Roles of c-type cytochromes in respiration in Neisseria meningitidis

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Three c-type cytochromes were identified in Neisseria meningitidis, based on predictions from genome sequences, that were hypothesized to be involved in electron transport to terminal electron acceptor reductases for oxygen (the cytochrome cbb3 oxidase) and nitrite (the nitrite reductase, AniA). Mutants were generated by allelic exchange with disrupted copies of the genes encoding these cytochromes and the phenotypes of the resultant mutants analysed. It was found that cytochrome cbb3 is required for in vivo nitrite reductase activity, whereas cytochromes c4 and c4 are both required for efficient growth using oxygen as an electron acceptor. Mutants in c4, c4, and c4+c4 have a decreased capacity to reduce oxygen, but there is a background oxygen-reduction activity, indicating that there may be other routes for electron transfer from the cytochrome bC1 complex to the cytochrome cbb3 oxidase, whereas cytochrome c4 appears to be the sole route of electrons to the nitrite reductase in N. meningitidis. Interestingly, cytochrome c4 is highly similar to a domain of copper nitrite reductases from various proteobacteria, whereas cytochrome c4 has high identity with a domain of the cytochrome cbb3 oxidase of Neisseria gonorrhoeae, yet these two proteins function in oxygen respiration and nitrite respiration, respectively. This highlights a limitation of predicting protein function from similarity to known proteins, i.e. very closely related protein domains in different organisms can have different redox partners.

INTRODUCTION

The β-proteobacterium Neisseria meningitidis is commonly identified as part of the commensal flora of the human nasopharyngeal mucosa. Very occasionally colonization is followed by invasion of the bloodstream by N. meningitidis, leading to life-threatening illness in the form of meningitis or septicaemia (van Deuren et al., 2000). The nasopharyngeal mucosa is habitat to a wide variety of other bacteria, including both aerobes and anaerobes (Brook, 2003). In previous work, we have determined that under aerobic conditions N. meningitidis is able to support respiration by reducing oxygen to water via the enzyme cytochrome cbb3 oxidase (which is the only oxygen reductase in N. meningitidis), and that when oxygen becomes limiting the bacterium expresses genes encoding a nitrite reductase (aniA) and a nitric oxide reductase (norB) that collectively catalyse the respiratory reduction of nitrite to nitrous oxide (Anjum et al., 2002). N. meningitidis is able to employ this partial denitrification pathway to support growth under micro-aerobic conditions in the presence of nitrite (Rock et al., 2005).

We have proposed an organization for the respiratory chain of N. meningitidis, based on genome sequence analysis and experimental analysis with specific inhibitors (Deedum et al., 2006). The nitric oxide reductase of N. meningitidis appears more similar to the quinol-oxidizing nitric oxide reductase (qNOR) than the cytochrome c-oxidizing NOR (cNOR) (de Vries & Schröder, 2002), and hence it was proposed that the nitric oxide reductase receives its electrons directly from the ubiquinone pool. This was confirmed experimentally by showing that nitric oxide reduction is insensitive to the cytochrome bc1 complex inhibitor myxothiazol. Contrastingly, the reduction of the other two electron acceptors (oxygen and nitrite) is very sensitive to myxothiazol. The enzymes responsible for these reductase reactions typically receive their electrons from c-type cytochromes in other micro-organisms, and hence it was proposed that these two enzymes terminate the electron-transport chain downstream of the cytochrome bc1 complex and c-type cytochromes (Deedum et al., 2006). The genome of N. meningitidis MC58 reveals the presence of genes encoding three putative c-type cytochromes that might mediate the transfer of electrons between the cytochrome bc1 complex and the reductases for oxygen and nitrite. These three c-type cytochromes are conserved within the genomes of other N. meningitidis strains and in Neisseria gonorrhoeae.
Gene NMB0717 (from *N. meningitidis* MC58) is predicted to encode a periplasmic mono-haem cytochrome with a molecular mass of 12.5 kDa. We call the putative product of this gene cytochrome *c*. A homologue of NMB0717, cytochrome c552 from *Thermus thermophilus*, has been proposed to transfer electrons between the cytochrome bc1 complex and ba3 oxidase in that organism (Muresanu et al., 2006). **Blast** searching reveals that the predicted protein sequences with closest similarity to NMB0717, outside of the *Neisseria* homologues, are predicted copper-type nitrite reductases in *Bdellovibrio bacteriovorus*, *Pseudoalteromonas haloplanktis* and several *Burkholderia* species. In these organisms, the gene for the copper nitrite reductase (homologous to the nitrite reductase gene, *aniA*, of *N. meningitidis*) is fused to a cytochrome domain homologous to NMB0717. This suggests a possible role for cytochrome *c* in transfer of electrons to nitrite reductase in *N. meningitidis*.

Gene NMB1805 is predicted to encode a periplasmic di-haem cytochrome with a molecular mass of 21.5 kDa. We call the putative product of this gene cytochrome *c*, consistent with the nomenclature for the homologous gene (also known as *cycA*) from *N. gonorrhoeae* (Turner et al., 2005). Cytochrome *c* homologues are found in many other proteobacteria and a crystal structure has been found for the protein from *Pseudomonas stutzeri* (Kadziola & Larsen, 1997). Both haem groups are hexacoordinated, consistent with a role in electron transfer, rather than enzyme catalysis.

Gene NMB1677 is predicted to encode a membrane-associated di-haem cytochrome with a molecular mass of 30 kDa. We call the putative product of this gene cytochrome *c*, consistent with the nomenclature for the homologous gene (also known as *cycB*) from *N. gonorrhoeae* (Turner et al., 2005). The protein contains a predicted N-terminal membrane span, followed by two soluble domains containing two covalently bound haems located within the periplasm. The second haem-containing domain of cytochrome *c* bears a striking similarity (74 % identity) to a region of the cytochrome *cbb3* oxidase subunit III (encoded by *ccoP*) from *N. gonorrhoeae*. *CcoP* from *N. gonorrhoeae* is predicted to contain three haem groups, whereas *CcoP*s from other organisms that have been characterized contain just two haem domains (Pitcher & Watmough, 2004). Indeed, the predicted *CcoP* from *N. meningitidis* contains two haems. The similarity of cytochrome *c* to a domain of the oxidase immediately suggests a role for cytochrome *c* in the electron transfer from cytochrome *bc1* to the cytochrome *cbb3* oxidase.

The possession of multiple *c*-type cytochromes as part of multiply branched respiratory chains is characteristic of many bacterial species. The unambiguous assignment of function to these cytochromes is often difficult due to their large apparent mass and apparent redundancy of function. The aim of the work presented in this paper was to investigate the roles of the three putative electron-carrier proteins of *N. meningitidis* in respiration in this organism, which is an important pathogen but which may also be viewed as a good model for analysis of branched respiratory metabolism due to its relatively small number of respiratory electron-acceptor reductases.

**METHODS**

**Bacterial strains, plasmids and growth conditions.** All strains of *N. meningitidis* used in this work were derived from *N. meningitidis* MC38 (McGuiness et al., 1991) (Table 1). *N. meningitidis* strains were routinely cultured at 37 °C in air supplemented with 5 % CO2 on Columbia agar plus 5 % (v/v) horse blood plates, or in liquid culture in Mueller–Hinton Broth (MHB) supplemented with 10 mM NaNHCO3. Aerobic culture was carried out in 5 ml of broth in 25 ml Sterilin McCartney bottles shaken at 200 r.p.m. Microaerobic culture was carried out using 20 ml of broth in a 25 ml Sterilin McCartney bottle, shaken at 90 r.p.m. and, where appropriate, supplemented with 6 mM NaNO2. Growth was monitored by measuring OD600 in a Jenway 6305 spectrophotometer. For whole-cell spectroscopy experiments cultures were supplemented with 5 mM glucose in order to provide a defined electron donor that could be included as physiological reductant in cuvettes. Antibiotics were used at the following concentrations: tetracycline 20 μg ml−1, erythromycin 50 μg ml−1, kanamycin 50 μg ml−1 and spectinomycin 50 μg ml−1.

**Construction of mutant strains.** The gene encoding cytochrome *c*5 (NMB0717) and 500 bp flanking on each side was amplified with primers c552F and c552R (Table 1) using Pfu polymerase (Promega). The product was cloned into pCR-Blunt II TOPO (Invitrogen). The product was cleaved with Bgl, which recognizes a site located centrally within the NMB0717 gene. Subsequently, the ends of the linearized plasmid were rendered blunt with Klenow fragment and the product was ligated with the spectinomycin resistance (*SpcR*) gene derived from pHP450 (Prentki & Krisch, 1984) to yield pTOPO_c5::SpcR. The gene encoding cytochrome *c*4 (NMB1805) and 500 bp flanking on each side was amplified with primers c554F and c554R (Table 1) and disrupted by essentially the same method as described for cytochrome *c*5 except that the gene was disrupted by digestion with Bsa361 (which recognizes a site located centrally within the NMB1805 gene). Insertion of an erythromycin resistance (*EryR*) gene [derived by PCR from a strain of *N. meningitidis* in which the gene for was disrupted by EryR (Rock et al., 2005)] yielded pTOPO_c4::EryR. The gene encoding cytochrome *c*5 (NMB1677) and 500 bp flanking on each side was amplified with primers c555F and c555R (Table 1) and disrupted by essentially the same method as described for cytochrome *c*4 except that the gene was disrupted by digestion with XmnI (which recognizes a site centrally within the NMB1677 gene) and insertion of a tetracycline resistance (*TetR*) gene derived from Tn916, yielding pTOPO_c5::TetR.

The recombinant plasmids containing disrupted copies of the genes encoding cytochromes were transformed into *N. meningitidis* MC58 using the method of Bogdan et al. (2002), selecting for recombinant strains using the appropriate antibiotic selection on plates, and verifying the correct chromosomal rearrangement by PCR.

**Gels and blotting.** Whole-cell extracts of *N. meningitidis* were prepared by harvesting 1 ml samples of cultures in late exponential phase by centrifugation, resuspending the pellets in 500 μl Tris/HCl (pH 8) + 1 % (w/v) n-dodecyl β-D-maltoside + 1 mg lysozyme ml−1 + 1 mg DNAse I ml−1, and subjecting the suspension to 8–10 cycles of freezing and thawing. Samples were separated by SDS-PAGE and blotted onto nitrocellulose membranes. Membranes were stained with Ponceau S to check for efficient protein transfer and...
The expression of \( c \)-type cytochromes was assessed using a chemiluminescence method (Vargas et al., 1993) to measure the peroxidase activity of haem groups covalently attached to protein. Five hundred microlitres of chemiluminescence detection reagents (SuperSignal West Dura substrate, Pierce) were mixed and subsequently exposed to X-ray film (for 5 s to 5 min) to achieve an optimum chemiluminescence signal. Bands due to cytochrome were identified using a chemiluminescence method (Vargas et al., 1993) to confirm the absence of a cytochrome band located near 550 nm. The lane containing extract from strain \( \text{N. meningitidis} \) \( c_x \) indicates the absence of a cytochrome band located near 550 nm, consistent with the absence of cytochrome \( c_x \) (which has a predicted molecular mass of 30 kDa). The lanes containing extracts from strains \( \text{N. meningitidis} \) \( c_x \) and \( c_x - c_4 \) lacked an intense band with a molecular mass of approximately 23 kDa, consistent with the absence of cytochrome \( c_x \) (predicted molecular mass 21.5 kDa) from these strains. There is no difference in the appearance of lanes between \( c_x \) and \( c_x - c_4 \). The lane containing extract from strain \( \text{N. meningitidis} \) \( c_x \) cannot be observed by this method.

### RESULTS

#### Construction and confirmation of mutants in cytochromes \( c_x, c_4 \) and \( c_5 \)

Mutant strains deficient in \( c_x, c_4, c_5 \) and \( c_x + c_4 \) were generated following transformation of the constructs described above into \( \text{N. meningitidis} \) MC58. In each case, the replacement of the wild-type copy of the gene with the copy containing an antibiotic resistance cassette was confirmed by PCR (data not shown). In order to obtain further biochemical confirmation, whole-cell extracts generated from each of the strains were run on SDS-PAGE, blotted onto nitrocellulose and stained for haem (Fig. 1a). The lane containing extract from strain \( \text{N. meningitidis} \) \( c_5 \) reveals the absence of a cytochrome band with molecular mass of approximately 33 kDa, consistent with the absence of cytochrome \( c_5 \) (predicted molecular mass 33 kDa). The lane containing extracts from strains \( \text{N. meningitidis} \) \( c_x \) and \( c_x - c_4 \) lacked an intense band with a molecular mass of 23 kDa, consistent with the absence of cytochrome \( c_4 \) (predicted molecular mass 21.5 kDa) from these strains. There is no difference in the appearance of lanes between \( c_x \) and \( c_x - c_4 \), indicating that a band due to cytochrome \( c_x \) cannot be observed by this method.

UV–visible reduced-minus-oxidized spectroscopy of intact cells of \( \text{N. meningitidis} \) wild-type yielded spectra consistent with the presence of \( c \)-type (\( x \) band located near 550 nm) and \( b \)-type (\( x \) band shoulder near 560 nm) cytochromes in this organism (Fig. 2). Comparison of wild-type versus strains deficient in \( c_x, c_4 \) and \( c_5 \) indicates the absence of...
Fig. 1. (a) Haem-stained blot of N. meningitidis extracts shows altered expression of cytochromes. Samples (13 µg) of total cell extracts from N. meningitidis wild-type MC58 and the mutants indicated (aerobically grown) were separated by 15% SDS-PAGE, blotted and stained for haem. (b) Western blot with anti-AnnA antibodies. The N. meningitidis strains were grown under microaerobic conditions plus nitrate. Gels were run as for (a).

specific cytochromes in each of the constructs (Fig. 2). The overall intensities of the redox difference spectra were decreased for the cytochrome-deficient strains compared to the wild-type. Furthermore, the positions of the α bands in these difference spectra are shifted compared to the wild-type. For N. meningitidis MC58, the α band is positioned at 555 nm, whilst the cα- and cα+ mutants have their α peak at 552 nm and the cα- mutant has an α band at 555 nm. The α band of the cα-cα- mutant is centred at 553 nm. It is notable that the mutation in cα causes a shift in the α band as well as a decrease in spectral intensity (for MC58 versus cα- and for cα- versus cα-cα-), providing evidence that cytochrome cα is expressed in wild-type N. meningitidis and absent from the cα mutant strains (despite giving no band on haem-stain blots).

Growth properties of cytochrome-deficient mutants of N. meningitidis

N. meningitidis MC58, cα-, cβ-, cγ- and cα-cα- were cultured under aerobic conditions and under microaerobic conditions in the presence and absence of 5 mM nitrite (Fig. 3). The growth rate of the cα- mutant was virtually the same as that of the wild-type during the exponential phase in aerobic culture (doubling time of 43 min), whereas the cα-, cα+ and cα-cα- mutants grew relatively poorly, with doubling times of 63 min, 130 min and 174 min, respectively (Fig. 3a). N. meningitidis MC58, cβ-, cγ- and cγ grew at similar rates to one another under microaerobic conditions in the absence but not the presence of nitrite (Fig. 3b, c). In the presence of nitrite, N. meningitidis MC58, cβ-, cγ- and cα-cα- had an exponential phase of growth, as expected for cultures that have nutrient sufficiency when nitrite is present, whereas the cγ- mutant had a linear growth curve, as would be expected for a strain that is limited by availability of a nutrient that is supplied at a constant rate, such as oxygen (Fig. 3c). This has been observed previously for strains of N. meningitidis that are unable to denitriify (Rock et al., 2005), and suggests that under these growth conditions the cytochrome cγ-deficient strain grows using the limiting nutrient oxygen and is unable to denitriify. Measurements of nitrite remaining in culture medium corroborated this proposition, since nitrite disappeared during the course of growth of all strains except N. meningitidis cα- (Fig. 3d). It is notable that N. meningitidis cα-, cγ- and cα-cα- grew to lower final cell densities than did N. meningitidis MC58, and yet utilized nitrite as quickly as or quicker than the wild-type. This is consistent with the relatively poor ability of these strains to grow aerobically (Fig. 3a), and indicates that under denitrifying conditions these strains use nitrite as the major electron sink for respiration whereas the wild-type combines nitrite and oxygen utilization simultaneously.

To test whether the impaired aerobic growth observed in mutants deficient in cα, cγ and cα+cγ was due to an inability to metabolize oxygen, the rate of oxygen uptake was measured in suspensions of N. meningitidis strains using a Clark-type oxygen electrode. The rate of oxygen uptake was measured for cα- and cγ- strains relative to wild-type following aerobic growth. The rates of oxygen uptake were 83 ± 5% and 59 ± 5% of the wild-type rate in strains cα- and cγ- respectively. The growth of N. meningitidis cα-cα- was so poor aerobically that we cultured the wild-type and cα-cα- strains under denitrifying conditions to analyse the relative oxygen respiration.
rate in this strain. The rate of oxygen uptake was $45 \pm 5\%$ of the wild-type rate in the $c_x^{-}c_4^{-}$ strain. Clearly both cytochromes $c_x$ and $c_4$ are involved in enabling N. meningitidis to utilize oxygen and to grow aerobically.

N. meningitidis $c_5^{-}$ failed to utilize nitrite during incubation under microaerobic conditions with nitrite. To determine whether this was due to an inability to respire nitrite or nitric oxide we grew strains MC58 and $c_5^{-}$ microaerobically in the absence of nitrite and then followed the accumulation of nitric oxide using an NO electrode after the addition of nitrite (Fig. 4). No nitric oxide accumulated from the $c_5^{-}$ strain, whereas, as expected, it accumulated immediately on adding nitrite to the wild-type. This indicates that the lesion in the $c_5$ mutant relates to nitrite reduction, not nitric oxide reduction. To assess whether the defect in nitrite reduction in N. meningitidis $c_5^{-}$ might be due to low nitrite reductase expression and/or activity rather than to a break in the electron-transport chain to the nitrite reductase we measured nitrite reductase expression and activity. Expression of nitrite reductase was assessed by Western blotting (Fig. 1b), which showed that AniA is expressed at similar levels in all strains. Using a methyl viologen-linked nitrite reductase assay in total cell extracts we found that N. meningitidis MC58 and $c_5^{-}$ had similar overall rates of nitrite reductase activity (data not shown). In the absence of cytochrome $c_5$ the electron-transport chain to nitrite reductase is disabled, presumably because cytochrome $c_5$ is an electron carrier between the cytochrome $bc_1$ complex and AniA nitrite reductase.

**Spectroscopic analysis of oxidation of N. meningitidis cytochromes by oxygen versus nitrite**

Like oxygen, nitrite was found to be capable of oxidizing cytochromes in N. meningitidis MC58 (but only after

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**Fig. 3.** Effect of deficiency in cytochromes on growth of N. meningitidis. Cultures of N. meningitidis wild-type MC58 (■—■) and mutants $c_x^{-}$ (□---□), $c_4^{-}$ (△---△), $c_5^{-}$ (●—●) and $c_5^{-}c_4^{-}$ (○---○) were grown under aerobic conditions (a), under microaerobic conditions without nitrite (b) and under microaerobic conditions plus 6 mM nitrite (c). In each case growth was monitored by measuring OD$_{600}$. Nitrite disappearance was monitored for microaerobic cultures supplemented with nitrite (d).

**Fig. 4.** Nitric oxide production in N. meningitidis wild-type MC58 but not the $c_5^{-}$ mutant strain. N. meningitidis MC58 and $c_5^{-}$ were grown under microaerobic conditions, and a 5 ml cell suspension was allowed to become anaerobic in a water-jacketed electrode chamber at 37 °C. Oxygen was monitored with a Clark-type electrode (dashed line). Nitric oxide was monitored with an NO electrode (solid line) before and after the addition of 5 mM nitrite.
DISCUSSION

In this study we investigated the roles of the three putative electron-carrier c-type cytochromes of *N. meningitidis* in respiratory electron transport during oxygen respiration and denitrification of nitrite to nitrous oxide. The evidence establishes that cytochrome *c*₅ and cytochrome *c*₄ are important for oxygen reduction and that cytochrome *c*₅ is necessary for the reduction of nitrite to nitric oxide. These findings run counter to the expectations based on similarity of the cytochromes to other proteins in sequence databases. Most notably, cytochrome *c*₅ is highly homologous to a cytochrome-containing domain of copper nitrite reductases from various proteobacteria, which had indicated that cytochrome *c*₅ might be involved in electron transfer to nitrite reductase in *N. meningitidis*, whereas the experimental finding was that mutation of cytochrome *c*₅ has no deleterious effect on nitrite reduction. Similarly, cytochrome *c*₅ (identified experimentally as required for nitrite reduction) is very similar to a domain of the cytochrome *cbb*₃ oxidase of *N. gonorrhoeae*, which had suggested that this protein might be important for oxygen respiration. This is an important caveat to bear in mind when predicting function of electron-transport proteins, i.e. very closely related protein domains in different organisms can have different redox partners.

The simplest explanation of the data we have obtained is that cytochrome *c*₅ is a mediator that carries electrons from the cytochrome *bc*₁ complex to the AniA nitrite reductase. Cytochromes *c*₅ and *c*₄ are not required for the reduction or oxidation of *c*₅. Is it feasible that cytochrome *c*₅ might be a direct electron donor to AniA nitrite reductase? AniA consists of a trimer of water-soluble subunits (Boulanger & Murphy, 2002) associated with the outer membrane via covalent attachment of N-terminal cysteine residues to fatty acid moieties (Clark *et al.*, 1987; Hoehn & Clark, 1992). It is presumed to be associated with the inner leaflet of the outer membrane, and hence located within the periplasmic compartment. To reduce AniA and drive nitrite reduction, electrons must be transported across the periplasm from the cytochrome *bc*₁ complex (in the inner membrane) to AniA. Can cytochrome *c*₅ span this gap? Analysis of the sequence of cytochrome *c*₅ indicates that it arose by a duplication event from an ancestral gene encoding a monohaem protein. There is no structure available for a dihaem cytochrome *c*₅, but structural information is available for a homologous monohaem cytochrome *c*₅ from *Shewanella putrefaciens* (Bartalesi *et al.*, 2002). This globular protein has a diameter of approximately 30 Å (3 nm), indicating that the dimeric cytochrome *c*₅ from *N. meningitidis* may span approximately 60 Å. *N. meningitidis* cytochrome *c*₅ is predicted to be attached to the membrane via a transmembrane helix, and thus it is anticipated that it can form a structure which protrudes up to approximately 60 Å into the periplasm from the inner membrane. The ingress of electrons to AniA occurs via a blue copper centre which is accessed from a site on the surface of AniA which is approximately 45 Å from the N-terminal face of the soluble protein structure (Boulanger & Murphy, 2002). Thus a complex of the globular domains of cytochrome *c*₅ and AniA could span some 105 Å across the periplasm. The width of the Gram-negative periplasm is approximately 170 Å, based on electron microscopy measurements (Matias *et al.*, 2003) and calculations based on the interaction of inner-membrane protein AcrB with outer-membrane protein TolC (Tamura *et al.*, 2005). Towards the N terminus of the mature AniA polypeptide there is a 35–40 residue region rich in alanine, proline and glutamate that may form an elongated unstructured linker that will allow AniA to get access to electrons from cytochrome *c*₅. It will be of interest to shorten this ‘linker region’ to determine whether it is required for allowing AniA to obtain electrons.

Haem staining was used successfully to identify cytochromes *c*₄ and *c*₅ in total extracts of *N. meningitidis*
strains. However, cytochrome \( c_5 \) could not be seen by this method. Haem staining relies on the peroxidase activity of the haem group, an activity that is affected by the naturation state of the protein folding around the haem group (Diederix et al., 2002). This activity varies between cytochromes and is presumably very low for cytochrome \( c_5 \). Spectroscopic measurements, however, showed a significant loss of \( c \)-type cytochrome from the \( c_5 \) mutant (Fig. 2), confirming that this is a major cytochrome in \( N. meningitidis \). The additive effects of mutations in \( c_5 \) and \( c_4 \) on oxygen respiration indicate that these two proteins operate as independent parallel pathways of electrons from the cytochrome \( b_{c1} \) complex to the cytochrome \( cbb_3 \) oxidase (Fig. 6). Additionally, there is residual oxidase activity in a \( c_5^{-}c_4^{-} \) mutant, indicating that there are alternative pathways to cytochrome \( cbb_3 \). Cytochrome \( c_5 \) may act as an alternative electron carrier to the oxidase, and it is noticeable that growth of a \( c_5^{-} \) mutant aerobically is slower than that of the wild-type at high optical densities in late exponential phase (Fig. 4a). We were unable to construct a \( c_5^{-}c_4^{-}c_5^{-} \) triple mutant, lending support to this proposition. An alternative route might involve the outer-membrane-associated cupredoxin Laz (lipid-modified azurin) (Gotschlich & Seiff, 1987; Kawula et al., 1987). Mutants deficient in the gene encoding Laz grew well aerobically (Wu et al., 2005; our unpublished data) but we were unable to generate a \( c_5^{-}c_4^{-}laz \) triple mutant (data not shown). The proposed electron-transport chain of \( N. meningitidis \) is summarized in Fig. 6.

Spectroscopic analysis following oxidation of reduced cytochromes in intact \( N. meningitidis \) with oxygen, nitrite and nitric oxide indicates that on oxidation of cells with nitrite the main chromophores that are oxidized are \( c_5 \) and nitric oxide. This indicates that on oxidation of cells with nitrite the main chromophores that are oxidized are \( c_5 \) and nitric oxide. It may also be related to the fact that nitrite reductase draws electrons from only cytochrome \( c_5 \) whereas oxygen oxidizes cytochromes \( cbb_3 \) and \( c_5 \) and possibly \( c_4 \). Furthermore, this spectroscopic observation is consistent with the finding that oxygen almost completely inhibits nitrite reduction in intact cells, whereas the reverse is not the case (Rock et al., 2005); i.e. oxygen is able to out-compete nitrite for electrons at the level of cytochrome \( c \).

In summary, we have identified the roles of three \( c \)-type cytochromes in the respiratory chain of \( N. meningitidis \). Respiration is crucial for survival of \( N. meningitidis \), and these cytochromes are highly conserved and extracytoplasmic, making them potential targets for the development of novel therapeutics against pathogenic neisseriae.

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