The biosynthesis of periplasmic electron transport proteins in methylotrophic bacteria

Pat M. Goodwin† and Christopher Anthony

Author for correspondence: Chris Anthony. Tel: +44 1703 594280. Fax: +44 1703 594459. e-mail: C.Anthony@Soton.ac.uk

Department of Biochemistry, University of Southampton, Southampton SO16 7PX, UK

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Electron transport in methylotrophs

Methylotrophic bacteria are characterized by their ability to grow on reduced C₁ compounds such as methane, methanol or methylamine and on related compounds such as dimethylamine and trimethylamine (Anthony, 1982). When Gram-negative methylotrophs grow on C₁ compounds a high proportion of their energy metabolism occurs in the periplasm, a feature they share with the chemolithotrophs (Anthony, 1986, 1992). This contrasts with the situation in typical aerobic, heterotrophic bacteria, in which most dehydrogenases (and therefore most energy metabolism) occur in the cytoplasm or cytoplasmic membrane. These dehydrogenases are usually either NAD⁺-linked or flavoproteins, and are coupled to an electron transport system involving ubiquinone and cytochrome b; the only periplasmic component is usually a small cytochrome c similar to that found in the intermembrane space of mitochondria. The unusual site of energy metabolism in methylotrophs is reflected in the high concentrations of their periplasmic electron transport proteins; in Methylobacterium extorquens, for example, the concentrations of the proteins involved specifically in methanol oxidation are about 0.5 mM (Beardmore-Gray et al., 1983; Anthony, 1986). Methylotrophs growing on methanol or methylamine therefore provide a valuable system for investigating the biosynthesis of periplasmic proteins. Some of the processes involved, of course, similar to those necessary for the synthesis of any protein that is not cytoplasmic; in addition, for electron transport proteins it is necessary to provide their redox active prosthetic groups. The development of methods for studying the genetics of methylotrophs (especially the Methylobacterium species and Paracoccus denitrificans), together with the recent elucidation of the structure of the unusual dehydrogenases involved in oxidation of methanol and methylamine, makes it an appropriate time to review this field.

This review will concentrate on the biosynthesis of electron transport proteins involved specifically in the aerobic oxidation of methanol and methylamine by way of quinoproteins. These are methanol dehydrogenase and its primary electron acceptor, cytochrome c₅₅; and methylamine dehydrogenase and its primary electron acceptor, which is normally amicyanin, a blue copper protein. These are all soluble, periplasmic proteins and electrons are usually transferred from the primary electron acceptors to typical membrane-bound terminal oxidases by way of a Class I c-type cytochrome (Fig. 1) (Anthony, 1992, 1993a). When methylotrophs are growing anaerobically in the presence of nitrate additional

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†Née P. M. Dunstan.

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**Fig. 1.** The periplasmic ‘methanol oxidase’ and ‘methylamine oxidase’ electron transport systems in methylotrophs. The quinoprotein dehydrogenases pass on electrons one at a time to the electron acceptors, liberating protons into the periplasm. The oxidase is cytochrome aa₃ or cytochrome cₒ. The dimensions of the periplasm, the periplasmic membrane and the proteins are approximately to scale. MDH, methanol dehydrogenase; MNDH, methylamine dehydrogenase; c₅₅, cytochrome c₅₅ (cytochrome c₅₅₁ in *P. denitrificans*); c₄₅₄ (cytochrome c₄₅₄ in *P. denitrificans*), a typical small Class I c-type cytochrome (this may be replaced by a blue copper protein like azurin in some bacteria); AMN, blue copper protein, amicyanin (this may be replaced in *M. methylophilus* by MauO, a c-type cytochrome). For reviews of the variety of electron transport chains in methylotrophs see Anthony (1992, 1993a).
periplasmic electron transport proteins are induced (Ferguson, 1988; Anthony, 1993a).

The events which occur during the biosynthesis of a periplasmic electron transport protein are summarized as follows, although after the first step (gene expression) the sequence is not necessarily in the order presented here.

(a) Expression of structural genes, genes required for synthesis of the prosthetic group, and genes encoding proteins involved in processing. The initial product of expression of a gene encoding a periplasmic protein is a preprotein with an N-terminal signal peptide.

(b) Transport of the unfolded preprotein across the membrane by a translocase system, directed by the signal peptide.

(c) Cleavage of the signal peptide from the preprotein.

(d) Folding of the protein, including proline isomerization reactions, the formation of the correct disulphide bridges and incorporation of metal ions essential for structure or for redox activity.

(e) Synthesis of prosthetic groups and their transport to the periplasm.

(f) Insertion of prosthetic groups or modification of residues on the preprotein to produce a redox active prosthetic group.

(g) Assembly of the subunits to form the mature protein.

The next section outlines the pathways involved in the transport of proteins into the periplasm in bacteria. This process has not been studied in methylotrophs but the mechanisms for translocation of most of their periplasmic proteins are likely to be similar to those operating in Escherichia coli. Specific aspects of the biosynthesis of the methanol and methylene oxidation systems are then described in the next two sections.

Translocation of proteins into the periplasm

Detailed bibliographies on this topic are provided in a number of recent reviews (Wickner et al., 1991; Hardy & Randall, 1993; Oliver, 1993; Pugsley, 1993; Wolin, 1994).

Signal peptides

As indicated above, proteins destined for export are recognized by the presence of an N-terminal signal peptide (Fig. 2), which is cleaved by a signal peptidase during or immediately after translocation. Typical signal peptides are 16–26 residues long and have the following features: a basic N-terminal region; a central hydrophobic sequence able to form an α helix; a non-helical C-terminal domain with a helix-disrupting residue (usually glycine or proline) at −6; and small side-chain residues at −3 and −1 (often alanine). This is the recognition site for signal peptidase I, which is responsible for removing the signal peptide from the preprotein after translocation.

The positively charged N-terminus of the signal peptide can react with negatively charged phospholipid head-groups in the membrane. Model studies indicate that the central apolar region can span the membrane as an α helix or β sheet, and that its interaction with the membrane could initiate protein export. However, it is not obvious how the sequences beyond the C-terminal of the signal peptide, which are generally hydrophilic, would get pulled into and across the membrane. It has been suggested that it is more likely that the signal peptide is required for interaction of the preprotein with specific 'pilot proteins' [SecB or a signal recognition particle (SRP); see below].

There are two other types of signal sequence, but these are less common. The 'lipoprotein signal peptide' is shorter than the standard sequence, contains a more hydrophobic central region and has a cysteine residue immediately after the cleavage site. It is cleaved by signal peptidase II. The third type, cleaved by type IV prepilin peptidase, is rare and has a highly conserved cleavage site (Q.R/K.G.F/M) between the N-terminal region and the central hydrophobic region.

Targeting of preproteins to the cytoplasmic membrane

In E. coli there are two ways in which preproteins can be targeted to the cytoplasmic membrane. There is probably considerable functional redundancy between these two pathways, although it is likely that any given protein will normally use only one of them.

The first pathway involves SecA and SecB, which are components of the general secretory (Sec) pathway (Pugsley, 1993). SecB is a molecular chaperone which binds to the preprotein during and/or after translation, preventing it from aggregating or folding into a stable state in the cytoplasm, and thus maintaining it in a conformation compatible with export. SecB probably does not recognize the signal peptide directly; instead it is thought that possession of this sequence slows down folding of the preprotein and enables the chaperone to bind to multiple sites on the nascent polypeptide. The SecB-preprotein complex then interacts with a peripheral membrane protein, SecA. This is a dimer with ATPase activity which can bind to preproteins and target them to the translocation apparatus in the membrane.

The second pathway, which is very similar to that by which eukaryotic proteins are targeted to the endoplasmic reticulum, has only recently been described in E. coli (Wolin, 1994). The eukaryotic pathway involves a cytoplasmic ribonucleoprotein SRP, its membrane-bound receptor, and GTP or ATP. The SRP is a complex rod-shaped particle consisting of six polypeptides and an RNA molecule of 300 nucleotides, which recognizes and binds signal sequences on nascent polypeptides. It targets the complex of ribosome plus nascent preprotein to the SRP receptor in the membrane. The complex is then transferred to the translocation apparatus and the SRP is released in a reaction requiring GTP hydrolysis. A ribonucleoprotein particle resembling SRP, together with a protein homologous to its receptor, have now been identified in E. coli; SecA is also probably necessary for
interaction with the translocation apparatus in this pathway.

In addition to the two pathways outlined here, it should be noted that there is some evidence for translocation mechanisms that are independent of signal peptides, Sec proteins and SRPs (Salmond & Reeves, 1993; Brandner & Donohue, 1994); because the precursors of the periplasmic proteins described in methylotrophic bacteria all have signal peptides, these mechanisms will not be further discussed.

**The translocation apparatus**

Once the preprotein has been targeted to the membrane it can interact with the integral membrane components of the translocation channel formed by SecE and SecY; a third protein (called band 1) is also thought to be involved. Translocation requires both ATP (for activity of SecA) and a protonmotive force. Two other proteins – SecD and SecF – are probably needed at a late stage in translocation and it has been suggested that they catalyse release of the polypeptide from the translocase and/or folding of the polypeptide on the face of the periplasmic side of the membrane. There are considerable structural and functional similarities between the translocation apparatus in prokaryotes and eukaryotes, indicating that it has been conserved during evolution.

**Cleavage of the signal peptide**

Following translocation the signal peptide is removed by one of the three specific membrane-bound signal peptidases mentioned earlier. Most preproteins destined for the periplasm have standard signal peptides and are cleaved by signal peptidase I (LepB), which has its active site in the periplasm. This does not belong to any of the four major classes of proteases and is thought to have a novel mechanism of catalysis, similar to that of the β-lactamases, whereby a carboxylate acts as the general base (Dalbey & von Heijne, 1992). The protein is released into the periplasm and the signal peptide is probably hydrolysed by a specific cytoplasmic peptidase (Novak et al., 1986).

**Folding of the periplasmic protein**

The preprotein crosses the membrane in the unfolded state and it might be expected that, on its release into the periplasm, molecular chaperones would be required to prevent unwanted folding pathways. However, at present there is little evidence for periplasmic, broad specificity chaperones equivalent to the cytoplasmic GroE (Wulfing & Pluckthun, 1994).

At least two of the steps in protein folding require catalytic activity, namely cis-trans prolyl isomerization and disulfide bond formation, the latter being common in periplasmic proteins but not in cytoplasmic proteins. There is good evidence that the periplasm of *E. coli* contains both prolyl isomerase (Liu & Walsh, 1990) and disulfide isomerase (for reviews see Bardwell & Beckwith, 1993; Bardwell, 1994; Loferer & Hennecke, 1994). The disulfide isomerase is a member of the thioredoxin superfamily and contains a very reactive disulphide bond which readily oxidizes free thiols, becoming reduced in the process. It is reoxidized by an integral membrane protein, DsbB. A third periplasmic thioredoxin-like protein, DsbC, is thought to enhance DsbA activity and may be particularly important in internal rearrangement (isomerization) reactions (Bardwell & Beckwith, 1993; Bardwell, 1994).
Synthesis of the methanol oxidation system

Methanol is oxidized to formaldehyde by methanol dehydrogenase, a quinoprotein which has pyrroloquinoline quinone (PQQ, Fig. 3) as its prosthetic group (for reviews see Anthony, 1986, 1993b). The enzyme is an αβ tetramer and its three-dimensional structure has recently been elucidated (Fig. 4) (Xia et al., 1992; Blake et al., 1994; White et al., 1993; Anthony et al., 1994; Ghosh et al., 1995). Each α subunit (66 kDa in M. extorquens AM1) contains one molecule of PQQ and one Ca²⁺ at its active site, and has two disulphide bonds. One of these is a novel type of bridge between adjacent cysteine residues; the bond itself is non-planar and the resulting structure is a novel eight-membered ring in contact with the plane of the PQQ in the active site. An intermediate during the reaction cycle is the free radical semiquinone form of PQQ and the function of the disulphide ring may be to protect this unstable form (Anthony et al., 1994). Each α subunit has three cis peptide bonds stabilized by the rings of proline side chains, which will require the activity of a prolyl isomerase for their formation. The main chain of the α subunit is wrapped around the outside of the β subunits.

The primary electron acceptor of methanol dehydrogenase is an unusual cytochrome, known as cytochrome ε₁ (cytochrome ε₁AM1 in P. denitrificans) (Anthony, 1992). The cytochrome from M. extorquens AM1 is about 19 kDa in size and, apart from its typical haem-binding site (Cys-Ser-Gly-Cys-His), its sequence has little homology with any other proteins. In particular the conserved features of other c-type cytochromes are absent; these include the positions of the haem site and the sixth ligand methionine, and the conserved lysine residues which interact with cytochrome oxidase (Nunn & Anthony, 1988). This last feature is not unexpected since cytochrome ε₁ mediates contact with...
electron transfer between methanol dehydrogenase and a typical Class I c-type cytochrome, which is the substrate for a cytochrome oxidase (Fig. 1).

Another periplasmic protein, known as the modifier protein or M-protein, interacts with methanol dehydrogenase. Formaldehyde can be oxidized by this enzyme, a reaction which must be strictly controlled, because in most methyloptrophs carbon is assimilated at the oxidation level of formaldehyde. M-protein appears to regulate this by decreasing the affinity of methanol dehydrogenase for formaldehyde (Long & Anthony, 1991).

The isolation and analysis of methanol oxidation (Mox) mutants has revealed that synthesis of the methanol oxidation system is a very complex process, requiring at least 25 genes. In summary, production of active periplasmic methanol dehydrogenase involves the following: synthesis and transport of PQQ; synthesis, transport and processing of prepeptides for the \( \alpha \) and \( \beta \) subunits; folding of these proteins in the periplasm; isomerization of prolines; insertion of disulphide bridges (including the special one at the active site); insertion of calcium and PQQ; wrapping \( \beta \) chains around the \( \alpha \) subunits; and association of the \( \alpha \beta_2 \) units to give the \( \alpha \beta_2 \) tetramer. Most of our knowledge of the genetics of this process has been obtained from investigation of \( M. \text{extorquens} \) AM1, \( M. \text{organophilum} \) XX, \( M. \text{organophilum} \) DSM760 and \( P. \text{denitrificans} \), and Fig. 5 compares the organization of \( \text{mox} \) genes in these organisms. Table 1 lists the \( \text{mox} \) genes found to date in a variety of methyloptrophs and their functions if known. A cluster of \( \text{mox} \) genes has also been identified in \( M. \text{methylotrophus} \) but these genes have not been characterized (Dawson & Goodwin, 1990). A model for the synthesis of active methanol dehydrogenase and cytochrome \( \epsilon_1 \) is presented in Fig. 6, and the details of this model are discussed in the following sections.

### Structural genes

In \( M. \text{extorquens} \) AM1 and \( P. \text{denitrificans} \), the structural genes encoding the \( \alpha \) and \( \beta \) subunits (\( \text{mxaF} \) and \( \text{mxaI} \)) are located in an operon together with \( \text{mxaG} \), the gene encoding cytochrome \( \epsilon_1 \) and \( \text{mxaJ} \), a gene of unknown function (Harms et al., 1987; Anderson et al., 1990; van Spanning et al., 1991). A putative \( \text{mxaF} \) promoter sequence (\(-35\) -AAGACA-, \(-10\) -TAGAA-) has recently been identified (Barta & Hanson, 1993; Chistoserdova et al., 1994). As expected, the polypeptide products of the structural genes contain typical signal sequences, which are cleaved on translocation to the periplasm (Fig. 2) (Nunn & Anthony, 1988; Nunn et al., 1989; Anderson et al., 1990).

The DNA sequence of \( \text{mxaJ} \) indicates that it encodes a precursor of a 30 kDa periplasmic protein which does not have significant homology with any known protein. In \( M. \text{methylotrophus} \) two forms of the methanol dehydrogenase have recently been isolated; one had the typical \( \alpha \beta_2 \) conformation, but the other contained a 32 kDa protein whose N-terminal amino acid sequence had homology with the predicted \( \text{mxaJ} \) gene product (Matsushita et al., 1993). It was therefore suggested that the \( \text{MxaJ} \) protein might be a component of methanol dehydrogenase, enabling it to function optimally in vivo. However, the possibility that \( \text{mxaJ} \) encodes a molecular chaperone essential for the assembly of active methanol dehydrogenase, as previously suggested (van Spanning et al., 1991), could not be ruled out.

### Synthesis of PQQ

PQQ is synthesized from glutamate and tyrosine (Houck et al., 1991) and must be transported into the periplasm before it can be incorporated into methanol dehydrogenase. At least seven \( \text{pqq} \) genes are necessary for this process (Morris et al., 1994) (see Fig. 5 and Table 1). Three of these (\( \text{pqqD}, \text{pqqG} \) and \( \text{pqqC} \) of \( M. \text{extorquens} \)) have been sequenced and shown to have homology with \( \text{pqq} \) genes of \( K. \text{pneumoniae} \) and \( A. \text{calcoaceticus} \), which both contain a PQQ-dependent glucose dehydrogenase (Morris et al., 1994). The functions of \( \text{pqqG} \) and \( \text{pqqC} \) are unknown but \( \text{pqqD} \) probably encodes a peptide precursor of PQQ. The predicted \( M. \text{extorquens} \) peptide is slightly larger than the products of the corresponding genes in \( K. \text{pneumoniae} \) and \( A. \text{calcoaceticus} \), comprising 29 amino acids, compared with 25 and 24 amino acids in the other two organisms. All three peptides contain a conserved sequence of seven amino acids, which includes glutamate and tyrosine residues, and these residues are probably the precursors of PQQ (Goosen et al., 1992; Meullenberg et al., 1992; Morris et al., 1994). Sequence analysis of the other genes in the \( \text{pqq} \) region of \( K. \text{pneumoniae} \) indicates that one encodes a protease and another a dipeptidase (Meullenberg et al., 1992); it has been suggested that these enzymes are involved in processing the peptide precursor of PQQ and there are presumably homologues in the methyloptrophs. The remaining \( \text{pqq} \) gene products are probably required for further processing or for transporting PQQ to the periplasm.

### Processing and assembly of methanol dehydrogenase

The \( \alpha \) and \( \beta \) subunits of methanol dehydrogenase are presumably transported into the periplasm by either the Sec or the SRP pathway. Once in the periplasm the \( \alpha \) subunits must associate with PQQ and calcium and then assemble with the \( \beta \) subunits to form an active enzyme. Because the PQQ is held by non-covalent bonds and is within the centre of the superbarrel it cannot be bonded directly to the unfolded \( \alpha \) chain and it cannot be added after complete folding of this chain. By contrast, the apoenzymes of some related quinoproteins such as glucose dehydrogenase readily associate with added PQQ after formation of the fully folded form of the enzyme. These enzymes differ from methanol dehydrogenase in two ways - they do not have a \( \beta \) subunit and consideration of their amino acid sequences indicates that they lack the surface fold that encloses the active site in methanol dehydrogenase, and prevents addition of PQQ into the \( \alpha \beta_2 \) tetrameric apoenzyme (Anthony et al., 1994).

At present little is known about the assembly of methanol dehydrogenase, but mutants of \( M. \text{extorquens} \) which are
Table 1. Genes involved in methanol oxidation in Gram-negative bacteria

Genes involved in methanol oxidation were originally designated *mox* (methanol oxidation) genes. Recently a new nomenclature has been adopted (Lidstrom et al., 1994), but *mox* is still used as a collective symbol for methanol oxidation genes. Genes involved in PQQ synthesis have been designated *pqg* genes and the remainder of the *mox* genes have been given a base symbol beginning with *mox* for methanol oxidation. The third letter is determined by the chromosomal linkage group. *Methylobacterium* species are pink facultative methylotrophs; *Methylphilus* species are obligate methylotrophs; *P. denitrificans* grows as a facultative methylotroph on C1 compounds by oxidizing them to CO2, and then assimilating this by the autotrophic pathway. All the other genera listed are methanotrophs.

### Designation Function Organism†

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<th>Function</th>
<th>Organism†</th>
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<td>Regulation</td>
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<td>Regulation</td>
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* The following genes may be equivalent: *mxaW* of *Methylobacterium organophilum* and *mxaX, mxaY* or *mxaZ* of *Paracoccus denitrificans*; *mxbA* and *mxbD*, *mxbM* or *mxbN*; *mxcA* and *mxcQ*, *mxcU* or *mxcE*.

† Key references for the genes listed above are as follows: 1, Harms et al. (1993); 2, Xu et al. (1993); 3, Nunn & Lidstrom (1986a); 4, Nunn & Lidstrom (1986b); 5, Anderson et al. (1990); 6, Machlin & Hanson (1988); 7, Harms et al. (1987); 8, Al-Taho et al. (1990); 9, Stephens et al. (1988); 10, Wachterbrulla et al. (1993); 11, Bastien et al. (1989); 12, van Spanning et al. (1991); 13, Harms (1993); 14, Richardson & Anthony (1992); 15, Morris & Lidstrom (1992); 16, Lee et al. (1991); 17, Day et al. (1990); 18, Laufer & Lidstrom (1993); 19, Biville et al. (1989); 20, Morris et al. (1994); 21, Nunn & Anthony (1988); 22, Nunn et al. (1989); 23, Matsushita et al. (1993).
defective in mxaA, mxaK or mxaL synthesize an inactive αβ2 tetrameric methanol dehydrogenase which contains PQQ and which can be converted to the active form on incubation with calcium (Richardson & Anthony, 1992). These genes must therefore be required for the insertion of calcium into methanol dehydrogenase and this step may occur after PQQ insertion. The products of mxaA, K and L are probably periplasmic and they could function as a calcium carrier and/or stabilize methanol dehydrogenase in an appropriate conformation which can bind calcium.

There are presumably a number of other gene products required for the folding and assembly of methanol dehydrogenase. These could include the MxaJ protein (see above) and proteins encoded by some or all of the other mox genes whose function has not yet been elucidated (Table 1).

**Regulation of methanol dehydrogenase synthesis**

In Methyllobacterium, methanol dehydrogenase is usually synthesized at low levels during growth on multicarbon substrates and induced on transfer to methanol medium. However, its synthesis is repressed during growth on a mixture of methanol and some heterotrophic substrates (Dunstan et al., 1972; O'Connor & Hanson, 1977; McNerney & O'Connor, 1980; Roitsch & Stolp, 1986). In P. denitrificans, methanol dehydrogenase synthesis is more strictly regulated and it has been suggested that it is inhibited by a catabolite-repression-like mechanism and induced by formaldehyde, i.e. by the product of methanol oxidation (DeVries et al., 1988). Thus regulation of the production of methanol dehydrogenase is complex and understanding the mechanism will require detailed genetic studies; these will be greatly helped by the recent development of promoter probe vectors (Morris & Lidstrom, 1992; Xu et al., 1993). One such vector has been used to demonstrate that the promoters of three mox genes were activated when M. organophilum was transferred from succinate to methanol medium. The three promoters investigated were for mxaF (which codes for the α subunit), mxaW (a gene of unknown function which is located upstream of mxaF and transcribed in the opposite direction) and mxcU (whose function is also unknown). It is likely that the promoters of some of the other mox genes are also regulated by methanol. It has been shown that activation of these methanol-regulated promoters requires one or more of the following regulatory genes: mxaB, mxbD, mxbN, mxeE and mxcQ (Xu et al., 1993). Three of these genes – mxaB, mxbD and mxbN – also regulate transcription of pqqD, but there is evidence that other mechanisms play a major part in the control of PQQ synthesis; these may involve transcriptional regulation of other pqq genes and/or post-transcriptional modification of one or more of the pqq gene products (Ramamoorthi & Lidstrom, 1995).
The products of the *mxa* regulatory genes have not been isolated but some of them may function as part of a signal transduction system. There is evidence that such a system operates in *P. denitrificans* and that three genes—*mxaX*, *mxaY* and *mxaZ*—are involved (Harms *et al.*, 1993). They are located upstream of *mxaF* and transcribed in the opposite direction. The *mxaZ* and *mxaY* genes form one transcriptional unit, possibly with *mxaX* as well, and one of these genes may be equivalent to the *mxaw* gene of *M. organophilum* (Lidstrom *et al.*, 1994).

The predicted amino acid sequences of *MxaY* and *MxaX* are homologous with the protein histidine kinases and response regulators of other bacterial signal transduction regulatory systems (for review of these see Parkinson, 1993). It has been suggested by Harms *et al.* (1993) that *MxaY* is a membrane histidine protein kinase which senses a signal (they propose this is formaldehyde) and is then autophosphorylated; *MxaY* then interacts with *MxaX*, which can then activate transcription of *mxaF*. The predicted amino acid sequence of the *mxaZ* gene product indicates that it is a membrane protein with one transmembrane segment but it has no homology with any known proteins and its function is unclear. It is not essential for the production of methanol dehydrogenase but may have a role in signal recognition and thus be required for maximum activation of the *mxaFJGI* operon.

**Production of cytochrome c₇**

**Haem biosynthesis.** There are two routes for the synthesis of 5-aminolevulinic acid (ALA), which is the precursor of the porphyrin skeleton of haem. The first involves the condensation of succinyl coenzyme A and glycine, which is catalysed by ALA synthase, and this pathway operates in *P. denitrificans* (Page & Ferguson, 1994). In the alternative C₇ pathway ALA is formed from glutamate, with glutamyl tRNA₁ as the first intermediate; as might be predicted, this pathway occurs in the obligate methylotroph *M. methylotrphus*, which cannot make succinate via the TCA cycle since it lacks 2-oxoglutarate dehydrogenase (Lloyd *et al.*, 1993).

**Post-translational processing of pre-cytochrome c₇**

This requires a number of gene products which are also needed for the production of other c-type cytochromes. Mutants of *M. extorquens* and *P. denitrificans* which are unable to make any c-type cytochromes have been isolated (Anthony, 1975; Willison & John, 1979; Harms *et al.*, 1985; Oozeer *et al.*, 1993), the *Methylbacterium* mutants falling into at least three complementation groups (Oozeer *et al.*, 1993). However, by analogy with *Rhodobacter capsulatus* and *Bradyrhizobium japonicum*, we would expect at least nine genes to be essential for the synthesis of cytochrome *c₇* in addition to its structural gene, *mxaG* (Rameiser *et al.*, 1991; Beckman *et al.*, 1992; Ritz *et al.*, 1993; Beckman & Kranz, 1993; Thonymeyer *et al.*, 1994a, b).

The predicted precursors of the c-types, including cytochrome *c₇*, have typical signal sequences, with signal peptidase I cleavage sites (Fig. 2), and they are presumably transferred across the membrane by the Sec or SRP pathway. One of the key steps in the processing of c-type cytochromes is the attachment of the haem group, and there is evidence from studies of mutants of *P. denitrificans* which are unable to synthesize cytochrome *c₇* and *c₅₅₀* that the apoproteins and haem are transported separately to the periplasm where they then combine (Page & Ferguson, 1989, 1990). Genes essential for cytochrome c biogenesis which are predicted to encode the components of an ABC transporter (which may be a specific haem transporter) have been identified in *B. japonicum*, *R. capsulatus* and *E. coli* (Rameiser *et al.*, 1991; Beckman *et al.*, 1992; Poole *et al.*, 1994).

In mitochondria the addition of haem to cytochrome c is catalysed by haem lyase but this enzyme has not yet been identified in bacteria. The haem-binding site (Cys-X-X-Cys-His) of the cytochrome c must be reduced before haem attachment can take place and a thioredoxin-like protein is probably required for this (Beckman & Kranz, 1993; Thonymeyer *et al.*, 1994b; Sambongi & Ferguson, 1994).

**Model for the synthesis of the ‘methanol oxidase’ system**

A model for the synthesis of active methanol dehydrogenase and cytochrome *c₇* is presented in Fig. 6. An environmental signal is recognized and transmitted by the *MxaX-MxaY* signal transduction system, resulting in the activation of the *mxaF* promoter. At least six other genes (*mxaB, mxbD, mxbM, mxbN, mxcE* and *mxaF*) are also involved in regulation of this promoter. The *mxaFJGI* operon is then expressed and the precursors of the α and β subunits of methanol dehydrogenase and cytochrome *c₇* are transported across the cytoplasmic membrane, with release of the signal peptides.

PQQ is synthesized in the cytoplasm from a peptide precursor encoded by *pqqD* and then transported into the periplasm. At least three genes (*mxaB, mxbD* and *mxbM*) regulate transcription of *pqqD* and at least six other genes (*pqqABCEFG*) encode products essential for PQQ production; they probably include a depeptidase and a protease involved in processing the precursor. Haem is also synthesized in the cytoplasm and then transported to the periplasm by an ABC transporter.

In the periplasm the α and β subunits of methanol dehydrogenase fold and assemble, and PQQ and calcium are inserted. Several gene products are likely to be involved in this process, including the *MxaA, MxaK* and *MxaL* proteins, which are essential for the insertion of calcium. Attachment of haem to apo-cytochrome *c₇* also occurs in the periplasm and a thioredoxin-like protein is required to maintain the haem-binding site in the reduced state.

**Synthesis of the methylamine oxidation system**

Methylamine is oxidized to formaldehyde by methylamine dehydrogenase, which was the first quinoprotein to have its structure determined by X-ray crystallography (Vellieux *et al.*, 1989). Remarkably, this enzyme is similar
to methanol dehydrogenase in having an unusual (but different) quinone prosthetic group, an $\alpha\beta_2$ tetrameric structure, and large ($\alpha$) subunits having a propeller fold arranged to form a superbarrel. The $\alpha$ subunit of methylamine dehydrogenase (40 kDa in *M. extorquens*) differs from that of methanol dehydrogenase, however, in having only a sevenfold radial symmetry and a centre occupied by amino acid residues and not by the prosthetic group (Vellieux et al., 1989; Chen et al., 1992b). This is not PQQ but another quinone structure, tryptophan tryptophylquinone (TTQ) (Fig. 3), which is formed by joining two tryptophan residues of the $\beta$ subunit (about 14 kDa in *M. extorquens*) which is tightly held together by six disulphide bridges (McIntire et al., 1991; Chen et al., 1991).

Methylamine dehydrogenase passes electrons to a specific electron acceptor, which is usually the blue copper protein amicyanin (about 12 kDa in *M. extorquens*) (for reviews see Anthony, 1993a; Davidson, 1993). Exciting possibilities for analysis of the interaction of these two proteins have recently arisen with the description of the X-ray structure (Fig. 1) (Anthony, 1993a). In some methylotrophs blue copper proteins have not been detected and it is assumed that a Class I cytochrome $c$ mediates directly between the methylamine dehydrogenase and the oxidase.

In *M. extorquens* a cluster of eleven genes, designated *mau* genes, has been identified (Fig. 7), eight of which – *mauF*, *mauB*, *mauE*, *mauD*, *mauA*, *mauC*, *mauG*, and *mauL* – are essential for growth on methylamine (Chistoserdov et al., 1994a; Lidstrom & Chistoserdov, 1993). Similar *mau* gene clusters are found in *P. denitrificans*, *Thiobacillus versutus*, *Methyllobacillus flagellatus* KT and *M. methylophilus* (Chistoserdov et al., 1992, 1994b; Ubbink et al., 1991). In *P. denitrificans* an additional gene essential for methylamine utilization – *mauR* – has recently been described; it is located next to *mauF*, but transcribed in the opposite direction (van Spanning et al., 1994). A model for synthesis of active methylamine dehydrogenase and amicyanin is presented in Fig. 8, and the details of the model are discussed in the following sections.

### Structural genes

The *mauB* and *mauA* genes encode the large and small subunits of methylamine dehydrogenase. As expected, the predicted gene products of *mauA* and *mauB* include a signal peptide, but that for *MauA* is longer than normal (57 amino acids compared with the usual 20–28) and has two other unusual features (Fig. 2) (Chistoserdov & Lidstrom, 1991). Before the region of positively charged amino acids at the N-terminal end there are 13 residues which are mostly hydrophilic, and near the peptidase recognition site is a region of positively charged amino acids, which would be expected to slow down translocation. This signal sequence does not function in *E. coli* when fused to *phoA* (the alkaline phosphatase reporter gene), and presumably has a special function in the processing of the $\beta$ subunit and/or its association with the $\alpha$ subunit. A similar signal sequence is present in the predicted polypeptide precursors of the $\beta$ subunits of *T. versutus*, *P. denitrificans* and *M. methylophilus* (Ubbink et al., 1991; Chistoserdov et al., 1992, 1994b).

The *mauC* gene encodes the precursor of amicyanin, which has a typical signal peptide. Not surprisingly, synthesis of amicyanin does not occur in the absence of copper in the medium, but there is evidence that iron is also essential for its production (Auton & Anthony, 1989). *M. methylophilus* W3A1 does not contain a *mauC* gene and it has been suggested that a cytochrome substitutes for amicyanin as the primary electron acceptor; this is possibly encoded by *mauO*, which is found at the end of the *mau* cluster in this organism (Chistoserdov et al., 1994b).

### Synthesis of the prosthetic group, TTQ

TTQ is derived from two tryptophan residues in the $\beta$ subunit (Fig. 3) and it has been suggested that its synthesis involves formation of an indole 6,7-dione or 6,7-hydroxyindole intermediate on one tryptophan residue, followed by cross-linking of the two residues (Lidstrom
A role for a c-type cytochrome in this pathway was first indicated by the observation that mutants unable to produce any c-type cytochromes are also impaired in the synthesis of active methylamine dehydrogenase (Anthony, 1975; Oozeer et al., 1993). It has been shown subsequently by Page & Ferguson (1993) that although such mutants are able to synthesize the α and β subunits, which are then transported to the periplasm, the β subunits do not react with a quinone stain. They therefore suggested that a c-type cytochrome-linked hydroxylase catalyses at least one step in quinone formation, and that this reaction occurs in the periplasm.

The mauG gene probably encodes a c-type cytochrome since the predicted amino acid sequence of its gene product has 29% homology with the cytochrome c peroxidase of Pseudomonas aeruginosa (Chistoserdov et al., 1994a). However, this cytochrome is not essential for quinone production since mutants defective in mauG make the β subunit, which reacts with a quinone stain. Peroxidases are known to cross-link indole groups and it has therefore been suggested that the MauG protein is involved in cross-linking the two tryptophan residues (Chistoserdov et al., 1994a). The mauL gene encodes a periplasmic protein which is also probable involved in cross-linking since mutants defective in this gene have a similar phenotype to MauG mutants. Further work is required to confirm this and to elucidate the other steps in TTQ formation.

The DNA sequences of mauM and mauN, neither of which is essential for methylamine utilization, indicate that they encode periplasmic and membrane proteins, respectively. They both have regions of homology with ferredoxin genes, and may encode iron–sulphur proteins involved in the postulated peroxidase reaction. Presumably other proteins provide their function in the mutants lacking them.

### Processing and assembly of methylamine dehydrogenase

Further processing of the subunits of methylamine dehydrogenase and their assembly in the periplasm to form the mature enzyme has not been studied. However, predictions from DNA sequence data indicate that the mauF and mauE genes of M. extorquens encode membrane proteins and that mauD encodes a periplasmic protein (Fig. 7). Mutants defective in these genes do not contain the β subunit and it has therefore been suggested that they are involved in the transport, processing and/or stabilization of this subunit (Lidstrom & Chistoserdov, 1993; Chistoserdov et al., 1994a). The precursor of the MauD protein of M. extorquens is unusual in that it has a lipoprotein peptide signal sequence (Fig. 2), but the equivalent preprotein of M. methylotrophus has a typical signal peptide.

### Regulation of methylamine dehydrogenase synthesis

Methylamine dehydrogenase and amicyanin are induced when cells are grown in medium containing methylamine or methylated amines and there is evidence that, in the obligate methylotroph M. methylotrophus, methylamine
dehydrogenase is repressed when methanol or NH₄⁺ is provided as an alternative carbon or nitrogen source (Dunstan et al., 1972; Large & Haywood, 1981; Auton & Anthony, 1989; Dawson et al., 1990). The predicted MauJ protein is cytoplasmic and, because it is not essential for growth on methylvamine, it has been postulated to have a regulatory role (Chistoserdov et al., 1994a). However, there was no evidence to support this hypothesis since MauJ mutants had levels of methylamine dehydrogenase activity similar to those in wild-type bacteria. The mauR gene described recently in P. denitrificans encodes a protein with homology to the LysR type transcriptional activators and is a better candidate for a regulatory gene in the methylamine oxidase system (van Spanning et al., 1994).

**A model for the synthesis of the ‘methylamine oxidase’ system**

A model for the synthesis of methylamine dehydrogenase and amicyanin is shown in Fig. 8. The mauB, mauA and mauC genes are expressed to form precursors of the α and β subunits of methylamine dehydrogenase and amicyanin. These are transported across the cytoplasmic membrane, although the abnormal signal sequence on the precursor of the β subunit probably slows down its transport. MauF and MauE, which are membrane proteins, may play a role in the transport process.

Although the exact pathway of TTQ synthesis is not known, at least two stages occur in the periplasm: the first is a cytochrome-c-dependent step essential for the formation of a quinone derivative of one of the trypophan residues, and the second is a peroxidase reaction, catalysed by MauG, resulting in cross-linking of the two trypophan residues which make up TTQ. The MauJ protein is also needed for this step and the ferredoxin-like proteins encoded by mauN and mauM may produce hydrogen peroxide for the peroxidase reaction. The MauD protein may be required to stabilize the β subunit during TTQ formation. Assembly of the methylamine dehydrogenase subunits to form an active enzyme occurs in the periplasm and presumably involves some as yet unidentified gene products.

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**References**


