

The carbon dioxide mineral sequestration analogues: examples from Tuscany (Italy)

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The Southern area of Tuscany (Italy) provides clear examples of natural analogues of carbon dioxide mineral sequestration. Our studies focused on the geological and geochemical characterization of the different natural manifestations of CO₂-trapping processes. Widespread serpentinite-hosted magnesite deposits have been investigated in the Southern Tuscany (Monti Livornesi, Colline Metallifere, Elba Island), together with shallower deposits of hydromagnesite in Montecastelli area. The magnesite deposits are a consequence of a relatively shallow hydrothermal circulation of Si- and CO₂-rich fluids intensively affecting serpentinite lenses, hosted by argillites [1].

The hydromagnesite incrustations (Figure 1), with the typically white rounded shape and vein or fracture fillings, represent an ongoing carbonation process on a gangue materials dumped from a serpentinite-hosted copper mine, close to Pomarance (Tuscany, Italy).

The study of these natural analogues complements laboratory experiments and possibly provides opportunity to constrain the boundary conditions and the mechanisms for CO₂-bearing phases to form. Here, we report a review of our geological mapping, petrological observation, mineralogical and geochemical analyses together with isotopical studies (C, O, Sr) of different outcrops in order to address: 1) the carbon source (deep versus atmospheric); 2) the fluid path-way during the alteration in relationship with the induced/reactivated fracturation; 3) the areal diffusion and the efficiency of the carbonation process; and 4) the mass balance of major and trace element during the alteration.



Figure 1: Example of hydromagnesite incrustation at Montecastelli

[1] Boschi (2009) *Chemical Geology* **Volume 265**, 209–226.

Eating Iron and Loving it: Ferrous Iron Metabolism in *Rhodospseudomonas palustris* TIE-1

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Iron is an essential element in biological systems, and its transport is thus a prime concern to all life. Iron also serves as an electron donor and acceptor for microbial respiration. However, a lot remains to be understood about these processes and we believe that studying iron specialists will provide fresh insight.

Rhodospseudomonas palustris TIE-1, is an α -proteobacterial iron specialist that uses energy from light and electrons from ferrous iron Fe(II) to support photoautotrophy (photoferrotrophy). *R. palustris* TIE-1 is the only genetically tractable photoferrotrophic microbe, and we are interested in employing molecular and geochemical analyses to better understand A) how it copes with high Fe(II) concentrations, and B) how electrons are transferred from Fe(II) to the photosynthetic reaction center.

Bioinformatics was used to interrogate the genome of *R. palustris* TIE-1 for putative Fe(II) transporters. The *pioABC* operon, the genetic locus essential for photoferrotrophy, was also included in this analysis. This locus might be responsible for both iron and electron transport. A combination of techniques such as heterologous complementation, mutant analysis, and immunofluorescence was used to confirm the role of the identified loci in Fe(II) transport. To assess the role of the Pio proteins in electron transfer from Fe(II) to the photosynthetic reaction center, novel bioelectrochemical reactors were devised. Our data indicate that *R. palustris* TIE-1 employs different membrane-bound Fe(II) transport systems under aerobic, anaerobic and photoferrotrophic conditions. Although the role of the Pio proteins in iron transport remains unclear, we demonstrate that they allow *R. palustris* TIE-1 to accept electrons from a poised electrode in the presence of light, supporting net carbon fixation and growth. We refer to this process as “photoelectrosynthesis” (PES).

This comprehensive study provides a better understanding of Fe(II) transport in α -proteobacteria. We also show that a pure phototrophic culture can perform PES, which has not been demonstrated previously. The role of the Pio proteins in PES brings to light the use of a common protein module to perform electron transfer reactions in unrelated bacteria. Ongoing studies are aimed at further understanding this process at the molecular level.