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Characterization of a novel cytochrome \( c_{GJ} \) as the electron acceptor of XoxF-MDH in the thermoacidophilic methanotroph \textit{Methylacidiphilum fumariolicum} SolV

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A B S T R A C T

Methanotrophs play a prominent role in the global carbon cycle, by oxidizing the potent greenhouse gas methane to CO\(_2\). Methane is first converted into methanol by methane monooxygenase. This methanol is subsequently oxidized by either a calcium-dependent MxaF-type or a lanthanide-dependent XoxF-type methanol dehydrogenase (MDH). Electrons from methanol oxidation are shuttled to a cytochrome redox partner, termed cytochrome \( c_G \). Here, the cytochrome \( c_L \) homolog from the thermoacidophilic methanotroph \textit{Methylacidiphilum fumariolicum} SolV was characterized. SolV cytochrome \( c_{GJ} \) is a fusion of a XoxG cytochrome and a periplasmic binding protein XoxJ. Here we show that XoxGJ functions as the direct electron acceptor of its corresponding XoxF-type MDH and can sustain methanol turnover, when a secondary cytochrome is present as final electron acceptor. SolV cytochrome \( c_{GJ} \) (XoxGJ) further displays a unique, red-shifted absorbance spectrum, with a Soret and Q bands at 440, 553 and 595 nm in the reduced state, respectively. VTVH-MCD spectroscopy revealed the presence of a low spin iron heme and the data further shows that the heme group exhibits minimal ruffling. The midpoint potential \( E^{\text{m},pH7} = +240 \text{ mV} \) is similar to other cytochrome \( c_G \) type proteins but remarkably, the midpoint potential of cytochrome \( c_{GJ} \) was not influenced by lowering the pH. Cytochrome \( c_{GJ} \) represents the first example of a cytochrome from a strictly lanthanide-dependent methylotrophic microorganism.

1. Introduction

Both aerobic and anaerobic methanotrophs play an important role in the global carbon cycle by oxidizing the greenhouse gas methane to CO\(_2\). Methane is mainly produced in anoxic environments through the anaerobic degradation of biomass by methanogenic archaea [1]. Before reaching the atmosphere, methane can be used as an electron donor by various microorganisms, which couple its oxidation to the reduction of nitrite, nitrate, metal-oxides, sulfate and oxygen [2–5]. Aerobic methanotrophs, with representatives in the Alpha- and Gammaproteobacteria [10] and Verrucomicrobia [11] have been intensely studied and are widespread in nature, from lakes sediment and peatlands to more extreme environments as permafrost and volcanic mudpots [12]. The first step in their metabolism is the oxygen-dependent activation of methane into methanol by methane monooxygenase [13]. Methanol is subsequently oxidized to formaldehyde by methanol dehydrogenase (MDH). MDH is quinoprotein with a pyrroloquinoline quinone (PQQ) prosthetic group. Formaldehyde can either be oxidized to formate and eventually CO\(_2\) or be assimilated into biomass via the RuMP or serine pathway. Instead of assimilation of formaldehyde, some methanotrophs utilize the Calvin-Benson-Bassham cycle for carbon fixation [4,11,12,14,15].

Methanol oxidation to formaldehyde was long believed to be solely catalyzed by the well-characterized calcium-dependent MDH (MxAFI) [16]. However, recent studies have identified an alternative MDH (XoxF), which is lanthanide-dependent [17–20]. These XoxF-type MDHs are widespread in nature and can be classified into multiple phylogenetic clades [21]. The same holds true for the physiological

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Abbreviations: MDH, Methanol dehydrogenase; ICP-MS, Inductively Coupled Plasma Mass Spectrometry; MMO, Methane monooxygenase; VTVH-MCD, variable temperature variable field magnetic circular dichroism

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electron acceptor of MDH, cytochrome cβ (MxaG/XoxG), which is usually encoded in the mxa or xox operon [21]. XoxG cytochromes are very divergent and can be clustered into four distinct clades [22]. Regardless of their diversity, the primary function of these cytochromes is most likely the same i.e. accept electrons from methanol oxidation by MDH and shuttle them to the next partner in the electron transfer chain.

The role as dedicated electron acceptor of MDH was first shown for the Mxa-type. Here cytochrome cβ was accepted electrons from MDH and donated them to cytochrome cβ, in which it turn donated electrons to a terminal oxidase [23]. More recently, XoxG has been shown to function as the dedicated electron acceptor of XoxF-MDH [24]. However, it was not clear how the electrons were subsequently transferred. The so far characterized cytochrome cβ’s contain one high potential, covalently bound, low-spin heme group with a His-Met coordinated iron [23–26]. Cytochrome cβ proteins have no sequence similarity to any other cytochrome. The sequence is unique with only the haem binding site CxxCH shared with all other cytochrome c’s. But remarkably, the 3D structures are very similar, with 3 large α-helices forming a haem cleft.

Another gene usually present in the MDH operon is MxaJ/XoxJ [21]. Recently, the MxaJ structure of M. amin sulfidivorans MP was resolved, which showed a “bi-lobate” folding architecture found in peri-plasmic binding proteins [27]. MxaJ might be involved in protein binding, rather than binding small molecules and could stabilize the interaction between MDH and pMMO or assist in conformational plasmic binding proteins [27]. MxaJ has been shown to function as the dedicated electron acceptor of XoxF-MDH [24]. However, it was not clear how the electrons were subsequently transferred. The so far characterized cytochrome cβ’s contain one high potential, covalently bound, low-spin heme group with a His-Met coordinated iron [23–26]. Cytochrome cβ proteins have no sequence similarity to any other cytochrome. The sequence is unique with only the haem binding site CxxCH shared with all other cytochrome c’s. But remarkably, the 3D structures are very similar, with 3 large α-helices forming a haem cleft.

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adjusted when no changes where observed (max. 15 min). Spectral changes in the Soret at 440 nm and the α-band at 595 nm were corrected for total spectrum shift by subtracting the absorbance of the closest isosbestic point at 455 nm and 611 nm, respectively. Those absorbance values were normalized and plotted against the potential. The midpoint potentials were determined by fitting the normalized amplitudes to the Nernst equation with one electron component using Origin version 9.1 (OriginLab Corp.).

2.4. Pyridine hemochrome assay

A pyridine hemochrome assay of cytochrome c\textsubscript{GJ} was performed as previously described by Berry and Trumpower [42]. Purified cytochrome c\textsubscript{GJ} (2.5 μM) was added to a 1 ml pyridine solution (20% v/v pyridine in 0.1 M NaOH) in a 1 cm path length suprasil quartz cuvette. The sample was oxidized by the addition of potassium hexacyanoferrate(III) after which a spectrum was recorded using a Cary 60 spectrophotometer (Agilent). Afterwards, the sample was reduced by adding an excess of sodium dithionite powder (~2 mg) and another spectrum was recorded. Reduced minus oxidized spectra were used to determine the location the α- and β-bands, 586 and 544 nm respectively.

2.5. Activity assays

Reduction of cytochrome c\textsubscript{GJ} by XoxF-type MDH (purified according to [17]) was monitored spectroscopically at the Soret band (440 nm) and the α-band (595 nm), using a Cary 60 spectrophotometer (Agilent). 5 μM cytochrome c\textsubscript{GJ} was incubated in 20 mM potassium phosphate pH 7.0 with 50 μM methanol and 0–300 mM NaCl. After one min, 50 mM XoxF MDH was added and the reaction was followed to the complete reduction of cytochrome c\textsubscript{GJ}. Assays were performed at 45 °C. To determine the optimal salt concentration of the assay, initial rates were plotted against the respective NaCl concentration.

Reduction of equine or bovine heart cytochrome c (Sigma) by cytochrome c\textsubscript{GJ} and XoxF-type MDH was assayed using the following protocol. 0.2 mM stock solutions of heart cytochromes were prepared fresh in 10 mM PIPES buffer pH 7.2 (1.4-Piperazinedithanesulfonic acid, Sigma) and amber tubes prior to use. Eu-MDH [43] and cytochrome c\textsubscript{GJ} were washed twice to remove salts and excess methanol by using spin filters (Vivaspin, Sartorius) with 30,000 or 10,000 MW cutoff. Reduction was followed at 45 °C and 550 nm using 96 well microtiter plates and the Epoch2 plate reader (BioTek). Each well contained 200 μl volume and 50 μM equine or bovine heart cytochrome c, 0.2 μM Eu-MDH, 0–1 μM cytochrome c\textsubscript{GJ} and 50 mM Methanol, all in 10 mM PIPES pH 7.2. Control reactions were run without Eu-MDH, methanol or cytochrome c\textsubscript{GJ} and neither of those showed reduction of the secondary electron acceptors, albeit traces of residual methanol led to a small reduction activity in the absence of excess methanol. To determine the amount of reduced heart cytochrome per minute, an extinction coefficient of 19.5 mM·cm\textsuperscript{-1} was determined at pH 7.2 by comparing the absorbance of the oxidized form of the fully reduced cytochrome (obtained by addition of 100 equivalents of sodium dithionite, we found the absorption to be both pH and buffer dependent and recommend to determine the extinction coefficient for the used conditions). This extinction coefficient is close to the reported value of 19.0 mM·cm\textsuperscript{-1} at pH 7.0 in 120 mM MOPS buffer [44].

2.6. UV–Vis and CD spectroscopy

The protein was washed with sodium phosphate buffer (20 mM, pH 7) to remove salts, methanol and degraded protein. A spin filter (Vivaspin, Sartorius) with 10,000 MW cutoff was used for this purpose. 200 μl cytochrome c\textsubscript{GJ} (72 μM) was diluted two times in buffer and the resulting protein solution was centrifuged at 4 °C for 4 min at 4500 rpm with a microclic fixed angle rotor from Heraeus. The flow through was discarded and the procedure repeated once. Then, 200 μl buffer was added and the solution was centrifuged for 8 min. After two subsequent additions of 200 μl buffer the solution was centrifuged for 10 and 15 minutes, respectively. This procedure yielded approximately 500 μl washed cytochrome c\textsubscript{GJ} with a concentration of 30 μM which was kept on ice in an amber Eppendorf vial until further use. A 1 mm path length Quartz suprasil cuvette with Teflon stopper was filled with washed cytochrome c\textsubscript{GJ} and the UV Vis recorded under ambient conditions (air, 25 °C) on a CARY60 spectrophotometer equipped with a xenon flash lamp. The same cuvette was then immediately transferred to a JASCO CD spectrometer and the spectrum recorded from 190 to 800 nm. CD-instrument parameters: Data pitch 0.1 nm, Instrument Name J-810-150S, Photometric Mode CD, HT, Sensitivity Standard, D.I.T. 1 s, Bandwidth 1.00 nm, Scanning Speed 500 nm/min, Manual Baseline correction, Accumulation Times 5. To fully reduce the cytochrome c\textsubscript{GJ} a 100 mM solution of Na2S2O4 was added (1.2 μl, 200 equiv.) to a solution of 200 μl washed cytochrome c\textsubscript{GJ}, and incubated on ice for 3 min. The UV Vis and CD spectra were then immediately recorded of the reduced cytochrome c\textsubscript{GJ} as described above. To oxidize, a 100 mM solution of K3[Fe(CN)6] was added (1.2 μl, 200 equiv.) to a solution of 200 μl washed cytochrome c\textsubscript{GJ}, and the mixture was incubated on ice for 5 min. The UV Vis and CD spectra were then immediately recorded of the oxidized cytochrome c\textsubscript{GJ} as described above.

2.7. Extinction coefficient determination

Extinction coefficients were determined from the absorbance values of the Soret and α-band of a 7 μM cytochrome c\textsubscript{GJ} solution. The protein concentration of purified cytochrome c\textsubscript{GJ} was determined using the absorbance at 280 nm and an extinction coefficient of 37,275 M\textsuperscript{-1}cm\textsuperscript{-1} determined according to the Edelhoch method [45].

2.8. Metal analysis by ICP-MS

To analyze the iron content, the purified SolV cytochrome c\textsubscript{GJ} was diluted in 65% nitric acid to a final concentration of 30% and heated at 100 °C for 180 min. After sample preparation, metal analysis was performed using an Inductively Coupled Plasma Mass Spectrometer (ICP-MS; I series, ThermoScientific). Height point calibration was performed with a dilution series of element standards (1000 ppm in 1% nitric acid, Merck). Combined with the absorbance values of the sample, before destruction, at 280 and 430 nm, the iron content of SolV cytochrome c\textsubscript{GJ} was determined to be 0.99 ± 0.06 mol Fe/mol protein (n = 4).

2.9. MCD spectroscopy

Protein samples of cytochrome c\textsubscript{GJ} were prepared by mixing 400 μl of cytochrome c\textsubscript{GJ} (72 μM) with 600 μl glycerol and loaded in a 0.62 cm path length nickel-plated copper sample cell with quartz windows. The MCD system used has a JASCO J815 spectropolarimeter and an Oxford Instruments SM4000 cryostat/magnet. Data were collected at increments of 0.5 Tesla (T) from 0 to 7.0 T and at temperatures of 1.5, 4.2, 6, 12, 24 and 48 K. Each spectrum was corrected for any natural CD by subtracting the zero-field spectrum of the sample and in addition by manual baseline correction using the isosbestic points at 352, 430 and 467 nm. The fitting of the VTVH data was achieved with the Fortran software VTVH 2.1.1. [46].

2.10. Mass spectrometry

Sample preparation for matrix assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) was performed according to Farhoud et al [47]. Briefly, the purified protein was run on SDS-PAGE and stained with Coomassie blue. The protein band was excised and cut into small blocks of 2 × 2 mm. After destaining, reduction and alkyllylation of cysteines was performed and the gel pieces
were incubated overnight in a trypsin solution (10 ng/ml trypsin) at 37 °C. Peptides were collected, mixed with an equal volume of 10 mg/ml 4-hydroxy-α-cyanocinnamic acid in 50% acetonitrile/0.05% trifluoroacetic acid and spotted onto a 96 wells stainless steel plate. A spectrum in the range of 600 to 3000 m/z was recorded using a Microflex LRF MALDI-TOF (Bruker) and analysed using the Mascot Peptide mass Fingerprint against the Methyloidiphilum fumariolicum SolV protein database. A peptide tolerance of 0.3 Da, methionine oxidation as a variable modification and one missed trypsin cleavage were allowed.

To determine the mass of the XoxGJ protein, linear mode MALDI-TOF MS using a Microflex LRF MALDI-TOF (Bruker) was performed on the undigested protein. XoxGJ was diluted 10 fold in matrix solution (10 mg/ml 3,5-dimethoxy-4-hydroxycinnamic acid in 50% acetonitrile/0.05% trifluoroacetic acid; Sigma). Calibration was performed with a cytochrome c (12,361.96 Da) and albumin (66,429.09 Da) standard (Sigma). The mass of XoxGJ was determined by taking the average of the monoisotopic masses found at MH+, M2H+ and M2H+, corrected for their respective charge.

2.11. Gel electrophoresis

4–15% SDS polyacrylamide gradient gels (PAGE [48];) were cast using model 475 gradient delivery system (Bio-Rad). Purified cytochrome cGJ was incubated in SDS sample buffer (62.5 mM Tris, 2% SDS, 50 mM TCEP, 10% glycerol, 0.005% bromophenol blue, pH 6.8) for 30 min at 50 °C before being loaded on the gel (CSH Protocols, 2006; doi:https://doi.org/10.1101/pdb.prot4540). After running, the gels were either stained with Coomassie Brilliant Blue or with a luminol based heme stain adapted from Mruk and Cheng [49]. After fixing the gel in 40% ethanol for 10 min it was incubated for 15 min in a luminol solution (5 mg luminol, 2 ml p-hydroxycoumaric acid (1 mg/ml in ethanol), 2 ml 1 M CAPS pH 11, 16 ml ultrapure water) after which 200 μl of 3% H2O2 was added. After an additional 5 min incubation, the gel was imaged using ChemiDoc (Bio-Rad) with the chemiluminescence program and an exposure time of 10 s.

3. Results and discussion

3.1. Genomic organization

The MDH operon in Methyloidiphilum fumariolicum SolV is organized as follows: xoxF, xoxJ, xoxGJ. This genomic organization is highly conserved in most methanotrophs utilizing either the MxaF- or XoxF-type MDH, of which the former also includes the mxaI gene encoding for the MDH small subunit [21]. Remarkable is the presence of a xoxGJ fusion, which is so far only present in Bradyrhizobium and thermophilic Verrucomicrobia species. Multiple sequence alignments and structural predictions of SolV XoxJ and the XoxJ part of the XoxGJ fusion protein with their MxaJ counterparts showed that although the overall sequence similarity is quite low, a similar fold can be adopted by SolV XoxJ (Fig. S1). The XoxJ part of the XoxGJ fusion is truncated compared to the other sequences and misses some of the secondary structure elements (Fig. S1). MxaJ has been postulated to facilitate the formation of functional complexes either between MDH and pMMO or MDH and MxaG [27]. The presence of a XoxGJ fusion protein would favor the latter role and although not all structural elements were conserved, the fusion of XoxJ with one of its proposed interaction partners, XoxG, a condensed structure might be sufficient for its function. The presence of an additional XoxJ in SolV might indicate separate distinct functions for both proteins, where one facilitates the interaction between MDH and the XoxG to which it is fused, the other facilitates binding of MDH to pMMO. In transcriptome analysis of SolV, both xoxJ and xoxGJ are expressed in the same order of magnitude for cells growing at μmax [35]. Cells grown under H2/NH4 conditions showed a twofold decrease in xoxJ expression, following the trend of the
decreased expression for the pmoCAB2 operon [35]. This suggests that XooJ is involved in a specific interaction of XoxF with one of the pMMO isoforms. XoxF has been shown to interact with PMMO in *M. buryatense* with a Kₐ value of 50 μM [50], which is considerably higher than the reported Kₐ value of 0.9 μM for MxaF with PMMO in *M. capsulatus* [51].

3.2. Purification of the XoxGJ fusion protein

The gene product of Mfumv2_1185, the cytochrome *c*₆ XoxGJ fusion protein from *Methylacidiphilum fumarolicum* SolV was purified as a yellowish protein (See Table 1 for an overview of characteristics). SDS-PAGE showed a major protein band with a mass of ~25 kDa (Fig. S2A), in agreement with the mass observed during size exclusion chromatography (~26 kDa), but slightly lower than theoretical mass of ~29 kDa calculated for the XoxGJ fusion protein on the basis of the gene sequence without leader peptide. Tryptic digestion of the gel band and analysis of the peptides using MALDI-TOF MS identified the protein as the gene product of Mfumv2_1185, with a Mowse score of 75 and 9 detected peptides resulting in a 31% coverage. A luminol-based heme stain after gel electrophoresis showed a strong signal for the 25 kDa XoxGJ band, suggesting the presence of a covalently attached heme moiety. Using linear mode MALDI-TOF MS on the undigested XoxGJ protein (Fig. S2B), the mass of the protein was determined at 29,746 ± 77 Da, close to the theoretical mass of the polypeptide (signal peptide removed) plus heme c of 29,783 Da.

3.3. Spectral characteristics

The spectrum of the cytochrome *c*₆ directly after purification suggests, due to its similarity to the dithionite reduced spectrum (Fig. 1, black trace), that it is mainly present in the reduced form containing iron(II) (Fig. 1, red trace). However, a small amount of iron(III) is present in the sample and thus a small band arising from the Met-Fe CT transition can be detected at 695 nm (Fig. 1C) [52], in agreement with the presence of a conserved methionine in a multiple sequence alignment of MxaG/XoxG (Fig. S3). It is notable to mention that the protein (washed using a spin filter to remove degraded protein and salts from the purification process) after storage is mainly in its oxidized form (Fig. 1, blue trace).

Interestingly, the spectra that were recorded directly after purification and the ones from the protein that had been stored at ~80 °C (independent of oxidation state) differed in that sense that the methionine to Fe(III) charge transfer transition had disappeared and even upon full oxidation did not reappear. It is likely that the methionine-ligation is lost upon storage. This “MetLoss” [54] behavior is not unusual for cytochromes and has been observed and studied for the cytochromes of *Methylobacterium extorquens* strains AM1 and many others [25,26,52,54-57]. Upon crystallization of the *Methylobacterium extorquens* cytochrome, the ligation at the iron changed from Met109 to His112, and this was proposed to be due to the high mobility of the loop containing these residues [25]. The same behavior has been demonstrated for cytochrome *c*₂ isolated from *Rhodospseudomonas palustris*, here the axial methionine ligand is replaced by an ammonia molecule during the crystallization process and this was also attributed to the high flexibility of the methionine-containing loop [56]. The lability of the ligation was further demonstrated for cytochrome *c*₆ from *Methylobacterium extorquens* AM1 which readily reacts with carbon monooxide [26].

The cytochrome *c*₆ isolated from SolV overall displays an unusual absorbance spectrum. Remarkably, the Soret band of the reduced protein is found at 440 nm, extremely red shifted for a cytochrome *c*₆. In addition, the quasi-allowed bands are observed at 552 and 595 nm in the reduced form. The absorption bands of the porphyrin ring of cytochrome *c*₆ from *Methylobacterium extorquens* AM1 (found at 549 nm and 416 nm) [25,26] and that from their cytochrome c-553 (553, 419 nm reduced and 414 nm oxidized) [58], are distinctly different to the cytochrome *c*₆ reported here, pointing towards a modification of or near the heme in the SolV protein. Not surprising is that the CT-band which arises from a methionine residue to iron(III) is not shifted and found at 695 nm as for the other systems (Fig. 1C). A recently reported XoxG homolog showed absorption peaks around 525 and 552 nm after reduction by dithionite [24]. Unfortunately, in this study the location of the Soret band was not reported. Two unusual c-type cytochromes, *c*₅₇₂ and *c*₅₇₉p, that also show red shifted absorbance spectra were previously purified from iron-oxidizing acidophilic microbial communities. Both cytochromes contained canonical CXXCH heme binding motifs and the authors speculated that the shifted spectra might be caused by oxidation of the porphyrin [59,60]. For the cytochrome *bd* oxidase a similar red-shifted spectrum was observed for one of the *b* hemes, termed *b*₅₉₅*. This red-shift is likely caused by a glutamate axial ligand of the heme [61]. To examine the effect of the axial ligands on the spectrum of cytochrome *c*₆, a pyridine hemochrome assay was performed [42]. Here, the heme ligands are replaced by pyridine molecules to eliminate their effect on the spectrum. The pyridine hemochrome assay of cytochrome *c*₆ showed an α-band at 586 nm and β-band at 544 nm in the reduced minus oxidized spectrum (Fig. 2). Compared to the α-band of a canonical heme c (550 nm), cytochrome *c*₆ still showed a large red-shift, which cannot be attributed to the axial heme ligands. The location of the α-band at 586 nm resembles that of a heme α, suggesting that one of the methyl groups of the porphyrin ring might be oxidized to a formyl group [42], as was suggested for cytochrome *c*₅₇₉p [59].

3.4. Electrochemical redox titration

Besides the axial ligands, changes in the absorption spectrum of
Hemes can be caused for example by heme distortion or changes in covalent attachment of the cysteine thiol groups. It has been suggested that distortion is one way to tune redox potential and it can either stabilize or destabilize a certain iron redox state and that the more the heme becomes distorted, the lower the reduction potential, albeit a clear correlation is lacking. Therefore we performed a spectrophotometric electrochemical redox titration of cytochrome $c_{GJ}$ at pH 7 and pH 4 in the range of +50 to +500 mV versus standard hydrogen electrode. This titration showed that the protein transitions from the completely oxidized to completely reduced form in a 150 mV redox span. Independent fitting of the relative absorbance changes of both the Soret and $\alpha$-band as a function of the potential, in the reducing and oxidizing direction, using the Nernst equation resulted in a midpoint potential of +240 mV at pH 7 and +255 mV at pH 4 (Fig. 3). This is similar to the midpoint potential of other cytochrome $c_{L}$’s at pH 7, which all fall in the range of ~200 mV to ~300 mV [23]. Thus it seems that the heme in SolV cytochrome $c_{GJ}$ is not particularly ruffled, since no effect on the redox potential is observed. The Methylobacterium extorquens AM1 cytochrome $c_{L}$ showed a strong pH dependence on its midpoint potential, increasing from 250 mV to 320 mV when the pH was dropped from 7 to 4 [26], whereas the SolV cytochrome $c_{GJ}$ was largely unaffected by this pH drop. The heme modification of SolV cytochrome $c_{GJ}$ might stabilize it at lower pH and prevent the increase in midpoint potential. This would allow the cytochrome to accept electrons from MDH and transfer them (via a second cytochrome) to the terminal oxidase (at ~ 300 mV) as efficiently at acidic as neutral conditions, whereas for Methylobacterium extorquens AM1 the increased midpoint potential to a value above that of the terminal oxidase would greatly hamper methanol fueled respiration.

3.5. VTVH-MCD spectroscopy

We further characterized cytochrome $c_{GJ}$ with VTVH-MCD spectroscopy to gain insight into the spin state of the iron center and to detect possible deviations from planarity of the heme ring [64]. MCD spectra of cytochrome $c_{GJ}$ were recorded in a phosphate buffer glycerol mixture at different temperatures ranging from 1.5 K to 48 K and different magnetic fields from 0.5 to 7 T (Fig. 4). The data were baseline corrected for instrument and spectral baseline. As mentioned above, after prolonged storage the iron is in the oxidized form. A full spectrum scan before and after reduction with sodium dithionite and temperature-dependent data at 7 T can be found in the supporting information (Figs. S4 and S5). No major transitions between 600 and 800 nm were observed.
observed. The spectra exhibit a large positive temperature-dependent Soret band with a crossover near 430 nm. The intense features in the low temperature MCD spectra are typical for a low spin iron(III) heme [53,65]. The VTVH data were fitted using the Program VTVH 2.0 and the best VTVH-fit was the summed data, where the maximum negative band was subtracted from the maximum positive band, which eliminates baseline correction errors. The fit is consistent with a simple Kramers doublet (S = 1/2) ground state, xz-polarization and gy, contributing the most towards MCD-intensity. There are very small contributions from Mxz and Myz as well as gx and gz, which is consistent with a small deviation from planarity (i.e. ruffling). This is also in line with the obtained redox potential that did not deviate from the usual range reported for cytochrome cGJ. The final values after fit of the Soret band were gx = 2.0000, gy = 2.0000, gz = 3.1775, Myz = 1.1397, Mxz = −0.0500, Myx = −0.0200 and a small zero field splitting of D = −0.0078 cm⁻¹.

3.6. Circular dichroism spectroscopy

The washed, oxidized and reduced samples shown above in Fig. 1 were also investigated with circular dichroism spectroscopy to assess integrity during reduction and oxidation. The far UV region spectra shown in Fig. S6 show that protein tertiary structure is minimally affected by the treatment with sodium dithionite or potassium hexacyanoferrate(III) and the oxidation state [66]. The Soret band feature in the CD, however, is dependent on the oxidation state of the iron with the positive features found at 427 and 420 nm for the reduced and oxidized forms respectively, and the negative features at 442 and 447 nm.

3.7. Physiological role of XoxF/GJ

The physiological role of cytochrome cGJ from SolV should be the same as that of other cytochrome cGJ’s i.e. accepting electrons from methanol oxidation by MDH. Hence, to test this function, the reduction state of cytochrome cGJ (5 μM) was followed at 440 nm and 595 nm, the absorbance maxima of the Soret and α-band respectively. After an initial 1 min incubation in the presence of 50 μM methanol to establish a baseline, 50 nM XoxF-type MDH was added (data not shown). MDH catalyzed the rapid oxidation of methanol, shuffling the electrons to cytochrome cGJ as observed by the complete reduction of cytochrome cGJ within minutes. A UV–Vis spectrum of MDH-mediated reduction of cytochrome cGJ can be found in Fig. S7. This demonstrates the direct interaction between MDH and cytochrome cGJ, both isolated from Methylacidiphilum fumaricicum SolV, without the need of a small electron carrier such as PMS or PES. Reduction of cytochrome cGJ by MDH has already been studied for several methylotrophs utilizing the MxtA-type MDH [23] and has recently been shown for its XoxF-type counterpart [24].

Usually, ionic interactions play a role between the binding of an enzyme to its redox partner and varying salt concentrations can favor binding and dissociation reactions, respectively. To determine the impact of salt concentrations for the MDH cytochrome cGJ couple, initial cytochrome cGJ reduction rates were plotted against NaCl concentration over a range of 0 to 300 mM (Fig. 5). The highest activity was observed at 0 mM NaCl and addition of higher concentrations of salt had an adverse effect on the initial rate until 150 mM NaCl, after which the rate was stabilizing. At low salt concentrations binding of the ferric form is likely optimal. This has been shown for MDH and cytochrome cGJ from Methylobacterium extorquens, where addition of 50 mM NaCl decreased the affinity of MDH for cytochrome cGJ with the Km value increasing from 3.5 to 31 μM [67]. This indicates that under the tested assay conditions binding of ferric cytochrome cGJ to MDH is the rate-limiting step. In addition to high levels of NaCl, EDTA is also known to inhibit the electron transfer between MDH and cytochrome cGJ as shown by Cox et al. [68].

![Graph showing effect of salt concentration on activity of XoxF-type MDH](image)

**Fig. 5.** Effect of salt concentration (0–300 mM NaCl) on the activity of XoxF-type MDH with cytochrome cGJ from Methylacidiphilum fumaricicum SolV as electron acceptor. Reduction of cytochrome cGJ (5 μM) was monitored spectroscopically at the Soret (440 nm) and α-band (595 nm), respectively. After an initial 1 min incubation of cytochrome cGJ in 20 mM potassium phosphate pH 7.0 with 50 μM methanol, the reaction was started by the addition of 50 mM XoxF-type MDH. Assays were performed at 45 °C. Activities are shown relative to the maximum activity of the respective wavelength. All datapoints are the means of three measurements and error bars indicate standard deviation.

After electrons are passed from MDH to cytochrome cL they are transferred to a second cytochrome, cytochrome cH which donates its electrons to a terminal oxidase to fuel respiration [23]. Another hypothesis is that methanol oxidation is coupled to methane oxidation either directly or via uphill electron transfer [69]. Metabolic flux analysis on M. buryatense showed that the only way to sustain observed growth and methane/oxygen consumption rates, was through the coupling of methanol oxidation to methane oxidation, although the exact mechanism could not be established [70]. In vitro assays however show that, just like reported for Methylophilus methylotrophus, Methylobacterium extorquens strains and Acetobacter methanolicus cytochrome cL [44,52,68,71], SolV cytochrome cGJ efficiently donates its electrons to a secondary cytochrome (Fig. S8). Both equine and bovine heart cytochrome c can be used as secondary electron acceptors to demonstrate this and the reduction of secondary cytochrome is monitored by an increase of absorbance at 550 nm. Increasing the concentration of cytochrome cGJ increased the rate of reduction of equine or bovine horse heart cytochrome c with a linear dependence between 0 and 1 μM. For this reduction both cytochrome cGJ and MDH are strictly necessary. A similar pathway for electron flow from methanol oxidation via two cytochromes to a terminal oxidase is thus possible in SolV. Furthermore, methanol addition to crude extract greatly stimulates oxygen consumption in crude cell extracts (data not shown), indicating methanol oxidation can readily fuel respiration.

4. Conclusions

In summary, a novel cytochrome cL homolog fused to a XoxJ periplasmic binding protein (the product of this fusion is termed here cytochrome cXoxJ) purified from Methylacidiphilum fumaricicum SolV functions as the direct electron acceptor of XoxF-type MDH. To the best of our knowledge, cytochrome cXoxJ is the first example of a cytochrome from a strictly lanthanide-dependent acidophilic methanotroph. It is readily oxidized by an additional cytochrome partner (e.g. bovine and equine heart cytochrome c), indicating it could fuel respiration via a terminal oxidase. Compared to canonical cytochrome c’s and specifically previously studied cytochrome cL’s, the SolV fusion protein has a red-shifted absorbance spectrum. This red-shift has also been observed in two cytochromes isolated from acidophilic iron oxidizing microbial
communities. It is possible that a heme-modification stabilizes the cytochrome function at acidic conditions. The midpoint potential of *Methylbacterium extorquens* AM1 cytochrome c₂ increased by +70 mV when the pH was lowered from 7 to 4, whereas the cytochrome c₅₅₃ from SolV was largely unaffected by this pH drop. This would allow SolV cytochrome c₅₅₃ to keep functioning under its natural, acidic conditions.

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**Conflict of interest**

The authors declare that they have no conflicts of interest with the content of this article.

**Appendix A. Supplementary data**

Supplementary data to this article can be found online at https://doi.org/10.1016/j.bpaa.2019.04.001.

**References**


