Analysis and modelling of respiratory metabolism in *Neisseria meningitidis*

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Abstract

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Chapter 1

Introduction

1.1 Biology and pathology of *Neisseria meningitidis*

Neisseria meningitidis is a Gram-negative, bean-shaped diplococcal bacteria[1], surrounded by a lipid membrane containing outer membrane proteins and lipopolysaccharides[1]. When pathogenic, the bacteria also has a polysaccharide capsule attached to the membrane[1]. It is non-spore forming, non-motile but piliated, and lives as a parasite, with humans being its only host[2]. *N. meningitidis* inhabits the mucosal membranes primarily in the respiratory tract, and it is estimated that up to 20-25% of the population have this bacteria in their nasopharynx while being asymptomatic[2–4].

The *Neisseria* genus contains a number of non-pathogenic species which are part of the normal human flora including *N. subflava*, *N. flavescens* and *N. lactamica*. Two species of *Neisseria* are the causative agents of human diseases, *N. meningitidis*, which causes bacterial meningitis and *N. gonorrhoea* which causes gonorrhoea. Being β-proteobacteria[2], the *Neisseria* genus is also related to a number of other pathogenic bacteria including *Bordetella* and *Burkholderia*. This taxa also includes nitrogen-fixing bacteria such as *Nitrosomonas*[5].

N. meningitidis is classified into 13 different serogroups based on the differences in lipopolysaccharides, capsules, outer membrane proteins and adhesion molecules[1,2,6]. 3 of these 13 serogroups are the main cause of meningococcal

meningitis, with serogroups B and C being the most prevalent[1]. Vaccines for Serogroup C are available, but serogroup B currently has no effective vaccine, as it mimics human antigens[2]. In addition to being the causative agent for meningococcal meningitis, *N. meningitidis* also causes septicaemia and the combination has a mortality rate of 10%[1,2].

Meningitis is caused by *N. meningitidis* entering the bloodstream and travelling to the meninges, a set of membranes that envelope the central nervous system, where the bacteria goes on to cause inflammation. Once it has entered the bloodstream, *N. meningitidis* is capable of switching its capsule by phase-variation to avoid host-immune detection[7,8]. After colonisation by the bacterium, in order to enter the bloodstream, it must first adhere to the mucosal tissue. This is facilitated by adhesion molecules on the outer membrane and by pili, with the latter being the primary source of adhesion[1,6]. Once the bacteria are adhered to the mucosal cells, additional contacts are made with the outer membrane proteins. Interestingly, the presence of the polysaccharide capsule, which is required for survival in the bloodstream, interferes with these additional contacts[2]. *N. meningitidis* invades the bloodstream by being endocytosed by the mucosal epithelial cells, a process which is triggered by the pili and outer membrane proteins on the bacteria.

N. meningitidis is able to survive in the bloodstream (typically an antimicrobial environment) mainly by virtue of its polysaccharide capsule as this is able to protect the bacteria against various immune responses by the host including complement-mediated bacteriolysis and phagocytosis by neutrophils[1]. Despite these protective features, specific antibodies *do* provide full protection against the bacteria, but the time taken for these antibodies to be produced means that the host has a period of at least 1 week in which it must rely on innate immune response[1]. Evidence suggests that systemic infection by *N. meningitidis* can only occur in hosts which are immunocompromised in some way, specifically if they do not have the serum bactericidal antibodies against capsular or non-capsular

antigens, or they are missing certain complement components[4]. A number of factors can increase the likelihood of contracting bacterial meningitis including smoking and travelling to epidemic regions[2]. In developed countries, the highest rates of invasive meningococcal meningitis are seen in infants and children less than 4 years-old, adolescents, military recruits and groups where crowding and new exposures occur such as college students living in dormitories, however the disease is capable of affecting all age groups[2].

There is evidence to suggest that much of the damage done to the host during a meningococcal infection is actually caused by the host in an attempt to rid itself of the bacteria[9]. A systemic infection causes a massive inflammatory response and the resulting quantities of cytokines produced eventually lead to organ dysfunction and the proteases produced by neutrophil activation also lead to endothelial injury[9].

Once *N. meningitidis* has entered the bloodstream, it goes on to invade the cerebro-spinal fluid (CSF), which serves as an excellent culture medium for the bacteria[4]. The host response to this infection is inflammation of the meninges, the membranes surrounding the central nervous system. This leads to a build-up of serous fluid in the brain causing cerebral swelling. Once the bacteria have entered the CSF, antimicrobial treatment is required otherwise the effects are almost invariably fatal[4].

Initially a meningococcal infection presents as a slight fever and chills, which may improve after 4-6 hours. Hemorrhagic skins lesions may appears between 8 and 18 hours, however roughly 20% of suffers never present with lesions. These skin lesions are possibly the most well known symptom of bacterial meningitis as they are characterised as a non-blanching (does not turn white under mild pressure) rash. The clearest evidence for meningococcal infection is a fever, stiff neck, aversion to bright light, vomiting, skin lesions and headaches. Unfortunately not all these symptoms may be present in all cases[4].

When meningococcal septicaemia occurs, renal function may be impaired as

a direct consequence of cardiac impairment. Septicaemia causes "capillary leak" which reduces cardiac output and increases the effort required to breathe normally. Reduced cardiac output can also affect the gastrointestinal tract leading to reduced function. Once treated these symptoms will usually subside as cardiac output improves[9].

In most cases the treatment for meningococcal meningitis is with antibiotics, where the primary aim is to achieve a rapid bactericidal effect in the CSF[1]. This treatment is suggested prior to positive identification of cultures of the bacteria obtained from the CSF as any delay is potentially life-threatening if the bacteria have indeed invaded the CSF[4].

1.2 Organisation of the respiratory chain of *N. meningitidis*

N. meningitidis is classified as an aerobe and as such has an oxidase pathway for reducing oxygen (O_2), but given that the environment in the nasopharynx is poor in oxygen, the bacteria must also be capable of respiring in a microaerobic environment. This is evidenced by the fact that bacterial isolates from the nasopharynx routinely contain both strict aerobes and strict anaerobes[10]. Genomic analysis of 2 strains of *N. meningitidis* shows that there are 3 terminal oxidases; 1 of each for reducing oxygen, nitrite (NO_2^-) and nitric oxide (NO)[11]. This analysis may be expanded as there are now many more genomes published. Experiments showed that under oxygen limiting conditions, *N. meningitidis* was capable of growth when nitrite was present in the media (Muller-Hinton Broth), and that nitrate (NO_3^-), the probable source for nitrite, had no effect on growth[11]. Additionally the bacteria require carbon dioxide, as shown by Tuttle and Scherp[12] and have 2 enzymes which catalyse the reduction of CO_2[4].

In vivo, nitrite is obtained as a product of digesting nitrate in food. There are a number of nitrate reducing enzymes present in the mouth and pharynx responsible for this[10]. Nitrite is also created by oxidation of nitric oxide, which is produced as a host signalling molecule and as a toxin as part of the host immune

response[10,13].

The respiratory pathway for reducing nitrite in *N. meningitidis* involves two steps; nitrite is reduced to nitric oxide, which is then further reduced to nitrous oxide. This represents incomplete reduction, as a further reduction step would reduce nitrous oxide to dinitrogen gas[10,14].

Reduction of oxygen is favourable over nitrite reduction due to the redox potential differences. The redox potential of O_2/H_2O is $+820mV$, NO_2^-/NO is $+348mV$, thus O_2 has a higher tendency to acquire electrons resulting in a electrochemically favourable reaction[15]. The electron flow towards the oxidase is also preferred physiologically as it liberates more energy by virtue of the translocation of more protons than the reduction of nitrite. The translocated protons are ultimately used in the synthesis of ATP molecules for energy. This results in reduction of oxygen in preference to nitrite when both are present (in most cases).

Reduction of oxygen in *N. meningitidis* is carried out by the oxygen reductase (oxidase) cytochrome *cbb*$_3$, a membrane-bound heme-copper oxidase[16]. *cbb*$_3$ is capable of binding oxygen and nitric oxide, which means that during nitrite reduction (denitrification), the oxidase can be competitively inhibited (chemically) by the intermediate product of denitrification. *cbb*$_3$ can be permanently damaged at high concentrations of NO and O_2, as they can both bind at the *cbb*$_3$ active site and react together to form peroxynitrite[17–19].

Nitrite is reduced by the nitrite reductase AniA, which is a copper containing reductase. This reduction does not involve translocation of protons, and thus does not produce any useable energy. Nitrite is reduced to nitric oxide which can then be further reduced by a nitric oxide reductase NorB. Since *N. meningitidis* is capable of reducing nitric oxide, a host toxin, directly, this may help it defend itself against part of the host immune response[10,20] as has been shown in tissue culture by Anjum et al.[19].

The reduction processes carried out by these enzymes are shown in the table in Table 1.1.

Reduction			Enzyme
NO_2^-	$\rightarrow$	NO	AniA
NO	$\rightarrow$	N_2O	NorB
O_2	$\rightarrow$	H_2O	*cbb*$_3$

Table 1.1: The reductions catalysed by the respiratory enzymes in *N. meningitidis*

The major source for electrons in both respiratory pathways is NADH, although electrons can also be obtained from pyruvate and lactate amongst others. These reduced substrates lead to reduction of ubiquinone to ubiquinol in the ubiquinone pool that exists within the bacteria. Ubiquinol is oxidised either by the cytochrome *bc*$_1$ complex or directly by the NorB enzyme whilst reducing NO to N_2O. Cytochrome *bc*$_1$ is oxidised by a number of intermediate cytochromes which act to transport electrons to the terminal oxidases; AniA and *cbb*$_3$. The c_5 cytochrome transports electrons from the *bc*$_1$ complex to AniA, and two cytochromes, $c_{2/x}$ and c_4, transport electrons to *cbb*$_3$. It is not understood why *cbb*$_3$ has 2 alternate cytochromes, and there is evidence to suggest that it can also be supplied, in a limited capacity, by the c_5 cytochrome as well[21]. The electron transport chain is shown graphically in Figure 1.1.

In addition to the difference in favourability between the two respiratory pathways, there is also a great deal of regulation, both at the enzymatic and transcriptional level. Chemical inhibition also plays a part in regulation as briefly mentioned previously. Expression of AniA is regulated by two processes, the reduction of oxygen and the presence of nitrite. The presence of oxygen down-regulates the expression of an activator of AniA expression. This activator is FNR (fumarate and nitrate reduction regulator), and the presence of oxygen effectively means that AniA expression is repressed by the reduced expression of FNR. In *N. meningitidis*, FNR appears to work slightly differently than in facultative anaerobes such as *E. coli*, in that FNR is still expressed at quite high concentrations of oxygen, and is itself down-regulated by a separate co-factor[22].

The presence of nitrite triggers the two component NarP/NarQ system which

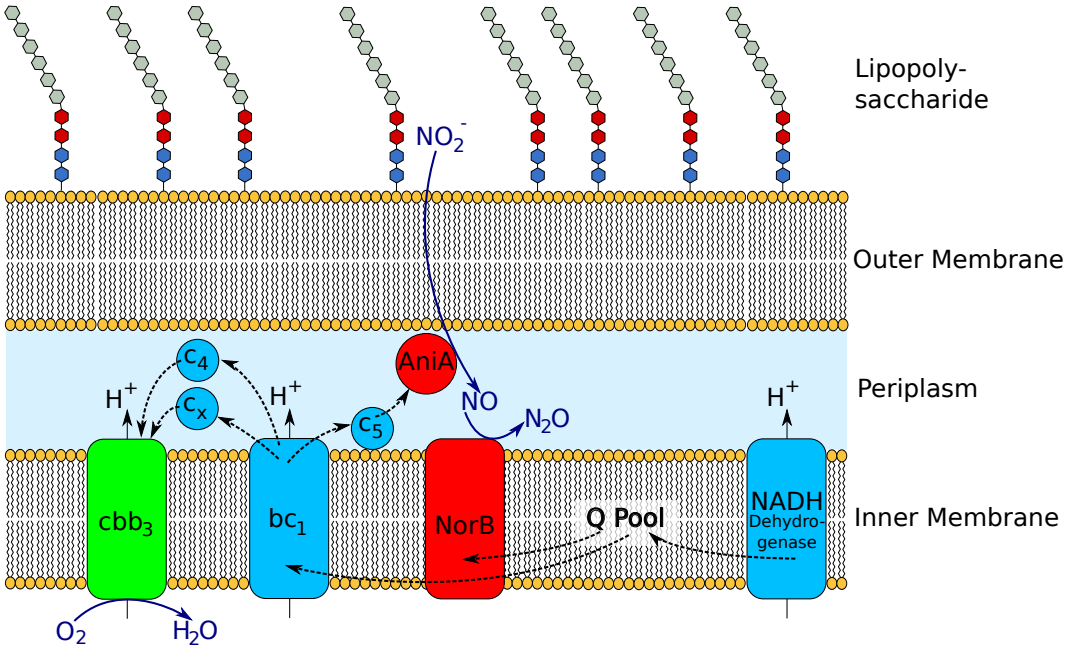

Figure 1.1: Layout of the components of the respiratory system in *Neisseria meningitidis*. Oxygen reducing components are shown in green, nitrogen reducing components in red. Components transporting electrons are coloured light blue, and their transport is indicated by dashed arrows. Respiratory substrates are shown in dark blue, with corresponding arrows linking them to their reducing enzymes. Components which produce membrane potential are also indicated.

activates expression of AniA in response to increasing levels of nitrite[10]. The activity of AniA is also controlled by the competition for electrons by the other reductase enzymes in the respiratory chain. Both NorB and *cbb$_3$* have a higher affinity for electrons than AniA, and as a result the presence of these enzymes (when active) has an inhibitory effect on AniA. The regulation of AniA is further complicated by the production of nitric oxide, and the presence of a protein, NsrR.

Nitric oxide has a direct inhibitory effect on the expression of AniA, as does the NsrR protein. Nitric oxide also inhibits the NsrR protein, leading to a derepresssion of AniA[20]. In the absence of nitric oxide, AniA is almost fully repressed by active NsrR. As NO concentrations increase, NsrR is inactivated allowing full activation of AniA. Once NO reaches a sufficiently high level it will begin to inhibit AniA[10,22].

NorB is less tightly regulated by respiratory components, as it is only acted upon by NsrR, however it is regulated by FNR and ArsR outside the respiratory

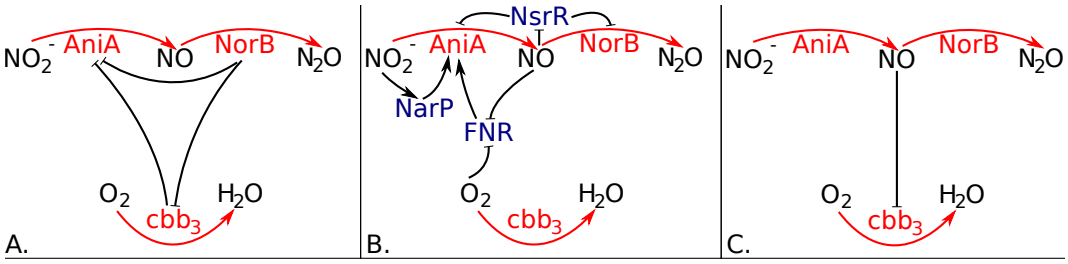

Figure 1.2: Regulation of respiratory components in *Neisseria meningitidis*. Enzymes and enzymatic reactions are shown in red. *A.* describes the regulation caused by competetion for electrons between the respiratory enzymes. *B.* shows the genetic regulation, which also involves a number of additional components in dark blue. *C.* shows chemical inhibition of the respiratory components.

chain[23]. This regulation by NsrR works in a similar way to how NsrR acts upon AniA. When there is no nitric oxide present, the NsrR acts to inhibit NorB since there is no substrate for it to reduce. In the presence of nitric oxide, NsrR is inhibited, leading to the activation of NorB which is now able to reduce NO to N_2O. In this case nitric oxide is acting as a de-repressor of NorB.

This complicated set of regulatory relationships between the different components of the respiratory pathways is shown in Figure 1.2.

1.3 Modelling

A limited amount of modelling has been carried out on bacterial respiratory chains, these focused on the denitrification pathway and treated the pathway as a simple electrical circuit[24]. An alternative approach involved modeling respiration using "P systems" which are probabilistic models of events. This assigned a probability of each reaction happening, dependant on the state of the system and then iterated through a given set of steps evaluating probabilities and altering values based on the outcome[25]. This approach to modelling was limited in that it was only predicting the quantities of 1 component in each of 2 "compartments"; oxygen in the cell membrane and carbon dioxide in the thylakoid membrane (the model was developed using cyanobacteria).

Since when modelling respiration in a cell, the most important factor is the change in concentration of components over time without any particular spatial

constraints, ordinary differential equations (ODEs) are an appropriate technique. In these systems the model does not change with regard to the spatial arrangement of any of the components. If the system requires changes in time *and* space, then partial differential equations (PDEs) would be necessary (and more complicated)[26].

Ordinary differential equations only depend on one variable; the time (t). In this case, the change in concentration over time for each component can be modelled as a single differential equation. For multiple components this leads to multiple differential equations with some that rely on the result of another (if the rate of one reaction is directly related to the concentration of another component). These ODEs must then be solved in parallel at a suitable timescale.

Complications arise when using differential equations if the processes are considered to be stochastic, as a differential equation model assumes that every component can have a continuous value, which is not the case as molecules are discrete. However if the system being modeled is sufficiently large, this effect can be ignored. If the reaction component size is small ($<$ 100s of molecules) stochastic simulation algorithms have to be used as described by Gillespie[27]. This method requires far more computation than solving ODEs, as the model will spend most of its time calculating values for reactions involving large molecules even though this is not necessary as the reaction is not stochastic. Additionally, the time interval used between reaction steps is usually very small, meaning the simulation progresses slowly[26].

A number of software packages exist that are capable of this type of modeling such as the Systems Biology Workbench[28] and COPASI[29]. These allow you to enter biochemical reactions in a format familiar to biologists, and have pre-defined libraries for types of reactions such as mass-action, or one with Michaelas-Menton kinetics etc. The mathematical equations are then derived automatically from the reactions and can be modified by hand if necessary. Parameters for the mathematical equations must be entered, and these will usually be derived from ex-

perimental data, or in some cases educated guesses (at least initially). Once a parameter set has been created, the modelling software can run a time-course using a relevant solver-algorithm. COPASI includes 4 solvers, LSODA (Livermore Solver for Ordinary Differential Equations)[30] for deterministic systems (such as ODEs), Gibson-Bruck[31] for stochastic systems and Runge-Kutta and LSODA for hybrid systems (where portions are not considered to be stochastic).

Chapter 2

Materials and Methods

2.1 *Neisseria meningitidis* strains used in this work

Name	Description	Source
MC58	Wild-Type Strain	McGuinness et al. [32]
ΔnorB::spc^r	Wild-Type with insertion of spectinomycin resistance cassette into *norB* gene	Heurlier et al. [20]
ΔnsrR::spc^r	Wild-Type with insertion of spectinomycin resistance cassette into *nsrR* gene	Rock et al. [22]
ΔnorB::spc^r-ΔnsrR::tet^r	Wild-Type with insertion of spectinomycin resistance cassette into *norB* and insertion of tetracyclin resistance cassette into *nsrR* genes	Heurlier et al. [20]
ΔaniA::spc^r-ΔnsrR::tet^r	Wild-Type with insertion of spectinomycin resistance cassette into *aniA* and insertion of tetracyclin resistance cassette into *nsrR* genes	Heurlier et al. [20]

Table 2.1: Bacterial strains and sources

2.2 Culturing *Neisseria meningitidis*

2.2.1 Growth of *Neisseria meningitidis*

N. meningitidis strains were grown on plates on Columbia Agar Base with defibrinated horse blood, and in liquid culture in Muller-Hinton Broth (MHB)

Plates were prepared by adding horse blood to a final concentration of 5% to molten agar, and poured into plastic petri dishes. After streaking with *N. meningitidis* the plates were incubated at 37°C in a 5% carbon dioxide/air mixture.

Aerobic liquid cultures were grown in 10ml MHB with 1% $NaHCO_3$ in plastic sterilin tubes, and incubated at 37°C at 200rpm. Microaerobic cultures were suspended in 20ml MHB, 1% $NaHCO_3$ in plastic sterilin tubes, incubated at 37°C at 100rpm.

2.2.2 Preparation of Antibiotic Selective Media

Liquid stock solutions of required antibiotics were either added directly to liquid culture, or, if growing on plates, to the molten agar when also adding horse blood. The final concentrations of antibiotics are given in Table 2.2.

Antibiotic	**Final concentration (μg/ml)**
Spectinomycin	50
Tetracyclin	2.5
Chloramphenicol	50

Table 2.2: Final antibiotic concentrations

2.2.3 Preparation of Frozen Bacterial Stocks

Bacteria were grown in liquid culture until late log phase prior to harvesting. Liquid cultures were then centrifuged at 4000g for 15 minutes, and the pellet was then resuspended in a 25% glycerol, 25% water and 50% MHB, all of which had been autoclaved beforehand. The bacterial stocks were then frozen at -80°C.

2.2.4 Streaking Plates for OD to CFU Ratio Calculation

Bacterial cultures were grown overnight and then transferred into aerobic liquid culture and samples taken throughout the day to obtain a range of different optical densities. The optical density was recorded at 600nm, and each sample was serially diluted to the following levels: 10^{-5}, 10^{-6} and 10^{-7}. 100μl of each of these dilutions was plated on a fresh blood agar plate and left to grow overnight. The following morning the number of colonies on each plate was counted and used to create a standard curve for Optical Density to Colony Forming Units.

2.3 Measuring Oxygen Concentration

Oxygen concentration in respiring cultures was measured using a Clark electrode[33] from Rank Brothers, Cambridge, UK. This electrode has a silver anode and a platinum cathode using a saturated potassium chloride solution as electrolyte. The electrode is set at the bottom of a 7ml reaction chamber separated from its contents by a thin teflon membrane. This membrane is permeable to dissolved oxygen, and is reduced by the electrode producing a measurable electrical current. The reaction chamber is maintained at 37°C by an attached waterbath. When performing experiments, 5ml of culture is added to the reaction chamber, which is stirred by use of a magnetic flea, and the chamber covered with a plastic stopper. The stopper has a number of holes through which the NO probe, or hamilton syringe can be inserted. Data is collected by attaching the electrode to an external data logger (Pico ADC20, Pico Technology).

2.3.1 Calibration of Oxygen Electrode

Calibration of the oxygen electrode assumes that anaerobic water will not produce any measurable current at the electrode. Oxygen saturated water contains 210μM Oxygen (ref needed). 5ml of ultrapure water was added to the electrode chamber, and then aerated to saturation by use of a pasteur pipette. The maximum value recorded by the data logger then corresponds to a concentration of

210μM Oxygen, with the relationship between mV as recorded against concentration being linear.

2.4 Measuring Nitric Oxide Concentration

Nitric Oxide concentration was measured using a Nitric Oxide probe (ISO-NOP, World Precision Intruments) connected to a Nitric Oxide Meter (ISO-NO mkII, World Precision Instruments). The NO probe is inserted through one of the holes in the plastic lid of the reaction chamber of the oxygen electrode assembly. The tip of the electrode should be immersed in the culture, with care being taken not to trap any air bubbles on the surface of the probe. The sensor is also attached to the same data logger as above. In this way both Oxygen and Nitric Oxide concentrations can be measured in parallel. See also these papers: Liu et al.[34] Bedioui and Villeneuve[35] Serpe and Zhang[36].

2.4.1 Calibration of Nitric Oxide Electrode

Calibration of the nitric oxide electrode

2.5 Measuring Nitrite Concentration (Griess Assay)

[37]

Chemicals

- 50ml 1% w/v Sulfanilamide in 1M HCl
- 50ml 0.02% w/v N.E.D. in 1M HCl

2.6 Nitric Oxide Production

Similar to the setup described by[38].

Chemicals

- 200ml $NaNO_2$ @ 2M - 27.6g in 200ml dH_2O

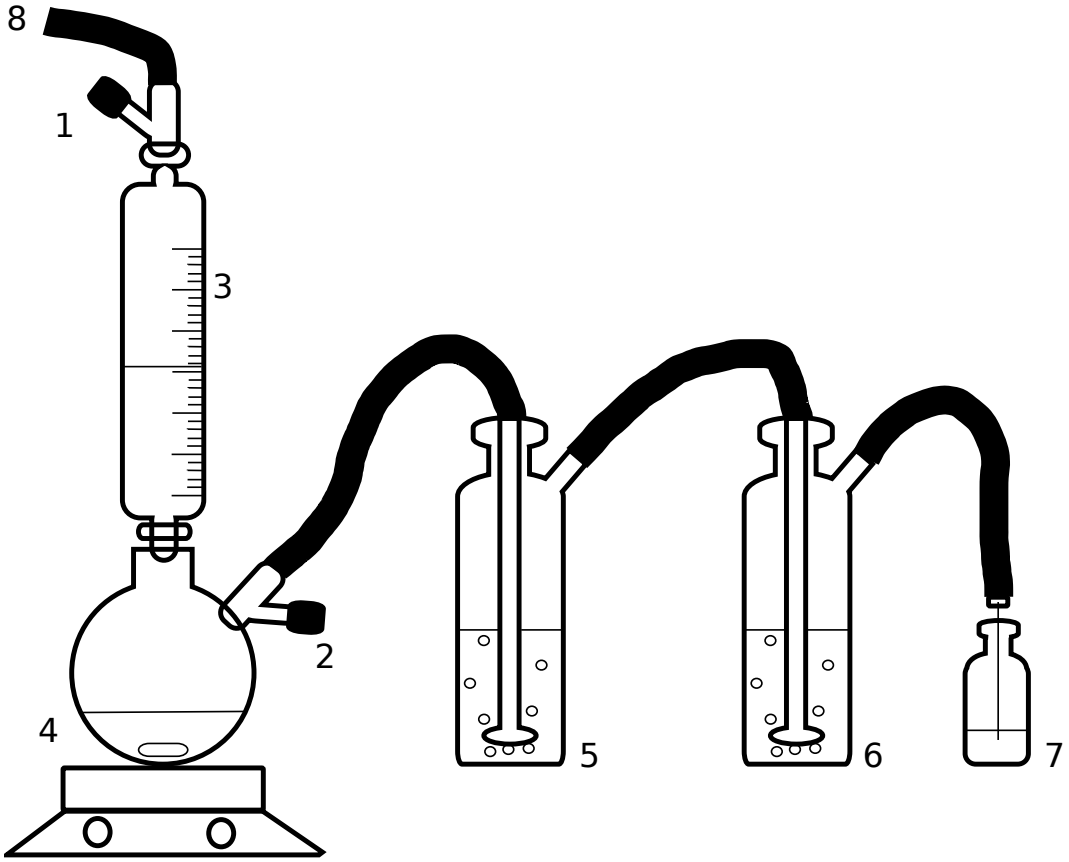

Figure 2.1: NO making apparatus. 1,2 - N_2 release valve. 3 - 50ml 4M H_2SO_4. 4 - 200ml 2M $NaNO_2$ stirring. 5 - 1M NaOH $\frac{2}{3}$ full. 6,7 - dH_2O $\frac{2}{3}$ full. 8 - To N_2 gas bottle.

- 50ml H_2SO_4 @ 4M - 11ml in 39ml dH_2O
- 200ml NaOH @ 1M - 8g in 200ml dH_2O

Procedure

- Set up system and sparge with N_2 gas for 15 minutes. Sparge 4M H_2SO_4 separately.
- Shut valve to N_2 hose (blue valve 1).
- Keep blue valve 2 open at all times.
- When sparged, add 25ml of 4M H_2SO_4 to 2M $NaNO_2$ and allow brown gas to bubble through to saturated solution vessel.
- Leave for at least 15 minutes allow 2M solution to cool.

- Remove needle and close sealing valve on saturated solution vessel.
- Clean up - allow 1-2 hours to allow reaction to finish. Sparge with N_2 to get rid of residual NO gas. Disassemble, wash in dH_2O and dry in oven.

Chapter 3

Parameter Estimation Methodologies

3.1 Simulated Annealing

3.2 Approximate Bayesian Computation by Sequential Monte Carlo

3.3 Metropolis Hastings Monte Carlo

Chapter 4

Model - Construction and Parameters

4.1 Construction

4.1.1 Converting Biological Reactions into Differential Equations

Where the reaction is describing a chemical process, the rate constant is given above the arrow, and the relevant enzyme shown in parentheses. Where the reaction is showing the addition of electrons (reduction), this is denoted by e^- below the arrow, the rate constant above, and the source of electrons in parentheses.

The equation that gives the change in oxygen concentration is

$$\frac{d[O_2]}{dt} = \beta(1 - [O_2]/K_O) - k_1[C_a][O_2]$$

$$\xrightarrow{\beta} \mathbf{O_2} \xrightarrow{k_1\ (C_a)} \mathrm{H_2O} \tag{4.1}$$

where β is the rate of passive diffusion of O_2 into the electrode chamber. This is inversely proportional to oxygen concentration in the chamber, and limited to the oxygen saturation concentration, K_O. This component of the equation is required to account for a peculiarity of the experimental set-up, whereby the rate of diffusion of oxygen into the system depends on the density of the bacterial culture, and is not insignificant. k_1 is the rate of reduction of oxygen by the oxygen

reductase *cbb*$_3$. This rate depends on the concentration of reduced (i.e. active) *cbb*$_3$, C_a and the concentration of O_2.

The equation for describing NO concentration changes is more complex as NO has a number of additional interactions in comparison to O_2. NO also interacts with *cbb*$_3$, in addition to being reduced from NO_2^-, reduced to N_2O and spontaneously lost from the electrode chamber. Currently this is the equation being used to model NO concentration.

$$\frac{d[NO]}{dt} = m_1[NO_2^-][A_a] - l_1[NO][B_a] - k_5[C_a][NO] + k_6[C_X] - \gamma[NO]$$

$$\begin{aligned} \mathrm{NO_2^-} &\xrightarrow{m_1\ (A_a)} \mathbf{NO} \xrightarrow{l_1\ (B_a)} \mathrm{N_2O} \\ \mathbf{NO} + \mathrm{C_a} &\xrightarrow{k_5} \mathrm{NO\text{–}C_X} \xrightarrow{k_6} \mathbf{NO} + \mathrm{C_a} \\ &\xrightarrow{\gamma} \mathbf{NO} \end{aligned} \tag{4.2}$$

The synthesis of NO is modelled by m_1 which is the rate of NO_2^- reduction by reduced (active) AniA. This also depends on the concentration of NO_2^- and reduced AniA (A_a). The reduction of NO requires l_1 which is the rate of reduction of NO by reduced (active) NorB. This depends on the concentration of NO and reduced NorB (B_a). Inhibition of *cbb*$_3$ by NO is modelled by the 3rd component of the equation. k_5 is the rate of inhibition of *cbb*$_3$ by NO. k_6 is the rate of recovery of inhibited *cbb*$_3$. γ is the rate of spontaneous loss of NO from the electrode chamber.

The reduction of nitrite is modelled by this equation

$$\frac{d[NO_2^-]}{dt} = -m_1[NO_2^-][A_a]$$

$$\mathbf{NO_2^-} \xrightarrow{m_1\ (A_a)} \mathrm{NO} \tag{4.3}$$

where m_1 is the rate of reduction of NO_2^- by reduced (active) AniA (A_a).

In addition to the rate of change of concentration of the respiratory substrates, the model also contains information about the state of the quinone pool, which is the upstream source of electrons into the respiratory chain. This is important because this affects the rate of reduction of the various enzymes which perform the substrate reductions. The equation for modelling the change in reduction state (activity) of the quinone pool is

$$\frac{d[Q_a]}{dt} = g([Q] - [Q_a]) - l_3[Q_a]([B] - [B_a]) - f[Q_a]([X] - [E])$$

$$\begin{aligned} &\xrightarrow[e^-]{g} \mathbf{Q_a} \\ \mathrm{B_i} &\xrightarrow[e^-]{l_3\ (\mathbf{Q_a})} \mathrm{B_a} \\ \mathrm{X\text{-}E} &\xrightarrow[e^-]{f\ (\mathbf{Q_a})} \mathrm{E} \end{aligned} \tag{4.4}$$

Q_a is the reduced quinone, and Q the total concentration of quinones in the system. g represents the rate of flow of electrons into the quinone pool from NADH. The rate of reduction of NorB by active quinones is given by l_3. NorB and reduced NorB are given by B and B_a respectively. As the quinones also reduce the cytochromes, this also needs to be modelled. f denotes the rate of reduction of cytochromes by the active quinones. Cytochromes and reduced cytochromes are given by X and E respectively.

Given that the concentration of active cytochromes changes, due to reduction by the quinone pool and oxidation by the downstream enzymes, and this concentration is a parameter in (4.4), it also needs to be included in the model, and this is given by the following equation

$$\frac{d[E]}{dt} = -k_3([C] - [C_a] - [C_X])[E] - m_3([A] - [A_a])[E] + f[Q_a]([X] - [E])$$

$$\begin{aligned} \mathrm{C_i} &\xrightarrow[e^-]{k_3\ (\mathbf{E})} \mathrm{C_a} \\ \mathrm{A_i} &\xrightarrow[e^-]{m_3\ (\mathbf{E})} \mathrm{A_a} \\ \text{X-E} &\xrightarrow[e^-]{f\ (Q_a)} \mathbf{E} \end{aligned} \tag{4.5}$$

where k_3 is the rate of reduction of the cytochrome c oxygen reductase (cbb_3) by the quinone pool (via c_x & c_4). C, C_a and C_X represent the overall concentration of cbb_3, reduced (active) cbb_3 and denatured cbb_3 respectively. m_3 is the rate of reduction of AniA by the cytochrome pool (via c_5). The concentration of active cytochromes increases by their reduction by the quinone pool.

To model the changes in concentration of the individual enzymes, cbb_3, AniA and NorB, the following equations are used:

$$\frac{d[C_a]}{dt} = k_3([C] - [C_a] - [C_X])[E] - k_1[C_a][O_2] - k_5[C_a][NO]$$

$$\begin{aligned} \mathrm{C_i} &\xrightarrow[e^-]{k_3\ (E)} \mathbf{C_a} \\ \mathrm{O_2} &\xrightarrow{k_1\ (\mathbf{C_a})} \mathrm{H_2O} \\ \mathrm{NO} + \mathbf{C_a} &\xrightarrow{k_5} \mathrm{NO\text{–}C_X} \end{aligned} \tag{4.6}$$

This equation models the concentration of reduced (active) cbb_3, and the following equation models the concentration of cbb_3 that has been denatured by NO.

$$\frac{d[C_X]}{dt} = k_5[C_a][NO] - k_6[C_X]$$

$$\mathrm{NO} + \mathrm{C_a} \xrightarrow{k_5} \mathrm{NO\text{–}}\mathbf{C_X} \xrightarrow{k_6} \mathrm{NO} + \mathrm{C_a} \tag{4.7}$$

Reduced (active) AniA concentrations are modelled by this equation

$$\frac{d[A_a]}{dt} = m_3([A] - [A_a])[E] - m_1[NO_2^-][A_a]$$

$$\begin{aligned} \mathrm{A_i} &\xrightarrow[e^-]{m_3\ (E)} \mathbf{A_a} \\ \mathrm{NO_2^-} &\xrightarrow{m_1\ (\mathbf{A_a})} \mathrm{NO} \end{aligned} \tag{4.8}$$

and reduced (active) NorB concentrations are modelled by this equation

$$\frac{d[B_a]}{dt} = l_3[Q_a]([B] - [B_a]) - l_1[NO][B_a]$$

$$\begin{aligned} \mathrm{B_i} &\xrightarrow[e^-]{l_3\ (Q_a)} \mathbf{B_a} \\ \mathrm{NO} &\xrightarrow{l_1\ (\mathbf{B_a})} \mathrm{N_2O} \end{aligned} \tag{4.9}$$

4.1.2 Assumptions and their Justifications

Assume that NO inhibits Reduced cbb3. It does according to Giuffre et al.[39]. Also, values are in the right ball park even though they are using aa3 rather than cbb3. $10^8 M^{-1}s^{-1}$ against around $50\mu M^{-1}s^{-1}$.

4.2 Parameters

Chapter 5

Oxygen reduction in *N. meningitidis*

5.1 Aerobic reduction of Oxygen

5.1.1 Introduction

5.1.2 Results

5.1.3 Discussion

Chapter 6

Nitric Oxide Reduction in *N. meningitidis*

Chapter 7

Nitrite Reduction in *N. meningitidis*

Chapter 8

AniA and NorB expression in *N. meningitidis*

8.1 Aerobic and Microaerobic Expression

8.1.1 Introduction

8.1.2 Results

8.1.3 Discussion

Chapter 9

The Completed Model

Appendix

References

1. van Deuren M, Brandtzaeg P, van der Meer JWM (2000) Update on Meningococcal Disease with Emphasis on Pathogenesis and Clinical Management. Clin Microbiol Rev 13: 144–166.

2. Stephens DS (2009) Biology and pathogenesis of the evolutionarily successful, obligate human bacterium Neisseria meningitidis. Vaccine 27: B71–B77.

3. Rosenstein NE, Perkins BA, Stephens DS, Popovic T, Hughes JM (2001) Meningococcal Disease. N Engl J Med 344: 1378–1388.

4. DeVoe IW (1982) The meningococcus and mechanisms of pathogenicity. Microbiol Mol Biol Rev 46: 162–190.

5. Madigan M, Martinko J, editors (2005) Brock Biology of Microorganisms. 11th ed., Prentice Hall.

6. Carbonnelle E, Hill DJ, Morand P, Griffiths NJ, Bourdoulous S, et al. (2009) Meningococcal interactions with the host. Vaccine 27: B78–B89.

7. Beddek AJ, Li MS, Kroll JS, Jordan TW, Martin DR (2009) Evidence for Capsule Switching between Carried and Disease-Causing Neisseria meningitidis Strains. Infect Immun 77: 2989–2994.

8. Moxon ER, Rainey PB, Nowak MA, Lenski RE (1994) Adaptive evolution of highly mutable loci in pathogenic bacteria. Current Biology 4: 24–33.

9. Pathan N, Faust SN, Levin M (2003) Pathophysiology of meningococcal meningitis and septicaemia. Arch Dis Child 88: 601–607.

10. Rock JD, Mahnane MR, Anjum MF, Shaw JG, Read RC, et al. (2005) The pathogen Neisseria meningitidis requires oxygen, but supplements growth by denitrification. Nitrite, nitric oxide and oxygen control respiratory flux at genetic and metabolic levels. Mol Microbiol 58: 800–9.

11. Rock JD, Moir JWB (2005) Microaerobic denitrification in Neisseria meningitidis. Biochem Soc Trans 33: 134–6.

12. Tuttle DM, Scherp HW (1952) Studies on the carbon dioxide requirement of Neisseria meningitidis. J Bacteriol 64: 171–182.

13. Lundberg JO, Weitzberg E, Cole JA, Benjamin N (2004) Nitrate, bacteria and human health. Nat Rev Micro 2: 593–602.

14. Deeudom M, Rock J, Moir J (2006) Organization of the respiratory chain of Neisseria meningitidis. Biochem Soc Trans 34: 139–42.

15. Deeudom M (2007) The electron transport chains of Neisseria meningitidis. Ph.D. thesis, University of York.

16. Preisig O, Zufferey R, Thony-Meyer L, Appleby C, Hennecke H (1996) A high-affinity cbb3-type cytochrome oxidase terminates the symbiosis- specific respiratory chain of Bradyrhizobium japonicum. J Bacteriol 178: 1532–1538.

17. Brown GC, Cooper C (1994) Nanomolar concentrations of nitric oxide reversibly inhibit synaptosomal respiration by competing with oxygen at cytochrome oxidase. FEBS Letters 356: 295–298.

18. Sharpe MA, Cooper CE (1998) Interaction of Peroxynitrite with Mitochondrial Cytochrome Oxidase. J Biol Chem 273: 30961–30972.

19. Anjum MF, Stevanin TM, Read RC, Moir JWB (2002) Nitric Oxide Metabolism in Neisseria meningitidis. J Bacteriol 184: 2987–2993.

20. Heurlier K, Thomson MJ, Aziz N, Moir JWB (2008) The nitric oxide (NO)-sensing repressor NsrR of Neisseria meningitidis has a compact regulon of genes involved in NO synthesis and detoxification. J Bacteriol 190: 2488–95.

21. Deeudom M, Koomey M, Moir JWB (2008) Roles of c-type cytochromes in respiration in Neisseria meningitidis. Microbiology 154: 2857–64.

22. Rock JD, Thomson MJ, Read RC, Moir JWB (2007) Regulation of denitrification genes in Neisseria meningitidis by nitric oxide and the repressor NsrR. J Bacteriol 189: 1138–44.

23. Isabella V, Wright LF, Barth K, Spence JM, Grogan S, et al. (2008) cis- and trans-acting elements involved in regulation of norB (norZ), the gene encoding nitric oxide reductase in Neisseria gonorrhoeae. Microbiology 154: 226–239.

24. Almeida JS, Reis MAM, Carrondo MJT (1997) A Unifying Kinetic Model of Denitrification. Journal of Theoretical Biology 186: 241–249.

25. Cavaliere M, Ardelean II (2006) Applications of Membrane Computing, chap. Modeling Respiration in Bacteria and Respiration/Photosynthesis Interaction in Cyanobacteria Using a P System Simulator, pp. 129–158. Springer.

26. Klipp E, Herwig R, Kowald A, Wierling C, Lehrach H (2005) Systems Biology in Practice. Concepts, Implementation and Application. WILEY-VCH Verlag GmbH & Co. KGaA, Weinheim.

27. Gillespie DT (1977) Exact stochastic simulation of coupled chemical reactions. The Journal of Physical Chemistry 81: 2340–2361.

28. Sauro HM, Hucka M, Finney A, Wellock C, Bolouri H, et al. (2003) Next Generation Simulation Tools: The Systems Biology Workbench and BioSPICE Integration. OMICS: A Journal of Integrative Biology 7: 355–372.

29. Hoops S, Sahle S, Gauges R, Lee C, Pahle J, et al. (2006) COPASI–a COmplex PAthway SImulator. Bioinformatics 22: 3067–3074.

30. Radhakrishnan K, Hindmarsh AC (1993) Description and Use of LSODE, the Livermore Solver for Ordinary Differential Equations. Tech. rep., NASA.

31. Gibson MA, Bruck J (2000) Efficient Exact Stochastic Simulation of Chemical Systems with Many Species and Many Channels. The Journal of Physical Chemistry A 104: 1876–1889.

32. McGuinness B, Barlow AK, Clarke IN, Farley JE, Anilionis A, et al. (1990) Deduced amino acid sequences of class 1 protein (PorA) from three strains of Neisseria meningitidis. Synthetic peptides define the epitopes responsible for serosubtype specificity. J Exp Med 171: 1871–1882.

33. Clark LC, Wolf R, Granger D, Taylor Z (1953) Continuous Recording of Blood Oxygen Tensions by Polarography. Journal of Applied Physiology 6: 189–193.

34. Liu X, Liu Q, Gupta E, Zorko N, Brownlee E, et al. (2005) Quantitative measurements of NO reaction kinetics with a Clark-type electrode. Nitric Oxide 13: 68 – 77.

35. Bedioui F, Villeneuve N (2003) Electrochemical Nitric Oxide Sensors for Biological Samples: Principle, Selected Examples and Applications. Electroanalysis 15: 5–18.

36. Serpe MJ, Zhang X (2007) The Principles, Development and Application of Microelectrodes for the In Vivo Determination of Nitric Oxide. In:

Michael AC, Borland LM, editors, Electrochemical Methods for Neuroscience, chap. 21, CRC Press.

37. Donald Nicholas DJ, Nason A (1957) Determination of nitrate and nitrite. In: Methods in Enzymology, vol. 3, pp. 981–984, Academic Press.

38. Aga RG, Hughes MN (2008) The Preparation and Purification of NO Gas and the Use of NO Releasers: The Application of NO Donors and Other Agents of Nitrosative Stress in Biological Systems. In: Poole RK, editor, Globins and Other Nitric Oxide-Reactive Proteins, Part A, vol. 436 of Methods in Enzymology, pp. 35 – 48, Academic Press.

39. Giuffre A, Barone MC, Mastronicola D, D'Itri E, Sarti P, et al. (2000) Reaction of Nitric Oxide with the Turnover Intermediates of Cytochrome c Oxidase: Reaction Pathway and Functional Effects. Biochemistry 39: 15446–15453.