Enhancing Reductive Dechlorination of Chloroethenes using Agri-Food Wastes

Camilla Valli[1], Sarah Zecchin[1], Laura Ferrari[2], M. Agosta[3], Lucia Cavalca[1]

[1] Department of Food, Environmental and Nutritional Sciences (DeFENS), University of Milan, Via Celoria 2, 20133 Milan, Italy
[2] Tauw Italia Srl, P.za L. Da Vinci 7, 20133 Milan, Italy
[3] Edison S.p.a., Foro Bonaparte 31, 20121 Milan, Italy

Corresponding author email: lucia.cavalca@unimi.it

ABSTRACT

Chloroethenes (CE) are widely used as solvents in industrial activities. Their intensive use and inadequate disposal methods have resulted in their penetration in permeable groundwater aquifers and affecting high-quality water availability worldwide (Bertolini et al., 2023). Although parental compounds such as tetrachloroethene (PCE) and trichloroethene (TCE) are toxic to humans, dehalogenation products 1,1- and 1,2(*cis-trans*)-dichloroethene (DCE) and vinyl chloride (VC) are carcinogenic. Biodegradation rate of bacterial organohalide respiration is limited by the availability of electron donors that limit the possibility to conduct complete dehalogenation to ethene. Adding fermentable reducing substrates that increase hydrogen and small organic acids, supports organo-halide respiring bacteria. Agrifood wastes represent a valuable source of bio-based substrates and enhance sustainability of bioremediation processes.

In this study, fermentable substrates (*i.e.* molasses, tomato extract, pomace, whey and pumpkin seed extract) were analyzed at a microcosm scale to evaluate their effects on reductive dehalogenation process. Real groundwater contaminated by 150-300 mg/L CE from landfill leachate was used. Physico-chemical parameters (pH, ORP, and chemical oxygen demand) and CE concentrations were monitored after 1, 4 and 6 month-incubation.

GC-MS analyses demonstrated CE biological dehalogenation over a 4-month incubation. The degradation efficiency of PCE was 70% higher in the presence of reducing substrates if compared to natural attenuation. Concurrently, the accumulation rate of VC was lower in all treatments added of waste-derived substrates, due to complete dehalogenation to ethene. Biomarkers for TCE and VC reductases *(tceA*, *vcrA)* and for *Dehalococcoides* 16S rRNA genes, quantified by real-time quantitative PCR, ranged from 10^7 to 10^9 gene copies/mL and were higher in substrate-amended trials. Molasses and tomato extract were more effective than other substrates in stimulating *Dehalococcoides* population growth and reductive dehalogenation genes *tceA* and *vcrA* compared to other substrates and natural attenuation. The impact of substrate addition on the microbial community is being investigated using 16S rRNA Illumina libraries. Data analyses are currently running.

Agri-food waste substrates, particularly molasses and tomato extract, significantly enhanced CE degradation and stimulated key dechlorinating bacteria. This approach not only promotes effective remediation of CE-contaminated sites but also provides a sustainable solution for waste valorization.

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References:

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