

Full Length Research Paper

BioRadBase: A database for bioremediation of radioactive waste

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Radioactive waste from different sectors such as nuclear energy, health care and food has become a discernible part of our environment. Several dumping methods are in routine practice to dispose radioactive wastes. Huge chemical and energy input in various skillful physico-chemical methods has limited their use while biological methods exploring the potential of micro-organisms could be a promising and eco-friendly approach to remediate radioactive pollutants. Bio-transformation, bio-accumulation and bio-sorption are key processes that have been tried for radionuclide remediation. BioRaDBase is the first database dedicated to micro-organisms which have been explored or engineered to remediate radioactive waste from the environment. The database serves as a comprehensive knowledgebase to search bacteria and fungi which have the ability to transform radioactive waste. This database would be a useful tool for the development of new bio-remediation technologies to clean up radioactive waste from the environment. The information in database has been managed under five classes, that is, type of radioactive waste, micro-organisms, genus listing, literature and waste management. The entries are also linked to external databases such as National Center for Biotechnology Information (NCBI), providing wide background information. Beside these, under the news section of the database, a user can connect to dedicated organizations working on issues like environmental protection, nuclear energy and radionuclide dumping. BioRaDBase can be accessed at <http://biorad.igib.res.in>.

Key words: Bioremediation of radioactive waste (BioRaDBase), radionuclides, biotransformation, biocrystallization, radioisotope, nuclear waste.

INTRODUCTION

Radionuclides in the environment are one of the major concerns to human health and ecotoxicology. Radioactive waste from sources like nuclear weapon fallout, nuclear energy generating industries, nuclear weapon reprocessing, medical use of radioisotopes, and

accidental release has become a part of our environment (Lloyd and Renshaw, 2005; Dighton et al., 2008). The remediation of radioactive waste is a serious challenge to the scientific community due to their inability to get destroyed. They can only be transformed into lesser toxic forms. (Hazzen and Tabak, 2005). Despite the potential risk of nuclear disasters, the demand of nuclear energy is ever rising, hence, the increase of radioactive pollutants in the environment might be expected in the near future. Owing to the environmental disturbance, high cost input and infeasibility of current clean-up technologies, bioremediation has been developed as a potential approach that can be implemented in radioactive waste remediation (Lloyd et al., 2002). Bioremediation is a

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Abbreviations: BioRaDBase, Bioremediation of radioactive waste database; PHP, hypertext preprocessor; EPA, environmental protection agency; NCBI, National Center for Biotechnology Information.

clean-up process for contaminated environmental site by using microbes to eliminate, detoxify, accumulate or transform the pollutant (Hazen and Tabak, 2005). Bioremediation of radio-nuclides is different from organic pollutants, where pollutant is degraded to innocuous compound or finally to CO₂ and water. Because radionuclides cannot be degraded, their remediation depends on the method of contamination that largely determines the bioavailability of the radionuclides. Microorganisms act on radionuclides present in radioactive waste by affecting its solubility, mobility and bioavailability. Until now, various micro-organisms from harsh and extreme habitats has been explored for their ability to catalyze the remediation of radioactive waste under *ex-situ* conditions. Bacteria from genus like *Geobacter*, *Deinococcus*, and *Shewanella* etc are well established in terms of radioactive waste remediation (Lloyd et al., 2002). A c-type cytochrome reductase has been studied in *Geobacter sulfurreducens* which plays an important role in the reduction of uranium (VI) to uranium (IV). Similar types of enzymes have also been found in other radionuclides which act as remediating bacteria and are named as *Shewanella* reductase, *Desulfovibrio vulgaris* reductase, and *Geobacter* reductase. The changes in the microbial community structure during the start-up of an *in-situ* biostimulation system for U (VI) reduction have shown that different functional populations play a role in U (VI) reduction as the level of U (VI) decreased. Hence, a specific microbial functional population can be stimulated and maintained *in-situ* in order to achieve a low uranium level in contaminated aquifers (Nostrand et al., 2011). *Shewanella oneidensis* have been reported to catalyze the reduction of a Co⁶⁰ chelated form, [Co (III)-EDTA] by using Mtr respiratory pathway. Thus, the understanding of such biochemical pathways, promotes the use of these bacteria as a tool for bioremediation (Hau et al., 2008). Fungi play a major role in radionuclide accumulation in terrestrial ecosystem. The capacity of fungi to accumulate radionuclide depends on the physical nature of radioactive source, fungal species and, presumably, their enzymatic potential. Soil saprophytic micro fungi, *Cladosporium cladosporioides* and *Penicillium roseopurpureum* have been shown to overgrow on radioactive 'hot particles' (<1147 Bq of γ -activity) and destroy them within 50 to 150 days (Zhdanova et al., 1991; Dighton et al., 2008). The accumulation of radionuclides such as ⁷Be, ⁶⁰Co, ⁹⁰Sr, ⁹⁵Zr, ⁹⁵Nb, ¹⁰⁰Ag, ¹²⁵Sb, ¹⁴⁴Ce, ²²⁶Ra and ²³⁸U has been reported in some mushroom species (Haselwandter and Berreck, 1994; Dighton et al., 2008). Similarly, differential bioreduction of Pu at contaminated sites could occur through biotic and abiotic means. However, biotic reduction is largely done by bacteria, while abiotic reduction was shown to be dependent on availability of complexing agent in soil (Deo et al., 2011). Bacterial cell surface plays a significant role in biocrystallization of uranium phosphate (Macaskie et al., 1996). Specific

bioaccumulation aspect of radioactive waste remediation shows the efficiency of *Pseudomonas aeruginosa* to accumulate uranium and thorium from plutonium contaminated pond (Premuzic et al., 1985). All of such studies justify the future aspect of micro-organisms based on remediation approach for radioactive waste treatment. Such microbial activities are of prime concern in disposing radioactive waste as they can change the mobility of radionuclides present in waste from deep geological dumping (Francis, 1998). During recent years, recombinant construct of bacteria like *Deinococcus radiodurans* has also been employed in the remediation process of radionuclides from radioactive waste (Daly, 2000).

Despite the fact that microbes have the potential to remediate radionuclides, limited work has been done on microbial enzyme systems involved. There is the need to encourage genomic and proteomic studies in order to fully understand the underlying mechanisms. Keeping these things in mind, we have developed a database that organizes information about microorganisms involved in remediation of radioactive waste in a systematic manner that provides researchers with easy access to relevant information about associated microorganisms.

METHODOLOGY

Dataset and database development

To structure the database, reference literature was collected from published research work on NCBI (<http://www.ncbi.nlm.nih.gov/>). Besides, this simple web access has also been performed. Database entries for section, type of radioactive waste and radioactive waste management were collected from the Department of Energy (DOE, US) <http://energy.gov/>, International Commission on Radiological Protection (ICRP) <http://www.icrp.org/>, and environmental protection agency (EPA) <http://www.epa.gov/>.

The MySQL (<http://www.mysql.com/>), a relational database management system was used for maintaining, storing and retrieval of curated data. Web interface for accessing the database was written in hypertext preprocessor (PHP) (<http://www.php.net/>) and JavaScript. The database was developed on a windows platform and hosted via an Apache Web Server (<http://www.apache.org/>). The database was copyrighted and maintained by the Institute of Genomics and Integrative Biology.

Database design and features

The present work BioRadBase, version 1.0 is a concerted effort was a concerted effort to extract and integrate the available data about micro-organisms involved in the remediation of radioactive waste. The BioRadBase web interface makes it feasible to access the available data by categorizing them into five classes on a single page (Figure 1). The first class "Type of waste", contains information of the radionuclides present in radioactive waste, their generation process, isotopic form, half life and categorization as low or high level radioactive waste depending on the residual radioactivity. Second class "Micro-organisms" includes species from bacteria and fungi involved in the detoxification or reduction process. The third class "Genus listing" describes the genus of all microbes involved in the remediation process. Each genus is linked to open database, in other words NCBI enables the users to further

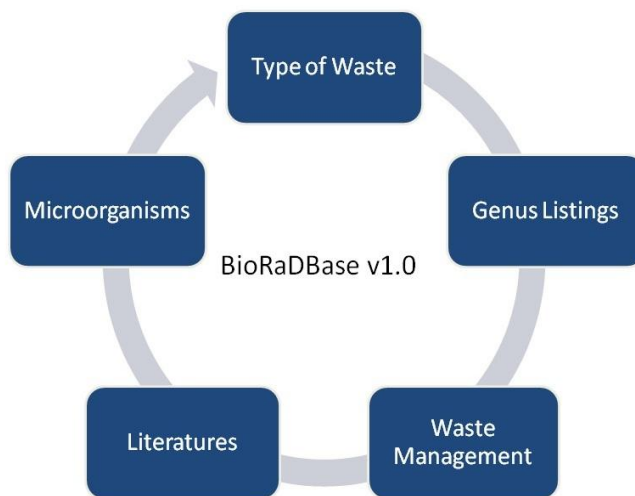


Figure 1 Structure of the Database

Thursday, February 17, 2011

Contributors Help Submit/Modify

uranium

Advance Search

Home

Type of Waste From Bacteria Listing = 68 records Show

Microorganisms From Fungi Listing = 9 records Show

Genus Listing From Waste Listing = 15 records Show

Publications

Waste Management

Organisms	Radioactive Material Utilize	Mechanism	Reference
<i>Acidovorax</i> sp.	Uranium	Reduction of U(VI) to U(IV)	Microbial transformations of radioactive waste and environmental restoration through bioremediation.
<i>Acinetobacter</i> RAQ-1	Uranium	Bind with uranium oxide	Developments in bioremediation of soils and sediments polluted with metals & radionuclides-1. Microbial processes and mechanisms affecting bioremediation of metals contamination and influencing metal toxicity and transport.
<i>Anaeromyxobacter</i> sp	Uranium	Reduction of U(VI) to U(IV)	Change in Bacterial community structure during in situ biostimulation of subsurface sediment cocontaminated with uranium and nitrates.
<i>Anaeromyxobacter dehalogenans</i> strain 2CFC	Uranium	Convert U (VI) to insoluble U (VI) form	Uranium Reduction and isotope fractionation by <i>Anaeromyxobacter dehalogenans</i> .
<i>Arthrobacter</i> sp.	Uranium	Bioprecipitation of U(VI)	Functional diversity and electron donor dependence of microbial population capable of U(VI) reduction in radionuclide contaminated subsurface sediments.
<i>Bacillus sphaericus</i>	Uranium	Bioaccumulation of Uranium	Complexation of uranium by cells and S layer sheets of <i>Bacillus sphaericus</i> .
<i>Thermoterrabacterium ferrireducens</i>	Uranium	Convert U (VI) to insoluble U (VI) form	Reduction of uranium (VI) phosphate during growth of the thermophilic bacterium <i>Thermoterrabacterium ferrireducens</i> .
<i>Cellulomonas flavigena</i> ATCC482	Uranium	Convert U (VI) to insoluble U (VI) form	Dissimilatory reduction of cr (VI), Fe(III), and U(VI) by cellulomonas isolates.
<i>Cellulomonas</i> sp. WS01	Uranium	Convert U (VI) to insoluble U (VI) form	Dissimilatory reduction of cr (VI), Fe(III), and U(VI) by cellulomonas isolates.
<i>Cellulomonas</i> sp. WS18	Uranium	Convert U (VI) to insoluble U (VI) form	Dissimilatory reduction of cr (VI), Fe(III), and U(VI) by cellulomonas isolates.
<i>Cellulomonas</i> sp. ES5	Uranium	Convert U (VI) to insoluble U (VI) form	Dissimilatory reduction of cr (VI), Fe(III), and U(VI) by cellulomonas isolates.
<i>Citrobacter</i>	Uranium	Extracellular polysaccharides make complex with Uranium	The removal of uranium from mining waste water using algal/microbial biomass.
<i>Clostridium acetobutylicum</i> (ATCC824)	Uranium	Reduction of U(VI)	Reduction of Uranium(VI) to U(IV) by Clostridia.
<i>Clostridium pasteurianum</i> (ATCC7040)	Uranium	Reduction of U(VI) to U(IV)	Reduction of Uranium(VI) to U(IV) by Clostridia.
<i>Clostridium sphenoides</i> (ATCC19403)	Uranium	Reduction of Uranium complexed with citric acid(U(VI) to U(IV)	Reduction of Uranium(VI) to U(IV) by Clostridia.
<i>Clostridium</i> sp.(ATCC53464)	Uranium	Reduction of Uranium complexed with citric acid(U(VI) to U(IV)	Reduction of Uranium(VI) to U(IV) by Clostridia.
<i>Clostridium</i> sp.	Uranium	Convert U (VI) to insoluble U (VI) form	XPS and XANES studies of uranium reduction by clostridium sp.
<i>Clostridium sphenoides</i> ATCC 19403	Uranium	Convert U (VI) to insoluble U (VI) form	Reductive precipitation and stabilization of uranium complexed with organic ligands by anaerobic bacteria.
<i>Dechloromonas</i> sp.	Uranium	Reduction of U(VI)	Functional diversity and electron donor dependence of microbial population capable of U(VI) reduction in radionuclide contaminated subsurface sediments.
<i>Deinococcus radiodurans</i> R1	Uranium	Convert U (VI) to insoluble U (VI) form	Reduction of Fe(III), Cr(VI), U(VI), and TC(VI) by <i>Deinococcus radiodurans</i> R1.
<i>D. radiodurans</i>	Uranium	Reduce U (VI)	bioremediation of metals and Radionuclides; What is it and How it works.
<i>Desulfomicrobium norvegicum</i> DSM 1741	Uranium	Convert U (VI) to insoluble U (VI) form	Enzymatic Iron and uranium reduction by sulfate-reducing bacteria.
<i>Desulfosporosinus</i> sp.	Uranium	reduced U(VI) to U(IV), in uranium mine sediments	Microbial populations stimulated for hexavalent uranium reduction in uranium mine sediments.

Figure 2a. General search using keyword "uranium".

Search: WASTE | FUNGI | **BACTERIA** | GENUS | REFERENCE | WASTE MANAGEMENT

Searching Bacteria

Custom Filter: Desulfovibrio vulgaris Whole words only

Search

All Fields
All Fields
Name
Radioactive Material
Mechanism
Reference

Name	Radioactive Material	Mechanism	Reference
Desulfovibrio vulgaris	Techneium	Tc(VII) reduction and precipitation	Reduction of Technetium by Desulfovibrio desulfuricans: Biocatalyst Characterization and Use in a Flowthrough Bioreactor.
Desulfovibrio vulgaris	Uranium	Reduce Fe (VI), U (VI), & sulfate reduction, using lactate, hydrogen, pyruvate as electron donor	Reduction of Uranium by Cytochrom c3 of Desulfovibrio vulgaris.
Desulfovibrio vulgaris	Radium	Dissolution of Radium	Microbial transformations of radioactive waste and environmental restoration through bioremediation.

Figure 2b. Advance search using keyword "Desulfovibrio vulgaris".

explore the information on related species widely. The fourth class, "Literature" presents the list of research papers used to extract information. Lastly, the fifth class "Waste management" categorized the radioactive waste as low level radioactive waste, high level radioactive waste and transuranic waste etc, depending on the radioactivity present in the waste along with disposal strategies as recommended by agencies like EPA. Besides the main content, database also updates the users with new achievements and advancements in this field briefly under the news section of database. BioRaDBase is enabled with search tool that specifies and fasten the search. The microbes can be searched for a particular radionuclide easily just by using search tool. An example of a key word search is shown in Figures 2a and b where the key word 'uranium' and 'Desulfovibrio vulgaris' respectively is searched against the database.

RESULTS AND DISCUSSION

BioRaDBase is a platform that provides scattered and unorganized information regarding radioactive waste remediation using micro-organisms in a comprehensive way. The present database satisfies the condition of working as a knowledge device that can motivates researchers to develop new microbial based technologies for remediation of radioactive wastes. Database will be extended further to keep pace with new scientific achievements in the field. In this work, we hope that BioRaDBase will serve the scientific community in designing effective and feasible bioremediation technologies for remediation of radioactive waste.

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