The thermoacidophilic methanotroph *Methylacidiphilum fumariolicum* SolV oxidizes subatmospheric H_2 with a high-affinity [NiFe] hydrogenase

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The trace amounts (0.53 ppmv) of atmospheric H_2 can be utilized by microorganisms to persist during dormancy. This process is catalyzed by certain Actinobacteria, Acidobacteria and Chloroflexi, and is estimated to convert 75 Tg H_2 annually, which is half of the total atmospheric H_2. This rapid atmospheric H_2 turnover is hypothesized to be catalyzed by high-affinity [NiFe] hydrogenases. However, apparent high-affinity H_2 oxidation has only been shown in whole cells, rather than for the purified enzyme. Here, we show that the membrane-associated hydrogenase from the thermoacidophilic methanotroph *Methylacidiphilum fumariolicum* SolV possesses a high apparent affinity ($K_{m(app)}$ = 140 nM) for H_2 and that methanotrophs can oxidize subatmospheric H_2. Our findings add to the evidence that the group 1h [NiFe] hydrogenase is accountable for atmospheric H_2 oxidation and that it therefore could be a strong controlling factor in the global H_2 cycle. We show that the isolated enzyme possesses a lower affinity (K_m = 300 nM) for H_2 than the membrane-associated enzyme. Hence, the membrane association seems essential for a high affinity for H_2. The enzyme is extremely thermostable and remains folded up to 95 °C. The ability to conserve energy from H_2 could increase fitness of verrucomicrobial methanotrophs in geothermal ecosystems with varying CH_4 fluxes. Group 1h [NiFe] hydrogenases could therefore contribute to mitigation of global warming, since CH_4 is an important and extremely potent greenhouse gas.