

## Supporting information

# Corrosion and Fate of Depleted Uranium Penetrators under Progressively Anaerobic Conditions in Estuarine Sediment

*Stephanie Handley-Sidhu<sup>◇</sup>, Paul J Worsfold<sup>◇</sup>, Christopher Boothman<sup>○</sup>, Jonathan R Lloyd<sup>○</sup>, Rebeca Alvarez<sup>○</sup>, Francis R Livens<sup>†○</sup>, David J Vaughan<sup>○</sup> and Miranda Keith-Roach<sup>◇\*</sup>*

### Summary

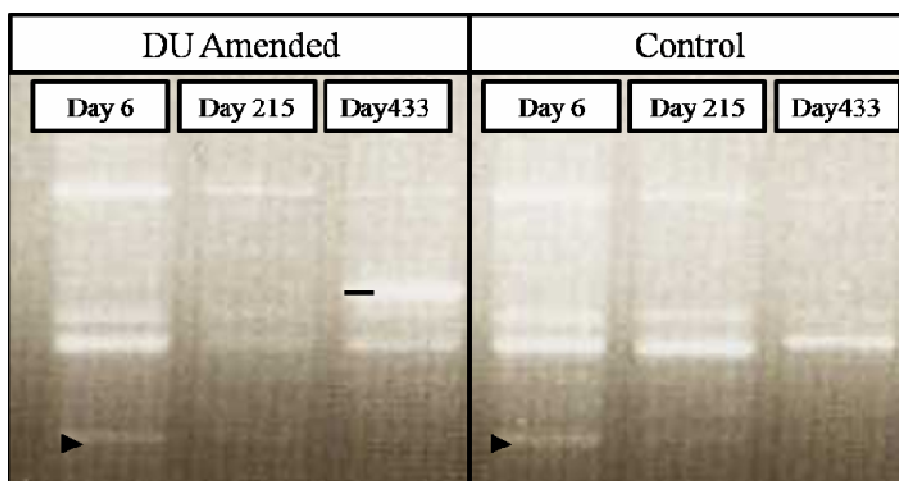
Pages = 5

Figure 1. Ribosomal intergenic spacer analysis (RISA) profile

Tables 1-3. DNA clone library sequencing results

Figure 2. Backscattered electron image and SEM/EDAX spectrum of U-rich particle.

**Figure 1.** Ribosomal intergenic spacer analysis (RISA) profiles for the DU contaminated and control high salinity microcosms, on days 6, 215 and 433, showing: (▶) the band that disappears over time as anaerobic conditions develop and (—) the band that appears by day 433 in the DU amended experiments.



**Table 1.** DNA clone library sequencing results for control Day 6 (A)

Clone	RFLP Type	Closest Matching Micro organism (accession Number)	Identities (% Match)	% Present	Phylogenetic Class
SSDUT0-1	1	Uncultured bacterium clone Fitz2_1 <a href="#">gb DQ256657.1</a>	207/256 (80%)	5.5%	Unknown
SSDUT0-2	2	Uncultured gamma proteobacterium clone Belgica2005/10-140-24 <a href="#">gb DQ351796.1</a>	914/931 (98%)	11.1%	Gammaproteobacteria
SSDUT0-3	3	Sediminibacter furfurosus <a href="#">dbj AB255369.1</a>	822/854 (96%)	3.6%	Flavobacteria
SSDUT0-4	4	Uncultured bacterium clone lka85 <a href="#">gb EF467579.1</a>	862/868 (99%)	1.9%	Unknown
SSDUT0-5	5	Lutimonas vermicola strain IMCC1616 <a href="#">gb EF108218.1</a>	857/890 (96%)	1.9%	Flavobacteria
SSDUT0-6	6	Loktanela agnita <a href="#">gb AY682198.1</a>	731/798(91%)	1.9%	Alphaproteobacteria
SSDUT0-7	7	Maribacter sp. EM44 <a href="#">gb EU443206.1</a>	867/883(98%)	3.6%	Flavobacteria
SSDUT0-8	8	Uncultured gamma proteobacterium clone Belgica2005/10-ZG-4 <a href="#">gb DQ351800.1</a>	913/918 (99%)	1.9%	Gammaproteobacteria
SSDUT0-9	9	Uncultured gamma proteobacterium clone NABOS_AG Gbact20 <a href="#">gb EU544853.1</a>	822/831 (98%)	5.5%	Gammaproteobacteria
SSDUT0-11	10	Uncultured bacterium clone IFD_64 <a href="#">gb DQ984548.1</a>	647/772 (83%)	1.9%	Unknown
SSDUT0-12	11	Loktanela tamlensis strain SSW-35 <a href="#">gb DQ533556.1</a>	846/879 (96%)	1.9%	Alphaproteobacteria
SSDUT0-13	12	Rhodobacteraceae bacterium DG1295 <a href="#">gb DQ486507.1</a>	810/881 (91%)	11.1%	Alphaproteobacteria
SSDUT0-14 SSDUT0-16	13, 14	Formosa algae clone SE60 <a href="#">gb AY771766.1</a>	878/905 (97%)	7.4%	Flavobacteria
SSDUT0-17	15	Uncultured bacterium clone P9X2b7G06 <a href="#">gb EU491232.1</a>	896/928 (96%)	1.9%	Unknown
SSDUT0-19	16	Formosa crassostrea strain KO3 <a href="#">gb EU328155.1</a>	794/891 (89%)	5.5%	Flavobacteria
SSDUT0-21	17	Gilvibacter sediminis <a href="#">dbj AB255368.1</a>	843/916(92%)	7.4%	Flavobacteria
SSDUT0-22	18	Gelidibacter sp. IMCC1914 <a href="#">gb EF108219.1</a>	871/881(98%)	3.6%	Flavobacteria
SSDUT0-24	19	Thiobacillus denitrificans ATCC 25259 <a href="#">gb CP000116.1</a>	839/872 (96%)	1.9%	Betaproteobacteria
SSDUT0-25	20	Dechloromarinus chlorophilus <a href="#">gb AF170359.1</a>   <a href="#">AF170359</a>	862/942 (91%)	1.9%	Gammaproteobacteria
SSDUT0-27	21	Agrobacterium ferrugineum <a href="#">dbj D88522.1</a>	858/884(97%)	3.6%	Alphaproteobacteria
SSDUT0-29	22	Uncultured actinobacterium clone Nubeena299 <a href="#">gb AY500123.1</a>	761/801 (95%)	1.9%	Actinobacteria
SSDUT0-35	23	Rhodobacter ovatus strain JA234T <a href="#">emb AM690348.2</a>	795/870 (91%)	1.9%	Alphaproteobacteria
SSDUT0-36	24	Uncultured bacterium clone FCPT679 <a href="#">gb EF516864.1</a>	945/961 (98%)	3.6%	Unknown
SSDUT0-38	25	Uncultured Planctomycetales QSSC8L-11 <a href="#">gb AF170771.1</a>	704/713 (98%)	1.9%	Planctomycetacia
SSDUT0-44	26	Uncultured marine bacterium clone SJC3.21 <a href="#">gb DQ071119.1</a>	916/925 (99%)	1.9%	Unknown
SSDUT0-45	27	Uncultured bacterium clone:S9JA-40 <a href="#">dbj AB154319.1</a>	897/910 (98%)	1.9%	Unknown
SSDUT0-51	28	Desulfobulbus mediterraneus <a href="#">gb AF354663.1</a>	822/878 93%)	1.9%	Deltaproteobacteria

**Table 2.** DNA clone library sequencing results for control Day 433 (B)

Clone	RFLP Type	Closest Matching Micro organism (accession Number)	Identities (% Match)	% Present	Phylogenetic Class
SSCT433-1	1	Uncultured spirochete clone Nubeena322 <a href="#">gb AY500097.1</a>	538/560 (96%)	1.8%	Spirochaetes
SSCT433-2	2	Pelobacter sp. clone A3b3 <a href="#">emb AJ271656.1 PSP271656</a>	872/881 (98%)	3.4%	Deltaproteobacteria
SSCT433-3	3	Uncultured gamma proteobacterium clone Belgica2005/10-140-1 <a href="#">gb DQ351774.1</a>	855/859 (99%)	7.0%	Gammaproteobacteria
SSCT433-4	4	Croceimarina litoralis strain IMCC1993 <a href="#">gb EF108214.1</a>	808/840 (96%)	1.8%	Flavobacteria
SSCT433-5	5	Silicibacter pomeroyi DSS-3 <a href="#">CP000031</a>	44/55 (80%)	1.8%	Alphaproteobacteria
SSCT433-6	6	Clostridium mesophilum strain SW408 <a href="#">gb EU037903.1</a>	755/823 (91%)	1.8%	Clostridia
SSCT433-7	7	Uncultured bacterium clone EPR3968-O8a-Bc13 <a href="#">gb EU491683.1</a>	901/913 (98%)	3.4%	Unknown
SSCT433-8	8	Uncultured eubacterium WCHA1-37 <a href="#">gb AF050577.1</a>	794/869 (91%)	1.8%	Unknown
SSCT433-9	9	Uncultured candidate division WS3 bacterium clone LD1-PA16 <a href="#">gb AY114313.1</a>	783/807 (97%)	3.4%	Unknown
SSCT433-10	10	Desulfobulbus rhabdoformis <a href="#">gb U12253.1 U12253</a>	844/917 (92%)	1.8%	Deltaproteobacteria
SSCT433-11	11	Uncultured spirochete clone 1E095 <a href="#">gb AY605146.1</a>	837/869 (96%)	1.8%	Spirochaetes
SSCT433-12	12	Uncultured bacterium clone:LS4-147 <a href="#">dbj AB234243.1</a>	887/912 (97%)	1.8%	Unknown
SSCT433-13	13	Tenacibaculum marinus strain A31 <a href="#">gb EU290161.1</a>	874/928 (94%)	10.5%	Flavobacteria
SSCT433-14	14	Olavius algarvensis sulfate-reducing endosymbiont <a href="#">gb AF328857.1 AF328857</a>	728/770 (94%)	3.4%	Deltaproteobacteria
SSCT433-15	15	Uncultured bacterium clone Flynn1_6 <a href="#">gb DQ256526.1</a>	770/792 (97%)	1.8%	Unknown
SSCT433-16	16	Acidovorax temperans <a href="#">gb AF078766.1 AF078766</a>	845/848 (99%)	1.8%	Betaproteobacteria
SSCT433-18	17	Uncultured Bacteroidetes bacterium clone OMEGA_pl_cont_7_A10 <a href="#">gb EU052266.1</a>	857/879 (97%)	5.2%	Unknown
SSCT433-20	18	Eudora adriatica <a href="#">emb AM945588.1</a>	763/802 (95%)	1.8%	Unknown
SSCT433-21	19	Uncultured delta proteobacterium <a href="#">dbj AB116504.1</a>	816/822 (99%)	8.7%	Deltaproteobacteria
SSCT433-23	20	Uncultured marine bacterium clone SJC3.21 <a href="#">gb DQ071119.1</a>	849/858 (98%)	8.7%	Unknown
SSCT433-25	21	Uncultured Azospirillum sp. clone BME95 <a href="#">gb DQ917835.1</a>	801/855 (93%)	1.8%	Alphaproteobacteria
SSCT433-26	22	Uncultured bacterium clone Asc-s-22 <a href="#">gb EF632644.1</a>	850/862 (98%)	1.8%	Unknown
SSCT433-27	23	Andersenella baltica strain BA141T <a href="#">emb AM712634.1</a>	778/788 (98%)	6.9%	Alphaproteobacteria
SSCT433-30	24	Uncultured bacterium clone Flynn2_14 <a href="#">gb DQ256506.1</a>	821/862 (95%)	1.8%	Unknown
SSCT433-35	25	Uncultured bacterium clone:S9JA-40 <a href="#">dbj AB154319.1</a>	899/924 (97%)	1.8%	Unknown
SSCT433-38	26	Uncultured gamma proteobacterium clone Belgica2005/10-ZG-8 <a href="#">gb DQ351804.1</a>	932/950 (98%)	5.2%	Gammaproteobacteria
SSCT433-39	27	Maribacter polysiphoniae strain LMG 23671 <a href="#">Temb AM497875.1</a>	869/894 (97%)	1.8%	Flavobacteria
SSCT433-47	28	Gelidibacter sp. IMCC1914 <a href="#">gb EF108219.1</a>	825/836 (98%)	1.8%	Flavobacteria
SSCT433-49	29	Uncultured bacterium clone:JS624-8 <a href="#">dbj AB121106.1</a>	734/793 (92%)	1.8%	Unknown
SSCT433-52	30	Uncultured candidate division WS3 bacterium clone LD1-PA13 <a href="#">gb AY114311.1</a>	849/894 (94%)	1.8%	Unknown

**Table 2.** DNA clone library sequencing results for DU-Amended Day 433 (C)

Clone	RFLP Type	Closest Matching Micro organism (accession Number)	Identities (% Match)	% Present	Phylogenetic Class
SSDUT433-1	1	Uncultured epsilon proteobacterium clone MC1_bact_cl30gb DQ295689.1	749/772 (97%)	3.6%	Epsilonproteobacteria
SSDUT433-2	2	Uncultured Desulfobulbaceae bacterium clone HT06Ba20 gb EU016446.1	945/959 (98%)	1.8%	Deltaproteobacteria
SSDUT433-3	3	Erythrobacter seohaensis gb AY562219.1	883/900 (98%)	1.8%	Alphaproteobacteria
SSDUT433-4	4	Olavius algarvensis sulfate-reducing endosymbgb AF328857.1 AF328857	910/969 (93%)	1.8%	Deltaproteobacteria
SSDUT433-5	5	Uncultured bacterium clone YE-QS-F49 gb DQ438317.1	912/927 (98%)	1.8%	Unknown
SSDUT433-6 SSDUT433-15	6, 12	Sulfurovum lithothropicum dbj AB091292.1	883/925 (95%)	36.4%	Epsilonproteobacteria
SSDUT433-7	7	Haemaphysalis longicornis symbiont 66 gb AY342036.1	835/936 (89%)	1.8%	Gammaproteobacteria
SSDUT433-8	8	Roseovarius sp. S6Vdbj AB114421.1	948/965(98%)	7.4%	Alphaproteobacteria
SSDUT433-12	9	Desulfobulbus mediterraneus strain NA62emb AJ866934.1	816/877 (93%)	1.8%	Deltaproteobacteria
SSDUT433-13	10	Thioalkalispira microaerophila strain ALEN 1gb AF481118.1	853/885 (96%)	1.8%	Gammaproteobacteria
SSDUT433-14	11	Pseudomonas lini strain B25 gb EU169168.1	853/914 (93%)	1.8%	Gammaproteobacteria
SSDUT433-16	13	Uncultured bacterium clone Kas27B gb EF203181.1	934/946 (98%)	3.6%	Unknown
SSDUT433-19	14	Desulfobacterium phenolicum strain DSM 3384emb AJ237606.1 DPH237606	865/940 (92%)	3.6%	Deltaproteobacteria
SSDUT433-20	15	Coxiella burnetii RSA 331 gb CP000890.1	856/970 (88%)	3.6%	Gammaproteobacteria
SSDUT433-22	16	Unidentified bacterium clone zdt-45e5 gb AC160099.1	941/1005 (93%)	1.8%	Unknown
SSDUT433-25	17	Uncultured delta proteobacterium clone CB13gb DQ831539.1	946/962 (98%)	5.6%	Deltaproteobacteria
SSDUT433-26	18	Uncultured bacterium clone Flynn1_17 gb DQ256717.1	940/954 (98%)	9.2%	Unknown
SSDUT433-27	19	Rhodobium pfennigii strain AR 2102 gb EU445271.1	838/908 (92%)	3.6%	Alphaproteobacteria
SSDUT433-30	20	Desulfobulbus mediterraneus gb AF354663.1	896/950 (94%)	1.8%	Deltaproteobacteria
SSDUT433-33	21	Arenibacter echinorum strain KMM 6047gb EF536749.1	834/843 (98%)	1.8%	Flavobacteria
SSDUT433-50	22	Uncultured bacterium clone SZB41 emb AM176874.1	850/893 (95%)	1.8%	Unknown
SSDUT433-51	23	Uncultured bacterium clone YE-QS-E44 gb DQ438270.1	814/817 (99%)	1.8%	Unknown

**Figure 2.** Backscattered electron image and SEM/EDAX spectrum of U-rich particle.

