Evaluation of the natural attenuation potential of a complex pollution plume (chlorate, perchlorate, 1,2dichloroethane and vinyl chloride) by autochthonous microbial communities

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Evaluation of the natural attenuation potential of a complex pollution plume (chlorate, perchlorate, 1,2dichloroethane and vinyl chloride) by autochthonous microbial communities

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Artificially synthetized chloride-based-oxyanions such as perchlorate (ClO_4^-) and chlorate (ClO_3^-), are used in a vast number of applications such as military and aerospace industry; they are also used as herbicides and in pyrotechnic applications. Due to their very high solubility, perchlorate and chlorate are readily transported in water systems and can thus end up in drinking water. Ingestion of perchlorate may affect iodine uptake by the human thyroid and thus thyroidal hormone production. Pollution by these oxyanions is an emerging problem in France and recent events of ground water contamination have increased concerns on the fate of these substances, thus encouraging research on its fate in the environment and effect on human health. As the transport of (liquid and gaseous) chloride is highly dangerous, it is generally transformed directly on site and thus other chloride molecules such as 1, 2 dichloroethane (DCA) which is a precursor of vinyl chloride (VC), can be found in the same locations.

The work we present here involves a site that once produced perchlorate, chlorate, DCA and VC. Due to historical losses, all of these substances are present in the groundwater. Following groundwater characterisation, the aim of the present study was to identify a naturel attenuation potential on site by researching specific genes involved in chlorate and perchlorate reduction and DCA or VC dehalogenation and then linking gene presence to activity using laboratory batch cultures.

After collecting biomass from 36 ground-water-samples, DNA was extracted and PCRs (polymerase chain reactions) were carried out to amplify genes coding for several enzymes; the *pcaA* gene coding for a alkane dehydrogenase, the *dhLA* gene coding for a haloalkanedehalogenase, the *pcrA* gene coding for a perchlorate reductase and the *cld* gene coding for a chlorite reductase. Moreover, global bacterial diversity was studied by amplifying the gene coding for RNA 16S and analysing diversity with an electrophoresis approach (DGGE, Denaturing Gel Gradient Electrophoresis). Bands of interest were purified and sequenced.

The gene-screening-results closely recovered zones where the chemicals had been detected in concentrations over 10µg/l and were especially precise for DCA and CV whereas for perchlorate and chlorate it suggested that the pollution span was once larger that presently. Degradation potentials, in batchs incubated at 15°C, demonstrated first chlorate reduction

then perchlorate reduction after a week's incubation in presence of an available carbon source (acetate and lactate) but no degradation in autotrophic conditions. DCA amounts also decreased in batchs but over a longer time span. Due to the pollution layout, where the perchlorate and chlorate plume encounters the DCA and VC one, experiments are presently being carried out to assess whether these organochlorides and/or their dechlorination metabolites can be used as a carbon source to fuel perchlorate and chlorate reduction, thus actively contributing to a naturel attenuation of this pollution. This potential could then be stimulated and used for *in situ* bioremediation. Indeed, total degradation of these molecules produces Cl^-, CO_2 and H_2O and which are harmless for the environment.