Nitrogen fixation by the verrucomicrobial methanotroph ‘Methylacidiphilum fumariolicum’ SolV

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The ability to utilize atmospheric nitrogen (N₂) as a sole nitrogen source is an important trait for prokaryotes. Knowledge of N₂ fixation by methanotrophs is needed to understand their role in nitrogen cycling in different environments. The verrucomicrobial methanotroph ‘Methylacidiphilum fumariolicum’ strain SolV was investigated for its ability to fix N₂. Physiological studies were combined with nitrogenase activity measurements and phylogenetic analysis of the nifDHK genes, encoding the subunits of the nitrogenase. ‘M. fumariolicum’ SolV was able to fix N₂ at low oxygen (O₂) concentration (0.5 %, v/v) in chemostat cultures. This low oxygen concentration was also required for an optimal nitrogenase activity [47.4 nmol ethylene h⁻¹ (mg cell dry weight)⁻¹]. Based on acetylene reduction assay and growth experiments, the nitrogenase of strain SolV seems to be extremely oxygen sensitive compared to most proteobacterial methanotrophs. The activity of the nitrogenase was not inhibited by ammonium concentrations up to 94 mM. This is believed to be the first report on the physiology of N₂ fixation within the phylum Verrucomicrobia.

INTRODUCTION

Biological N₂ fixation is essential to life. In this process nitrogen is taken from its relatively inert molecular form (N₂) in the atmosphere and converted into ammonium according to the equation N₂ + 8 H⁺ + 8 e⁻ + 16 ATP → 2 NH₃ + H₂ + 16 ADP + 16 P; (Dixon & Kahn 2004; Howard & Rees, 1996). The micro-organisms performing this process are known as diazotrophs and they provide about 60 % of the annual nitrogen input into the biosphere (Newton, 2007). Diazotrophs are found in the domains Bacteria and Archaea and their lifestyle varies from free-living, loosely associated to symbiotic. The first methane-oxidizing bacteria, or methanotrophs, capable of N₂ fixation were isolated in 1964, referred to as Pseudomonas methanitrificans (Davis et al., 1964). Methanotrophs form an important sink for the greenhouse gas methane but the coupling between the methane and nitrogen cycles is poorly understood (Murrell & Jetten, 2009).

The microbial oxidation of methane may be coupled to the reduction of sulfate, nitrite or oxygen (Boetius et al., 2000; Hanson & Hanson, 1996; Raghoebarsing et al., 2006). Oxygen-consuming obligate aerobic methanotrophs are widespread in many natural environments (Conrad, 2009; Hanson & Hanson, 1996), where they feed on the methane produced by methanogens in the anoxic zones of these ecosystems. Until recently, all methanotrophs could be phylogenetically placed into 13 genera, belonging to the Gammaproteobacteria (type I) and the Alphaproteobacteria (type II) (Hanson & Hanson, 1996). However, in 2007, three research groups independently described novel thermoacidophilic methanotrophs isolated from geothermal areas in Italy, New Zealand and Russia (Dunfield et al., 2007; Islam et al., 2008; Pol et al., 2007). These methanotrophs represented a distinct phylogenetic lineage within the phylum Verrucomicrobia and they belong to a single genus for which the name ‘Methylacidiphilum’ was proposed (Op den Camp et al., 2009). Environmental clone libraries show that there is a large biodiversity in verrucomicrobia and they are encountered in many ecosystems, such as soils, peat bogs, acid rock drainage and landfill leachate, often in relatively high numbers, but having an unknown physiology (Wagner & Horn, 2006). However, the verrucomicrobial methanotrophs were obtained in pure cultures and a complete genome sequence was published for ‘Methylacidiphilum infernorum’ strain V4 (Hou et al., 2008) while a draft genome analysis was done for ‘Methylacidiphilum fumariolicum’ strain SolV (Pol et al., 2007). As nitrogen is one of the compounds that limits bacterial growth in most ecosystems, the ability to utilize N₂ as a sole nitrogen source is an important trait. Knowledge of N₂ fixation by methanotrophs will help us...
to understand their role in carbon and nitrogen cycling in different environments. Although it was first assumed that only type II and the type I moderately thermophilic *Methylococcus* strains were capable of N\(_2\) fixation (Oakley & Murrell, 1988), later the presence of both *nifH* gene fragments and acetylene reduction activity was demonstrated in a variety of type I and type II strains (Auman et al., 2001). Genetic and biochemical evidence was provided to show that N\(_2\) fixation capabilities are broadly distributed among methanotrophs. Recently, it was also demonstrated that the deep-sea anaerobic methane-oxidizing Archaea fix N\(_2\) and share the products with their sulfate-reducing bacterial symbionts (Dekas et al., 2009).

Preliminary growth experiments and genome analyses indicated that also the *Methylacidiphilum* strains should be able to fix N\(_2\) (Op den Camp et al., 2009). The genomes of strain SoV and strain V4 show a complete set of necessary genes for N\(_2\) fixation (Op den Camp et al., 2009; Hou et al., 2008). Most of these genes and their organization in putative operons resemble those of *Methylococcus capsulatus* Bath (Ward et al., 2004), a gammaproteobacterial methanotroph that has been shown to fix N\(_2\) (Oakley & Murrell, 1991). The aim of this study was to elucidate N\(_2\) fixation by *Methylacidiphilum fumarolicum* SoV in more detail. Physiological studies were combined with nitrogenase activity measurements and analysis of the *nifH* gene encoding one of the subunits of the nitrogenase.

**METHODS**

**Organism.** *Methylacidiphilum fumarolicum* strain SoV used in this study was originally isolated from the volcanic region Campi Flegrei, near Naples, Italy (Pol et al., 2007). The pH and temperature optima for growth were 2 and 55 °C, respectively.

**Medium composition for growth.** The medium used in this study to grow strain SoV contained: in g L\(^{-1}\), MgCl\(_2\)-6H\(_2\)O, 0.08; CaHPO\(_4\)-2H\(_2\)O, 0.44; Na\(_2\)SO\(_4\), 0.14; K\(_2\)SO\(_4\), 0.35; (NH\(_4\))\(_2\)SO\(_4\), 0.26; plus 1 ml L\(^{-1}\) trace element solution (Schönheit et al., 1979) and 2 % (v/v) autoclaved fangaia soil extract (liquid obtained from the Fangai mud pool at Pozzuoli in Italy), unless stated otherwise. The medium was adjusted to pH 2 with 1 M H\(_2\)SO\(_4\) before autoclaving. To prevent precipitation, CaHPO\(_4\)-2H\(_2\)O was dissolved in fangaia soil extract and was sterilized separately and added to the bulk of the medium after autoclaving and cooling. The concentration of ammonium (NH\(_4\)\(^+\)) in the fangaia soil extract may vary from 1 to 28 mM. Most of the experiments were performed with an extract containing 28 mM.

**Gas and ammonium analyses.** Methane (CH\(_4\)), oxygen (O\(_2\)), nitrogen (N\(_2\)) and carbon dioxide (CO\(_2\)) were analysed on an Agilent series 6890 gas chromatograph equipped with a Porapak Q and a Molecular Sieve column and a thermal conductivity detector as described before (Ettwig et al., 2008). Ethylene (C\(_2\)H\(_4\)) and acetylene (C\(_2\)H\(_2\)) were analysed with a Varian star 3400 gas chromatograph using a flame-ionization detector and a Porapak N column (30 m x 0.250 mm) with helium (He) as carrier gas. The injection detector and oven temperature were 125, 250 and 90 °C, respectively. The gas chromatographs were calibrated quantitatively for each gas by injecting dilutions of pure gases or mixtures. For all gas analyses 100 μl gas samples were injected with a glass syringe. Ammonium concentrations were measured using the o-phthaldialdehyde (OPA) method (Taylor et al., 1974).

**Batch cultivation.** The effect of O\(_2\) concentration on N\(_2\) fixation by strain SoV was tested in 1.1 serum bottles, sealed with red butyl rubber stoppers. The batch incubations were performed in 50 ml nitrogen-free medium, without fangaia soil extract. The medium was inoculated with cells obtained from the early stationary phase and the inoculum size was always adjusted to achieve the same low initial optical density (OD\(_{600}\)), varying between 0.08 and 0.12. The gas composition in the headspace was adjusted to 13 % and 8 % (v/v) for CH\(_4\) and CO\(_2\), respectively. O\(_2\) concentrations between 1 and 10 % (v/v) were tested. The experiment was started by incubating the bottles at 50 °C with shaking at 200 r.p.m. During the experiment, gas samples were removed from the bottle headspace and analysed as described above.

**Chemostat cultivation.** The growth yield and stoichiometry of CH\(_4\) conversion to CO\(_2\) of strain SoV were determined using a chemostat, under N\(_2\)-fixing conditions. The chemostat, liquid volume 300 ml, was operated at 55 °C with stirring at 750 r.p.m. with a stirrer bar. The chemostat was supplied with medium at a flow rate of 5.1 ml h\(^{-1}\), using a peristaltic pump. The cell-containing medium was removed automatically from the chemostat by a peristaltic pump when the liquid level reached the sensor in the reactor. Supply of CH\(_4\) (0.72 ml min\(^{-1}\), N\(_2\) (0.46 ml min\(^{-1}\)) and CO\(_2\) (2.1 ml min\(^{-1}\)) took place by mass flow controllers through a sterile filter and sparged into the medium just above the stirrer bar. An O\(_2\) sensor in the liquid was coupled to an ADI1030 Biocounter (Applikon) regulating the O\(_2\) mass controller to achieve a O\(_2\) saturation of 0.5 %. After steady state was reached, CH\(_4\) and O\(_2\) consumption and CO\(_2\) production were determined by measuring the going and outgoing gas flows and the gas concentrations. The ingoing gas mixture now contained (all v/v) 14 % CH\(_4\), 19 % O\(_2\), 12 % N\(_2\) and 54 % CO\(_2\) at a flow rate of 3.8 ml h\(^{-1}\). The outgoing gas passed through a sterile filter with a flow rate of 2.8 ml h\(^{-1}\), and contained (all v/v) 3 % CH\(_4\), 2.8 % O\(_2\), 16 % N\(_2\) and 79 % CO\(_2\). To determine the dry weight concentration, triplicate 5 ml samples from the culture suspension were filtered through preweighed 0.45 μm filters and dried to constant weight in a vacuum oven at 70 °C.

**Nitrogenase assay.** Acetylene (C\(_2\)H\(_2\)) reduction has been shown to be a suitable assay for N\(_2\) fixation in methanotrophs (Dalton & Whittenbury, 1976; Murrell & Dalton, 1983; Toukdarian & Lidstrom, 1984). The nitrogenase activity assay was performed in 120 ml serum bottles, sealed with grey butyl rubber stoppers. The black rubber stoppers proved to be inhibitory. For this assay 0.5–2 ml culture was inoculated with cells obtained from the early stationary phase and the nitrogen-free medium, without fangaia soil extract. The medium was autoclaved and cooling. The concentration of ammonium (NH\(_4\)\(^+\)) in the fangaia soil extract may vary from 1 to 28 mM. Most of the experiments were performed with an extract containing 28 mM.

**Phylogenetic analysis.** Representative *nifH*, *nifD* and *nifK* gene sequences, encoding the functional proteins of the nitrogenase complex, were obtained from GenBank. The genes were also extracted from the preliminary genome data of strain SoV (GenBank accession no. GU299762). Conceptual translations into amino acids were performed and a concatenated set was created for alignment and phylogenetic analysis using MEGA 4 (Tamura et al., 2007). The evolutionary history was inferred using the neighbour-joining method (Saitou & Nei, 1987). The bootstrap consensus tree inferred

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from 500 replicates was taken to represent the evolutionary history of the taxa analysed (Felsenstein, 1985).

RESULTS AND DISCUSSION

N2 fixation in batch cultures

Although N2 fixation by the recently discovered methanotrophic verrucomicrobia is claimed on the basis of preliminary data (Dunfield et al., 2007) and the presence of their genetic potential (Op den Camp et al., 2009) there are no reports that show N2 fixation.

Batch incubations of *M. fumariolicum* SolV in nitrogen-free medium (and without fangaia soil extract) showed that this methanotroph was able to fix N2. When *M. fumariolicum* cells from batch cultures in the late exponential phase (when ammonium was already depleted) were transferred to medium with N2 as the sole source of nitrogen, and incubated at our standard oxygen concentrations (5–10 %, v/v) some increase in OD_{600} was observed but this increase did not last long. We subsequently used cells that had reached the stationary phase. Transfers of these cells (at 5–10 %, v/v, O2) never showed any growth within 10 weeks. However, when the initial oxygen concentration was reduced to 2 % (v/v) an increase in OD_{600} could be observed (Fig. 1a), indicating N2 fixation. In batch cultures such low oxygen concentrations cannot be maintained because of rapid oxygen consumption. Even at low cell densities (OD_{600} 0.1), repeated additions of oxygen were necessary and concentrations fluctuated accordingly (Fig. 1b). This variation was also described by Dedysh et al. (2004). Such incubations at around 2 % (v/v) O2 in the headspace resulted in linear growth (Fig. 1a). After decreasing the oxygen concentration to 1.3 % (v/v) and below, a short exponential growth phase was observed (Fig. 1b), but was experimentally difficult to reproduce. It was observed that in such bottles growth accelerated when oxygen concentrations dropped below 1 % (v/v) and slowed down after adjusting the oxygen concentration to 1.5 % (v/v).

In the above-described experiments, it took 13 days before the bacteria started to grow. When these (already) N2-fixing cultures were transferred into fresh nitrogen-free medium, their lag phase was reduced to 1 day. The long adaptation is probably required for induction of the nitrogenase. As there is no free nitrogen available for this protein synthesis, the organism probably relies on the recycling of other proteins or the presence of some stored nitrogen. When the stationary-phase cultures were transferred to ammonium-containing medium, exponential growth started within 1 day, indicating that the long lag phase is not caused by inactivation of metabolism.

When a N2-free argon (Ar) gas phase was used no growth was observed, further supporting the conclusion that an active N2-fixing metabolism was present (Fig. 1a).

The requirement of low oxygen concentration for N2 fixation has also been demonstrated for *Methylobacter luteus* (<2%, v/v), *Methylocystis* strain T-1 (<6%, v/v) and *Methylococcus capsulatus* Bath (<10%, v/v) by batch cultivation under N2-fixing condition (Dedysh et al., 2004; Murrell & Dalton, 1983; Takeda, 1988). In contrast some other known methanotrophs are able to fix N2 at higher oxygen concentrations, e.g. *Methylosinus trichosporium* OB3b (15–17 %, v/v) and *Methylocapsa acidiphila* B2T (atmospheric oxygen concentration) (Dedysh et al., 2002, 2004).

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**Fig. 1.** (a) Batch cultivation of strain SolV in nitrogen-free medium with nitrogen gas as nitrogen source. Incubation with oxygen concentrations of between 0.5 and 1.5 % (A), between 1 and 2 % (■), 5 % (□) and 10 % (△); and the control with 1 % oxygen in the absence of nitrogen (●). (b) Due to practical limitations it was not possible to keep the oxygen concentration (○) constant in the batch bottles and frequent additions were required (arrows).
Nitrogenase assays

The N₂-fixing *M. fumariolicum* cells described above were tested for nitrogenase activity. The acetylene reduction assay showed that these growing cultures indeed possessed nitrogenase activity. After 3 h of incubation with acetylene, linear ethylene production started and continued for more than 8 h at rates of 11.1 nmol h⁻¹ (mg dry weight cells)⁻¹ for the cells growing at around 1% (v/v) O₂. A linearly growing culture (up to 2%, v/v, O₂) showed a lower nitrogenase activity of 3.7 nmol h⁻¹ (mg dry weight cells)⁻¹. Consistently, both the growth experiments and nitrogenase activity assays showed the detrimental effects of oxygen at concentration above 1% (v/v).

The non-growing control culture with argon gas, where oxygen concentration was kept constant at around 1% (v/v), also showed nitrogenase activity. After 3 h of incubation with acetylene, this culture showed linear ethylene production for more than 8 h at a rate of 5.5 nmol h⁻¹ (mg dry weight cells)⁻¹. This activity represents the induction of the nitrogenase. The 3 h incubation time required before linear ethylene production started was also observed for *Methylococcus capsulatus* Bath (Zhivotchenko et al., 1995).

The differences in nitrogenase activity between the cultures grown at 1–2% (v/v) O₂ and below 1% (v/v) O₂ can be explained as a toxic effect of oxygen. Nitrogenase is known to be an oxygen-sensitive enzyme and can be irreversibly damaged by oxygen (Robson & Postgate, 1980). So it is plausible that part of the activity of this enzyme is lost during growth at 1–2% (v/v) O₂, resulting in the linear growth observed.

Our results are in accordance with the concept that molecular oxygen is an important repressor of the transcription of *nif* genes (Rudnick et al., 1997) and that the presence of N₂ is not needed for their activation.

N₂-fixing chemostat cultures

In contrast to batch cultures, chemostat cultivation has the advantage of much better oxygen control, especially at low concentrations. A chemostat with medium containing 2% (v/v) fangaia soil extract (resulting in an initial ammonium concentration of 0.5 mM) was inoculated with *M. fumariolicum* SolV. In the first period of incubation (about 7 days), no medium was supplied to the chemostat; the oxygen concentration in the medium in the chemostat was controlled at 0.5% saturation. Exponential growth was observed for 2 days. The maximum growth rate (μmax) was 0.07 h⁻¹ (corresponding to a doubling time of 10 h), which is identical to that of a batch culture with 5–10% (v/v) O₂ and indicates that oxygen is not limiting growth at 0.5% saturation. Growth ceased (at an OD₆₀₀ of 0.35) when the amount of ammonium from the fangaia soil extract was depleted (<5 µM, Fig. 2a). After 1 day of adaptation the cells resumed exponential growth, but now with N₂ as the only nitrogen source, at a μmax of 0.025 h⁻¹ (doubling time 27 h) (Fig. 2a). The rapid onset of N₂ fixation is in contrast to the long lag phase in batch incubations, where only stationary-phase, nitrogen-depleted cells were able to start N₂ fixation. Apparently the actively growing cells in a chemostat are able to synthesize the nitrogenase protein more rapidly than the fully depleted stationary-phase cells in batch culture. After an OD₆₀₀ of 2 was reached, exponential growth ceased and the culture showed linear growth up to OD₆₀₀ 3.6, most likely due to CH₄ gas–liquid transfer limitations (Fig. 2a). At that time (day 7) the influent and effluent pumps of the chemostat were switched on. The chemostat was now supplied with medium, at a dilution rate of 0.017 h⁻¹ (doubling time 40 h), well below the μmax observed in the batch phase. Although the soil extract added to the medium contains ammonium, the ammonium concentration in the chemostat remained below the detection limit (<5 µM). A stable steady state was reached in about 18 days (Fig. 2b). In the presence of ammonium, N₂ fixation was not expected. Cells will start to fix N₂ when the availability of nitrogen compounds becomes limiting, as was demonstrated for *Methylococcus capsulatus* Bath by Zhivotchenko et al. (1995). Furthermore, ammonium is an important repressor of the transcription of *nif* genes, as was observed for diazotrophic species of proteobacteria (Rudnick et al., 1997).

The μmax of strain SolV under N₂-fixing conditions was 2.8 times slower compared to growth on ammonium as nitrogen source (Pol et al., 2007). This was expected, because N₂-fixation is an endergonic process, which needs...
about 16 mol ATP per N₂ molecule fixed (Dixon & Kahn, 2004). Accordingly, the growth yield of 3.5 g dry weight cells per mol CH₄ under N₂ fixing conditions was almost two times lower than the yield with ammonium as nitrogen source (6.4 g dry weight per mol CH₄; Pol et al., 2007). CH₄ was converted to CO₂ according to the stoichiometry 

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\text{CH}_4 + 1.62 \text{O}_2 \rightarrow 0.87 \text{CO}_2 + 1.5 \text{H}_2\text{O} + 0.13 \text{CH}_2\text{O} \quad \text{(biomass)}
\]

When compared to the stoichiometry of ammonium-grown cells (Pol et al., 2007), a slightly higher consumption of oxygen and production of carbon dioxide was found, which coincides with the lower cell yield.

N₂ fixation by cells of strain SolV grown in chemostat cultures was confirmed by nitrogenase activity assays. The incubation with acetylene showed linear ethylene production for more than 4 h at a rate of 47.4 nmol h⁻¹ (mg dry weight cells⁻¹). The rate is sufficient to sustain N₂ assimilation in chemostat cultures with a doubling time of 40 h. Similar nitrogenase activity values were reported for type II and type X methanotrophs (Murrell & Dalton, 1983). The activity rate of the chemostat-grown cells is four times higher than for cells growing in batch culture at <1% O₂, indicating that 1% (v/v) O₂ is still detrimental for N₂ fixation. In contrast to the inhibitory effect of ammonium on N₂ fixing in growing cultures, concentrations of ammonium up to 94 mM did not have an effect on the acetylene reduction activity of the nitrogenase. Rates were linear for more than 2 h. This was also observed for several species of proteobacteria able to fix N₂ (Rudnick et al., 1997). However, Murrell & Dalton (1983) suggested that ammonium may affect the activity of nitrogenase and not the synthesis of this enzyme.

**Oxygen optimum of SolV nitrogenase activity**

The nitrogenase assay performed under 1% (v/v) O₂ resulted in nonlinear ethylene production, with both batch-grown cells and chemostat-grown cells. Fig. 3(a) shows ethylene production by batch-grown cells with pulse-wise addition of small amounts of oxygen. The effect of oxygen concentration on ethylene accumulation is clearly visible: e.g. addition of oxygen at day 3 slowed down production while the decreasing oxygen concentration from this point onwards resulted in an increase. This effect was explained by oxygen inhibition and was similar to the oxygen effect on growth in the N₂-fixing batch incubations described above.

To determine the optimum oxygen concentration for the SolV nitrogenase activity in whole cells, acetylene and oxygen in the headspace were set to be 2% (v/v) and 0.1–8% (v/v), respectively. The optimal oxygen concentration for SolV nitrogenase activity was found to be 0.5% (v/v) (Fig. 3b). At lower oxygen concentrations the activity decreased, possibly due to oxygen limitation for energy generation. Nitrogenase activity was still observed at oxygen concentrations up to 1% (v/v), but at oxygen concentrations above 2% (v/v) no nitrogenase activity was detected. This is in agreement with the results of batch incubations, where no growth was observed at head-space oxygen concentrations above 2% (v/v) (Fig. 1a) and favours the 0.5% O₂ saturation we used for the chemostat culture liquid medium as being optimal for growth under N₂-fixing conditions. The oxygen requirement for nitrogenase activity for other methanotrophs was 6% (v/v) for *Methylococcus capsulatus* Bath, 2% (v/v) for *Methylosinus* strain 6 and 0.5–1% (v/v) for *Methylocystis* strain T-1.

![Graph](Fig. 3. (a) Effect of oxygen concentration (○) on nitrogenase activity (▲) of a N₂-fixing batch culture of strain SolV. Additions of oxygen are indicated by the arrows. (b) Cell suspensions of N₂-fixing strain SolV were incubated at different oxygen concentrations, with methanol as the oxidizable carbon substrate. Ethylene production from acetylene was measured (■); 100% activity is equal to 47.4 nmol C₂H₄ h⁻¹ (mg dry weight)⁻¹.)
If we compare the nitrogenase assay with growth experiments in nitrogen-free medium, no activity of nitrogenase was observed in assays at oxygen concentrations above 1% (v/v), while growth was observed even at 2% (v/v) O₂. This might be explained as a result of metabolic activity, which reduces the oxygen concentration in the cells.

Phylogenetic analysis of the nitrogenase

From the preliminary genome data it was clear that the important genes for N₂ fixation were present in strain SolV. The genes encoding the structural protein \( \text{nifH} \), \( \text{nifD} \) and \( \text{nifK} \) and the genes encoding cofactor biosynthesis \( \text{nifE} \), \( \text{nifN} \) and \( \text{nifX} \) are located in a putative operon (see Supplementary Fig. 1, available with the online version of this paper). BLASTP searches with the translated genes from the operon revealed 89 ± 6% identity with the proteins of the closely related ‘Methylacidiferum infernorum’ V4. Proteins from \( \alpha \) - and \( \gamma \)-proteobacterial methanotrophs showed 72 ± 10% identity. The Fe-protein from strain SolV, encoded by \text{nifH} \( \alpha \), was shown to possess the cysteines involved in 4Fe–4S cluster coordination and the residues of the two Walker motifs (Howard & Rees, 1996). The other two structural proteins, encoded by \text{nifD} \( \alpha \) and \text{nifK} \( \alpha \), also contain the conserved residues depicted by Howard & Rees (1996).

Based upon NifH phylogeny the verrucomicrobial gene product can be grouped with Cluster I NifH proteins (Zehr et al., 2003; Supplementary Fig. S2). This cluster contains the conventional Mo-containing NifH proteins. The nitrogenase is believed to be an evolutionarily conserved protein complex (Howard & Rees, 1996). The high degree of sequence similarity among nitrogenase proteins may suggest either an early origin or lateral gene transfer among prokaryotic lineages (Postgate & Eady, 1988). Although the early origin is supported by phylogenetic analysis of large sets of nitrogenase and 16S rRNA gene sequences (Postgate & Eady, 1988; Young, 1992), comparative genomics analysis supports a scenario in which nitrogenases could have been dispersed by lateral gene-transfer mechanisms. The relation of verrucomicrobial nitrogenase to that of the Archaea and Proteobacteria was investigated by analysis of a concatenated set of the translated structural genes \( \text{nifH} \), \( \text{nifD} \) and \( \text{nifK} \), taken from representative available bacterial genome sequences. Two cyanobacteria were chosen as an outgroup. The neighbour-joining phylogenetic tree (Fig. 4)
calculated from the alignment showed that the verrucomicrobial nitrogenases group with those of Proteobacteria and acidophilic *Leptospirillum* species, the latter being members of the phylum *Nitrospirae* that inhabit acid mine drainage. This finding seems to be more supportive of the lateral gene transfer scenario also in view of the grouping in the tree with a proteobacterial acidophile, *Acidithiobacillus ferrooxidans*. Based on growth experiments and the acetylene reduction assay, diazotrophy was demonstrated for *Acidithiobacillus ferrooxidans* and *Leptospirillum ferrooxidans* (Mackintosh, 1978; Norris et al., 1995). It is believed that the acidophilic biofilms in acid mine drainage receive limited fixed carbon and nitrogen from external sources and therefore have to fix atmospheric CO₂ and N₂ (Tyson et al., 2005). For the Solfatara ecosystem less is known about the nitrogen availability. We have observed a high variety of ammonium concentrations in soil extract (see above).

**Conclusion**

‘*Methylocacidiphilum funariolicum*’ SoIV was able to fix N₂ under low oxygen concentration (0.5% O₂ saturation) in chemostat cultures at a dilution rate of 0.017 h⁻¹. Based on the acetylene reduction assay and the growth experiment we conclude that the nitrogenase of strain SoIV is extremely oxygen sensitive compared to most other proteobacterial methanotrophs. To our knowledge, this is the first report on the physiology of N₂ fixation within the phylum *Verrucomicrobia*.

**REFERENCES**


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