

Bioremediation potential of immobilized aerobic consortia dechlorinating 1,2-DCA

E.M. Petta^{1*}, L. Scirè Calabrisotto^{1*}, I. Cruciata¹, M.C. Citarrella², M. Tagliavia^{1,3}, A. Vassallo⁴, G. Carpani⁵, R. Scaffaro², V. Catania⁶ and P. Quatrini¹

¹Department of Biological, Chemical and Pharmaceutical Sciences and Technologies (STeBiCeF), University of Palermo, Italy ²Department of Engineering, University of Palermo, Italy ³Institute for Biomedical Research and Innovation – National Research Council (IRIB-CNR), Palermo, Italy ⁴School of Biosciences and Veterinary Medicine, University of Camerino, Italy ⁵Environmental and Biological Laboratories, Eni S.p.A., S. Donato Milanese, Milan, Italy ⁶Department of Earth and Marine Sciences (DiSTeM), University of Palermo, Italy

*These authors contributed equally to this work

Corresponding author e-mail: elisamaria.petta@unipa.it / laura.scirecalabrisotto@unipa.it

1,2-dichloroethane (1,2-DCA) is a persistent and probably carcinogenic groundwater contaminant. Under suitable conditions, 1,2-DCA can be biodegraded by specialized microorganisms by anaerobic and aerobic pathways that can be exploited in bioremediation. Although anaerobic pathways are usually more studied, hydrolytic aerobic biodegradation seems a promising alternative. Currently, the only known hydrolytic pathway is mediated by the key enzyme haloalkane dehalogenase Dh1A, encoded by the *dhlA* gene, carried by a few isolates within the Xanthobacteriaceae family¹. In this work, the dechlorinating potential of newly isolated aerobic 1,2-DCA degrading consortia was evaluated to be exploited in bioremediation strategies based on bioaugmentation with immobilized degrading bacteria.

Six 1,2-DCA dechlorinating consortia were isolated from 1,2-DCA contaminated groundwater through enrichment cultures on mineral salt medium amended with 1,2-DCA as sole carbon source and subsequent transfer on solid medium. Chemical monitoring performed over time (on four of the six consortia) by Cl⁻ release assay and Gas Chromatography-Mass Spectrometry (GC-MS) revealed stable 1,2-DCA removal capacity by all consortia. The Whole Genome Sequencing revealed the presence of genera including known aerobic 1,2-DCA degraders (*Ancylobacter*, *Starkeya*, *Xanthobacter*) and other genera whose role in the consortia is yet unclear. All consortia carried a *dhlA* gene fragment 100% identical to that of other known aerobic 1,2-DCA degraders, and other genes involved in the hydrolytic 1,2-DCA degradative pathway. The consortia were tested for the ability to form 1,2-DCA-degrading biofilms on biodegradable biopolymeric polylactic acid (PLA) scaffolds made by electrospinning². Scanning Electron Microscopy observations and GC-MS monitoring revealed the consortia can form a biodegrading biofilm on biopolymeric scaffolds that maintains its properties after being transferred to a new system.

Successful immobilization on biopolymeric supports suggests the potential application of the dechlorinating consortia-scaffold system as a bioremediation device.

¹Munro et al., (2016). Appl. Environ. Microbiol. 82(17), 5298-5308.

²Catania et al., (2020) New Biotechnology 58, 25-31;