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.

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

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

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

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

Cell suspensions of the micro-organism catalysed the reduction of methylene blue with H,, indicating that the methanogen contained an enzyme which activates molecular hydrogen.

\[
\text{H}_2 \rightarrow 2\text{e}^- + 2\text{H}^+ \quad E_0' = -414 \text{mV}
\]

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 CO, the cell suspensions of the methanogen isolated by Stephenson & Stickland (1933a) catalysed the reduction of carbon monoxide, formaldehyde (added as hexamethylenetetramine) and methanol to methane with H,, albeit at much lower rates than the reduction of CO,. 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 H, to H,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, 1951). 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. Kluyver (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 the book on Methanogenesis: Ecology, Physiology, Biochemistry & Genetics edited by Ferry (1993a), to the 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 10⁸ 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. The concentration of atmospheric methane has increased steadily during the last 300 years from 0.7 p.p.m. to 1.7 p.p.m., owing probably in large part to the expanded cultivation of rice and ruminant livestock. 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 catabolic 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: Methanobacteriales, Methanococcales, Methanomicrobiales, Methanopyrales and Methanosaicales. Of these, only the Methanosarcinales can ferment acetate to CO₂ and CH₄ and grow on methanol, methylthioles or methylamines as sole energy source. In turn, hyperthermophilic species are only found among the Methanobacterales, Methanococcales and Methanopyrales (Boone et al., 1993).

The DNA sequence of the total genome has, until now, been determined for two methanoarchaea, for Methanococcus jannaschii (Bult et al., 1996) and for Methanobacterium thermoautotrophicum (strain ΔH) (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.

\[
\begin{align*}
\text{Glucose} & \rightarrow 3\text{CO}_2 + 3\text{CH}_4 \quad \Delta G^\circ = -418.1 \text{ kJ mol}^{-1} \\
\text{Glucose} + 2\text{H}_2\text{O} & \rightarrow 2\text{CH}_3\text{COO}^- + 2\text{H}^+ + 2\text{CO}_2 + 4\text{H}_2 \quad \Delta G^\circ = -215.7 \text{ kJ mol}^{-1} \\
\text{Glucose} + 2\text{H}_2\text{O} & \rightarrow 2\text{CH}_3\text{COO}^- + 2\text{HCOO}^- + 4\text{H}^+ + 2\text{H}_2 \quad \Delta G^\circ = -208.7 \text{ kJ mol}^{-1}
\end{align*}
\]

These fermentations are brought about by strictly anaerobic bacteria and/or protozoa. In a second step, the products of glucose fermentation are then converted to methane, the rate of conversion being such that the concentrations of acetate (< 1 mM), formate (< 0.1 mM) and H₂ (< 1 μM) in the anaerobic sediments remain very low (Zinder, 1993).

\[
\begin{align*}
\text{CH}_3\text{COO}^- + \text{H}^+ & \rightarrow \text{CO}_2 + \text{CH}_4 \quad \Delta G^\circ = -36 \text{ kJ mol}^{-1} \\
4\text{H}_2 + \text{CO}_2 & \rightarrow \text{CH}_4 + 2\text{H}_2\text{O} \quad \Delta G^\circ = -131 \text{ kJ mol}^{-1} \\
4\text{HCOO}^- + 4\text{H}^+ & \rightarrow \text{CH}_4 + 3\text{CO}_2 + 2\text{H}_2\text{O} \quad \Delta G^\circ = -144.5 \text{ kJ mol}^{-1}
\end{align*}
\]
**Table 1.** Reactions and enzymes known to be involved in methane formation from acetate in the *Methanosarcinales* (Ferry, 1993b, 1995, 1997a)

<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 thio kinase (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</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 → CH₃S-CoM + H₂SPT</td>
<td>Methyl-H₂SPT: coenzyme M methyltransferase (energy conserving) (mtrEDCBAFGH)</td>
<td>Fischer et al. (1992); Lu et al. (1995); Lienard et al. (1996); Lienard &amp; Gottschalk (1998)</td>
</tr>
<tr>
<td>CH₃S-CoM + H₂S-CoB → CoM-S-CoB + CH₃</td>
<td>Methyl-coenzyme M reductase</td>
<td>Thauer et al. (1993); Springer et al. (1995)</td>
</tr>
<tr>
<td>CoM-S-CoB + 2[H] → H₂S-CoM + H₂S-CoB</td>
<td>Heterodisulphide reductase (bdrDE)</td>
<td>Heiden et al. (1993); Peer et al. (1994); Künel et al. (1998)</td>
</tr>
<tr>
<td>CO₂ + 2[H] → 2H⁺ + 2e⁻</td>
<td>H₂S-CoM + H₂S-CoB</td>
<td>From Thauer et al. (1977).</td>
</tr>
<tr>
<td><strong>ΔG°v</strong> values add up to -38 kJ mol⁻¹, which is very similar to the <strong>ΔG°v</strong> = -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.</td>
<td>From Thauer et al. (1977).</td>
<td></td>
</tr>
<tr>
<td>† From Thauer (1990); CO₂ in the gaseous state at 10⁵ Pa. <strong>E°v</strong> was determined by Grahame &amp; DeMoll (1995) to be -270 mV and <strong>ΔG°v</strong> 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 <strong>ΔG°v</strong> = +41.3 kJ mol⁻¹ appears unrealistically endergonic. Note, however, that in the reaction four products are formed from two substrates. <strong>ΔG°v</strong> is thus highly concentration dependent. At 0.1 mM concentrations of all substrates and products (pH₅ = 10 Pa), <strong>ΔG°v</strong> = -26.6 kJ mol⁻¹ and <strong>E°v</strong> = -430 mV (Thauer, 1990).</td>
<td>‡ From Thauer (1990); CO₂ in the gaseous state at 10⁵ Pa. <strong>E°v</strong> was determined by Grahame &amp; DeMoll (1995) to be -270 mV and <strong>ΔG°v</strong> 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 <strong>ΔG°v</strong> = +41.3 kJ mol⁻¹ appears unrealistically endergonic. Note, however, that in the reaction four products are formed from two substrates. <strong>ΔG°v</strong> is thus highly concentration dependent. At 0.1 mM concentrations of all substrates and products (pH₅ = 10 Pa), <strong>ΔG°v</strong> = -26.6 kJ mol⁻¹ and <strong>E°v</strong> = -430 mV (Thauer, 1990).</td>
<td></td>
</tr>
<tr>
<td>§ The nickel iron-sulphur corrinoid enzyme is isolated from <em>Methanosarcina</em> spp. as a multienzyme complex composed of five different subunits (Grahame &amp; DeMoll, 1996; Maupin-Furlow &amp; Ferry, 1996a, b); ferredoxin appears to be the physiological electron acceptor (Fischer &amp; Thauer, 1990; Peer et al., 1994; Ferry, 1995, 1997a). The encoding genes in <em>Methanosarcina thermophila</em> are organized in a transcription unit, cdhABCXDE, X being an open reading frame of unknown function (Maupin-Furlow &amp; Ferry, 1996b). CdHA and CdHB are predicted to be nickel iron-sulphur proteins and CdHD and CdHE to harbour the corrinoid prosthetic group.</td>
<td>§ From Weiss et al. (1994).</td>
<td></td>
</tr>
<tr>
<td><strong>²</strong> From Thauer et al. (1993).</td>
<td><strong>²</strong> From Thauer et al. (1993).</td>
<td></td>
</tr>
<tr>
<td>†† Membrane-associated enzyme purified from methanol-grown <em>Methanosarcina bacteri</em> 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 EchABCDFE, Ech being an E. coli hydrogenase-3-type hydrogenase (Künkel et al., 1998). HdrE is a b-type cytochrome (Künkel et al., 1997, 1998).</td>
<td>†† Membrane-associated enzyme purified from methanol-grown <em>Methanosarcina bacteri</em> 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 EchABCDFE, Ech being an E. coli hydrogenase-3-type hydrogenase (Künkel et al., 1998). HdrE is a b-type cytochrome (Künkel et al., 1997, 1998).</td>
<td></td>
</tr>
</tbody>
</table>

H-S-CoM, coenzyme M; H-S-CoB, coenzyme B; H₂SPT, tetrahydrocorrinapterin, which is the modified tetrahydromethanopterin (for structures see Fig. 3) present in the *Methanosarcinales* (Gorris & van der Drift, 1994).

**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)

<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 (<em>fwdHFGDACB and fmdECB</em>§)</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>Methenyl-H₃MPT* + H⁺ → methylene-H₃MPT + H₂</td>
<td>H₂-forming methylene-H₃MPT dehydrogenase (<em>hmd</em>)</td>
<td>Schwöer et al. (1993b); Schleicher et al. (1994, 1995); Klein et al. (1995a, b); Berkesell &amp; Thauer (1995); Hartmann et al. (1996a, b); Thauer et al. (1996)</td>
</tr>
<tr>
<td>Methylene-H₃MPT + F₄₂₀H₂ → CH₄ + H₂O</td>
<td>F₄₂₀-dependent methylene-H₃MPT reductase (<em>mer</em>)</td>
<td>Vaupel &amp; Thauer (1995); Nolling et al. (1995a); Kunow et al. (1993)</td>
</tr>
<tr>
<td>CH₃S-CoM + H₂ + S-CoM → CH₃S-CoM + H₂O</td>
<td>Methyl-coenzyme M reductase (<em>mcrBDCGA and mtrBDGA</em>)**</td>
<td>Bonacker et al. (1993); Goubeaud et al. (1997); Shima et al. (1997); Ermler et al. (1997b); Becker &amp; Ragsdale (1998)</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 10⁶ Pa.

‡ Calculated for 2[H] = 1H₂ at 10⁶ 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 (Kasler & Schönheit, 1989a, b).

§ *fwd* denotes the genes encoding the tungsten enzyme and *fmd* the molybdienzyme 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 + F₄₂₀ → F₄₂₀H₂; ΔG° = −11 kJ mol⁻¹; the E⁰ 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).
to consist of two parts (Fig. 1): an oxidative part in which coenzyme M (H-S-CoM, 2-thioethanesulphonate) and coenzyme B (H-S-CoB, 7-thioheptanoyloxytrione-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).

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

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), N₅-, méthylethyltrahydrodormethanopterin (CH₂₃-H₄MPT) or N₅-, méthylethyltrahydrosarcinapterin (CH₂₃-H₅SPT) 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: tetrahydrosarcinapterin in the *Methanosarcinales* and *Methanococcales* and tathioprin and/or thiotrimerin 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 \(\Delta G^{\text{rev}} = -30 \text{ kJ mol}^{-1}\) 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 \((\Delta G^{\text{rev}} = +31.8 \text{ kJ mol}^{-1})\) (Thauer et al., 1977). The reduction of the heterodisulphide with acetyl-CoA \((\Delta G^{\text{rev}} = +0 \text{ kJ mol}^{-1})\) (calculated from \(E_0^\text{rev}\) values given in Table 1) and with 2-propanol \((\Delta G^{\text{rev}} = -15 \text{ kJ mol}^{-1})\) 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 \((\Delta G^{\text{rev}} = -19 \text{ kJ mol}^{-1})\) is also 'pushed' by the preceding reaction, the irreversible hydrolysis of arginine to citrulline and NH₃ \((\Delta G^{\text{rev}} = -37.7 \text{ kJ mol}^{-1})\) (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).

---

†† From Weiss et al. (1994).

* Membrane-associated multi-enzyme complex composed of eight different subunits, MtrA–H, MtrA harbouring a corrinoid prosthetic group (Harms et al., 1995). Energy conservation proceeds via an electrochemical Na⁺ potential (Gätterl et al., 1994). For literature on the enzyme complex from *Methanosarcina* spp., see Table 1.

* mcr denotes the genes encoding the iso-enzyme 1 and mrt the iso-enzyme II. Both iso-enzymes are isolated as multi-enzyme complexes composed of three different subunits, McrABG or MrtABG, in an \(\alpha_2\beta_2\gamma_2\) configuration. For literature on the enzyme complex from *Methanosarcina* spp., see Table 1.

‡‡ Calculated for [H] = H₂ at 10⁵ Pa.

### Table 1

<table>
<thead>
<tr>
<th>Substrate</th>
<th>Energy Change (kJ mol⁻¹)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Acetate</td>
<td>-34</td>
</tr>
<tr>
<td>Formate</td>
<td>-43.5</td>
</tr>
<tr>
<td>Ethanol</td>
<td>-35</td>
</tr>
<tr>
<td>Methanol</td>
<td>-34</td>
</tr>
</tbody>
</table>

**References**

1. *Methanobacterium thermoautotrophicum* (AGO' configuration. For literature on the enzyme complex from *Methanosarcina* spp., see Table 1.

2. The enzyme is purified from *Methanobacterium thermoautotrophicum* in a complex with the F₄₃0 non-reducing hydrogenase (Setzke et al., 1994).

3. From Weiss et al. (1994).

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Marjory Stephenson Prize Lecture

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2381
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:

\[ H_2 + 2e^- + 2H^+ \rightarrow 2H_2 \]

\[ 2e^- + 2H^+ + CoM-S-S-CoB \rightarrow H-S-CoM + H-S-CoB \]

\[ E'_o = -200 \text{ mV} \]

---

**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>CH₃OH + H₂ → CH₄ + H₂O</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Δ𝐺° = −27.5 kJ mol⁻¹</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CH₃-S-CoM + H₂ → CH₄ + H₂CO</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Δ𝐺° = −45 kJ mol⁻¹</td>
<td></td>
<td></td>
</tr>
<tr>
<td>H2C=S-CoM + 2[H] → CH₄ + H₂CO</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>CH₃OH + H₂ → CH₃-S-CoM + H₂O</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Δ𝐺° = −27.5 kJ mol⁻¹</td>
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<tr>
<td>CH₃-S-CoM + H₂ → CH₄ + H₂O</td>
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<tr>
<td>Δ𝐺° = +30 kJ mol⁻¹</td>
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<tr>
<td>CH₃OH + H₂SPT → CH₃H₂SPT + H₂O</td>
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<tr>
<td>Δ𝐺° = +2.5 kJ mol⁻¹</td>
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<tr>
<td>CH₃H₂SPT + F₄20 →</td>
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</tr>
<tr>
<td>methyl-H₂SPT + F₄20H₂</td>
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<tr>
<td>Δ𝐺° = +6.2 kJ mol⁻¹</td>
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<tr>
<td>methyl-H₂SPT + F₄20H₂ +</td>
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<tr>
<td>H⁺ → methyl-H₂SPT + F₄20H₂</td>
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</tr>
<tr>
<td>Δ𝐺° = −5 kJ mol⁻¹</td>
<td></td>
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</tr>
<tr>
<td>Methenyl-H₂SPT + H₂O →</td>
<td></td>
<td></td>
</tr>
<tr>
<td>formyl-H₂SPT + H⁺</td>
<td></td>
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</tr>
<tr>
<td>Δ𝐺° = +46 kJ mol⁻¹</td>
<td></td>
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<tr>
<td>Formyl-H₂SPT + MFR →</td>
<td></td>
<td></td>
</tr>
<tr>
<td>formyl-MFR + H₂SPT</td>
<td></td>
<td></td>
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<tr>
<td>Δ𝐺° = +4.4 kJ mol⁻¹</td>
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<tr>
<td>Formyl-MFR → CO₂ + MFR + 2[H]</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Δ𝐺° = −16 kJ mol⁻¹</td>
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</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 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 E° 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 polyferrodoxin (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.
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 thermoautotrophicum (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 Nölling 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) F₁₂₀-reducing Ni/Fe-hydrogenase (Vaupel & Thauer, 1998); (ii) F₁₂₀ non-reducing hydrogenase of unknown physiological electron acceptor — in Methanobacteria spp., one of the subunits from the enzyme is a cytochrome b (Deppenmeier, 1995; Deppenmeier et al., 1995; Kumazawa et al., 1994; Kenner & 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 F420 and the oxidation of F420H2 in the energy metabolism of methanogenic archaea

F420 is a 5’ deazaflavin derivative found in relatively high concentration in methanogenic archaea (Gorris & van der Drift, 1994). F420 in methanogens is converted to inactive F420P by denylation and F420 to F430 by deamination 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>1. Reduction of F420</td>
<td></td>
<td></td>
</tr>
<tr>
<td>F420-reducing hydrogenase</td>
<td>All hydrogenotrophic methanogens</td>
<td>Sorgenfrei et al. (1997a, b); Vaupel &amp; Thauer (1998); Nolling &amp; Reeve (1997); Grahame &amp; Stadman (1993)</td>
</tr>
<tr>
<td>F420-dependent formate dehydrogenase</td>
<td>Methanogens growing on formate</td>
<td>Keltjens &amp; Vogels (1993)</td>
</tr>
<tr>
<td>F420-dependent methylene-H4,MPT dehydrogenase</td>
<td>Methanogens growing on methanol, methylthiols or methamines</td>
<td>Thauer et al. (1996); Afting et al. (1998)</td>
</tr>
<tr>
<td>F420-dependent methylene-H4,MPT reductase</td>
<td>Methanogens growing on methanol, methylthiols or methamines</td>
<td>Klein et al. (1996); Widdel &amp; Frimmer (1995); Berk et al. (1996)</td>
</tr>
<tr>
<td>H2-forming methylene-H4,MPT dehydrogenase plus F420-dependent methylene-H4,MPT dehydrogenase</td>
<td>Most hydrogenotrophic methanogens of the orders Methanobacterales, Methanococcales and Methanopyrales</td>
<td>Berk et al. (1996); Thauer et al. (1996); Widdel &amp; Frimmer (1995)</td>
</tr>
<tr>
<td>F420-dependent alcohol dehydrogenase</td>
<td>Methanogenium liminatans, Methanoculleus thermophilicus, Methanococcus organophilum, Methanobacterium palustre, Methanocorpusculum spp.</td>
<td>See Table 2</td>
</tr>
<tr>
<td>NADP-dependent alcohol dehydrogenase plus F420-dependent NADP reductase</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

2. Oxidation of F420H2

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Organism</th>
<th>Most recent literature</th>
</tr>
</thead>
<tbody>
<tr>
<td>F420-dependent methylene-H4,MPT dehydrogenase</td>
<td>Methanogens reducing CO2 to methane</td>
<td>See Table 2</td>
</tr>
<tr>
<td>F420-dependent methylene-H4,MPT reductase</td>
<td>Methanogens reducing CO2 to methane</td>
<td>Haase et al. (1992); Abken &amp; Deppenmeier (1997); Abken et al. (1998a, b)</td>
</tr>
<tr>
<td>F420H2 dehydrogenase complex</td>
<td>Methanosarcina mazei, Methanolobus tindarius</td>
<td>Vaupel (1993)</td>
</tr>
<tr>
<td>F420-dependent hydrogenase</td>
<td>Methanogens of the orders Methanococcales and Methanobacterales growing on formate and lacking F420H2, dehydrogenase complex</td>
<td></td>
</tr>
</tbody>
</table>

Hedderich et al., 1992; Nolling et al., 1995c) or a 45 kDa flavoprotein (Wasserfallen et al., 1995; Nolling et al., 1995c); (iii) Escherichia coli hydrogenase-3-type Ni/Fe-hydrogenase of unknown physiological electron acceptor (Kinkel et al., 1998); and (iv) a metal-free hydrogenase, the H2-forming methyleneetetrahydro-methanopterin dehydrogenase, which together with the F420-dependent methyleneetetrahydro-methanopterin dehydrogenase catalyses the reduction of F420 with H2 (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 dehydrogenases can be involved in heterodisulphide reduction with H2: with inside-out vesicles from Methanosarcina mazei it has been shown that both F420-dependent (Deppenmeier et al., 1990a, b) and F420-independent (Deppenmeier et al., 1991) reduction of the heterodisulphide with H2 are coupled with the phosphorylation of ADP (Deppenmeier et al., 1996; Abken et al., 1998a, b).

**Heterodisulphide reduction with F420H2**

Cell extracts of Methanosarcina mazei and of Methanolobus tindarius catalyse the reduction of heterodisulphide with reduced F420, the coenzyme of many dehydrogenases in methanogenic archaea (Table 4). (F420 is a 5’ deazaflavin derivative with an E° = −360 mV present in relatively high concentrations in these organisms; Gorris & van der Drift, 1994). For the reduction of the heterodisulphide with F420H2, 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 F420H2 dehydrogenase complex catalysing
the reduction of methanophenazine with F_{430}H_2, the reduction being coupled with phosphorylation of ADP (Abken et al., 1998a, b; Bämmer et al., 1998). Such an F_{430}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 F_{430}H_2 dehydrogenase complex and not growing on H_2 and CO_2, heterodisulphide reduction with F_{430}H_2 probably proceeds via H_2 as intermediate (Vaupel, 1993).

**Coupling with ATP synthesis**

As indicated, methyl transfer from NAD-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 A_5A_3 ATPase (Wilsms et al., 1996; Inatomi, 1996; Ruppert et al., 1998) and there is indirect evidence also for the presence of an Na^+-translocating F_5F_0 ATPase (Becher & Müller, 1994). *Methanobacterium* spp. and *Methanococcus* spp. harbour only one A_5A_3 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 [g (mol CH_4)^{-1}] increases with decreasing H_2 concentrations (Schönheit et al., 1980; Morgan et al., 1997; for regulation see Pihl et al., 1994; Nölling et al., 1995a, b; Nölling & 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 kJ mol^{-1} at 10^5 Pa H_2 to only approximately -30 kJ 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-oxoglutarate, 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_2S 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_8/H_2S couple and that of the heterodisulphide/H-S-CoM + H-S-CoB couple are both in the order of -200 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 methylotrophic z 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-methanogens, 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 and H-S-CoB to succinate and CoM-S-S-CoB (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)

<table>
<thead>
<tr>
<th>Reaction</th>
<th>Enzyme system</th>
<th>Most recent literature</th>
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<tbody>
<tr>
<td>CH₂H₂MTP + H-S-CoM → CH₃-S-CoM + H₂MTP</td>
<td>N⁵-Methyl-H₂MTP: coenzyme M methyltransferase (energy conserving)</td>
<td>Supperich et al. (1993); Gärtner et al. (1993, 1994); Weiss et al. (1994); Harms et al. (1995); Harms &amp; Thauer (1996a, 1997, 1998); Lu et al. (1995); Lienard et al. (1996); Lienard &amp; Gottschalk (1998)</td>
</tr>
<tr>
<td>CH₂NH₂ + H-S-CoM → CH₃-S-CoM + NH₃</td>
<td>Monomethylamine: coenzyme M methyltransferase</td>
<td>Burke &amp; Krzycki (1995, 1997); Burke et al. (1998)</td>
</tr>
<tr>
<td>CH₃-S-CoM + CH₃NH₂</td>
<td>Trimethylamine: coenzyme M methyltransferase (MtbA + MtmBC)†</td>
<td>Ferguson &amp; Krzycki (1997); Wassenaar et al. (1996)</td>
</tr>
<tr>
<td>(CH₃)₂NH + H-S-CoM → CH₃-S-CoM + (CH₃)₂NH₂</td>
<td>Tetramethylamine: coenzyme M methyltransferase (MtqA + MtqC)†</td>
<td>Asakawa et al. (1998); Tanaka (1994)</td>
</tr>
<tr>
<td>CH₃-S-CoM + CH₃-S-H</td>
<td>Methylthiol: coenzyme M methyltransferase§ (MtsAB)</td>
<td>Paul &amp; Krzycki (1996); Tallant &amp; Krzycki (1996)</td>
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</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 MtbB are zinc enzymes (Sauer & Thauer, 1997); MtC, MtmC, MtqC and MtsB have been shown to be corrinoid proteins harbouiring 6-hydroxybenzimidazolyl cobamide as prosthetic group.
‡ Obtained from ΔG° for the reaction of methane to methane with H₂ calculated from the free energies of formation from the elements tabulated in Thauer et al. (1977) and from ΔG° of −85 kJ mol⁻¹ for methyl-coenzyme M reduction with H₂ to CH₄ and coenzyme M (Thauer et al., 1993).
§ Also catalyses the methylation of coenzyme M with methylmercaptopropanol (95%), methylmercaptopropionate (80%), mercaptopropanol (10%), methylmercaptoethanol (8%) and methylidene (170%) (Tallant & Krzycki, 1997) and the methylation of mercaptoethanol (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-(methylene)propionate (Kₚ = 1.3 mM; Vₚmax = 1.3 μM mg⁻¹), ethyl-coenzyme M (Kₚ = 1.3 mM; Vₚmax = 7.4 μM mg⁻¹), methylseleno-coenzyme M (Kₚ = 0.3 mM; Vₚmax = 35 μM mg⁻¹) and difluoromethyl-coenzyme M (Kₚ = 2.5 mM; Vₚmax = 20 μM mg⁻¹) were reduced (methyl-coenzyme M: Kₚ = 0.1 mM; Vₚmax = 11 μM 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 (Kₚ = 8 μM) and 2-chloroethanesulphonate (Kₚ = 70 μM) (Gunsalus et al., 1978), 3-bromopropanesulphonate (Kₚ = 50 nM), 4-bromobutanesulphonate (Kₚ = 6 μM) and 2-azidoethanesulphonate (Kₚ = 1 μM).
It has been proposed and evidence has been reported that the physiological electron donor for methyl-coenzyme M reduction could possibly be a larger molecule which contains coenzyme B covalently bound through a mixed anhydride linkage to a sugar moiety (Sauer et al., 1990; Sauer, 1991). This is presently no longer considered to be very likely. Recently, methyl-coenzyme M reductase was isolated from *Methanobacterium thermoautotrophicum* under very mild conditions and then crystallized. The purified enzyme contained coenzyme B bound in its active site. In the crystal structure, the threonine phosphate moiety of coenzyme B could clearly be resolved. The phosphate group of the threonine phosphate moiety was not covalently bound to any other molecule (Ermiller 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 (Ellenson et al., 1982), which is a nickel porphinoid, 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 Methanoarchaeales) 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,
Methanobacteriales, the genes encoding the three sub-units 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\(^{\text{237}}\)), a histidine (1-N-methyl-His\(^{\text{227}}\)), a cysteine (S-methyl-Cys\(^{\text{102}}\)) and a glutamine (2-methyl-Gln\(^{\text{489}}\)) are methylated and instead of a glycine there appears to be a thioglycine (Gly\(^{\text{244}}\)) (Ermler et al., 1997b).

**Coenzyme F\(_{430}\): the prosthetic group of methyl-coenzyme M reductase**

The first report on coenzyme F\(_{430}\) (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\(_{430}\), in which it was incorporated, and that F\(_{430}\) contained mol\(^{-1}\) 1 mol nickel. In the same year, biosynthetic evidence was provided by Dietert et al. (1980b) that F\(_{430}\) 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\(_{430}\) is the prosthetic group of methyl-coenzyme M reductase (Ellefson et al., 1982). Until now, coenzyme F\(_{430}\) 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\(_{430}\). Nickel brings up to five number of different metals found in the centre of biological cyclic tetrapyrroles. Up to the discovery of F\(_{430}\), the different metals known to occur were iron in haems and in sirohaem, magnesium in chlorophylls, cobalt in corrinoids and copper in turacin, the pigment of turaco bird 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\(_{430}\) is by far the most highly reduced or saturated amongst all known tetrapyrroles (Fig. 6). Coenzyme F\(_{430}\) 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\(_{430}\) 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\(_{430}\) is derived from dihydro-sirohydrochlorin, which is also the biosynthetic precursor of sirohaem and B\(_{12}\) (Thauer & Bonacker, 1994; Hungerer et al., 1996).

**Coenzyme F\(_{430}\): properties relevant to the catalytic mechanism of methyl-coenzyme M reductase**

Coenzyme F\(_{430}\) 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\(_{430}\) 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\(_{12}\)) (Kräutler et al., 1998) (Fig. 7).

F\(_{430}\) as isolated in the Ni(II) oxidation state can be reduced to the Ni(I) oxidation state. In aqueous solution, the standard redox potential \(E^\circ\) 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 \(-640\) mV (Lexa & Saveant, 1983; Daas et al., 1995).

Ni(II) in \(F_{430}\) can be methylated with methyl iodide, methyltosylate or methylsulphonium ions (but not with methylthioethers) (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, 1992). 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)/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 \(0\) 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-
obcob(II)alamin with electron donors more positive than \(-650\) 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 stereocconfiguration (Lin & Jaun, 1992).

Methyl-Ni(II) \(F_{430}\) spontaneously protonolyses to yield CH₄ and Ni(II) \(F_{430}\) (Lin & Jaun, 1991). It is an electrophilic substitution which is predicted to proceed with retention of stereocconfiguration. To the contrary, methylcob(II)alamin dissociates to a methyl radical and cob(II)alamin rather than to protonolys 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 methylcob(II)reductase catalyses the reduction of the methyl group of methyl-coenzyme M to methane with inversion of stereocconfiguration, 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* ΔH requires the addition of at least two proteins, designated A2 and A3a, 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.

\[
\text{MCR (inactive)} \xrightarrow{\Delta H} \text{MCR (0.1% active)}
\]

\[
\text{Ti(III), pH 7} \xrightarrow{\text{ATP}} \text{MCR (0.1% active)}
\]

The sequence of *atu*, the A2-encoding gene, predicts that A2 is a 59 kDa ATP-binding protein related to the ABC family of proteins that participates in energy-dependent transport processes (Kuhner et al., 1993).

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 proteins, ATP and an electron donor), the inactive enzyme was incubated with [methyl-\(^{14}H\), thio-\(^{35}S\)]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 CH₄ (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 all the MCR molecules present must have been activated under the assay conditions. The finding that only 0.1% of the maximal possible specific activity was reached (see above) and that it took more than 100 turnovers for 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, A₃α 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 inactive methyl-coenzyme M reductase preparations contained F₄₃⁰ in the Ni(II) oxidation state.

A first breakthrough was the finding that the specific activity of methyl-coenzyme M reductase was 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 MCRred₁ 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 MCRox₁ 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).

\[ \text{MCRox₁ (inactive)} \rightarrow \text{MCRred₁ (100% active)} \]

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 F₄₃⁰ 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 MCRred₂ 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 reductase 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 MCRoxl-silent, MCRred2-silent,
MCRoxl-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(II) 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 crystallized 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
Camnack, 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 α and α' and subunits β and β', and by
the fact that, except for subunits γ and γ', each subunit
contacts all other subunits of the multisubunit complex
(Ermel 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 (Ermel et al., 1997b).

Binding of coenzyme F₄₃₀

F₄₃₀ is bound at the bottom of the 30-Å-long channel
such that its tetrapyrole 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 dihydrosiro-
hydrochlorin, is only accessible from the rear face
(Crane et al., 1995, 1997a, b). The tetrapyrole 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 tetrapyrole plane and is coordinated to
six ligands arranged in a nearly optimal octahedral
configuration. The four equatorially located nitrogen
atoms of the tetrapyrole ring have distances to the
corectetrapyrrole plane of F₄₃₀ is bound to 1.2 Å for ring
A, 1.2 Å for ring B, 1.9 Å for ring C and 1.2 Å for ring D (Fig.
8). As the fifth ligand the side chain oxygen of Glu147 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 Glu147 is the axial ligand (Ermel et al.,
1997b) as to be expected thermodynamically and as seen
also in other proteins (Roach et al., 1997). Glu147 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 tetrapyrole ring plane of F₄₃₀, is
occupied by the thiol group of coenzyme M, which is
positioned almost parallel to the tetrapyrole 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 Tyr233 and Tyr587 and a water
molecule that bridges coenzyme M and B. The ethyl
moiety is embedded between the lactam ring of the Ni
porphyrinoid 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
Fig. 8. Coenzyme $F_{430}$ 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 (MCR$_{ox1-silent}$). 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 $F_{430}$ with its thiol group bound to Ni(II) in the active site of methyl-coenzyme M reductase (MCR$_{ox1-silent}$). Structure at 1.45 Å resolution. The oxygen of Gln$^{147}$ is seen to approach the Ni from the rear face of $F_{430}$ 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 (MCR$_{ox1-silent}$). 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 $\alpha$, $\alpha'$ and $\beta$ (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 Waal's contact with several hydrophobic residues. The thiol group of coenzyme B is positioned at a distance of 8.7 Å from the nickel of $F_{430}$ and 6.2 Å from the coenzyme M thiol sulphur. It interacts with the side chain of nitrogen of Asn$^{248}$, the main chain peptide nitrogen of Val$^{262}$ and the bridging water molecule mentioned above. Asn$^{248}$ is within hydrogen bond distance of the sulphur that is presumed to replace the backbone carbonyl oxygen of the modified Gly$^{2445}$ (see below).

Five modified amino acids in the active site region

The electron density map revealed five modified amino acids located in subunits $\alpha$ and $\alpha'$ at or very near the active site region, 1-N-methyl-His$^{257}$, 4-methyl-Arg$^{271}$, 2-methyl-Gln$^{200}$, S-methyl-Cys$^{2452}$ and Gly$^{2445}$, where
the carbonyl oxygen appears to be substituted by sulphur (Ermel 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 MCRoxl.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 Phe$^{230}$, Tyr$^{233}$, Phe$^{244}$, Phe$^{261}$ and Tyr$^{267}$ flanked further by hydrophobic and aromatic residues (Ermel 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 H$_2$ synthase 1 (Picot et al., 1994) and methylmalonyl-CoA mutase (Mancia et al., 1996).

Crystal structure of methyl-coenzyme M reductase in the MCR$_{\text{silent}}$, MCR$_{\text{red2-silent}}$ and MCR$_{\text{ox2-silent}}$ states

The structure of the MCR$_{\text{silent}}$ state was refined in the resolution range 2.0–10.0 Å with the use of the MCR$_{\text{ox1-silent}}$ structure for initial phase determination (Ermel et al., 1997b). The two enzyme states exhibit nearly identical overall structures. The model of the MCR$_{\text{silent}}$ structure is mainly distinguished from that of MCR$_{\text{ox1-silent}}$ by binding of the oxidized instead of the reduced forms of coenzyme M and coenzyme B (Fig. 10). A superposition of the structures reveals that the reduced coenzyme B in MCR$_{\text{ox1-silent}}$ and the coenzyme B moiety of the heterosulphide in MCR$_{\text{silent}}$ align perfectly except that the sulphur is turned slightly towards coenzyme M. In contrast to coenzyme B, coenzyme M has moved more than 4 Å away from its position in the MCR$_{\text{ox1-silent}}$ state. The thiol group is shifted perpendicular and the sulphonate group parallel to the tetrapyrrole plane of F$_{430}$ resulting in a 90° rotation of coenzyme M. In this position, one oxygen atom of the sulphonate is axially coordinated with the nickel and contacts the hydroxyl group of Tyr$^{267}$. The distance between nickel and oxygen is 2.1 Å. The second oxygen atom is hydrogen bonded to the lactam ring of F$_{430}$ and to the hydroxyl group of Tyr$^{267}$ and the third to a water molecule located at the former binding site of the sulphonate.

The structures of methyl-coenzyme M reductase in the MCR$_{\text{red2-silent}}$ and MCR$_{\text{ox2-silent}}$ states have, in the meantime, also been resolved but have not yet been completely refined. Available information indicates that in the MCR$_{\text{red2-silent}}$ state, the active site of methyl-coenzyme M reductase is probably devoid of both coenzyme M and coenzyme B. The 30-Å-long channel leading into the active site pocket is more open and the residues of the α-, α', β- and γ-subunits forming the channel are more flexible. In the MCR$_{\text{ox2-silent}}$ state, methyl-coenzyme M reductase appears to contain bound coenzyme B but not coenzyme M (W. Grabarse, unpublished results).

Catalytic mechanism proposed for methyl-coenzyme M reductase

The crystal structures display inactive states of methyl-coenzyme M reductase with coenzyme F$_{430}$ in the Ni(II) oxidation state. Nevertheless, the arrangement of the coenzymes and the protein environment, combined with the catalytic properties of the enzyme and the chemical properties of free coenzyme F$_{430}$, allow for conclusions about the active site and the catalytic mechanism (Ermel et al., 1997b).

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(I) oxidation state. This is deduced from the finding that methyl-coenzyme M reductase only exhibits activity when assayed in its Ni(I) oxidation form (either MCR$_{\text{ox1}}$ or MCR$_{\text{red2}}$ 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 (Ermel 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 F$_{430}$. 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; Berkesel, 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(I). In the MCR$_{\text{ox1-silent}}$ structure, coenzyme M probably mimics the binding position of methyl-coenzyme M with respect to the binding mode of the sulphate 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 sulfurs of coenzyme M and coenzyme B. Model building studies indicate, however, that the two sulfurs 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 MCRoxl-silent structure reveals an interaction between the thiol group of coenzyme B and two hydrogen donors, the amide and peptide nitrogen of Asn₁₄¹ and Val₁₄₈, 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. Tyr₂₃₃ and Tyr₆₃₇ 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 sulphinate oxygen of the coenzyme M moiety binds to the Ni(II) atom of F₄₃₀ as in the MCRoxl-silent state. Coordination of the sulphinate 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 sulphinate oxygen might even be used as a driving force to push the heterodisulphide out of the channel. It is not evident at present when, 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 Tyr₂₃₃ or Tyr₆₃₇ 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 °) (Manske & Klar, 1992.). The H⁺ would be replenished by the dissociation of coenzyme B.

\[
\text{CH₂-S-CoM + H⁺ + Ni(I) F₄₃₀} \rightarrow \text{CH₃-Ni(III) F₄₃₀ + H-S-CoB} \\
\text{H-S-CoB} \rightarrow \text{H⁺ + S-CoB}
\]

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 thiol radical cation.

\[
\text{CH₃-Ni(III) F₄₃₀ + H-S-CoM} \rightarrow \text{CH₃-Ni(II) F₄₃₀ + H-S-CoM⁺}
\]
CH₃Ni(II)F₄₃₀ spontaneously protonolyses to CH₄ and Ni(II)F₄₃₀. The H⁺ could be provided by the coenzyme M thiol radical cation, which is more acidic than coenzyme M.

CH₃Ni(II)F₄₃₀ + H⁺ \rightarrow CH₄ + Ni(II)F₄₃₀

H⁻S-CoM⁻ \rightarrow H⁺ + 'S-CoM

Protonolysis is essentially irreversible and thus probably pulls the preceding reactions and pushes the successive reactions. The coenzyme M thiol radical could react with the thiolate of coenzyme B, generating a disulphide radical anion.

'S-CoM + 'S-CoB \rightarrow CoM-S-'S-CoB⁻

A prerequisite is a loosening of the interaction between the sulphonate moiety of coenzyme M and the protein matrix, enabling a shift of coenzyme M towards coenzyme B. The disulphide radical anion has a redox potential (Lenz & Giese, 1997) negative enough for the reduction of Ni(II)F₄₃₀ to Ni(I)F₄₃₀.

Ni(II)F₄₃₀ + CoM-S-'S-CoB⁻ \rightarrow Ni(I)F₄₃₀ + CoM-S-S-CoB

Electron transport from the disulphide anion radical to the nickel could be via the modified Gly²⁴⁴, a thiglycine, which interacts with the thiol group of coenzyme B, generating a disulphide radical anion. 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.

H-S-CoB + X \rightarrow 'S-CoB + XH

The electron acceptor X cannot be Ni(II)F₄₃₀ as has been proposed since the enzyme is only active in its Ni(I)F₄₃₀ reduced form (Goubeaud et al., 1997). Therefore, there must be a second redox active group capable of oxidizing coenzyme B to the coenzyme B thiol 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 Gly²⁴⁴, a thiglycine, which interacts with the thiol group of coenzyme B via the side chain nitrogen of Asn²⁴⁸¹ and which could be susceptible to reduction to the thiketyl radical X⁻ (Buckel & Keese, 1995; Buckel, 1996). Probably the protonated thioketone would be reduced to the protonated thiketyl (XH) since this reaction is energetically more favourable as deduced from the thermodynamics of the reduction of ketones to ketals in the protonated and unprotonated forms (Lenz & Giese, 1997).

The coenzyme B thiol 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(I)F₄₃₀ and which could be susceptible to reduction to the thiketyl radical X⁻ (Buckel & Keese, 1995; Buckel, 1996). Probably the protonated thioketone would be reduced to the protonated thiketyl (XH) since this reaction is energetically more favourable as deduced from the thermodynamics of the reduction of ketones to ketals in the protonated and unprotonated forms (Lenz & Giese, 1997).

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 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 CH₃Ni(III)F₄₃₀ rather than CH₂Ni(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 thiol radical to the CoM-S(CH₃)-S-CoB sulphuranyl radical (Jaun, 1990; Berkessel, 1991; Tada & Masuzawa, 1997).

CH₂S-CoM + 'S-CoB \rightarrow CoM-S-(CH₃)⁻S-CoB

The catalytic cycle would be closed by electron transfer from X⁻ to Ni(II)F₄₃₀.

X⁻ + Ni(II)F₄₃₀ \rightarrow X + Ni(I)F₄₃₀

Via endergonic XH dissociation to X⁻ + H⁺, the two last reactions could be thermodynamically tightly coupled.

The salient feature of mechanism 2 is that it involves transient methyl radical intermediates and does not involve CH₂Ni(III)F₄₃₀ as intermediate in the catalytic cycle. Transient methyl radical intermediates could possibly account for the presumed methylation of His²⁵⁷, Arg²⁷¹, Gln³⁴⁰ and Cys³⁴².

Future studies will have to show which of the proposed catalytic mechanisms is correct or whether both are wrong. Unfortunately, one can only disprove but not prove a catalytic mechanism (Stinson, 1995).

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 methanogenesis 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., 1992) and 4 (Andrews et al., 1997) of the formate hydrogenlyase 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 Elsden and Hans-Günter Schlegel for providing me with literature on M. Stephenson.

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