Biochemistry of methanogenesis: a tribute to Marjory Stephenson

Rudolf K. Thauer

Keywords: methanogenesis and methanogenic archaea, methyl-coenzyme M reductase and its crystal structure, coenzyme F₄₃₀, coenzyme M, coenzyme B

Historical overview

In 1933, Stephenson & Stickland (1933a) published that they had isolated from river mud, by the single cell technique, a methanogenic organism capable of growth in an inorganic medium with formate as the sole carbon source.

\[ 4\text{HCOO}^- + 4\text{H}^+ \rightarrow \text{CH}_4 + 3\text{CO}_2 + 2\text{H}_2\text{O} \]
\[ \Delta G^0 = -144.5 \text{ kJ mol}^{-1} \]

Methane formation from formate was shown to occur in a stepwise manner, by the preliminary decomposition of formic acid into \( \text{CO}_2 \) and \( \text{H}_2 \), followed by a reduction of \( \text{CO}_2 \) by \( \text{H}_2 \), suggesting that formate was not an intermediate in the reduction of \( \text{CO}_2 \) to methane.

\[ \text{HCOO}^- + \text{H}^+ \rightarrow \text{H}_2 + \text{CO}_2 \]
\[ \Delta G^0 = -3.5 \text{ kJ mol}^{-1} \]

\[ 4\text{H}_2 + \text{CO}_2 \rightarrow \text{CH}_4 + 2\text{H}_2\text{O} \]
\[ \Delta G^0 = -131 \text{ kJ mol}^{-1} \]

Cell suspensions of the micro-organism catalysed the reduction of methylene blue with \( \text{H}_2 \), indicating that the methanogen contained an enzyme which activates molecular hydrogen.

\[ \text{H}_2 \rightarrow 2\text{e}^- + 2\text{H}^+ \]
\[ E'_0 = -414 \text{ mV} \]

This enzyme had been discovered by Stephenson & Stickland (1931a) 2 years before in a number of bacterial species and was named by them 'hydrogenase'.

The paper by Stephenson & Stickland (1933a) is considered to mark the beginning of the modern era for study of methanogenesis (Wolfe, 1993). It is the first report on the isolation in pure culture of a methanogen and the first study of an enzyme and of reactions involved in methanogenesis.

Besides \( \text{CO}_2 \), the cell suspensions of the methanogen isolated by Stephenson & Stickland (1933a) catalysed the reduction of carbon monoxide, formaldehyde (added as hexamethylene-tetramine) and methanol to methane with \( \text{H}_2 \), albeit at much lower rates than the reduction of \( \text{CO}_2 \). It is significant that the cell suspensions did not yield methane from compounds of two or more carbon atoms. The cell suspensions did, however, slowly reduce sulphate with \( \text{H}_2 \) to \( \text{H}_2\text{S} \), a property not encountered by any other methanogen isolated since then. It therefore seems possible that, in spite of all efforts to purify it, the culture obtained by Stephenson & Stickland (1933a) was contaminated with one of the sulphate reducers abundantly present in the river mud (Stephenson & Stickland, 1931b) from which the methanogen was isolated (Elsden & Pirie, 1949).

The following review summarizes what we presently know about the biochemistry of methanogenesis, emphasis being put on the enzyme methyl-coenzyme M reductase catalysing the methane-forming reaction proper. It is a tribute to Marjory Stephenson, who discovered hydrogenase in these micro-organisms. Marjory Stephenson died 50 years ago on 12 December 1948 at the age of only 63 (Elsden & Pirie, 1949; Robertson, 1949; Woods, 1950; Elsden, 1981). She had worked for 30 years in the Cambridge Biochemical Laboratory headed by Frederick Gowland Hopkins (Stephenson, 1948) on various aspects of the chemistry of bacteria (Stephenson, 1932, 1933, 1934, 1935). The 3rd edition of her book on Bacterial Metabolism (Stephenson, 1949) is a treasury of knowledge very worth reading even today, 50 years later. Marjory Stephenson was the second woman to be elected to the Royal Society of London (Mason, 1992, 1996) and a cofounder of the Society for General Microbiology, of which she was the second president (Postgate, 1995).
In this review, with the exception of a few papers describing discoveries, only publications on the biochemistry of methanogenesis are cited that have appeared since 1993: these contain reference to earlier and often more important papers, many of which have come from the laboratories of A. J. Kluver (Kamp et al., 1959), H. A. Barker (Barker, 1956), T. Stadtman (Stadtman, 1967; Grahame & Stadtman, 1993), R. Wolfe (Wolfe, 1991, 1996), J. D. Ferry (Ferry, 1993b, 1995, 1997a), G. Gottschalk (Deppenmeier et al., 1996), A. Klein (Sorgenfrei et al., 1997a), J. Reeve (Reeve et al., 1997) and G. Vogels (Keltjens & Vogels, 1993). A historical overview of methanogenesis has recently been published by Wolfe (1993). The reader is also referred to a review by Daniels (1993) and by Blaut (1994) and three more recent reviews by the author (Weiss & Thauer, 1993; Thauer et al., 1993; Thauer, 1997).

**Methanogens: where they live, what they do and who they are**

Methane is an end product of the microbial decomposition of organic matter in anaerobic freshwater environments such as lake sediments and the intestinal tract of animals. Estimates are that presently about 1% of the plant material formed per year by photosynthesis from CO₂ is remineralized via methane, more than 10⁶ tons of the combustible gas being intermediately generated. Roughly two-thirds of the methane diffuses into aerobic zones, where it is oxidized by methanotrophic bacteria. A few percent is buried, leading to the formation of methane deposits, but most of the rest escapes to the atmosphere where it is photochemically converted to CO₂, CH₄, or reduced to methane with H₂ as exemplified for methanol:

\[
\begin{align*}
4\text{CH}_3\text{OH} + 2\text{H}_2\text{O} & \rightarrow 3\text{CH}_4 + 1\text{CO}_2 + 4\text{H}_2 \\
\Delta G^\circ & = -106.5 \text{ kJ (mol CH}_4\text{)}^{-1} \\
\text{CH}_3\text{OH} + \text{H}_2 & \rightarrow \text{CH}_4 + \text{H}_2\text{O} \\
\Delta G^\circ & = -112.5 \text{ kJ mol}^{-1} 
\end{align*}
\]

Methanogenesis is the only way that methanogenic archaea can obtain energy for growth and these are the only organisms known to produce methane as a catastrophic end product.

Despite the high specialization, not all methanogens are phylogenetically closely related. This is reflected, for example, in differences in cell wall composition (Sprott & Beveridge, 1993; Kandler & König, 1998). Methanogens can also have very different optimal growth conditions; thus some thrive optimally at temperatures below 20 °C and others at or near the temperature of boiling water (Boone et al., 1993).

Methanogens taxonomically all belong to the archaean kingdom of *Euryarchaeota*. They are classified in five orders each phylogenetically related to another as distantly as the *Cyanobacteria* to the *Proteobacteria*. The five orders are: *Methanobacteria*, *Methanococcales*, *Methanomicrobiales*, *Methanopyrales* and *Methanosarcinales*. Of these, only the *Methanosarcinales* can ferment acetate to CO₂ and CH₄ and grow on methanol, methylthiols or methylamines as sole energy source. In turn, hyperthermophilic species are only found among the *Methanobacteria*, *Methanococcales* and *Methanopyrales* (Boone et al., 1993).

The DNA sequence of the total genome has, until now, been determined for two methanarchaea, for *Methanococcus jannaschii* (Bult et al., 1996) and for *Methanobacterium thermoautotrophicum* (strain AH) (Smith et al., 1997). Recently, the sequence for *Archaeoglobus fulgidus* has also been published (Klenk et al., 1997). This sulphate-reducing archaean is phylogenetically most closely related to the *Methanosarcinales* with which it has many biochemical features in common.

\[
\begin{align*}
\text{CH}_3\text{COO}^- + \text{H}^+ & \rightarrow \text{CO}_2 + \text{CH}_4 & \Delta G^\circ & = -36 \text{ kJ mol}^{-1} \\
\text{4H}_2 + \text{CO}_2 & \rightarrow \text{CH}_4 + 2\text{H}_2\text{O} & \Delta G^\circ & = -131 \text{ kJ mol}^{-1} \\
\text{4HCOO}^- + 4\text{H}^+ & \rightarrow \text{CH}_4 + 3\text{CO}_2 + 2\text{H}_2\text{O} & \Delta G^\circ & = -144.5 \text{ kJ mol}^{-1} 
\end{align*}
\]

The organisms mediating these methane-forming reactions were originally thought to be bacteria, but are now recognized as belonging to a separate phylogenetic domain, the *Archaea*. Methanarchaea are highly specialized. They can only use acetate, H₂ and CO₂, formate and/or other C₁ compounds such as methanol, methylthiols and methylamines as energy substrates, the C₁ compounds being either disproportionated to CO₂ and CH₄ or reduced to methane with H₂ as exemplified for methanol:

\[
\begin{align*}
\text{4CH}_3\text{OH} + 2\text{H}_2\text{O} & \rightarrow 3\text{CH}_4 + 1\text{CO}_2 + 4\text{H}_2\text{O} & \Delta G^\circ & = -106.5 \text{ kJ (mol CH}_4\text{)}^{-1} \\
\text{CH}_3\text{OH} + \text{H}_2 & \rightarrow \text{CH}_4 + \text{H}_2\text{O} & \Delta G^\circ & = -112.5 \text{ kJ mol}^{-1} 
\end{align*}
\]

Methanogenesis is the only way that methanogenic archaea can obtain energy for growth and these are the only organisms known to produce methane as a catastrophic end product.

Despite the high specialization, not all methanogens are phylogenetically closely related. This is reflected, for example, in differences in cell wall composition (Sprott & Beveridge, 1993; Kandler & König, 1998). Methanogens can also have very different optimal growth conditions; thus some thrive optimally at temperatures below 20 °C and others at or near the temperature of boiling water (Boone et al., 1993).

Methanogens taxonomically all belong to the archaean kingdom of *Euryarchaeota*. They are classified in five orders each phylogenetically related to another as distantly as the *Cyanobacteria* to the *Proteobacteria*. The five orders are: *Methanobacteria*, *Methanococcales*, *Methanomicrobiales*, *Methanopyrales* and *Methanosarcinales*. Of these, only the *Methanosarcinales* can ferment acetate to CO₂ and CH₄ and grow on methanol, methylthiols or methylamines as sole energy source. In turn, hyperthermophilic species are only found among the *Methanobacteria*, *Methanococcales* and *Methanopyrales* (Boone et al., 1993).

The DNA sequence of the total genome has, until now, been determined for two methanarchaea, for *Methanococcus jannaschii* (Bult et al., 1996) and for *Methanobacterium thermoautotrophicum* (strain AH) (Smith et al., 1997). Recently, the sequence for *Archaeoglobus fulgidus* has also been published (Klenk et al., 1997). This sulphate-reducing archaean is phylogenetically most closely related to the *Methanosarcinales* with which it has many biochemical features in common.
The reactions and enzymes known to be involved in methane formation from acetate in the *Methanosarcinales* (Ferry, 1993b, 1995, 1997a)

H-S-CoM, coenzyme M; H-S-CoB, coenzyme B; \(H_2\)SPT, tetrahydrocorrinoid, which is the modified tetrahydromethanopterin (for structures see Fig. 3) present in the *Methanosarcinales* (Gorris & van der Drift, 1994).

<table>
<thead>
<tr>
<th>Reaction</th>
<th>Enzyme (gene)</th>
<th>Most recent literature</th>
</tr>
</thead>
<tbody>
<tr>
<td>Acetate + CoA → acetyl-CoA + H₂O</td>
<td>Acetate kinase (ack) and phosphotransacetylase (pta) in <em>Methanosarcina</em> spp. or acetate thiokinase (acs) in <em>Methanosaeta</em> spp.</td>
<td>Latimer &amp; Ferry (1993); Singh-Wissmann &amp; Ferry (1995); Eggen et al. (1991a)</td>
</tr>
<tr>
<td>Acetyl-CoA + H₂SPT → CH₃H₂SPT + CO₂ + CoA + 2[H]</td>
<td>Carbon-monoxide dehydrogenase/acetyl-CoA synthase (cdhABCDE)</td>
<td>Grahame (1993); Sowers et al. (1993); Lu et al. (1994); Grahame &amp; DeMoll (1995, 1996); Eggen et al. (1991b, 1996); Grahame et al. (1996); Maupin-Furlow &amp; Ferry (1996a, b)</td>
</tr>
<tr>
<td>CH₃H₂SPT + H₂S-CoM → CH₃₂-S-CoM + H₂SPT</td>
<td>Methyl-H₂SPT: coenzyme M methyltransferase (mtrEDCBAFGH)</td>
<td>Fischer et al. (1992); Lu et al. (1995); Lienard et al. (1996); Lienard &amp; Gottschalk (1998)</td>
</tr>
<tr>
<td>CH₃₂-S-CoM + H₂-S-CoB → CoM-S-S-CoB + CH₃</td>
<td>Methyl-coenzyme M reductase (mcrBDGCA)</td>
<td>Thauer et al. (1993); Springer et al. (1995)</td>
</tr>
<tr>
<td>CoM-S-S-CoB + 2[H] → H₂-CoM + H₂-S-CoB</td>
<td>Heterodisulphide reductase (hdrDE)</td>
<td>Heiden et al. (1993); Peer et al. (1994); Künkel et al. (1998)</td>
</tr>
</tbody>
</table>

*ΔG²⁰ values add up to -38 kJ mol⁻¹, which is very similar to the ΔG²⁰ = -36 kJ mol⁻¹ calculated for CH₃COO⁻ + H⁺ → CH₄ + CO₂ from free energy of formation data (Thauer et al., 1977). See also the first footnotes to Tables 2 and 3.

† From Thauer et al. (1977).

‡ From Thauer (1990); CO₂ in the gaseous state at 10⁶ Pa. \(E'_0\) was determined by Grahame & DeMoll (1995) to be -270 mV and \(ΔG²⁰\) to be +28 kJ mol⁻¹, values not consistent with the overall thermodynamics of methanogenesis from acetate (see first footnote), from CO₂ (Table 2) and from methanol (Table 3). At first sight, a \(ΔG²⁰ = +413\) kJ mol⁻¹ appears unrealistically endergonic. Note, however, that in the reaction four products are formed from two substrates. \(ΔG²⁰\) is thus highly concentration dependent. At 0.1 mM concentrations of all substrates and products (\(pH = 10\) Pa), \(ΔG²⁰ = -2.6\) kJ mol⁻¹ and \(E' = -430\) mV (Thauer, 1990).

§ Calculated for 2[H] = 1H₂ at 10⁶ Pa.

|| The nickel iron-sulphur corrinoid enzyme is isolated from *Methanosarcina* spp. as a multi-enzyme complex composed of five different subunits (Grahame & DeMoll, 1996; Maupin-Furlow & Ferry, 1996a, b); ferredoxin appears to be the physiological electron acceptor (Fischer & Thauer, 1990; Peer et al., 1994; Ferry, 1995, 1997a). The encoding genes in *Methanosarcina thermophila* are organized in a transcription unit, cdhABCDE, X being an open reading frame of unknown function (Maupin-Furlow & Ferry, 1996b). CdHA and CdHB are predicted to be nickel iron-sulphur proteins and CdhD and CdhE to harbour the corrinoid prosthetic group.

‖ From Weiss et al. (1994).

†† The enzyme is isolated as a multi-enzyme complex of three different subunits, McrABG, in an \(αβγ\) configuration.

†‡ Membrane-associated enzyme purified from methanol-grown *Methanosarcina Barkeri* is a complex of two different subunits, HdrDE (Künkel et al., 1997), and from acetate-grown cells is a complex of eight different subunits, HdrDE and EchABCDF, Ech being an *E. coli* hydrogenase-3-type hydrogenase (Künkel et al., 1998). HdrE is a \(b\)-type cytochrome (Künkel et al., 1997, 1998).

---

**Energy metabolism of methanoarchaea**

The reactions and enzymes known to be involved in methane formation from acetate, from CO₂ and from methanol are summarized in Tables 1–3.

The energy metabolism of methanogens can be viewed...
Table 2. Reactions and enzymes known to be involved in methane formation from CO₂ (Thauer et al., 1993)

MFR, methanofuran; H-S-CoM, coenzyme M; H-S-CoB, coenzyme B; H₄MPT, tetrahydromethanopterin, which is a tetrahydrofolate (H₄F) analogue found instead of H₂F in the Methanobacteriales (for structures see Fig. 3). In the other orders, modified forms of H₄MPT are present: tetrahydrodrosarcinopterin in the Methanosarcinales and Methanococcales and tattiopterin and/or thermopterin in the Methanomicrobales (Gorris & van der Drift, 1994). F₄₃₀ is a S'-deazaflavin derivative found in relatively high concentrations in methanogenic archaebacteria (Gorris & van der Drift, 1994). See also the legend to Table 4.

<table>
<thead>
<tr>
<th>Reaction*</th>
<th>Enzyme (gene)</th>
<th>Most recent literature</th>
</tr>
</thead>
<tbody>
<tr>
<td>CO₂ + MFR + 2[H] → formyl-MFR</td>
<td>Formylmethanofuran dehydrogenase ([fwd]HFGDACB and fmdECB)$</td>
<td>Schmitz et al. (1994); Bertram &amp; Thauer (1994); Bertram et al. (1994a, b); Wasserfallen (1994); Hochheimer et al. (1995, 1996); Vorholt et al. (1996, 1997b); Vorholt &amp; Thauer (1997); Holm &amp; Sander (1997)</td>
</tr>
<tr>
<td>Formyl-MFR + H₄MPT → formyl-H₄MPT + MFR</td>
<td>Formylmethanofuran: H₄MPT formyltransferase ([fr])</td>
<td>Shima et al. (1995, 1996); Lehmacher (1994); Ermler et al. (1997a); Kunow et al. (1996)</td>
</tr>
<tr>
<td>Methenyl-H₄MPT⁺ + F₄₃₀H₂ → methylene-H₄MPT + F₄₃₀H₂</td>
<td>F₄₃₀-dependent methylene-H₄MPT dehydrogenase ([mtd])</td>
<td>Klein et al. (1993b); Kunow et al. (1993); Klein &amp; Thauer (1995, 1997); Mukhopadhyay et al. (1995)</td>
</tr>
<tr>
<td>Methenyl-H₄MPT⁺ + H₂ → methylene-H₄MPT + H₂</td>
<td>H₂-forming methylene-H₄MPT dehydrogenase ([hmd])</td>
<td>Schwörrer et al. (1993b); Schleucher et al. (1994, 1995); Klein et al. (1995a, b); Berkeskel &amp; Thauer (1995); Hartmann et al. (1996a, b); Thauer et al. (1996)</td>
</tr>
<tr>
<td>Methylene-H₄MPT + F₄₃₀H₂ → CH₄ + H₂MPT + F₄₃₀</td>
<td>F₄₃₀-dependent methylene-H₄MPT reductase (mer)</td>
<td>Vaupel &amp; Thauer (1995); Nolling et al. (1995a); Kunow et al. (1993)</td>
</tr>
<tr>
<td>CH₃S-CoM + H₂ → CH₃-CoM + CH₄</td>
<td>Methyl-coenzyme M reductase ([mcr]BDCGA and mrtBDCGA)**</td>
<td>Bonacker et al. (1993); Goubeaud et al. (1997); Shima et al. (1997); Ermler et al. (1997b); Becker &amp; Ragsdale (1998)</td>
</tr>
<tr>
<td>H₂S-CoM + H₂</td>
<td>Heterodisulphide reductase ([hda], [hdaBC])††</td>
<td>Hedderich et al. (1994); Setzke et al. (1994)</td>
</tr>
</tbody>
</table>

*ΔG° values from Thauer et al. (1993). They add up to −130·7 kJ mol⁻¹, which is almost identical to the ΔG° = −131 kJ mol⁻¹ calculated for 4H₂ + CO₂ → CH₄ + 2H₂O from free energy of formation data (Thauer et al., 1977).
† From Bertram & Thauer (1994); determined at 60 °C; CO₂ in the gaseous state at 10⁵ Pa.
‡ Calculated for 2[H⁺] = 1H⁺ at 10⁵ Pa. The direct electron donor is probably a polyferredoxin (Vorholt et al., 1996). The endergonic reduction of CO₂ with H₂ to formylmethanofuran is driven by the electrochemical Na⁺ potential involving reversed electron transport (Kaesler & Schönheit, 1989a, b).
§ [fwd] denotes the genes encoding the tungsten enzyme and [fmd] the molybdenum enzyme in Methanobacterium thermoautotrophicum (Hochheimer et al., 1996). The latter enzymes are isolated from Methanobacterium thermoautotrophicum as multienzyme complexes composed of the subunits FwdABC and FwdA + FmdBC, respectively. FwdB and FmdB contain bound molybdopterin-guanine dinucleotide and tungsten and molybdenum, respectively (Hochheimer et al., 1996).
|| H₂ + F₄₃₀ → F₄₃₀H₂; ΔG° = −11 kJ mol⁻¹; the E° of the F₄₃₀/F₄₃₀H₂ couple is −360 mV (Thauer et al., 1993) and that of the H⁺/H₂ couple is −414 mV (Thauer et al., 1977).
to consist of two parts (Fig. 1): an oxidative part in which coenzyme M (H-S-CoM, 2-thioethanesulfonate) and coenzyme B (H-S-CoB, 7-thioheptanoylthreonine-phosphate) (for structures see Fig. 4) are oxidized to the heterodisulphide CoM-S-S-CoB; and a reductive part in which the heterodisulphide of coenzyme M and coenzyme B is re-reduced.

**Oxidative part**

In this part, methyl-coenzyme M is a central intermediate (Taylor & Wolfe, 1974a, b; Shapiro & Wolfe, 1980; Lovley et al., 1984). It is formed from coenzyme M and acetate, CO₂ or reduced C₁ compounds such as methanol, methylthiols and methylamines via the pathways shown in Fig. 2. Methyl-coenzyme M is subsequently reduced with coenzyme B to methane with the concomitant formation of the heterodisulphide of coenzyme M and coenzyme B (Bobik et al., 1987; Ellermann et al., 1988).

\[
\text{CH}_3\text{-S-CoM} + \text{H-S-CoB} \rightarrow \text{CH}_4 + \text{CoM-S-S-CoB}
\]

\[\Delta G^\circ = -45 \text{ kJ mol}^{-1}\]

As far as known the exergonic reaction, which is catalysed by methyl-coenzyme M reductase and which proceeds essentially irreversibly, is not coupled with energy conservation (Thauer et al., 1993).

In methanogenesis from CO₂ (Escalante-Semerena et al., 1984) and from acetate (Fischer & Thauer, 1989), N²-methylene-tetrahydrodromethanopterin (CH₃-H₄MPT) or N²-methylene-tetrahydro-sarcinapterin (CH₃-H₄SPT) is an intermediate in methyl-coenzyme M formation (Fig. 2). [Tetrahydrodromethanopterin (H₄MPT) is the tetrahydrofolate (H₄F) analogue found instead of H₂F in the Methanobacteriales (for structures see Fig. 3). In the other orders, modified forms of H₄MPT are present: tetrahydro-sarcinapterin in the Methanosarcinales and Methanococcales and tathioprotein and/or thermoprotein in the Methanomicrobiales (Gorris & van der Drift, 1994; see also White, 1998).] The methyl group of CH₃-H₄MPT is transferred to coenzyme M in an exergonic reaction (\[\Delta G^\circ = -30 \text{ kJ mol}^{-1}\)] coupled with energy conservation via an electrochemical sodium potential across the cytoplasmic membrane (Becher et al., 1992a, b; Becher & Müller, 1994; Müller & Gottschalk, 1994; Lienard et al., 1996; Lienard & Gottschalk, 1998).

Despite this fact, methyl-coenzyme M formation from acetate or CO₂ is most probably not associated with a net phosphorylation of ADP since the first step in methanogenesis from acetate (Table 1) and that from CO₂ (Table 2) are endergonic reactions which in order to proceed are predicted to consume more energy than is conserved in the methyl transfer reaction.

**Reductive part**

Since the generation of the heterodisulphide in the oxidative part of the energy metabolism apparently is not coupled with net ATP formation, the energy required for growth of methanogens must be generated in the reductive part, the exergonic reduction of the heterodisulphide (Fig. 1), and indeed it has been shown that the reduction of the heterodisulphide is coupled with phosphorylation of ADP via the chemiosmotic mechanism involving an electrochemical H⁺ potential as intermediate (Peinemann et al., 1990; Deppenmeier et al., 1990a, b, 1991; Sparling et al., 1993). Dependent on the methanogenic growth substrate, the electrons for the reduction derive from the oxidation of either H₂, the carbonyl group of acetyl-CoA, formate, ethanol or 2-propanol or of one of the reduced C₁ compounds methanol, methylthiols or methylamines. Under standard conditions, the free energy change associated with heterodisulphide reduction with H₂ is \(-40 \text{ kJ mol}^{-1}\), with formate is \(-43.5 \text{ kJ mol}^{-1}\), with ethanol (acetate as product) is \(-35 \text{ kJ mol}^{-1}\) and with methanol (CO₂ as product) is \(-34 \text{ kJ mol}^{-1}\), which is sufficient to drive the phosphorylation of 1 mol ADP (\[\Delta G^\circ = +31.8 \text{ kJ mol}^{-1}\]) (Thauer et al., 1977). The reduction of the heterodisulphide with acetyl-CoA (\[\Delta G^\circ = +0 \text{ kJ mol}^{-1}\]) (calculated from \(E^\circ\) values given in Table 1) and with 2-propanol (\[\Delta G^\circ = -15 \text{ kJ mol}^{-1}\]) is much less exergonic. Under the conditions in the cell, the free energy change \(\Delta G\) is, however, probably considerably more negative since the reduction is ‘pushed’ by irreversible formation of the heterodisulphide from methyl-coenzyme M and coenzyme B. Such a coupling is not unusual: e.g. in the arginine dihydrolase pathway operative in many bacteria and archaea, the energy-conserving formation of ornithine, CO₂ and NH₃ from citrulline (\[\Delta G^\circ = -19 \text{ kJ mol}^{-1}\]) is also ‘pushed’ by the preceding reaction, the irreversible hydrolysis of arginine to citrulline and NH₃ (\[\Delta G^\circ = -37.7 \text{ kJ mol}^{-1}\]) (Thauer et al., 1977). There is evidence that heterodisulphide reduction with H₂ is coupled with the synthesis of more than 1 mol ATP (Deppenmeier et al., 1996).

---

[^1]: From Weiss et al. (1994).
[^2]: *Mcr* denotes the genes encoding the isoenzyme 1 and *mrt* the isoenzyme II. Both isoenzymes are isolated as multienzyme complexes composed of three different subunits, MCrABG or MrtABG, in a \(\alpha_2\beta_2\gamma_2\) configuration. For literature on the enzyme complex from *Methanosarcina* spp., see Table 1.
[^3]: Calculated for \([\text{H}_2] = 10^4 \text{ Pa}\).
[^4]: The enzyme is purified from *Methanobacterium thermoautotrophicum* in a complex with the \(\text{F}_{100}\) non-reducing hydrogenase (Setzke et al., 1994).
**Table 3. Reactions and enzymes known to be involved in methane and CO₂ formation from methanol in Methanosarcina spp. (Keltjens & Vogels, 1993)**

Only methanogens of the family Methanosarcinaceae are capable of methanol disproportionation to CH₄ and CO₂. For abbreviations, see Tables 1 and 2.

<table>
<thead>
<tr>
<th>Reaction*</th>
<th>Enzyme (gene)</th>
<th>Most recent literature</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Methane formation</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ΔG° = −27.5 kJ mol⁻¹</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CH₃S-CoM + H₂S-CoB → CoM-S-S-CoB + CH₄</td>
<td>Methyl-coenzyme M reductase <em>(mcrBDCGA)</em></td>
<td>See Table 1</td>
</tr>
<tr>
<td>ΔG° = −45 kJ mol⁻¹</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CoM-S-S-CoB + 2[H] → H₂S-CoM + H₂-CoB</td>
<td>Heterodisulphide reductase <em>(hdrDE)</em></td>
<td>Heiden et al. (1994); Künkel et al. (1997)</td>
</tr>
<tr>
<td>Eᵣ = −200 mV</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ΔG° = −40 kJ mol⁻¹</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2. CO₂ formation</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ΔG° = −27.5 kJ mol⁻¹</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CH₃S-CoM + H₂SPT → H₂S-CoM + CH₄</td>
<td>Methyl-H₂SPT:coenzyme M methyltransferase <em>(energy conserving)</em> <em>(mtrEDCBAFGH)</em></td>
<td>See Table 1</td>
</tr>
<tr>
<td>ΔG° = +30 kJ mol⁻¹</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CH₃OH + H₂SPT → CH₃H₂SPT + H₂O</td>
<td>Enzyme has not yet been identified unambiguously</td>
<td>Keltjens &amp; Vogels (1993)</td>
</tr>
<tr>
<td>ΔG° = +2.5 kJ mol⁻¹</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CH₃H₂SPT + F₄₂₀ → methylene-H₂SPT + F₄₂₀H₂</td>
<td>F₄₂₀-dependent methylene-H₂SPT reductase <em>(mer)</em></td>
<td>Ma &amp; Thauer (1990); Te Brømmelstroet et al. (1991)</td>
</tr>
<tr>
<td>ΔG° = +6.2 kJ mol⁻¹</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Methylene-H₂SPT + F₄₂₀ + H⁺ → methenyl-H₂SPT¹ + F₄₂₀H₂</td>
<td>F₄₂₀-dependent methylene-H₂SPT dehydrogenase <em>(mtd)</em></td>
<td>Enßle et al. (1991); Te Brømmelstroet et al. (1991)</td>
</tr>
<tr>
<td>ΔG° = −5.9 kJ mol⁻¹</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Methenyl-H₂SPT + H₂O → formyl-H₂SPT + H⁺</td>
<td>Methenyl-H₂SPT cyclohydrolase <em>(mch)</em></td>
<td>Te Brømmelstroet et al. (1990); Vaupel et al. (1998)</td>
</tr>
<tr>
<td>ΔG° = +4.6 kJ mol⁻¹</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Formyl-H₂SPT + MFR → formyl-MFR + H₂SPT</td>
<td>Formylmethanofuran:H₂SPT formyltransferase <em>(fr)</em></td>
<td>Kunow et al. (1996)</td>
</tr>
<tr>
<td>ΔG° = +4.4 kJ mol⁻¹</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Formyl-MFR + MFR → CO₂ + MFR + 2[H]</td>
<td>Formylmethanofuran dehydrogenase <em>(fmdEFACDB)</em></td>
<td>Vorholt et al. (1996)</td>
</tr>
<tr>
<td>Eᵣ = −530 mV</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ΔG° = −16 kJ mol⁻¹</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*ΔG°* values from Thauer et al. (1993) and Keltjens & Vogels (1993). They add up to ΔG° = −319 kJ mol⁻¹ for 4CH₃OH + 2H₂O → 3CH₄ + 1CO₂ + 4H₂O, which is very close to ΔG° = −319.5 kJ mol⁻¹ calculated from free energy of formation data (Thauer et al., 1977).

† Calculated from 2[H] = 1H₂ at 10⁸ Pa.

‡ F₄₂₀H₂ → F₄₂₀ + H₂; ΔG° = +11 kJ mol⁻¹; the Eᵣ of the F₄₂₀/F₄₂₀H₂ couple is −360 mV (Thauer et al., 1993) and that of the H⁺/H₂ couple is −414 mV (Thauer et al., 1977).

§ The direct electron acceptor is probably a polyferredoxin (Vorholt et al., 1996). The exergonic dehydrogenation of formylmethanofuran is coupled with energy conservation via an electrochemical Na⁺ gradient (Kaesler & Schönheit, 1989a, b). See also Table 2.

Heterodisulphide reduction with H₂

The reduction of the heterodisulphide with the primary electron donors involves at least two enzymes, a dehydrogenase and a heterodisulphide reductase, and an electron transport chain connecting the two enzymes as schematically exemplified for heterodisulphide reduction with H₂:

H₂ → 2e⁻ + 2H⁺

2e⁻ + 2H⁺ + CoM-S-S-CoB → H₂S-CoM + H₂-CoB

Eᵣ = −200 mV

2382
The heterodisulphide reductase (Hdr), first discovered by Hedderich & Thauer (1988), is a novel type of disulphide reductase catalysing the reduction of the heterodisulphide in two successive one-electron steps and probably involving thyl radical intermediates (Künkel et al., 1997; Heim et al., 1998). The enzyme complex, composed of at least two different subunits, has been characterized from Methanobacterium thermotrophicum (Hedderich et al., 1990, 1994; Setzke et al., 1994), from Methanosarcina barkeri (Heiden et al., 1993, 1994; Künkel et al., 1997, 1998) and from Methanosarcina thermophila (Peet et al., 1994). Heterodisulphide reductase HdrDE from Methanosarcina spp. is a cytochrome b (HdrE)-containing enzyme (Heiden et al., 1993, 1994; Künkel et al., 1997); methanophenazine is most probably the direct electron donor, the oxidation of reduced methanophenazine with heterodisulphide being coupled with energy conservation (Abken et al., 1998a, b; Bäumer et al., 1998). The enzyme HdrABC from Methanobacterium spp. is an iron–sulphur protein (Hedderich et al., 1994; Setzke et al., 1994). The direct electron donor is not yet known (see Nolling et al., 1995c).

Hydrogenotrophic methanogens can contain up to four different types of hydrogenases and of each type, several isoenzymes (Thauer et al., 1993; Sorgenfrei et al., 1997a, b; Künkel et al., 1998; for topology see Braks et al., 1994): (i) F₁209-reducing Ni/Fe-hydrogenase (Vaupel & Thauer, 1998); (ii) F₁20 non-reducing hydrogenase of unknown physiological electron acceptor — in Methanosarcina spp., one of the subunits from the enzyme is a cytochrome b (Deppenmeier, 1995; Deppenmeier et al., 1995); Kumazawa et al., 1994; Kemner & Zeikus, 1994a, b) and in Methanobacterium spp., which are devoid of cytochromes, the electron acceptor is possibly either a 44 kDa polyferredoxin (Reeve et al., 1989;
**Table 4.** Dehydrogenases catalysing the reduction of $F_{420}$ and the oxidation of $F_{420}H_2$ in the energy metabolism of methanogenic archaea

$F_{420}$ is a 5'-deazaflavin derivative found in relatively high concentration in methanogenic archaea (Gorris & van der Drift, 1994). $F_{420}$ in methanogens is converted to inactive $F_{320}$ by adenylation and $F_{320}$ to $F_{420}$ by deadenylation in response to different growth conditions (Vermeij et al., 1994, 1995, 1996).

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Organism</th>
<th>Most recent literature</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>1. Reduction of $F_{420}$</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$F_{420}^+$-reducing hydrogenase</td>
<td>All hydrogenotrophic methanogens</td>
<td>Sorgenfrei et al. (1997a, b); Vaupel &amp; Thauer (1998)</td>
</tr>
<tr>
<td>$F_{420}$-dependent formate dehydrogenase</td>
<td>Methanogens growing on formate</td>
<td>Nölling &amp; Reeve (1997); Grahame &amp; Stadman (1993)</td>
</tr>
<tr>
<td>$F_{420}$-dependent methylene-$H_4$MPT dehydrogenase</td>
<td>Methanogens growing on methanol, methylthiols or methylamines</td>
<td>Keltjens &amp; Vogels (1993)</td>
</tr>
<tr>
<td>$F_{420}$-dependent methylene-$H_4$MPT reductase</td>
<td>Methanogens growing on methanol, methylthiols or methylamines</td>
<td>Keltjens &amp; Vogels (1993)</td>
</tr>
<tr>
<td>$H_2$-forming methylene-$H_4$MPT dehydrogenase plus $F_{420}$-dependent methylene-$H_4$MPT dehydrogenase</td>
<td>Most hydrogenotrophic methanogens of the orders Methanobacteriales, Methanococcales and Methanopyrales</td>
<td>Thauer et al. (1996); Afting et al. (1998)</td>
</tr>
<tr>
<td>$F_{420}$-dependent alcohol dehydrogenase</td>
<td>Methanogenium liminatans, Methanoculleus thermophilius, Methanobacterium palustre, Methanocorpusculum spp.</td>
<td>Klein et al. (1996); Widdel &amp; Frimmer (1995); Berk et al. (1996)</td>
</tr>
<tr>
<td>NADP-dependent alcohol dehydrogenase plus $F_{420}$-dependent NADP reductase</td>
<td></td>
<td>Berk et al. (1997); Widdel &amp; Frimmer (1995)</td>
</tr>
<tr>
<td><strong>2. Oxidation of $F_{420}H_2$</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$F_{420}$-dependent methylene-$H_4$MPT dehydrogenase</td>
<td>Methanogens reducing CO$_2$ to methane</td>
<td>See Table 2</td>
</tr>
<tr>
<td>$F_{420}$-dependent methylene-$H_4$MPT reductase</td>
<td>Methanogens reducing CO$_2$ to methane</td>
<td>See Table 2</td>
</tr>
<tr>
<td>$F_{420}H_2$ dehydrogenase complex</td>
<td>Methanoscarcina mazei, Methanolobus tindarius</td>
<td>Haase et al. (1992); Abken &amp; Deppenmeier (1997); Abken et al. (1998a, b)</td>
</tr>
<tr>
<td>$F_{420}$-dependent hydrogenase</td>
<td>Methanogens of the orders Methanococcales and Methanobacteriales growing on formate and lacking $F_{420}H_2$ dehydrogenase complex</td>
<td>Vaupel (1993)</td>
</tr>
</tbody>
</table>

Hedderich et al., 1992; Nölling et al., 1995c) or a 45 kDa flavoprotein (Wasserfallen et al., 1995; Nölling et al., 1995c); (iii) *Escherichia coli* hydrogenase-3-type Ni/Fechydrogenase of unknown physiological electron acceptor (Kinkel et al., 1998); and (iv) a metal-free hydrogenase, the $H_2$-forming methylenetetrahydrogenoterin dehydrogenase, which together with the $F_{420}$-dependent methylenetetrahydrogenoterin dehydrogenase catalyses the reduction of $F_{420}$ with $H_2$ (Thauer et al., 1996; Reeve et al., 1997). Both enzymes are induced during growth under conditions of nickel deprivation (Afting et al., 1998).

There are indications that at least two of the hydrogenases can be involved in heterodisulphide reduction with $H_2$: with inside-out vesicles from *Methanosarcina mazei* it has been shown that both $F_{420}$-dependent (Deppenmeier et al., 1990a, b) and $F_{420}$-independent (Deppenmeier et al., 1991) reduction of the heterodisulphide with $H_2$ are coupled with the phosphorylation of ADP (Deppenmeier et al., 1996; Abken et al., 1998a, b).

**Heterodisulphide reduction with $F_{420}H_2$**

Cell extracts of *Methanosarcina mazei* and of *Methanolobus tindarius* catalyse the reduction of heterodisulphide with reduced $F_{420}$, the coenzyme of many hydrogenases in methanogenic archaea (Table 4). ($F_{420}$) is a 5'-deazaflavin derivative with an $E^0 = -360$ mV present in relatively high concentrations in these organisms; Gorris & van der Drift, 1994.) For the reduction of the heterodisulphide with $F_{420}H_2$, besides heterodisulphide reductase an additional enzyme is required: *Methanosarcina* spp. (Deppenmeier et al., 1990a, b; Abken & Deppenmeier, 1997) and *Methanolobus tindarius* (Deppenmeier et al., 1990b; Haase et al., 1992) have been shown to contain a membrane-associated $F_{420}H_2$ dehydrogenase complex catalysing
the reduction of methanophenazine with \( \text{F}_{440} \text{H}_2 \), the reduction being coupled with phosphorylation of ADP (Abken et al., 1998a, b; Bümer et al., 1998). Such an \( \text{F}_{440} \text{H}_2 \) dehydrogenase complex is also found in *Archaeoglobus* sp. (Kunow et al., 1993, 1994; Klenk et al., 1997), but is apparently lacking in *Methanococcus* spp. (Bult et al., 1996; and *Methanobacterium* sp. (Smith et al., 1997) as deduced from the genome sequences. In methanogens lacking the \( \text{F}_{440} \text{H}_2 \) dehydrogenase complex and not growing on H\(_2\) and CO\(_2\), heterodisulphide reduction with \( \text{F}_{440} \text{H}_2 \) probably proceeds via H\(_2\) as intermediate (Vauple, 1993).

**Coupling with ATP synthesis**

As indicated, methyl transfer from \( \text{N}^5\)-methyltetrahydromethanopterin to coenzyme M in the oxidative part of the energy metabolism is coupled with the build-up of an electrochemical Na\(^+\) gradient (Becher et al., 1992a, b; Lienard et al., 1996). In turn, the reduction of the heterodisulphide in the reductive part is coupled with electrogenic H\(^+\) translocation (Peinemann et al., 1990; Deppenmeier et al., 1990a, b, 1991; Sparling et al., 1993). *Methanosarcina* spp. have been shown to contain an H\(^+\)-translocating \( \text{A}_{3} \text{A}_{1} \) ATPase (Wilms et al., 1996; Inatomi, 1996; Ruppert et al., 1998) and there is indirect evidence also for the presence of an Na\(^+\)-translocating \( \text{F}_{440} \text{A}_{1} \text{A}_{1} \) ATPase (Becher & Müller, 1994). *Methanobacterium* spp. and *Methanococcus* spp. harbour only one \( \text{A}_{3} \text{A}_{1} \) ATPase as deduced from the genome sequences (Bult et al., 1996; Smith et al., 1997). It is not known whether this ATPase is Na\(^+\)- or H\(^+\)-translocating. There is evidence for both (Chen & Konisky, 1993; Sparling et al., 1993; Smigan et al., 1994). Methanogens contain an Na\(^+\)/H\(^+\) antiporter capable of interconversion of the electrochemical H\(^+\) and Na\(^+\) potentials (Schönheit & Beimborn, 1983; Deppenmeier et al., 1996).

The stoichiometry of coupling of methanogenesis with ADP phosphorylation appears not to be constant. Evidence is available that during growth of methanogens on H\(_2\) and CO\(_2\) the growth yield \( \text{g} / (\text{mol} \text{CH}_4) \text{ mole}^{-1} \) increases with decreasing H\(_2\) concentrations (Schönheit et al., 1980; Morgan et al., 1997; for regulation see Pihl et al., 1994; Nolling et al., 1995a, b; Nolling & Reeve, 1997), indicating that at low H\(_2\) concentrations coupling of heterodisulphide reduction with ADP phosphorylation is tighter than at high H\(_2\) concentrations. With decreasing H\(_2\) concentrations the free energy change associated with CO\(_2\) reduction to methane decreases from \(-131 \text{ kJ} \text{ mol}^{-1} \) at 10\(^6\) Pa H\(_2\) to only approximately \(-30 \text{ kJ} \text{ mol}^{-1} \) at the H\(_2\) concentrations prevailing in methanogenic ecosystems where the H\(_2\) partial pressure is only between 1 and 10 Pa.

**Other heterodisulphide-generating reactions**

Methyl-coenzyme M reduction with coenzyme B is not the only reaction in which the heterodisulphide is regenerated. Most methanogens contain a fumarate reductase which catalyses the reduction of fumarate with H-S-CoM and H-S-CoB to succinate and CoM-S-S-CoB (Bobik & Wolfe, 1989; Heim et al., 1998). This reaction is involved in the biosynthesis of 2-oxo-glutarate, which, in the methanogens containing the fumarate reductase, is synthesized via reductive carboxylation of succinyl-CoA (Tersteegen et al., 1997; Thompson et al., 1998).

**Analogy between heterodisulphide reduction and sulphur reduction**

Many anaerobic bacteria and archaea can grow with elemental sulphur as terminal electron acceptor in the energy metabolism (Schauder & Kröger, 1993). Sulphur reduction to H\(_2\)S is coupled with energy conservation as evidenced by growth on H\(_2\) and S\(^0\). In elemental sulphur, which at room temperature is S\(_8\), the sulphur atoms are connected via S-S bonds just as the two sulphurs in heterodisulphide. The redox potential of the S\(^0\)/H\(_2\)S couple and that of the heterodisulphide/H-S-CoM+ H-S-CoB couple are both in the order of \(-200 \text{ mV} \) (Thauer et al., 1977). Methanogens and sulphur-reducing micro-organisms thus have in common that they both live at the expense of S-S bond reduction. Methanogens differ, however, from sulphur reducers in that they are independent of an external sulphur source as electron acceptor since they can reoxidize the 'reduced sulphur' with CO\(_2\) or one of the other methanogenic carbon substrates, which themselves are concomitantly reduced to methane.

**Methyl-coenzyme M, an intermediate unique to methanogenesis**

Coenzyme M and methyl-coenzyme M have, until now, only been found in methanogenic archaea (Balch & Wolfe, 1979). The same holds true for the enzymes catalysing the formation of methyl-coenzyme M (Table 5) and for methyl-coenzyme M reductase. All the other enzymes and coenzymes involved in methanogenesis, maybe with exception of coenzyme B, are also present in sulphate-reducing archaea (Vorholt et al., 1995, 1997a; Klenk et al., 1997). Recently, tetrahydromethanopterin and tetrahydromethanopterin-dependent enzymes were even found in a methylo trophic x-proteobacterium (Chistoserdova et al., 1998), indicating that some of the methanogenic enzymes and coenzymes are not as unique to the archaeal kingdom as previously thought. Also of interest is the recent finding that several non-methanogenic, including *Bacillus subtilis*, contain genes encoding a putative heterodisulphide reductase, the function of which remains to be elucidated (Heim et al., 1998).

Coenzyme M is the smallest coenzyme known to date. The enzymes catalysing its methylation and reductive demethylation are highly specific for its structure. 2-Selenoethanesulphonate and 3-thiopropionate can in part substitute for H-S-CoM in its function, 3-thiopropanesulphonate cannot (Gunsalus et al., 1978; Wackett et al., 1987; Tallant & Krzycki, 1996, 1997).
Table 5. Reactions and enzymes known to be involved in the formation of methyl-coenzyme M (Keltjens & Vogels, 1993)

For abbreviations, see Table 2.

<table>
<thead>
<tr>
<th>Reaction</th>
<th>Enzyme system</th>
<th>Most recent literature</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \text{CH}_3\text{H}_4\text{MPT} + \text{H}-\text{S-CoM} \rightarrow \text{CH}_2\text{S-CoM} + \text{H}_4\text{MPT} )</td>
<td>( \text{N}^3\text{Methyl-H}_4\text{MPT}:\text{coenzyme M methyltransferase (energy conserving)} ) (MtrA–H)</td>
<td>( \text{Stupperich et al.} (1993); \text{Gärtner et al.} (1993, 1994); \text{Weiss et al.} (1994); \text{Harms et al.} (1995); \text{Harms &amp; Thauer} (1996a, 1997, 1998); \text{Lu et al.} (1995); \text{Lienard et al.} (1996); \text{Lienard &amp; Gottschalk} (1998)</td>
</tr>
<tr>
<td>( \Delta \text{G}^\circ = -30 \text{ kJ mol}^{-1} )</td>
<td></td>
<td></td>
</tr>
<tr>
<td>( \text{CH}_3\text{OH} + \text{H}-\text{S-CoM} \rightarrow \text{CH}_2\text{S-CoM} + \text{H}_2\text{O} )</td>
<td>( \text{Methyl-Coenzyme M methyltransferase (MT2)} ) activity (Grahame, 1989; Yeliseev + Obtained from AGO' for methylamine reduction to methane with H(_2), calculated from the free energies of formation from the elements 6-hydroxybenzimidazolyl cobamide as prosthetic group.</td>
<td>( \text{Sauer et al.} (1997); \text{Sauer &amp; Thauer} (1997, 1998)</td>
</tr>
<tr>
<td>( \Delta \text{G}^\circ = -27.5 \text{ kJ mol}^{-1} )</td>
<td></td>
<td></td>
</tr>
<tr>
<td>( \text{CH}_3\text{NH}_2^+ + \text{H}-\text{S-CoM} \rightarrow \text{CH}_2\text{S-CoM} + \text{NH}_4^+ )</td>
<td>( \text{Monomethylamine:coenzyme M methyltransferase} )</td>
<td>( \text{Burke &amp; Krzycki} (1995, 1997); \text{Burke et al. (1998)}</td>
</tr>
<tr>
<td>( \Delta \text{G}^\circ = -5.1 \text{ kJ mol}^{-1} )</td>
<td></td>
<td></td>
</tr>
<tr>
<td>( \text{CH}_3\text{S-CoM} + \text{CH}_2\text{NH}_2^+ )</td>
<td>( \text{Dimethylamine:coenzyme M methyltransferase} )</td>
<td>( \text{Wassenaar et al. (1996, 1998)}</td>
</tr>
<tr>
<td>( \Delta \text{G}^\circ = -2.5 \text{ kJ mol}^{-1} )</td>
<td></td>
<td></td>
</tr>
<tr>
<td>( \text{CH}_2\text{S-CoM} + \text{CH}_2\text{NH}_2^+ )</td>
<td>( \text{Trimethylamine:coenzyme M methyltransferase} )</td>
<td>( \text{Ferguson &amp; Krzycki} (1997); \text{Wassenaar et al. (1996)}</td>
</tr>
<tr>
<td>( \Delta \text{G}^\circ = -6.3 \text{ kJ mol}^{-1} )</td>
<td></td>
<td></td>
</tr>
<tr>
<td>( \text{CH}_2\text{S-CoM} + \text{CH}_2\text{NH}_3^+ )</td>
<td>( \text{Tetramethylamine:coenzyme M methyltransferase} )</td>
<td>( \text{Asakawa et al.} (1998); \text{Tanaka (1994)}</td>
</tr>
<tr>
<td>( \Delta \text{G}^\circ = ? )</td>
<td></td>
<td></td>
</tr>
<tr>
<td>( \text{CH}_2\text{S-CoM} + \text{CH}_2\text{S}-\text{H} )</td>
<td>( \text{Methylthiol:coenzyme M methyltransferase} )</td>
<td>( \text{Paul &amp; Krzycki} (1996); \text{Tallant &amp; Krzycki (1996, 1997)}</td>
</tr>
<tr>
<td>( \Delta \text{G}^\circ \approx 0 \text{ kJ mol}^{-1} )</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

* From Weiss et al. (1994).
| † | | |
| ‡ | | |

† For activity in cell extracts the presence of a methyltransferase-activating protein (MAP), reduced ferredoxin and ATP are additionally required (Daas et al., 1993, 1994, 1996a, b). MtaA (= MT2-M), MtbA (= MT2-A), MtqA and MtsA exhibit methylcobalamin:coenzyme M methyltransferase (MT2) activity (Grahame, 1989; Yeliseev et al., 1993; Ferguson et al., 1996; Wassenaar et al., 1996) and show sequence similarity (LeClerc & Grahame, 1996; Harms & Thauer, 1996b; Paul & Krzycki, 1996; Asakawa et al., 1998). MtaA and MtbA are zinc enzymes (Sauer & Thauer, 1997); MtqC, MtqB, MtqC and MtbB have been shown to be corrinoid proteins harbouring 6-hydroxybenzimidazolyl cobamide as prosthetic group.

‡ Obtained from \( \Delta \text{G}^\circ \) for methylene reduction to methane with \( \text{H}_2 \) calculated from the free energies of formation from the elements tabulated in Thauer et al. (1977) and from \( \Delta \text{G}^\circ \) of \(-85 \text{ kJ mol}^{-1}\) for methyl-coenzyme M reduction with \( \text{H}_2 \) to \( \text{CH}_4 \) and coenzyme M (Thauer et al., 1993).

§ Also catalyses the methylation of coenzyme M with methylmercaptopropanol (95\%), methylmercaptopropionate (80\%), mercaptomethanol (10\%), methylmercaptoethanol (8\%) and methyl iodide (170\%) (Tallant & Krzycki, 1997) and the methylation of mercaptobenzyl (27\%) and 2-mercaptopropanol (66\%) (Tallant & Krzycki, 1996).

### Methyl-coenzyme M reductase, its substrate and inhibitors

Methyl-coenzyme M and coenzyme B are the substrates of methyl-coenzyme M reductase, methane and heterodisulphide its products (Bobik et al., 1987; Ellermann et al., 1988) (Fig. 4). From the methyl-coenzyme M analogues tested in cell extracts of Methanobacterium thermoautotrophicum, only 2-(methylthio)propionate (\( K_m = 1.3 \text{ mM} \); \( V_{max} = 1.3 \text{ mM} \) mg\(^{-1}\)) and ethyl-coenzyme M (\( K_m = 1.3 \text{ mM} \); \( V_{max} = 7.4 \text{ mM} \) mg\(^{-1}\)), methyl-seleno-coenzyme M (\( K_m = 0.3 \text{ mM} \); \( V_{max} = 35 \text{ mM} \) mg\(^{-1}\)) and difluoromethyl-coenzyme M (\( K_m = 2.5 \text{ mM} \); \( V_{max} = 20 \text{ mM} \) mg\(^{-1}\)) were reduced (methyl-coenzyme M: \( K_m = 0.1 \text{ mM} \); \( V_{max} = 11 \text{ mM} \) mg\(^{-1}\)) (Wackett et al., 1987). Interestingly, trifluoromethyl-coenzyme M and trifluoromethyl-seleno-coenzyme M (Wackett et al., 1987) and 2-(dimethylsulphonium)ethanesulphonate (Gunsalus et al., 1978) were not reduced, neither were 2-(methoxy)ethanesulphonate, propyl-coenzyme M and 3-(methylthio)propanesulphonate; these compounds were even inhibitors (Gunsalus et al., 1978; Wackett et al., 1987). Other inhibitors based on the methyl-coenzyme M structure are 2-bromoethanesulphonate (\( K_i = 8 \mu\text{M} \)) and 2-chloroethanesulphonate (\( K_i = 70 \mu\text{M} \)) (Gunsalus et al., 1978), 3-bromopropanesulphonate (\( K_i = 50 \text{nM} \)), 4-bromobutanesulphonate (\( K_i = 6 \mu\text{M} \)) and 2-azidoethanesulphonate (\( K_i = 1 \mu\text{M} \)).
be resolved. The phosphate group of the threonine phosphate moiety was not covalently bound to any other molecule (Ermler et al., 1997b).

**Molecular properties of methyl-coenzyme M reductase and of its isoenzyme**

Methyl-coenzyme M reductase (MCR) has an apparent molecular mass of approximately 300 kDa. It is composed of three different subunits, α (McrA), β (McrB) and γ (McrG), in an αβγ arrangement (Gunsalus & Wolfe, 1980). The enzyme contains 2 mol of tightly but not covalently bound coenzyme F430 mol⁻¹ (Ellefson et al., 1982), which is a nickel porphinoïd, the structure of which is shown in Fig. 5. The enzyme as purified generally also contains 2 mol H-S-CoM (Hartzell et al., 1987) and 2 mol H-S-CoB (Noll & Wolfe, 1986). The enzyme can be reconstituted from its subunits in the presence of coenzyme F430, albeit with very low specific activity (Hartzell & Wolfe, 1986).

*Methanobacterium thermoautotrophicum, Methanothermus fervidus* and *Methanococcus jannaschii* (probably all members of the *Methanobacteriales* and *Methanococcales*) have been shown to contain besides MCR a genetically distinct isoenzyme of methyl-coenzyme M reductase designated MRT (Rospert et al., 1990; Brenner et al., 1993; Lehmacher & Klenk, 1994; Bult et al., 1996; Nolling et al., 1996). The expression of the two isoenzymes is differentially regulated by the growth conditions (Bonacker et al., 1992; Pihl et al., 1994; Reeve et al., 1997; Pennings et al., 1997).

The genes encoding the three subunits of the isoenzyme I (MCR) form a transcription unit (*mcrBDCGA*) which additionally contains two open reading frames encoding two polypeptides, McrC and McrD, of molecular masses below 20 kDa (Cram et al., 1987; Bokranz & Klein, 1987).
Methanobacteriales, the genes encoding the three subunits of the isoenzyme II (MRT) also form a transcription unit (mrtBDGA) which, however, contains additionally only one open reading frame encoding a protein with sequence similarity to McrD (Nolling et al., 1996). In Methanococcus jannaschii, mrtD is separated from the mrtBGA operon by approximately 37 kbp. The function of the mcrC, mcrD and mrtD gene products is not known (Reeve et al., 1997). A possibility could be that they are involved in post-translational modification of the α subunit, which, in the native enzyme, is extensively modified as revealed by crystal structure analysis: an arginine (4-methyl-Arg\textsuperscript{271}), a histidine (1-N-methyl-His\textsuperscript{235}), a cysteine (S-methyl-Cys\textsuperscript{452}) and a glutamine (2-methyl-Gln\textsuperscript{400}) are methylated and instead of a glycine there appears to be a thiglycine (Gly\textsuperscript{444})(Ermel et al., 1997b).

Coenzyme F\textsubscript{430}, the prosthetic group of methyl-coenzyme M reductase

The first report on coenzyme F\textsubscript{430} (Fig. 5) is by Gunsalus & Wolfe (1978), who observed in cell extracts of Methanobacterium thermoautotrophicum a low-molecular-mass non-fluorescent compound with an absorption maximum at 430 nm. In 1979, Schönheit and others discovered that growth of methanogens is dependent on nickel. Diekert et al. (1980a) and Whitman & Wolfe (1980) then showed that the nickel was in part required for the synthesis of F\textsubscript{430}, in which it was incorporated, and that F\textsubscript{430} contained mol\textsuperscript{-2} 1 mol nickel. In the same year, biosynthetic evidence was provided by Diekert et al. (1980b) that F\textsubscript{430} is a nickel tetrapyrrole, the structure of which was subsequently elucidated in collaboration with the group of A. Eschenmoser at the ETH Zürich (Pfaltz et al., 1982; Färber et al., 1991). Finally, in 1982 it was found that F\textsubscript{430} is the prosthetic group of methyl-coenzyme M reductase (Ellefson et al., 1982). Until now, coenzyme F\textsubscript{430} has been found only in methanogenic archaea in which it is always present (Diekert et al., 1981) and in which its only function appears to be the prosthetic group of methyl-coenzyme M reductase.

The presence of a ligand nickel atom is the striking feature of coenzyme F\textsubscript{430}. Nickel brings up to five different metals found in the centre of biological cyclic tetrapyroles. Up to the discovery of F\textsubscript{430}, the different metals known to occur were iron in haem and in sirohaem, magnesium in chlorophylls, cobalt in corrinoids and copper in tuarcin, the pigment of tuarcobird feathers. Another striking feature is the state of reduction of the pyrrole ring system. One encounters the interesting fact, possibly related to its anaerobic evolution and function, that coenzyme F\textsubscript{430} is by far the most highly reduced or saturated amongst all known tetrapyrroles (Fig. 6). Coenzyme F\textsubscript{430} has only five double bonds, of which two pairs are conjugated, but they are separated by two single bonds and so do not form a larger conjugated bond system. The yellow colour of coenzyme F\textsubscript{430} in contrast to the red colour of porphyrins and corrinoids, is no doubt related to this low degree of conjugation (Friedmann et al., 1991).

Biosynthetically, coenzyme F\textsubscript{430} is derived from dihydro-sirohydrochlorin, which is also the biosynthetic precursor of sirohaem and B\textsubscript{12} (Thauer & Bonacker, 1994; Hungerer et al., 1996).

Coenzyme F\textsubscript{430}, properties relevant to the catalytic mechanism of methyl-coenzyme M reductase

Coenzyme F\textsubscript{430} is released from methyl-coenzyme M reductase upon denaturation with perchloric acid or trichloroacetic acid. In the released coenzyme, nickel is in the Ni(II) oxidation state. For the understanding of the function of coenzyme F\textsubscript{430} in methyl-coenzyme M reductase, the following properties of the non-protein-bound cofactor are considered to be of importance (Jaun, 1993; Won et al., 1993; Telser, 1998; see also Stolzenberg & Zhang, 1997; Pandiyan et al., 1997; Schmid et al., 1996, 1997; Jäger & Rudolph, 1997). They are discussed in comparison to those of cobalamin (B\textsubscript{12}) (Kräutler et al., 1998) (Fig. 7).

F\textsubscript{430} as isolated in the Ni(II) oxidation state can be reduced to the Ni(I) oxidation state. In aqueous solution, the standard redox potential \( E^0 \) of the Ni(II)/Ni(I) couple is between −600 mV and −700 mV (Jaun & Pfaltz, 1986; Holliger et al., 1993) and is thus in the same
order as that of the cob(II)alamin/cob(I)alamin couple, which is $-640 \text{ mV}$ (Lexa & Saveant, 1983; Daas et al., 1995).

Ni(II) in $F_{430}$ can be methylated with methyl iodide, methyltosylate, methylhalides or methylsulphonium ions (Jaun & Pfaltz, 1988; Lin & Jaun, 1992), yielding a methyl-Ni(II) metalloorganic compound (Lin & Jaun, 1991). With methyltosylate, primarily methyl-Ni(III) $F_{430}$ must be formed (Jaun, 1993), just as methylcob(III)alamin is formed upon methylation of cob(I)alamin. Methyl-Ni(III) $F_{430}$ is, however, a very labile compound which is predicted to be almost instantaneously reduced to methyl-Ni(II) $F_{430}$ by any electron donor available (Jaun, 1993). Upon methylation of Ni(II) $F_{430}$, only methyl-Ni(II) $F_{430}$ rather than methyl-Ni(III) $F_{430}$ can be detected (Lin & Jaun, 1991). Based on the $E^0$ of the Ni(II) $F_{430}$/Ni(II) $F_{430}$ redox couple (Jaun, 1990), the $E^0$ of the methyl-Ni(III)/methyl-Ni(II) couple is estimated to be much more positive than $0 \text{ V}$. In this property, $F_{430}$ differs significantly from cobalamin, the methylated form of which [methylcob(III)alamin] is stable and resistant towards reduction to methyl-

cob(II)alamin with electron donors more positive than $-650 \text{ mV}$. Methylation of Ni(II) $F_{430}$ to methyl-Ni(III) $F_{430}$ is a nucleophilic substitution which is predicted to proceed with inversion of stereoconfiguration (Lin & Jaun, 1992).

Methyl-Ni(II) $F_{430}$ spontaneously protonolyses to yield CH$_4$ and Ni(II) $F_{430}$ (Lin & Jaun, 1991). It is an electrophilic substitution which is predicted to proceed with retention of stereoconfiguration. To the contrary, methylcob(II)alamin dissociates to a methyl radical and cob(I)alamin rather than to protonolysate to methane and cob(II)alamin.

These properties of $F_{430}$ indicate that the nickel porphinoind is a good methyl group reduction catalyst and differs in this property from cobalamin, which is a good methyl transfer catalyst. They are probably relevant to the catalytic mechanism of methyl-coenzyme M reductase: there is evidence that the enzyme only becomes active upon reduction of its prosthetic group from the Ni(II) to the Ni(I) oxidation state (Goubeaud et al., 1997). Furthermore, there is evidence that methyl-coenzyme M reductase catalyses the reduction of the methyl group of methyl-coenzyme M to methane with inversion of stereoconfiguration, consistent with Ni(II) $F_{430}$ methylation and methyl-Ni(II) $F_{430}$ protonolysis as steps in the catalytic cycle (Ahn et al., 1991).

**Activation of methyl-coenzyme M reductase by reduction to the Ni(I) oxidation state**

Methyl-coenzyme M reductase isolated from cells of methanogenic archaea is more or less inactive (Gunsalus & Wolfe, 1980; Brenner et al., 1993). The enzyme purified from *Methanobacterium thermoautotrophicum* $\Delta$H requires the addition of at least two proteins, designated A$_2$ and A$_3\alpha$, of ATP and of Ti(III) citrate for activation in vitro. Even in their presence, however, only less than 0.1% of the specific activity in vivo is reached.

The sequence of *MCR (inactive) $\rightarrow$ A$_2$A$_3\alpha$ MCR (0.1% active) $\rightarrow$ Ti(III), pH 7 ATP*

It was mentioned above that MCR as isolated in its inactive form contains tightly bound 2 mol coenzyme M (Hartzell et al., 1987). When in the presence of the activating system (A$_2$, ATP and an electron donor), the inactive enzyme was incubated with [methyl-\textsuperscript{3}H, tio-\textsuperscript{235}S]methyl-coenzyme M and component B, the coenzyme M moiety of methyl-coenzyme M was found to slowly exchange into the enzyme-bound coenzyme M during turnover, 150–160 mol CH$_4$ (mol enzyme)$^{-1}$ having to be formed before the exchange into the 2 mol bound coenzyme M was complete (Hartzell et al., 1987). In the absence of the activating system and of component
B or in the presence of 2-bromoethanesulphonate, neither an exchange nor methane formation was observed. Apparently exchange was dependent on enzyme turnover. The finding of complete exchange indicates that the MCR molecules present were not all activated at the same time and that they lost activity again after several turnovers.

The enzyme purified from the Marburg strain of Methanobacterium thermoautotrophicum shows residual activity (0.1 U mg⁻¹) in the absence of A₂, A₃a and ATP (Ankel-Fuchs & Thauer, 1986). In the presence of an appropriate reductant, the specific activity even increases to 1 U mg⁻¹, which is 2% of that expected from in vivo data (Ellermann et al., 1989). EPR spectroscopic analysis revealed that these enzyme preparations were essentially EPR silent, as were the cells from which the enzyme was purified. This indicates that the inactive methyl-coenzyme M reductase preparations contained F₄₃₅ in the Ni(II) oxidation state.

A first breakthrough was the finding that the specific activity of methyl-coenzyme M reductase is much higher in extracts prepared from cells of Methanobacterium thermoautotrophicum reduced with 100% H₂ prior to harvest. Such reduced cells and the methyl-coenzyme M reductase enriched from such cells exhibited a nickel-based EPR spectrum designated MCRₐ₇ and the spin concentration of the signal correlated with the specific activity. The highest spin concentration reached was between 10 and 20% and the highest specific activity was between 10 and 20 U per mg purified methyl-coenzyme M reductase (Rospert et al., 1991; Bonacker et al., 1993).

The final breakthrough was the finding that purified methyl-coenzyme M reductase in the MCRox₂ state (see below) can be activated to a specific activity of 100 U mg⁻¹ by reduction with Ti(III) citrate at pH 10. The reduced enzyme exhibited an axial MCRred₁ signal with a spin concentration near to 100% (Goubeaud et al., 1997).

\[
\text{MCRox₁ (inactive) } \xrightarrow{\text{Ti(III);pH 10}} \text{MCRred₁ (100% active)}
\]

Methyl-coenzyme M reductase with a specific activity of 100 U mg⁻¹ shows an EPR spectrum very similar and a characteristic UV/visible spectrum almost identical to that of non-protein-bound coenzyme F₄₃₅ in the Ni(I) oxidation state (Goubeaud et al., 1997). From this finding, it is concluded that the MCRred₁ signal of methyl-coenzyme M reductase is derived from its Ni(I) reduced prosthetic group. From the correlation of the specific activity with the MCRred₁ spin concentration it is deduced that the prosthetic group of methyl-coenzyme M reductase has to be in the Ni(I) oxidation state for the enzyme to be active.

**EPR-signal-exhibiting forms of methyl-coenzyme M reductase:** MCRred₁, MCRred₂, MCRox₁ and MCRox₂

As already indicated, active methyl-coenzyme M reductase exhibits the EPR spectrum MCRred₁. The signal is induced in cells of Methanobacterium thermoautotrophicum growing on 80% H₂/20% CO₂ by switching to gassing with 100% H₂. The axial signal builds up within 10 min. Upon further gassing with 100% H₂, a second methyl-coenzyme M reductase derived signal appears, designated MCRred₂, which is rhombic rather than axial [Albracht et al., 1988; for a Ni(I) macrocyclic complex exhibiting a rhombic EPR spectrum see Suh et al., 1996]. Cell extracts of such reduced cells also show a high specific activity and also exhibit the MCRred₁ signal. Upon addition of coenzyme M to the cell extracts, the MCRred₂ signal increases; upon addition of methyl-coenzyme M, the MCRred₂ signal is converted to the MCRred₁ signal (Rospert et al., 1991, 1992).

When gassing of growing Methanobacterium thermoautotrophicum cultures is switched from 80% H₂/20% CO₂ to 80% N₂/20% CO₂, a methyl-coenzyme M reductase derived EPR signal is induced which differs significantly from the MCRred₁ and MCRred₂ signals and which was designated MCRox₁ (Albracht et al., 1986, 1988). This signal is also induced when the cultures of Methanobacterium thermoautotrophicum growing on 80% H₂/20% CO₂ are supplemented with Na₂S (50 mM) (Becker & Ragsdale, 1998). The methyl-coenzyme M reductase in the MCRox₁ form can be purified. The pure enzyme shows only very low specific activity but can be activated by reduction with Ti(III) citrate at pH 10 to the MCRred₁ form (Goubeaud et al., 1997) (see above).

When cultures of Methanobacterium thermoautotrophicum growing on 80% H₂/20% CO₂ are supplemented with Na₂SO₃ (10 mM) or Na₂S₂O₄ (10 mM), a methyl-coenzyme M reductase derived novel EPR signal is induced which is designated MCRox₂. The enzyme in this form can be isolated but is inactive. It cannot be activated by reduction with Ti(III) (Becker & Ragsdale, 1998).

**EPR-silent forms of methyl-coenzyme M reductase:** MCRsilent, MCRred₁-silent, MCRred₂-silent, MCRox₁-silent and MCRox₂-silent

Different EPR-silent forms of methyl-coenzyme M reductase have to be discriminated. These forms all have in common that they show only very little activity and are not susceptible to activation by reduction with Ti(III) at pH 10 to the MCRred₁ form. (Residual activity may be due to the presence of traces of EPR active forms.)

The methyl-coenzyme M form referred to as MCRsilent is the one obtained by isolation from cells of Metha-
anobacterium thermoautotrophicum harvested without prior gassing with 100% H2 or 20% CO2/80% N2. The forms designated MCRred1 silent, MCRred2 silent, MCRox1 silent and MCRox2 silent are generated spontaneously from the respective EPR active forms when stored under strictly anaerobic conditions at 4 °C: the spin concentration of the different EPR signals decreases by 50% within only a few hours. In the presence of traces of O2, the MCRred1 and MCRred2 signals are instantaneously quenched (Rospert et al., 1991, 1992) whereas the decay rate of the MCRox signals is similar under anaerobic and aerobic conditions (Goubeaud et al., 1997; Becker & Ragsdale, 1998). The latter finding suggests that the MCRox forms of methyl-coenzyme M reductase could contain F430 in the Ni(III) oxidation state. Interestingly, the two MCRox forms exhibit a UV/visible spectrum more closely related to that of Ni(I1) F430 than to Ni(I) F430 or Ni(III) F430 (Jaun, 1990, 1993).

Crystal structure of methyl-coenzyme M reductase in the MCRox-silent state

First crystals of methyl-coenzyme M reductase were obtained in 1991 by Rospert (1991) for the isoenzyme I from Methanobacterium thermoautotrophicum (Marburg). From this time on the enzyme from various methanogens and from various different preparations was crystalized and tested for defraction. Beginning 1996, the first good crystals were obtained from a highly purified preparation of methyl-coenzyme M reductase isoenzyme I in the MCRox state from Methanobacterium thermoautotrophicum (Marburg strain) (Shima et al., 1997). The crystal structure was solved in the MCRox silent state to 1.4 Å resolution (1 Å = 0.1 nm) (Ermler et al., 1997b; see also Ferry, 1997b; and Cammack, 1997). The primary structure of the enzyme had previously been resolved by Bokranz et al. (1988).

Methyl-coenzyme M reductase in the MCRox silent state contains bound 2 mol coenzyme F430, 2 mol reduced coenzyme M and 2 mol reduced coenzyme B as revealed by the X-ray structure.

Overall structure

It is characterized by a series of α helices arranged in a compact form with an ellipsoidal shape of about 120 by 85 by 80 Å. The subunits are mutually tightly associated, as indicated by extended interface areas, particularly between subunits a and a’ and subunits b and b’, and by the fact that, except for subunits γ and γ’, each subunit contacts all other subunits of the multisubunit complex (Ermler et al., 1997b).

Two independent active sites

There are two binding sites, roughly 50 Å apart, for coenzyme F430, coenzyme M and coenzyme B, forming two separated structurally identical active sites. In each binding site the three coenzymes are embedded inside a narrow channel, 30 Å long, and at the narrowest part 6 Å in diameter, extending from the protein surface deeply into the interior of the protein complex (see the diagram in Fig. 11). The channel and the coenzyme-binding sites are formed by residues of subunits α, α’, β and γ (and equivalently α’, α, β’ and γ’), indicating that one trimer is not sufficient to accomplish the enzymic reaction (Ermler et al., 1997b).

Binding of coenzyme F430

F430 is bound at the bottom of the 30-Å-long channel such that its tetrapyrrole plane points with its front face (reduced pyrrole rings A, B, C and D clockwise) (see Fig. 5) roughly towards the mouth of the channel, whereas its rear face points to the channel bottom. Thus only the front face is accessible to the substrate. Interestingly, in sulphite reductase the prosthetic group sirohaem, which as F430 is biosynthetically derived from dihydrosirohydrochlorin, is only accessible from the rear face (Crane et al., 1995, 1997a, b). The tetrapyrrole ring of coenzyme F430 is bound in a rather flat conformation to the enzyme as predicted for the free coenzyme F430 in the hexagonally coordinated Ni(II) state (Farber et al., 1991; Jaun, 1993). The Ni atom present as Ni(II) sits almost exactly in the tetrapyrrole plane and is coordinated to six ligands arranged in a nearly optimal octahedral configuration. The four equatorially located nitrogen atoms of the tetrapyrrole ring have distances to the nickel of 2.14 Å for ring A, 2.11 Å for ring B, 2.10 Å for ring C and 1.99 Å for ring D (Fig. 8). As the fifth ligand the side chain oxygen of Glnn147 protrudes from a long loop to the rear face of F430 and approaches the Ni(II) atom to 2.3 Å (Fig. 9). The 1.45 Å electron density map demonstrates that the oxygen and not the nitrogen of the side chain Glnn147 is the axial ligand (Ermler et al., 1997b) as to be expected thermodynamically and as seen also in other proteins (Roach et al., 1997). Glnn147 is embedded in the protein matrix such that it will probably not be able to move away when F430 is reduced from the Ni(II) to the Ni(I) oxidation state in which the Ni(I) is preferentially tetraplanarily coordinated (Jaun, 1993; Telser et al., 1997). By the enforced axial fifth ligand the nucleophilicity of the Ni(I) in F430 is predicted to be increased, facilitating the nucleophilic substitution of the methyl group of coenzyme M.

Binding of coenzyme M

In MCRox silent, the sixth coordination site of nickel, located in front of the tetrapyrrole ring plane of F430, is occupied by the thiol group of coenzyme M, which is positioned almost parallel to the tetrapyrrole plane in contact with its front face (Fig. 9). The thiol group binds axially to the nickel (2.42 Å distance) and interacts with the hydroxyl group of Tyr232 and Tyr562 and a water molecule that bridges coenzyme M and B. The ethyl moiety is embedded between the lactam ring of the Ni porphinoid and the phenyl ring of Phe423. Coenzyme M is anchored to the polypeptide chain by its negatively charged sulphonate group, forming a salt bridge to the

Marjory Stephenson Prize Lecture

2391
Fig. 8. Coenzyme F₄₃₀ in the Ni(II) oxidation state as viewed by looking from outside through the 30-Å-long channel into the active site pocket of methyl-coenzyme M reductase (MCRₙₙ₁₁-silent). The front face (reduced pyrrole rings A, B, C and D clockwise) is seen. Structure at 1.45 Å resolution.

Fig. 9. Coenzyme M located in front of the tetrapyrrole ring plane of F₄₃₀ with its thiol group bound to Ni(II) in the active site of methyl-coenzyme M reductase (MCRₙₙ₁₁-silent). Structure at 1.45 Å resolution. The oxygen of Gln₁⁴⁷ is seen to approach the Ni from the rear face of F₄₃₀ to 2.3 Å.

Fig. 10. Heterodisulphide of coenzyme M and coenzyme B bound via an oxygen of its sulphonate group to Ni(II) in the active site of methyl-coenzyme M reductase (MCRₙₙ₁₁-silent). Structure at 1.75 Å resolution.

**Binding of coenzyme B**

With its elongated conformation, coenzyme B fits accurately into the most narrow segment of the channel formed by residues of subunits α, α' and β (see also the diagram in Fig. 11a). Coenzyme B is anchored to the protein mainly by salt bridges between the negatively charged L-threonine phosphate moiety and five positively charged amino acids. The heptanoyl arm is in van der Waals contact with several hydrophobic residues. The thiol group of coenzyme B is positioned at a distance of 8.7 Å from the nickel of F₄₃₀ and 6.2 Å from the coenzyme M thiol sulphur. It interacts with the side chain of nitrogen of Asn₂₄₈, the main chain peptide nitrogen of Val₂₄₈ and the bridging water molecule mentioned above. Asn₂₄₈ is within hydrogen bond distance of the sulphur that is presumed to replace the backbone carbonyl oxygen of the modified Gly²₄₁₅ (see below).

**Five modified amino acids in the active site region**

The electron density map revealed five modified amino acids located in subunits α and α' at or very near the active site region, 1-N-methyl-His₂₃⁷, 4-methyl-Arg₂₇¹, 2-methyl-Gln₂⁰⁰, S-methyl-Cys₂⁵² and Gly₂⁴₄, where
the carbonyl oxygen appears to be substituted by sulphur (Ermler et al., 1997b).

**Exclusion of bulked water from the active site**

When coenzyme B is bound to the enzyme the active site is shielded from bulk solvent. The sole water molecule found in the active site region of MCRox1.silent between coenzyme M and coenzyme B should be displaced after binding of the more bulky methyl-coenzyme M. The active site is lined up by an annular arrangement of Phe230, Tyr233, Phe244, Phe356 and Tyr357 flanked further by hydrophobic and aromatic residues (Ermler et al., 1997b). These amino acids are completely conserved in all methyl-coenzyme M reductases (Nölling et al., 1996). Methane formation from methyl-coenzyme M and coenzyme B thus takes place in a greasy pocket and probably does not involve water molecules. These conditions would allow for radical intermediates. Solvent-inaccessible active sites coated by non-polar aromatic residues and attainable by a channel have been observed in several radical-based enzymes such as galactose oxidase (Ito et al., 1991), prostaglandin H2 synthase 1 (Picot et al., 1994) and methylmalonyl-CoA mutase (Mancia et al., 1996).

**Crystal structure of methyl-coenzyme M reductase in the MCRsilent, MCRred2-silent and MCRox2-silent states**

The structure of the MCRsilent state was refined in the resolution range 2.0–10.0 Å with the use of the MCRox1.silent structure for initial phase determination (Ermler et al., 1997b). The two enzyme states exhibit nearly identical overall structures. The model of the MCRsilent structure is mainly distinguished from that of MCRox1.silent by binding of the oxidized instead of the reduced forms of coenzyme F and coenzyme B (Fig. 10). A superposition of the structures reveals that the reduced coenzyme B in MCRox1.silent and the coenzyme B moiety of the heterodisulphide in MCRsilent align perfectly except that the sulphur is turned slightly towards the tetrapyrrole plane of Fγ30, resulting in a 90° rotation of the reduced form (either MCRred1 or MCRred2 state) (Rospert et al., 1991, 1992; Goubeaud et al., 1997).

First the structure of the enzyme–substrate complex and of the enzyme–product complex and their formation and dissociation, respectively, will be discussed. Then two alternative mechanisms for the conversion of the enzyme–substrate to the enzyme–product complex will be proposed.

**Enzyme–substrate/product complex**

In Fig. 11, diagrams of the enzyme–substrate complex and of the enzyme–product complex are given. The prosthetic group is shown in the Ni(II) oxidation state. This is deduced from the finding that methyl-coenzyme M reductase only exhibits activity when assayed in its Ni(II) Fγ30 reduced form (either MCRred1 or MCRred2 state) (Rospert et al., 1991, 1992; Goubeaud et al., 1997).

The diagram in Fig. 11 shows that the prosthetic group of methyl-coenzyme M is accessible only through a narrow channel and only by methyl-coenzyme M (Ermler et al., 1997b). Through this channel methyl-coenzyme M must enter before coenzyme B binds since upon coenzyme B binding the channel is completely locked. This is consistent with an ordered ternary complex kinetic mechanism displayed by the enzyme (Bonacker et al., 1993).

Coenzyme B is able to penetrate the 30-Å-long channel only with its aliphatic arm and its arm is not long enough for its thiol group at the end to reach the Ni of Fγ30. A distance of 8.7 Å remains. A direct reaction of the coenzyme B thiol group with nickel, as has previously been proposed (Jaun, 1990; Berkessel, 1991), can therefore be excluded. Methyl-coenzyme M is, however, anchored in the active site to the protein matrix with its sulphonate group relative to the prosthetic group such that both the methyl group and the thioether sulphur could directly interact with the Ni(II). In the MCRox1.silent structure, coenzyme M probably mimics the binding position of methyl-coenzyme M with respect to the binding mode of the sulphonate moiety but
presumably not with respect to the binding mode of the thiol group. A Ni-S-CoM intermediate in the catalytic cycle is not attractive because of the long distance of 6.2 Å between the sulphurs of coenzyme M and coenzyme B. Model building studies indicate, however, that the two sulphurs of coenzyme M and coenzyme B come in van der Waal's contact when the methyl group of methyl-coenzyme M is placed in van der Waal's distance of the potentially attacking nickel (Fig. 11a) (Ermler et al., 1997b). Therefore, a Ni-CH₃ intermediate proposed from free coenzyme F₄₃₀ studies (Lin & Jaun, 1991; Jaun, 1993) appears to be compatible with the steric requirements of the active site.

From the structure of the enzyme-substrate complex shown in Fig. 11(a) it is evident that the H⁺ required for methane formation from methyl-coenzyme M is lastly provided by coenzyme B. The MCR₁看一下结构 reveals an interaction between the thiol group of coenzyme B and two hydrogen donors, the amide and peptide nitrogen of Asn₄₁₈ and Val₄₈₉, which would facilitate the cleavage of the H⁺ and permit the presence of a thiolate anion. However, the coenzyme B sulphur is probably too far away from the methyl group of methyl-coenzyme M for direct hydrogen transfer. Tyr₃₃₅ and Tyr₈₆₇ are positioned in the active site such that they could mediate this transfer (Ermler et al., 1997b).

The structure of the enzyme-product complex shown in Fig. 11(b) considers that the heterodisulphide cannot leave the enzyme when the sulphonate oxygen of the coenzyme M moiety binds to the Ni(II) atom of F₄₃₀ as in the MCR₁看一下 state. Coordination of the sulphonate oxygen to nickel is prevented when nickel is present as nucleophilic Ni(I) (Jaun, 1993; Telser et al., 1997). The repulsion between Ni(I) and the sulphonate oxygen might even be used as a driving force to push the heterodisulphide out of the channel. It is not evident at present where, and how the methane gets out (Ermler et al., 1997b).

Both mechanisms of the conversion of the enzyme-substrate complex (Fig. 11a) to the enzyme-product complex (Fig. 11b) in the following to be discussed are based on the assumption that the methyl group of methyl-coenzyme M is transferred to Ni(I) of the prosthetic group before being reduced to methane and that the methyl group of methyl-coenzyme M has to be somehow activated in order that the transfer to Ni(I) F₄₃₀ can proceed (Jaun, 1993).

**Mechanism 1**

It is assumed that methyl transfer from methyl-coenzyme M to Ni(I) yields CH₃-Ni(III) F₄₃₀ involving protonation of methyl-coenzyme M by Tyr₃₃₅ or Tyr₈₆₇ to the sulphonium cation in the transition state. A precedent for such a protonation is found in the crystal structures of *ortho*-hydroxyphenyl- or *ortho*-hydroxybenzyl thioethers, giving rise to 5- and 6-membered rings, respectively, but also in the crystal structures of 3,4-dihydro-6-hydroxy-4,5,7,8-pentamethyl-2H-1-(benzothio)pyran (d S-H = 2.55 Å, O-H-S = 148 °) (Burton et al., 1985) and 2,3,7,8-tetrahydroxythianthrene (d S-H = 2.53 Å, O-H-S = 167 °) (Mansel & Klar, 1992). The H⁺ would be replenished by the dissociation of coenzyme B.

\[
\text{CH}_3\text{-S-CoM} + \text{H}^+ + \text{Ni(I)} \rightarrow \text{CH}_3\text{-Ni(III) F}_{430} + \text{H-S-CoM}
\]

\[
\text{H-S-CoB} \rightarrow \text{H}^+ + \text{S-CoB}
\]

The CH₃-Ni(III) F₄₃₀ formed by methylation of Ni(I) F₄₃₀ with methyl-coenzyme M is a strong one-electron oxidant and is therefore predicted to oxidize the protonated leaving group to the coenzyme M thyl radical cation.

\[
\text{CH}_3\text{-Ni(III) F}_{430} + \text{H-S-CoM} \rightarrow \text{CH}_3\text{-Ni(II) F}_{430} + \text{H-S-CoM}^+
\]
Reduction of a thioketone to the corresponding thio-ketyl with the disulphide radical anion should be in hydrogen bond interaction with both the coenzyme B yields CH,-Ni(I1) F430 rather than CH3-Ni(II1) in radical reactions (Jaun, 1993). Methylation that are also consistent with most of the findings. Only one alternative is discussed here. It considers that Ni(1) should quench the MCRred, EPR signal rather than methyl-coenzyme M in the absence of coenzyme B. The catalytic cycle in the alternative mechanism is therefore assumed to start with the formation of the coenzyme B thiol radical by one electron oxidation of coenzyme B.

\[ \text{CH}_3 \text{-CoB} + \text{X} \rightarrow \text{S-CoB} + \text{XH} \]

The electron acceptor X cannot be Ni(II) F430 as has been proposed since the enzyme is only active in its Ni(I) reduced form (Goubeaud et al., 1997). Therefore, there must be a second redox active group capable of oxidizing coenzyme B to the coenzyme B thyl radical, and indeed there is evidence for two independent redox active groups in methyl-coenzyme M reductase (Rospert, 1991; Rospert et al., 1992). This group could be the modified Gly445, a thio glycine, which interacts with the thiol group of coenzyme B via the side chain nitrogen of Asn441 and which could be susceptible to reduction to the thiolyl radical X- (Buckel & Keese, 1995; Buckel, 1996). Probably the protonated thioketone would be reduced to the protonated thiolyl (XH) since this reaction is energetically more favourable as deduced from the thermodynamics of the reduction of ketones to ketyl in the protonated and unprotonated forms (Lenz & Giese, 1997).

The coenzyme B thyl radical would react with methyl-coenzyme M, generating the above-mentioned sulphuranyl radical. From the sulphuranyl radical, the methyl radical would be transferred to Ni(1) generating the heterodisulphide and CH3-Ni(II) F430, which would protonolyse to Ni(II) F430 and CH4.

Mechanism 1 has several features in common with that proposed for ribonucleotide reductase (Lenz & Giese, 1997).

An argument against mechanism 1 is that it predicts that methyl-coenzyme M in the absence of coenzyme B should quench the MCRred EPR signal rather than stabilize it (Rospert et al., 1992; Goubeaud et al., 1997).

**Mechanism 2**

One can hypothesize alternative catalytic mechanisms that are also consistent with most of the findings. Only one alternative is discussed here. It considers that Ni(I) F430 with its unpaired electron is a radical and is most reactive in radical reactions (Jaun, 1993). Methylation of Ni(I) F430 with most methyl donors thus directly yields CH3-Ni(II) F430 rather than CH2-Ni(III) F430 (Lin & Jaun, 1991; Jaun, 1993). For methyl-coenzyme M to react with Ni(I) F430 in this manner, it has to be activated such that a homolytic cleavage of the S-methyl bond is favoured, e.g. by reaction of methyl-coenzyme M with the coenzyme B thyl radical to the CoM-S(CH3)-S-CoB sulphuranyl radical (Jaun, 1990; Berkessel, 1991; Tada & Masuzawa, 1997).

\[ \text{CH}_3 \text{-CoM} + \text{X} \rightarrow \text{S-CoB} \rightarrow \text{CoM-S-(CH}_3\text{)-S-CoB} \]

The electron acceptor X cannot be Ni(II) F430 as has been proposed since the enzyme is only active in its Ni(I) reduced form (Goubeaud et al., 1997). Therefore, there must be a second redox active group capable of oxidizing coenzyme B to the coenzyme B thyl radical, and indeed there is evidence for two independent redox active groups in methyl-coenzyme M reductase (Rospert, 1991; Rospert et al., 1992). This group could be the modified Gly445, a thio glycine, which interacts with the thiol group of coenzyme B via the side chain nitrogen of Asn441 and which could be susceptible to reduction to the thiolyl radical X- (Buckel & Keese, 1995; Buckel, 1996). Probably the protonated thioketone would be reduced to the protonated thiolyl (XH) since this reaction is energetically more favourable as deduced from the thermodynamics of the reduction of ketones to ketyl in the protonated and unprotonated forms (Lenz & Giese, 1997).

The catalytic cycle in the alternative mechanism is therefore assumed to start with the formation of the coenzyme B thyl radical by one electron oxidation of coenzyme B.

\[ \text{H-S-CoB} + \text{X} \rightarrow \text{S-CoB} + \text{XH} \]

The electron acceptor X cannot be Ni(II) F430 as has been proposed since the enzyme is only active in its Ni(I) reduced form (Goubeaud et al., 1997). Therefore, there must be a second redox active group capable of oxidizing coenzyme B to the coenzyme B thyl radical, and indeed there is evidence for two independent redox active groups in methyl-coenzyme M reductase (Rospert, 1991; Rospert et al., 1992). This group could be the modified Gly445, a thio glycine, which interacts with the thiol group of coenzyme B via the side chain nitrogen of Asn441 and which could be susceptible to reduction to the thiolyl radical X- (Buckel & Keese, 1995; Buckel, 1996). Probably the protonated thioketone would be reduced to the protonated thiolyl (XH) since this reaction is energetically more favourable as deduced from the thermodynamics of the reduction of ketones to ketyl in the protonated and unprotonated forms (Lenz & Giese, 1997).

**From hydrogenase to methyl-coenzyme M reductase**

It has been a long way from the first demonstration of an enzyme, of hydrogenase, in methanogens in 1933 by Stephenson & Stickland (1933a) to the crystal structure of methyl-coenzyme M reductase in 1997 and there is still a good way to go until the biochemistry of methanogenesis is completely understood. Many ques-
tions remain to be answered. For methyl-coenzyme M reductase, the most pertinent questions are, what functions do the five amino acid modifications in the enzyme have and how are these modifications brought about? The answers to these questions could be the key to the understanding of the catalytic mechanism of the methane-forming enzyme. Fortunately, recently a genetic system for archaea of the genus *Methanosarcina* has become available (Metcalf et al., 1997) now allowing these problems to be also tackled with genetic methods.

The work of my group on the biochemistry of methane genesis started with growth experiments and the discovery that growth of methanogens is dependent on nickel (Schönheit et al., 1979). This led to the finding that coenzyme F₄₃₀ is a nickel porphinoid (Diekert et al., 1980a, b), that carbon monoxide dehydrogenase from methanogens contains nickel (Hammel et al., 1984) and that the hydrogenases first described by Marjory Stephenson (Stephenson & Stickland, 1931a) are nickel enzymes (Graf & Thauer, 1981; Albracht et al., 1982; Albracht, 1994) (for recent reviews on nickel enzymes including methyl-coenzyme M reductase see Cammack & van Vliet, 1998; Maroney et al., 1998). Later we found that methanogens also contain a metal-free hydrogenase (Zirngibl et al., 1990; Thauer et al., 1996) and just recently that methanogens contain a fourth type of hydrogenase (Künkel et al., 1998) that shows sequence similarity to hydrogenase 3 (Sauter et al., 1997) and 4 (Andrews et al., 1997) of the formate hydrogenylase from *E. coli*, an enzyme complex first studied in detail in the laboratory of Marjory Stephenson now almost 70 years ago (Stickland, 1929; Stephenson & Stickland, 1932, 1933b; Woods, 1936). With respect to my research, I, therefore, feel myself in the scientific tradition of Marjory Stephenson. And there is even a genealogical connection: I learned to grow methanogens from Greg Zeikus when he was in Marburg for a sabbatical (Zeikus et al., 1977). He himself had obtained his training from Ralph Wolfe in Urbana (Zeikus & Wolfe, 1972), who discovered methyl-coenzyme M reductase (Wolfe, 1991). The first work of Ralph Wolfe on methanogens is together with Sidney Eldsen (Knight et al., 1966), who had been a student of Marjory Stephenson in the Cambridge Biochemistry Laboratory (Wolfe, 1991) where in 1933 the modern era of methanogenesis began (Wolfe, 1993). I am therefore very much indebted to the Society for General Microbiology for having chosen me to give the 1998 Marjory Stephenson Lecture.

Acknowledgements

This work was supported by the Max-Planck-Gesellschaft, the Deutsche Forschungsgemeinschaft and by the Fonds der Chemischen Industrie. I want to thank Sidney Eldsen and Hans-Günter Schlegel for providing me with literature on M. Stephenson.

References


Becher, B., Müller, V. & Gottschalk, G. (1992b). N₅-methyltetrahydrodihydronitrosothiopurin reductase coenzyme M methyltransferase of...


Crane, B. R., Siegel, L. M. & Getzoff, E. D. (1997a). Structures of the sioheme- and Fe-4S-4-containing active center of sulfite reductase in different states of oxidation: heme activation via...


roles of methylcobamide: coenzyme M methyltransferase iso-
zymes in metabolism of methanol and methylamines in Meth-


H₂ conversion rates in H₂O and D₂O. J Biol Inorg Chem 1, 446–450.


Klein, A. R. & Thauer, R. K. (1995). Re-face specificity at C14a of methylenetetrahydromethanopterin and Si-face specificity at C5 of coenzyme F₄₃₀ for coenzyme F₄₃₀-dependent methylene-


2402


