reductases. The question then is what they do, presuming that they do bear an important biological function – a reasonable assumption given their high expression levels in M. oxyfera. It is tempting to speculate that the modified proteins can bind two NO molecules, rearrange N-O bonds with the aid of the hemes and non-heme metal (iron or otherwise), and recombine both N and O atoms such that N\(_2\) and O\(_2\) are made. In other words, the enzymes would act as an NO dismutase. At this stage, this is speculation. The proof can only come from the purification and rigorous characterization of these intriguing enzymes.

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