



The role of bacterial biomineralization on the pedogenesis of magnetic Apennines paleosols

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It is known that the soil magnetic properties are sensitive indicators of soil-forming processes. However, even where soils have developed on the same substrate and over the same timescale, great differences in magnetic properties can result over short distances. A soil may become magnetically enhanced if there is conversion of some of the weakly magnetic Fe-oxyhydroxides or other Fe sources into strongly ferrimagnetic minerals such as magnetite and maghemite. There are many theories explaining soil magnetic susceptibility: chemical weathering, sedimentary rocks, inherited magnetite, fires, and bacterial mineralization. Although the biological contribution to pedogenic magnetic content is well documented, the metabolic processes of Fe-reducing bacteria are still largely unknown.

In this work soils evolved from ammonitic limestone dating back 170-183 million years ago (Middle/Early Jurassic, Aalenian/Toarcian stage) and characterized by opposite magnetic properties were collected from Mount Zuccarello in Central Apennines (Italy), from 880 to 990 m a.s.l. and investigated for their chemical properties, morphological characteristics and microstructures of magnetic minerals, powder X-ray diffractometry (XRD), X-Ray fluorescence with DP-6000 Delta Premium PXRF (Olympus-Innov-X, Waltham, MA USA) and microscopy (SEM-EDX). The magnetic soil revealed a higher content of maghemite as compared to the non-magnetic soil, likely derived from magnetite oxidation. Furthermore, the correlation between the contents of magnetic minerals and organic matter suggests that an efficient Fe³⁺ reduction occurred, with a consequent magnetite formation. This would have been made possible because of an adequate supply of oxidizable organic matter. As Fe²⁺ production occurs upon (temporary) wetting of soil portions and subsequent respiratory depletion of oxygen, investigation of the bacteria population harbouring these soils occurred after their isolation under both aerobic and anaerobic (microaerophilic) conditions. Both types of bacteria were identified and characterized for their ability to bind and reduce Fe³⁺. Furthermore, the total DNA was extracted and the entire bacterial community was assessed by means of pyrosequencing of the 16S rRNA genes.