"Gheorghe Asachi" Technical University of Iasi, Romania

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CHARACTERIZATION OF MICROBIAL COMMUNITIES IN GROUNDWATER FROM LOMBARDIA (ITALY) POLLUTED BY ARSENIC

Lucia Cavalca[1,2], Patrizia Zaccheo[3], Anna Corsini[1], Ben Abbas[2], Paolo Mulotto[1], Vincenza Andreoni[1], Gerard Muyzer[1,4]

[1]*Dipartimento di Scienze e Tecnologie Alimentari e Microbiologiche (DiSTAM), University of Milano, via Celoria 2, Milano, Italy, I-20133;* [2]*Department of Biotechnology, Delft University of Technology, Julianalaan 67, 2628 BC Delft, The Netherlands* [3]*Dipartimento di Produzione Vegetale (DiProVe), University of Milano, via Celoria 2, Milano, Italy, I-20133* [4]*Department of Aquatic Microbiology, Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, 1090 GE Amsterdam, The Netherlands*

Abstract

Human exposure to arsenic (As) typically occurs through drinking water and the World Health Organization indicates a maximum threshold of 10 μg L^{-1} in drinking water. The aims of the work were 1) to investigate the relationships between groundwater microbial populations and water characteristics and 2) to envisage an origin of As contamination.

Water samples were collected from 10 sites (six wells and four piezometers, Cremona, Italy), chosen from ARPA Lombardia (Regional Agency for Health Prevention and Environmental Protection) dataset, based on their different levels of As pollution. Samples from piezometers showed neutral pH value, significantly higher concentrations of total dissolved iron (Fe) and manganese (Mn) and significantly higher values of electrical conductivity (EC) than samples from wells. These latter samples had a mean pH value of 7.8. The total As concentration in groundwater samples ranged from 0.7 to 171 μg L^{-1}. Samples from eight out of 10 sites exceeded the 10 μg L^{-1} As threshold (D.Lgs. 31/2001). AsIII was dominant in all the samples and AsIII/AsV ratio ranged from 3.6 to 6.7.

Denaturing gradient gel electrophoresis (DGGE) and Pyrotag sequence were used to characterize six microbial groundwater communities by analysing 16S rRNA genes amplified from environmental DNA. Sequence of dominant DGGE bands showed significant similarities with those of uncultured bacteria related to chemolithoautrophic denitrifying, nitrite-oxidizing, sulfur-oxidising, sulfate-reducers and methylophilic strains. A *Nitrospira*-related sequence was found in three out of six groundwater samples reflecting the widespread of these nitrifiers in natural ecosystems. No sequence was directly related to known As strains, possibly because their number was below the detection limit. By Pyrotag sequence analysis Betaproteobacteria (retrieved in five out of the six samples), Delta and Epsilonproteobacteria (in four samples), and Alphaproteobacteria (in three samples) were found as the mostly represented classes. Pyrotag sequence analysis allowed the detection of Fe (*Gallionella* sp.) and of Mn (*Hyphomicrobium* sp.) oxidizers and Fe reducers (*Geobacter* sp.). In addition to the 16S rRNA genes, genes related to the AsV respiratory reductase (*Arr*A) and the AsV reductase (*ArsC*) were found in some groundwater samples.

Dissimilatory AsV respiring, AsV reducing and Fe reducing bacteria could be responsible for As mobilization in groundwaters from Lombardia, although the presence of AsV in reducing environment suggests also activity of AsIII-oxidizing bacteria.

Acknowledgment