

#: In development *: New

Microbial groups		
Detection	Target gene	Remark
Total Bacteria	Bacterial 16S rRNA	
Total Archaea	Archaeal 16S rRNA	
Denitrifying bacteria	Nitrate reductase (<i>narG</i>)	NO ₃ → NO ₂
Denitrifying bacteria	Nitrite reductase (<i>nirS</i> or <i>nirK</i>)	NO ₂ → NO
Denitrifying bacteria	Nitrous oxide reductase (<i>nosZ</i>)	N ₂ O → N ₂
Nitrogen fixation bacteria*	Nitrogen reductase (<i>nifH</i>)	N ₂ → N-biomass
Nitrifying bacteria*	Ammonia mono-oxygenase (<i>amoA</i>)	NH ₄ ⁺ → NH ₃
Ammonification bacteria*	Urease (<i>ureC</i>)	N-biomass → NH ₄ ⁺ / NH ₃
Annamox bacteria*	16S rRNA of <i>Scalindua brodea</i>	NO ₂ + NH ₄ ⁺ → N ₂
Iron-reducing bacteria	Geobacteriales 16S rRNA	
Sulphate-reducing bacteria	Sulfite-reductase (<i>dsrA</i> or <i>dsrB</i>) Adenosine-5'-phosphosulphate reductase (<i>aspA</i>)*	
Hydrogen-consuming bacteria	Fe-hydrogenase (<i>hydA</i>) NiFeSe-hydrogenase (<i>hysA</i>)	(e.g. Microbiological influenced corrosion, MIC)
Methanogenic Archaea	Methyl-CoM reductase (<i>mcrA</i>)	
Pathogenic bacteria		
Detection	Target gene	Remark
Cyanobacteria	Cyanobacteria 16S rRNA Microcystis 16S rRNA <i>Synthase toxine (mcyD)</i>	
<i>Legionella</i> sp.	5s rRNA <i>mipA</i>	<i>Legionella</i> group <i>Legionella pneumophila</i>
<i>Enterobacteriaceae</i>	<i>Enterobacteriaceae</i> 23S rRNA	Indicator of faecal contamination
<i>Escherichia coli</i>	Glucuronidase (<i>uidA</i>)	Indicator of faecal contamination
Biological transformation of pollutants		
Detection	Target gene	Remarks
Mineral oil#	Alkane mono-oxygenase (<i>alkA</i> and <i>alkB</i>)	Alkane hydroxylation
BTEX (benzene, toluene, ethyl benzene, xylene)#	Catechol-1,2-dioxygenase Catechol-2,3-dioxygenase	Aerobic ring-cleavage
PAH (polycyclic aromatic hydrocarbons)#	α subunit of the PAH-ring hydroxylating dioxygenases (PAH-RHDα) for Gram Positive (PAH-RHDα GP) Gram Negative (PAH-RHDα GN)	
MTBE (methyl <i>tert</i> -butyl ether)	MTBE mono-oxygenase (<i>mdpA</i>) Isobutyryl-CoA mutase (<i>icmA</i>)*	MTBE → TBA Degradation of 2-HIBA
TEX (toluene, ethyl benzene, xylene)	Benzylsuccinyl-CoA synthase (<i>bssA</i> # and SRB- <i>bssA</i> #)	Anaerobic ring-cleavage
1,2-dichloroethane	Haloalkane dehalogenase (<i>dhIA</i>)	Hydrolytic dechlorination
PCE & TCE (tetrachloroethene, trichloroethene)	16S rRNA specific for <i>Dehalococcoides</i> , <i>Desulfitobacterium</i> , <i>Sulfurospirillum</i> , <i>Dehalobacter</i> , <i>Desulfuromonas</i> and/or <i>Desulfomonile</i>	Anaerobic reductive dechlorinating bacteria
pTCE (trichloroethene)	Trichloroethene reductase (<i>tceA</i>)	TCE → cis-DCE
Cis-DCE & VC1	<i>Dehalococcoides</i> spp. 16S rRNA	Anaerobic dechlorinating bacteria
VC 1	Vinylchloride reductase (<i>vcrA</i> and <i>bvcA</i>)	Anaerobic, VC → ethene
VC*2	Exoxyalkane coenzyme M transferase (<i>etrE</i>)	Aerobic VC degradation

1 Bas van der Zaan, Fredericke Hannes, Nanne Hoekstra, Huub Rijnaarts, Willem m.de Vos, Hauke Smidt and Jan Gerritse, 2010, Correlation of *Dehalococcoides* 16S rRNA and chloroethene-reductive dehalogenase genes with geochemical conditions in chloroethene-contaminated groundwater in Applied and Environmental Microbiology, Vol. 76, (3), p.843-850

2 Sara Picone, Fredericke Hannes, Jan Gerritse, Tim Grotenhuis, Huub Rijnaarts, (article in preparation) Aerobic vinyl chloride degradation in unsaturated soil batches