

# Carbon Monoxide-Dependent Methyl Coenzyme M Methylreductase in Acetotrophic *Methosarcina* spp.

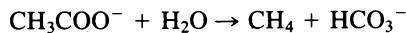
MICHAEL J. K. NELSON AND JAMES G. FERRY\*

Department of Anaerobic Microbiology, Virginia Polytechnic Institute and State University, Blacksburg, Virginia 24061

Received 30 May 1984/Accepted 21 August 1984

Cell extracts of acetate-grown *Methanosarcina* strain TM-1 and *Methanosarcina acetivorans* both contained CH<sub>3</sub>-S-CoM methylreductase activity. The methylreductase activity was supported by CO and H<sub>2</sub> but not by formate as electron donors. The CO-dependent activity was equivalent to the H<sub>2</sub>-dependent activity in strain TM-1 and was fivefold higher than the H<sub>2</sub>-dependent activity of *M. acetivorans*. When strain TM-1 was cultured on methanol, the CO-dependent activity was reduced to 5% of the activity in acetate-grown cells. *Methanobacterium formicicum* grown on H<sub>2</sub>-CO<sub>2</sub> contained no CO-dependent methylreductase activity. The CO-dependent methylreductase of strain TM-1 had a pH optimum of 5.5 and a temperature optimum of 60°C. The activity was stimulated by the addition of MgCl<sub>2</sub> and ATP. Both acetate-grown strain TM-1 and acetate-grown *M. acetivorans* contained CO dehydrogenase activities of 9.1 and 3.8 U/mg, respectively, when assayed with methyl viologen. The CO dehydrogenase of acetate-grown cells rapidly reduced FMN and FAD, but coenzyme F<sub>420</sub> and NADP<sup>+</sup> were poor electron acceptors. No formate dehydrogenase was detected in either organism when grown on acetate. The results suggest that a CO-dependent CH<sub>3</sub>-S-CoM methylreductase system is involved in the pathway of the conversion of acetate to methane and that free formate is not an intermediate in the pathway.

The acetotrophic methane-producing bacteria metabolize acetate as follows:



Studies with deuterated acetate have shown that the methyl group is transferred intact to CH<sub>4</sub> (19). It has been hypothesized (12) that acetate is cleaved by a mechanism analogous to a reversal of the pathway proposed for the biosynthesis of acetate in *Clostridium thermoaceticum*. In the biosynthetic pathway, a protein with carbon monoxide dehydrogenase activity is thought to be involved in the reduction of CO<sub>2</sub> to an enzyme-bound, reduced C<sub>1</sub> intermediate which then reacts with a methyl donor to form acetate (10, 14, 18). A similar mechanism may be utilized for the synthesis of acetate for cellular carbon by the H<sub>2</sub>-CO<sub>2</sub>-utilizing methanogen *Methanobacterium thermoautotrophicum* (25).

Recent reports are consistent with an involvement of CO dehydrogenase in the pathway of methanogenesis from acetate. *Methanosarcina barkeri* MS, adapted to grow on acetate, contained fivefold more CO dehydrogenase activity than cells grown on methanol or H<sub>2</sub>-CO<sub>2</sub> (12); this enzyme may constitute up to 5% of the total protein in acetate-grown cells (13). High levels of CO dehydrogenase are also present in *Methanotherix soehngenii* (11), an acetotroph unable to utilize H<sub>2</sub>-CO<sub>2</sub> for methanogenesis.

Coenzyme M (2-mercaptoethanesulfonate; HS-CoM) is the terminal methyl carrier for the formation of methane from methanol and CO<sub>2</sub> (16, 23, 26). Methanogenic organisms grown on either substrate contain H<sub>2</sub>-dependent 2-(methylthio)ethanesulfonate (CH<sub>3</sub>-S-CoM) methylreductase (H<sub>2</sub>-methylreductase), which reductively demethylates CH<sub>3</sub>-S-CoM to form methane, with H<sub>2</sub> as the electron donor (1, 4, 5, 7, 8). The H<sub>2</sub>-methylreductase of *M. thermoautotrophicum* is a complex system composed of several separable protein and nonprotein components (17). Acetate-grown *M. barkeri* 227 also contains a H<sub>2</sub>-methylreductase system;

however, methanol-grown or H<sub>2</sub>-CO<sub>2</sub>-grown cells contain similar levels of H<sub>2</sub>-methylreductase activity (1). Acetate-grown *M. barkeri* 227 is able to metabolize H<sub>2</sub>-CO<sub>2</sub> (6); thus, the H<sub>2</sub>-methylreductase system of this organism may only be present as a component of the H<sub>2</sub>-CO<sub>2</sub> pathway.

Two acetotrophic methane-producing organisms, *Methanosarcina* strain TM-1 (30) and *Methanosarcina acetivorans* (24), were chosen by our laboratory for biochemical studies of the dissimilation of acetate to methane. When grown on acetate, these organisms are unable to utilize H<sub>2</sub>-CO<sub>2</sub> for methanogenesis, simplifying the study of acetate metabolism. It was recently shown that the methyl group of acetate is transferred to HS-CoM during methanogenesis from acetate by *Methanosarcina* strain TM-1 (15), implicating CH<sub>3</sub>-S-CoM methylreductase in the formation of methane from acetate. Here we report on the CH<sub>3</sub>-S-CoM methylreductase systems of *Methanosarcina* strain TM-1 and *M. acetivorans*. The results show that CO serves as a novel electron donor for the CH<sub>3</sub>-S-CoM methylreductase systems of these organisms when grown on acetate.

## MATERIALS AND METHODS

**Organisms and culture conditions.** *Methanosarcina* strain TM-1 (30) was obtained from S. H. Zinder, and *M. acetivorans* ATCC 35395 (24) was obtained from K. R. Sowers. Both organisms were cultured on acetate as large-scale cultures (10 liters) with a pH auxostat system (K. R. Sowers, M. J. Nelson, and J. G. Ferry, *Curr. Microbiol.*, in press) similar to that used for the cultivation of methanogenic bacteria on formate (21). Acetic acid (10 M) was automatically added to fermentors by a pH controller; this maintained both a constant pH (7.0) and a constant acetate concentration (50 mM). The basal medium for strain TM-1 contained the indicated concentrations (in grams per liter) of the following constituents: NH<sub>4</sub>Cl, 1.44; K<sub>2</sub>HPO<sub>4</sub>, 1.13; KH<sub>2</sub>PO<sub>4</sub>, 1.13; NaCl, 0.45; MgSO<sub>4</sub> · 7H<sub>2</sub>O, 0.09; CaCl<sub>2</sub> · 2H<sub>2</sub>O, 0.06; yeast extract (Difco Laboratories), 0.5; Trypticase (BBL Microbiology Systems), 0.5; Fe(NH<sub>4</sub>)<sub>2</sub>(SO<sub>4</sub>)<sub>2</sub>, 0.01; cysteine · HCl, 0.27; Na<sub>2</sub>S · 9H<sub>2</sub>O, 0.27; Antifoam C, 0.5; and resazurin,

\* Corresponding author.

0.001. Trace elements and vitamin solutions (29) were each added at a final concentration of 1% (vol/vol). *M. acetivorans* was cultured in maintenance medium as previously described (24); the basal medium contained (concentrations in grams per liter) the following: NaCl, 23.4; MgSO<sub>4</sub>, 6.3; yeast extract, 1.0; Trypticase, 1.0; NH<sub>4</sub>Cl, 0.5; KCl, 0.8; CaCl<sub>2</sub> · 2H<sub>2</sub>O, 0.14; Na<sub>2</sub>HPO<sub>4</sub>, 0.6; cysteine · HCl, 0.25; Na<sub>2</sub>S · 9H<sub>2</sub>O, 0.25; and resazurin, 0.001. Sodium acetate (50 mM) or methanol (100 mM) was added as the substrate. When methanol was utilized, additional methanol (2 g/liter) was added each day during growth. *Methanobacterium formicum* JF-1 was cultured on H<sub>2</sub>-CO<sub>2</sub> (80%:20%, gas phase) as previously described (21) with the basal medium described for strain TM-1 but without yeast extract and Trypticase and with sodium formate (6.1 g/liter). All cells were harvested in a continuous-flow centrifuge (Cepa type LE) under a stream of N<sub>2</sub>, and the resulting cell paste was frozen and stored in liquid nitrogen.

**Anaerobic procedures.** The general anaerobic procedures for the preparation of cell extracts and for assays were as previously described (21). All containers and solutions used for anaerobic procedures were made O<sub>2</sub> free by repeated vacuum degassing and replacement with O<sub>2</sub>-free gas (N<sub>2</sub>, H<sub>2</sub>, or CO). All gasses used were scrubbed for trace amounts of O<sub>2</sub> by passage through reduced BASF catalyst R3-11 (Chemical Dynamics) or a solution of 2 mM reduced methyl viologen.

**Preparation of cell extracts.** Cell extracts were prepared anaerobically under an H<sub>2</sub> atmosphere by suspension of frozen cells in twice their weight of anaerobic breakage buffer, passage of the suspension through a French pressure cell at 135 MPa (20,000 lb/in<sup>2</sup>), and collection of the broken cell mixture directly in sealed, H<sub>2</sub>-filled centrifuge tubes. The mixture was then centrifuged at 27,000 × *g* (4°C) for 20 min; the resulting supernatant solution (15 to 35 mg of protein per ml) was removed from the tubes and stored in liquid nitrogen until use. Breakage buffer consisted of 50 mM potassium *N*-tris(hydroxymethyl)methyl-2-aminoethanesulfonate buffer (pH 7.0) containing 10 mM 2-mercaptoethanol, 10 mM MgCl<sub>2</sub>, 5% (vol/vol) glycerol, and 0.01 mg of DNase I (Sigma Chemical Co.) per ml.

**Enzyme assays.** CH<sub>3</sub>-S-CoM methylreductase assays were performed anaerobically in sealed, calibrated, 5-ml serum vials (Wheaton Scientific) that contained the appropriate gas at 1 atm (101 KPa) of pressure and were placed in a reciprocating (60-rpm) shaker water bath at 40°C, except as otherwise indicated. The standard assay (0.5 ml) contained 100 mM potassium 2-(*N*-morpholino)ethanesulfonate (pH 6.0), 2 mM ATP, 20 mM MgCl<sub>2</sub>, 5 mM CH<sub>3</sub>-S-CoM, cell extract, and the appropriate electron donor. The CO utilized (99.5% CO; Matheson Gas) contained 0.05% H<sub>2</sub> as a contaminant. Control assays that contained N<sub>2</sub> with up to 0.25% H<sub>2</sub> showed no significant CH<sub>3</sub>-S-CoM methylreductase activity. For formate-dependent reactions, 2 to 20 mM sodium formate was included as indicated in the reaction mixture, which was equilibrated with N<sub>2</sub>. An N<sub>2</sub> gas phase was also used for control assays with no electron donor. Cell extracts were equilibrated with H<sub>2</sub> for 10 min before H<sub>2</sub>-dependent reactions were initiated. Cell extracts for other assays were equilibrated with N<sub>2</sub> in the same manner. Reactions were initiated by the addition of the cell extract. Gas samples (50 μl) were taken with a gas-tight syringe at several time intervals, CH<sub>4</sub> was determined, and assay rates were calculated from the linear portion of the time course obtained. The reaction rates are reported as net rates after subtraction of the reaction rates of N<sub>2</sub> controls. Methane was analyzed by

gas chromatography with a Varian 3700 gas chromatograph equipped with a Porapak QS column, nitrogen carrier gas (15 ml/min), and flame ionization detector.

Hydrogenase and formate dehydrogenase assays were performed as previously described (21, 22) with methyl viologen as the electron acceptor. Assays were also performed with coenzyme F<sub>420</sub> (F<sub>420</sub>), FAD, FMN, NAD<sup>+</sup>, or NADP<sup>+</sup> (45 μM) substituted for methyl viologen. These assays were done the same way as the methyl viologen assays except that the reduction of the electron acceptor was monitored spectrophotometrically at the appropriate wavelength for the electron acceptor used. The following extinction coefficients (mM<sup>-1</sup> cm<sup>-1</sup>) were used: F<sub>420</sub>, *E*<sub>420</sub> = 42.5; FAD, *E*<sub>450</sub> = 11.3; FMN, *E*<sub>450</sub> = 12.2; NAD<sup>+</sup>, *E*<sub>340</sub> = 6.2; and NADP<sup>+</sup>, *E*<sub>340</sub> = 6.2. In all cases one unit of activity equals the amount of enzyme required to reduce 1 μmol/min of the electron acceptor used. Control assays were performed without electron donors (N<sub>2</sub> atmosphere), and reaction rates were corrected for endogenous reduction of the electron acceptor by the cell extract. CO dehydrogenase assays were performed the same way as the hydrogenase assays but under an atmosphere of 100% CO.

**Protein determination.** Protein was assayed by the method of Bradford (2) with bovine serum albumin as the standard.

**Chemicals.** F<sub>420</sub> was purified from extracts of *M. formicum* as previously described (22). CH<sub>3</sub>-S-CoM was synthesized as previously described (20) and isolated as the ammonium salt. All other chemicals were obtained commercially.

## RESULTS

**Electron donors for CH<sub>3</sub>-S-CoM methylreductase.** Both *Methanosarcina* strain TM-1 and *M. acetivorans* were grown on acetate, and extracts of the cells were tested for CH<sub>3</sub>-S-CoM methylreductase activity with CO, H<sub>2</sub>, or formate as the potential electron donor. *M. formicum*, a methanogen incapable of utilizing acetate for methanogenesis, was grown on H<sub>2</sub>-CO<sub>2</sub>, and extracts of this organism were tested in a similar manner for comparison with the two acetotrophs.

A CO-dependent CH<sub>3</sub>-S-CoM methylreductase (CO-methylreductase) activity was present in extracts of acetate-grown strain TM-1 (Fig. 1). After a brief lag, the rate of methane formation was constant and was dependent upon the presence of both CH<sub>3</sub>-S-CoM and CO. The specific activity was similar (89%) to that of the H<sub>2</sub>-methylreductase activity in extracts of H<sub>2</sub>-CO<sub>2</sub>-grown *M. formicum* (Table 1). Acetate-grown strain TM-1 also contained H<sub>2</sub>-methylreductase activity (Fig. 1 and Table 1) that was equal to the CO-methylreductase activity. Assays continued for more than 2 h produced stoichiometric amounts of methane (90 to 100% of the theoretical amount) from CH<sub>3</sub>-S-CoM with either CO or H<sub>2</sub> as the electron donor. Formate was not utilized as an electron donor in the CH<sub>3</sub>-S-CoM methylreductase system of strain TM-1.

Significant CO-methylreductase activity was also present in extracts of acetate-grown *M. acetivorans*, although the amount was lower than that in strain TM-1 (Fig. 2 and Table 1). Unlike strain TM-1, the H<sub>2</sub>-methylreductase activity in this organism was only 20% that of the CO-methylreductase activity. Little methane was formed from CH<sub>3</sub>-S-CoM when 20 mM formate was the electron donor (Fig. 2 and Table 1), and no significant methane formation occurred when 2 mM formate was used (Fig. 2). Thus, free formate did not support significant CH<sub>3</sub>-S-CoM methylreductase activity in either acetotroph.

*M. formicum* utilizes H<sub>2</sub> and formate as electron donors

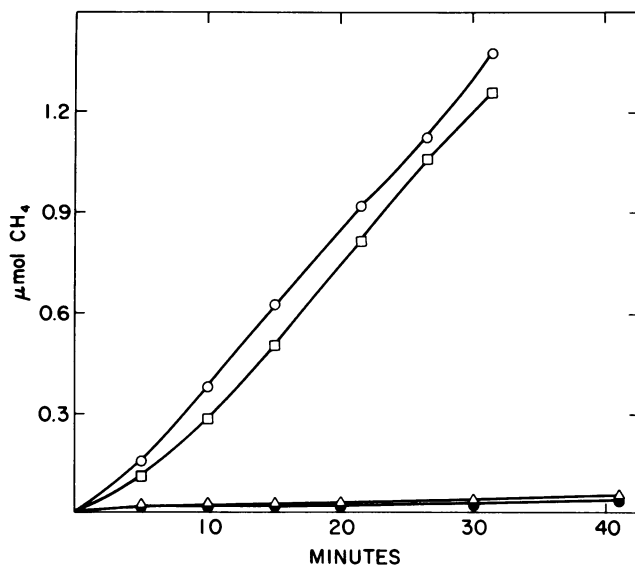


FIG. 1. Time course of methane formation by the  $\text{CH}_3\text{-S-CoM}$  methylreductase system in acetate-grown *Methanosarcina* strain TM-1 with  $\text{CO}$ ,  $\text{H}_2$ , or formate as the electron donor. Each standard assay contained  $100\ \mu\text{l}$  ( $1.5\ \text{mg}$  of protein) of strain TM-1 cell extract with the following electron donors:  $\text{CO}$ ,  $\circ$ ;  $\text{H}_2$ ,  $\square$ ; sodium formate ( $20\ \text{mM}$ ),  $\triangle$ ; no electron donor or either  $\text{CO}$  or  $\text{H}_2$  in the absence of  $\text{CH}_3\text{-S-CoM}$ ,  $\bullet$ .

for the reduction of  $\text{CO}_2$  to methane. Both  $\text{H}_2$  and formate supported substantial  $\text{CH}_3\text{-S-CoM}$  methylreductase activity in extracts of this organism, but  $\text{CO}$ -methylreductase was not detected (Table 1). Thus, both acetate-grown methanogens contained  $\text{CO}$ -methylreductase systems, but the non-acetate utilizer contained no detectable  $\text{CO}$ -methylreductase.

*Methanosarcina* strain TM-1 was cultured on methanol as an alternate substrate and tested for  $\text{H}_2$ -methylreductase and  $\text{CO}$ -methylreductase (Table 1). Methanol-grown and acetate-grown strain TM-1 contained similar  $\text{H}_2$ -methylreductase activities. However, methanol-grown strain TM-1 contained only 5% of the  $\text{CO}$ -methylreductase activity in acetate-grown cells. Thus, the ability to use  $\text{CO}$  as an electron donor for the  $\text{CH}_3\text{-S-CoM}$  methylreductase system is correlated with growth on acetate.

**Properties of the  $\text{CO}$ -methylreductase of *Methanosarcina* strain TM-1.**  $\text{CO}$ -methylreductase activity occurred over a broad pH range, with optimal activity between pH 5.2 and 6.0 (Fig. 3A). Activities were similar at pH 6.5 in either buffer tested. The activity increased with temperature up to

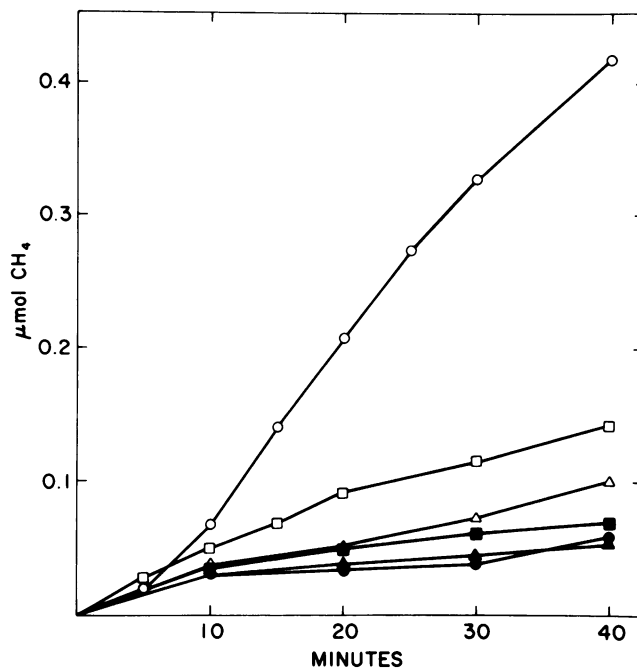


FIG. 2. Time course of methane formation by the  $\text{CH}_3\text{-S-CoM}$  methylreductase system in acetate-grown *M. acetivorans* with  $\text{CO}$ ,  $\text{H}_2$ , or formate as the electron donor. Each standard assay contained  $100\ \mu\text{l}$  ( $3.2\ \text{mg}$  of protein) of *M. acetivorans* cell extract with the following electron donors:  $\text{CO}$ ,  $\circ$ ;  $\text{H}_2$ ,  $\square$ ; sodium formate ( $20\ \text{mM}$ ),  $\triangle$ ; no electron donor, sodium formate ( $2\ \text{mM}$ ), or  $\text{H}_2$  in the absence of  $\text{CH}_3\text{-S-CoM}$ ,  $\bullet$ ;  $\text{CO}$  in the absence of  $\text{CH}_3\text{-S-CoM}$ ,  $\blacksquare$ ; sodium formate ( $20\ \text{mM}$ ) in the absence of  $\text{CH}_3\text{-S-CoM}$ ,  $\blacktriangle$ .

$60^\circ\text{C}$  (Fig. 3B). The  $\text{CO}$ -methylreductase of strain TM-1 was stimulated by the addition of  $\text{MgCl}_2$  and ATP, although substantial activity was obtained without the addition of either component. Activity was stimulated 182% by the addition of  $4\ \text{mM}$  ATP in the presence of  $22\ \text{mM}$   $\text{MgCl}_2$ . In the presence of  $2\ \text{mM}$  ATP, maximum activity was obtained in the presence of  $12\ \text{mM}$   $\text{MgCl}_2$ .

**Oxidoreductase activities.** Extracts of strain TM-1 and *M. acetivorans* were assayed for  $\text{CO}$  dehydrogenase, hydrogenase, and formate dehydrogenase with the nonspecific electron acceptor methyl viologen (Table 2). When cultured on acetate, both strain TM-1 and *M. acetivorans* contained high amounts of  $\text{CO}$  dehydrogenase activity; the rates were 96- and 40-fold greater, respectively, than that of  $\text{CO}$  dehydrogenase activity in extracts of  $\text{H}_2\text{-CO}_2$ -grown *M. formicicum*. As expected (21), *M. formicicum* contained substantial hy-

TABLE 1.  $\text{CH}_3\text{-S-CoM}$  methylreductase activities in *Methanosarcina* strain TM-1, *M. acetivorans*, and *M. formicicum* with  $\text{H}_2$ ,  $\text{CO}$ , or formate as the electron donor<sup>a</sup>

Organism	Growth substrate	Sp act (nmol of $\text{CH}_4$ /min per mg) with electron donor:		
		$\text{H}_2$	$\text{CO}$	Formate
<i>Methanosarcina</i> strain TM-1	Acetate	$29.9 \pm 1.5$	$30.2 \pm 2.4$	ND <sup>b</sup>
	Methanol	$20.1 \pm 0.4$	$1.4 \pm 0.2$	
<i>M. acetivorans</i>	Acetate	$0.70 \pm 0.10$	$3.6 \pm 0.20$	$0.27 \pm 0.12$
<i>M. formicicum</i>	$\text{H}_2\text{-CO}_2$	$33.9 \pm 4.7$	ND	$38.4 \pm 6.2$

<sup>a</sup> Standard methylreductase assays were performed in an atmosphere of  $\text{H}_2$  or  $\text{CO}$  or with  $20\ \text{mM}$  sodium formate in an atmosphere of  $\text{N}_2$ . Assays were initiated by the addition of  $100\ \mu\text{l}$  of cell extract of strain TM-1 ( $1.5$  to  $1.7\ \text{mg}$  of protein), *M. acetivorans* ( $3.2\ \text{mg}$  of protein), or *M. formicicum* ( $1.5\ \text{mg}$  of protein). Each assay was repeated a minimum of three times.

<sup>b</sup> ND, Nondetectable. Minimum detectable level,  $0.09\ \text{nmol/min per mg}$ .

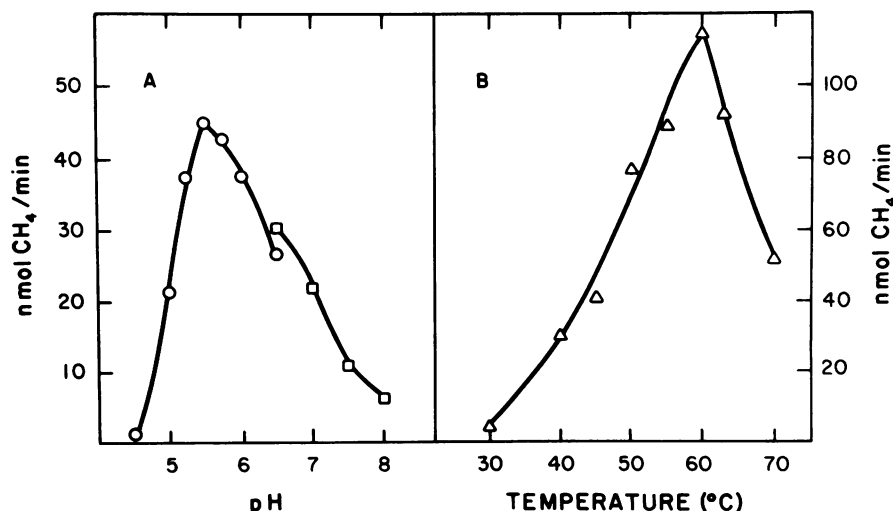


FIG. 3. Temperature and pH profiles of the CO-methylreductase of *Methanosarcina* strain TM-1. (A) Activity versus pH with 100 mM 2-(*N*-morpholino)ethanesulfonate (O) or *N*-tris(hydroxymethyl)methyl-2-aminoethanesulfonate (□) buffer in the assay mixture, adjusted to the indicated pH with KOH. (B) Activity versus temperature. All other conditions were as indicated for the standard assay. Each assay contained 100  $\mu$ l (1.5 mg of protein) of acetate-grown strain TM-1 cell extract.

drogenase and formate dehydrogenase activities, although the CO dehydrogenase activity was low. Hydrogenase was also present in acetate-grown strain TM-1, which had H<sub>2</sub>-methylreductase activity. *M. acetivorans*, which had low H<sub>2</sub>-methylreductase activity (Fig. 2 and Table 1), contained little hydrogenase. No formate dehydrogenase was detected in either acetate-grown acetotroph when assayed with methyl viologen (Table 2) or FAD, FMN, or F<sub>420</sub> (data not shown).

The CO dehydrogenase activity in acetate-grown strain TM-1 increased linearly with the CO concentration up to 1 mM when assayed with methyl viologen. These results indicate that the apparent  $K_m$  for CO was  $>1$  mM with the assay conditions used.

The CO dehydrogenase and hydrogenase activities in methanol-grown strain TM-1 were both ca. 20% of the respective activities in acetate-grown cells (Table 2). Although this represents a significant decrease for both enzymes, substantial amounts of activity were still present.

The hydrogenase and CO dehydrogenase activities in extracts of both acetate-grown organisms were also assayed with several physiological electron acceptors. NAD<sup>+</sup> was not reduced with either CO or H<sub>2</sub> in either acetotroph. NADP<sup>+</sup> was slowly reduced with either H<sub>2</sub> or CO at the same rate (0.01  $\mu$ mol/min per mg) in strain TM-1. Only CO

donated electrons for NADP<sup>+</sup> reduction (0.003  $\mu$ mol/min per mg) in *M. acetivorans*. Both FAD and FMN were rapidly reduced with either CO or H<sub>2</sub> in strain TM-1 (Table 3). F<sub>420</sub> was also rapidly reduced with H<sub>2</sub> strain TM-1, but the reduction of F<sub>420</sub> with CO was much slower. Thus, although flavins or F<sub>420</sub> were reduced by H<sub>2</sub>, only flavins were readily reduced by CO. Similar results for the reduction of F<sub>420</sub> and flavins in the presence of CO were obtained in *M. acetivorans* (Table 3). The reduction of F<sub>420</sub>, FAD, or FMN with H<sub>2</sub> was not detected in extracts of *M. acetivorans*.

## DISCUSSION

In this study, we investigated potential electron donors for the CH<sub>3</sub>-S-CoM methylreductase systems in acetate-grown *Methanosarcina* strain TM-1 and *M. acetivorans*. A novel feature of the CH<sub>3</sub>-S-CoM methylreductase systems in these organisms is the ability to use CO as the electron donor when grown on acetate. Based on our results and the recent finding that CH<sub>3</sub>-S-CoM is an intermediate in the conversion of acetate to methane (15), a pathway for methanogenesis from acetate is postulated in Fig. 4. In this pathway, the methyl group of acetate is transferred to HS-CoM, forming CH<sub>3</sub>-S-CoM as the terminal methyl carrier. Other methyl carriers may be involved before HS-CoM. The carboxyl

TABLE 2. Methyl viologen-linked hydrogenase, CO dehydrogenase, and formate dehydrogenase in extracts of *Methanosarcina* strain TM-1, *M. acetivorans*, and *M. formicicum*

Organism	Growth substrate	Sp. act <sup>a</sup> with electron donor:		
		H <sub>2</sub>	CO	Formate
<i>Methanosarcina</i> strain TM-1	Acetate	8.4 $\pm$ 1.0	9.1 $\pm$ 1.9	ND <sup>b</sup>
	Methanol	1.9 $\pm$ 0.2	1.7 $\pm$ 0.05	
<i>M. acetivorans</i>	Acetate	0.070 $\pm$ 0.004	3.8 $\pm$ 0.5	ND
<i>M. formicicum</i>	H <sub>2</sub> -CO <sub>2</sub>	129 $\pm$ 25	0.095 $\pm$ 0.007	8.2 $\pm$ 0.3

<sup>a</sup> Expressed as micromoles of methyl viologen reduced per minute per milligram. Assays were performed as described in the text. Aliquots of extracts containing 15 to 650  $\mu$ g of protein were assayed. Each assay was repeated a minimum of three times. Endogenous activities with no added electron donor were  $<0.005$ ,  $<0.002$ , and  $<0.06$   $\mu$ mol/min per mg for assays of strain TM-1, *M. acetivorans*, and *M. formicicum*, respectively.

<sup>b</sup> ND, Nondetectable. Minimum detectable level,  $5 \times 10^{-4}$   $\mu$ mol/min per mg.

TABLE 3. F<sub>420</sub>, FAD-, and FMN-linked hydrogenase and CO dehydrogenase in extracts of acetate-grown *Methanosarcina* strain TM-1 and *M. acetivorans*

Organism	Electron donor	Sp act <sup>a</sup> with electron acceptor:		
		F <sub>420</sub>	FAD	FMN
<i>Methanosarcina</i> strain TM-1	H <sub>2</sub>	0.15 ± 0.03	0.41 ± 0.03	0.50 ± 0.04
	CO	0.01 <sup>b</sup>	2.1 ± 0.2	1.9 ± 0.7
<i>M. acetivorans</i>	H <sub>2</sub>	ND <sup>c</sup>	ND	ND
	CO	0.03 <sup>b</sup>	0.77 ± 0.13	0.57 ± 0.002

<sup>a</sup> Expressed as micromoles of electron acceptor reduced per minute per milligram. Assays were performed as described in the text. Aliquots of extracts containing 15 to 650 μg of protein were assayed. Each assay was repeated a minimum of three times. Endogenous activities with no added electron donor were <0.0002 and <0.002 μmol/min per mg for F<sub>420</sub> and flavin assays, respectively.

<sup>b</sup> Maximum activity out of eight assays.

<sup>c</sup> ND, Nondetectable. Minimum detectable level, 4 × 10<sup>-4</sup> μmol/min per mg.

group of acetate is converted to an unidentified, bound C<sub>1</sub> intermediate before oxidation to CO<sub>2</sub>. High concentrations of exogenous CO may also form this bound C<sub>1</sub> intermediate. The oxidation of the C<sub>1</sub> intermediate by a protein with CO dehydrogenase activity provides the reducing equivalents necessary for the reduction of CH<sub>3</sub>-S-CoM to CH<sub>4</sub>. The reducing equivalents are transferred from the CO dehydrogenase to the CH<sub>3</sub>-S-CoM methylreductase by a presently unidentified electron carrier(s).

The low affinity for CO of the CO dehydrogenase in strain TM-1 in the present study and similar findings for the CO dehydrogenase in acetate-grown *M. barkeri* (13) suggest that free CO is not an intermediate in the acetate dissimilation pathway. However, high concentrations of free CO may equilibrate with a component of the pathway, forming a physiological C<sub>1</sub> electron donor for the methylreductase (Fig. 4). Furthermore, evidence has been presented that a bound C<sub>1</sub> intermediate formed from CO is incorporated into the carboxyl group of acetate during its biosynthesis in the H<sub>2</sub>-CO<sub>2</sub> utilizer *M. thermoautotrophicum* (25). A protein with CO dehydrogenase activity is also required for acetate formation by *C. thermoaceticum* from physiological C<sub>1</sub> donors (18).

The following results were consistent with an involvement of components of the CO-methylreductase system in the pathway of methanogenesis from acetate. (i) High levels of CO dehydrogenase activity were present in both acetate-grown organisms. *M. formicicum*, grown on H<sub>2</sub>-CO<sub>2</sub>, contained only 1% of the CO dehydrogenase activity present in acetate-grown strain TM-1. Activities reported for other nonacetate utilizers (3, 9) were from 2 to 4% of those in strain TM-1. (ii) High levels of CO-methylreductase activity were also present in both acetate-grown organisms, suggesting its involvement in a major metabolic pathway. The CO-methylreductase activities in these organisms were comparable to the H<sub>2</sub>-methylreductase activities reported for H<sub>2</sub>-CO<sub>2</sub>-utilizing methanogenic organisms (1, 5, 7). (iii) A CO-methylreductase system was not present in the nonacetate utilizer *M. formicicum*. (iv) When strain TM-1 was cultured on methanol as an alternate energy source, the CO-methylreductase activity was 5% of that in acetate-grown cells. It was previously reported that cell suspensions of methanol-grown strain TM-1 produce CH<sub>4</sub> from acetate at 3% of the rate in acetate-grown cells (S. H. Zinder, Abstr. Annu. Meet. Am. Soc. Microbiol. 1982, I88, p. 109).

The possibility exists that in the pathway of methanol utilization for methanogenesis, an oxidized C<sub>1</sub> intermediate identical to that formed during the oxidation of the C-1 of acetate is formed from methanol (presumably at the step just before the final two-electron oxidation to CO<sub>2</sub>) and subse-

quently consumed in a manner identical to that in the acetate utilization pathway. If this were the case, methanol-grown cells should also contain substantial CO-methylreductase activity. The results of the present study suggest that this is not the case and that the CO-methylreductase system may be uniquely associated with the conversion of acetate to methane.

Although the CO-methylreductase specific activity in methanol-grown strain TM-1 decreased to 5% of that in acetate-grown cells, the CO dehydrogenase specific activity decreased to only 19% of that in acetate-grown cells. Thus, the decreased CO dehydrogenase activity in methanol-grown cells apparently cannot account for the much larger decrease in the CO-methylreductase activity. Possible explanations for these results which are consistent with both CO dehydrogenase and CO-methylreductase involvement in methanogenesis from acetate are the following. (i) The CO dehydrogenase was constitutive, but another inducible component(s) of the CO-methylreductase system limited the CO-methylreductase activity in methanol-grown cells. (ii) More than one CO dehydrogenase was present in strain TM-1, but only one coupled to the CH<sub>3</sub>-S-CoM methylreductase system, and it was the absence of the other enzyme that was responsible for the decreased CO dehydrogenase activity and loss of CO-methylreductase activity in methanol-grown cells.

Possible mechanisms for the transfer of reducing equivalents from CO to CH<sub>3</sub>-S-CoM include the intermediate formation of formate or H<sub>2</sub>, with subsequent utilization by a formate dehydrogenase- or hydrogenase-dependent CH<sub>3</sub>-S-CoM methylreductase system. The absence of detectable formate dehydrogenase activity and the inability of formate to support significant methylreductase activity in either acetotroph indicate that free formate is not an intermediate

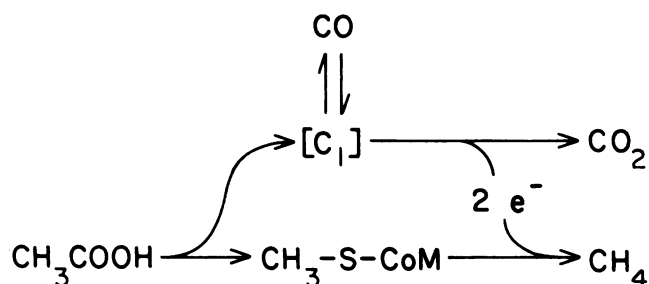


FIG. 4. Proposed pathway for the conversion of acetate to methane and CO<sub>2</sub>. A hypothetical bound C<sub>1</sub> intermediate in the production of CO<sub>2</sub> from the C-1 of acetate or from CO is represented as [C<sub>1</sub>].

in the CO-methylreductase systems in these organisms. These results also suggest that formate is not a free intermediate in the electron flow from acetate to methane, as proposed previously (27). The presence of a H<sub>2</sub>-methylreductase system in the acetotrophic organisms studied raises the question of whether H<sub>2</sub> is an intermediate in the CO-methylreductase system. If H<sub>2</sub> were produced from CO, followed by uptake by the H<sub>2</sub>-methylreductase system, the H<sub>2</sub>-methylreductase activity should be equal to or greater than the CO-methylreductase activity. The H<sub>2</sub>-methylreductase activity in *M. acetivorans* was 20% of the CO-methylreductase activity, suggesting that the transfer of electrons from CO to CH<sub>3</sub>-S-CoM does not involve free H<sub>2</sub>.

At present, the physiological electron acceptor for the CO dehydrogenase coupled to the CH<sub>3</sub>-S-CoM methylreductase system is unknown. The preliminary evidence suggests that F<sub>420</sub> and pyridine nucleotides are not involved. However, both FAD and FMN were readily reduced by CO, suggesting that a flavin or flavoprotein may be linked to the CO dehydrogenase. FAD was shown to be required for the H<sub>2</sub>-methylreductase system in *M. thermoautotrophicum* (17).

Some of the properties examined for the CO-methylreductase system in cell extracts of the thermophilic acetotroph strain TM-1 were similar to those reported for the H<sub>2</sub>-methylreductase system in cell extracts of the thermophilic H<sub>2</sub>-CO<sub>2</sub> utilizer *M. thermoautotrophicum* (7). Both systems had a similar pH optimum and temperature optimum. Like the H<sub>2</sub>-methylreductase system in *M. thermoautotrophicum*, the CO-methylreductase system in strain TM-1 was stimulated by the addition of ATP and MgCl<sub>2</sub>. However, the CO-methylreductase in strain TM-1 was active without the addition of ATP. This is in contrast to H<sub>2</sub>-methylreductase activities reported for several other methanogens, including *M. thermoautotrophicum* (7). The ATP-independent activity of the CO-methylreductase was more consistent with the H<sub>2</sub>-methylreductase activity in *Methanobacterium bryantii* (28), which also contained substantial activity without the addition of ATP because of the endogenous synthesis of ATP by the extracts tested. Whether the ATP-independent activity of the CO-methylreductase in the present study was the result of endogenous ATP was not examined.

The results of the present study are consistent with the hypothesis that the biochemistry of the conversion of acetate to methane involves steps analogous to a reversal of the acetate biosynthesis pathways of acetogenic anaerobes and H<sub>2</sub>-CO<sub>2</sub>-utilizing methanogenic bacteria. Cell extracts of acetate-grown methanogenic bacteria readily lose the ability to produce methane from acetate (unpublished data), which has precluded the in-depth study of the biochemistry of the acetate dissimilation pathway. Our results suggest that the CO-methylreductase system is involved in the terminal steps of the conversion of acetate to methane and CO<sub>2</sub>. Studies of this system should prove useful in the understanding of the pathway of the conversion of acetate to methane. Experiments are presently under way to further characterize the CO-methylreductase system in acetotrophic methane-producing bacteria.

#### ACKNOWLEDGMENTS

We thank Kevin Sowers for assistance in the culturing of *M. acetivorans* and *Methanosarcina* strain TM-1.

This investigation was supported by Gas Research Institute Basic Research grant 5082-260-0710.

#### LITERATURE CITED

1. Baresi, L., and R. S. Wolfe. 1981. Levels of coenzyme F<sub>420</sub>, coenzyme M, hydrogenase, and methylcoenzyme M methylre-

- ductase in acetate-grown *Methanosarcina*. Appl. Environ. Microbiol. 41:388-391.
2. Bradford, M. M. 1976. A rapid and sensitive method for quantitation of microgram quantities of protein utilizing the principle of protein-dye binding. Anal. Biochem. 72:248-254.
3. Daniels, L., G. Fuchs, R. K. Thauer, and J. G. Zeikus. 1977. Carbon monoxide oxidation by methanogenic bacteria. J. Bacteriol. 132:118-126.
4. Ellefson, W. L., and R. S. Wolfe. 1980. Role of component C in the methylreductase system of *Methanobacterium*. J. Biol. Chem. 255:8388-8389.
5. Ellefson, W. L., and R. S. Wolfe. 1981. Component C of the methylreductase system of *Methanobacterium*. J. Biol. Chem. 256:4259-4262.
6. Ferguson, T. J., and R. A. Mah. 1983. Effect of H<sub>2</sub>-CO<sub>2</sub> on methanogenesis from acetate or methanol in *Methanosarcina* sp. Appl. Environ. Microbiol. 46:348-355.
7. Gunsalus, R. P., and R. S. Wolfe. 1978. ATP activation and properties of the methyl coenzyme M reductase system in *Methanobacterium thermoautotrophicum*. J. Bacteriol. 135:851-857.
8. Gunsalus, R. P., and R. S. Wolfe. 1980. Methyl coenzyme M reductase from *Methanobacterium thermoautotrophicum*. Resolution and properties of the components. J. Biol. Chem. 255:1891-1895.
9. Hammel, K. E., K. L. Cornwell, G. B. Diekert, and R. K. Thauer. 1984. Evidence for a nickel-containing carbon monoxide dehydrogenase in *Methanobrevibacter arboriphilicus*. J. Bacteriol. 157:975-978.
10. Hu, S.-I., H. L. Drake, and H. G. Wood. 1982. Synthesis of acetyl coenzyme A from carbon monoxide, methyltetrahydrofolate, and coenzyme A by enzymes from *Clostridium thermoacetatum*. J. Bacteriol. 149:440-448.
11. Kohler, H.-P., and A. J. B. Zehnder. 1984. Carbon monoxide dehydrogenase and acetate thiokinase in *Methanoxithrix soehngenii*. FEMS Microbiol. Lett. 21:287-292.
12. Krzycki, J. A., R. H. Wolkin, and J. G. Zeikus. 1982. Comparison of unithrophic and mixotrophic substrate metabolism by an acetate-adapted strain of *Methanosarcina barkeri*. J. Bacteriol. 149:247-254.
13. Krzycki, J. A., and J. G. Zeikus. 1984. Characterization and purification of carbon monoxide dehydrogenase from *Methanosarcina barkeri*. J. Bacteriol. 158:231-237.
14. Ljungdahl, L. G., and H. G. Wood. 1982. Acetate biosynthesis, pp. 165-202. In D. Dolphin (ed.), Vitamin B<sub>12</sub>, vol. 2. John Wiley & Sons, Inc., New York.
15. Lovley, D. R., R. H. White, and J. G. Ferry. 1984. Identification of methyl coenzyme M as an intermediate in methanogenesis from acetate in *Methanosarcina* spp. J. Bacteriol. 160:521-525.
16. McBride, B. C., and R. S. Wolfe. 1971. A new coenzyme of methyl transfer, coenzyme M. Biochemistry 10:2317-2324.
17. Nagle, D. P., and R. S. Wolfe. 1983. Component A of the methylreductase system of *Methanobacterium*: resolution into four components. Proc. Natl. Acad. Sci. U.S.A. 80:2151-2155.
18. Pezacka, E., and H. G. Wood. 1984. The synthesis of acetyl-CoA by *Clostridium thermoacetatum* from carbon dioxide, hydrogen, coenzyme A and methyltetrahydrofolate. Arch. Microbiol. 137:63-69.
19. Pine, M. J., and H. A. Barker. 1956. Studies on the methane fermentation. XII. The pathway of hydrogen in the acetate fermentation. J. Bacteriol. 71:644-648.
20. Romesser, J. A., and W. E. Balch. 1980. Coenzyme M: preparation and assay. Methods Enzymol. 67:545-552.
21. Schauer, N. L., and J. G. Ferry. 1980. Metabolism of formate in *Methanobacterium formicicum*. J. Bacteriol. 142:800-807.
22. Schauer, N. L., and J. G. Ferry. 1982. Properties of formate dehydrogenase in *Methanobacterium formicicum*. J. Bacteriol. 150:1-7.
23. Shapiro, S., and R. S. Wolfe. 1980. Methyl-coenzyme M, an intermediate in methanogenic dissimilation of C<sub>1</sub> compounds by *Methanosarcina barkeri*. J. Bacteriol. 141:728-734.
24. Sowers, K. R., S. F. Baron, and J. G. Ferry. 1984. *Methanosarcina acetivorans* sp. nov., an acetotrophic methane-producing bacterium isolated from marine sediments. Appl. Environ.

- Microbiol. **47**:971-978.
25. **Stupperich, E., K. E. Hammel, G. Fuchs, and R. K. Thauer.** 1983. Carbon monoxide fixation into the carboxyl group of acetyl coenzyme A during autotrophic growth of *Methanobacterium*. FEBS Lett. **152**:21-23.
  26. **Taylor, C. D., and R. S. Wolfe.** 1974. Structure and methylation of coenzyme M (HSCH<sub>2</sub>CH<sub>2</sub>SO<sub>3</sub>). J. Biol. Chem. **249**:4879-4885.
  27. **Vogels, G. D., and C. M. Visser.** 1983. Interconnection of methanogenic and acetogenic pathways. FEMS Microbiol. Lett. **20**:291-297.
  28. **Whitman, W. B., and R. S. Wolfe.** 1983. Activation of the methylreductase system from *Methanobacterium bryantii* by ATP. J. Bacteriol. **154**:640-649.
  29. **Wolin, E. A., M. J. Wolin, and R. S. Wolfe.** 1963. Formation of methane by bacterial extracts. J. Biol. Chem. **238**:2882-2886.
  30. **Zinder, S. H., and R. A. Mah.** 1979. Isolation and characterization of a thermophilic strain of *Methanosarcina* unable to use H<sub>2</sub>-CO<sub>2</sub> for methanogenesis. Appl. Environ. Microbiol. **38**:996-1008.