

Abstract

Microbial diversity within uranium (U) ore deposits, host rocks and soils from U mines at Jharkhand, India were investigated by culture independent molecular analysis of 16S rRNA genes. Aerobic heterotrophic bacteria isolated from U ore were characterized for their uranium and other heavy metal resistance and U accumulation capacity. Impact of U ore contamination on agricultural soil bacterial diversity was elucidated through microcosm based study. Clone library analysis followed by sequencing of major ribotypes revealed that each sample harbor distinct autochthonous bacterial community. U ores were predominated by lineages of *Acinetobacter* and unclassified *Pseudomonadales*; *Limnobacter*, *Diaphorobacter* and unclassified member of β -*Proteobacteria* followed by α -*Proteobacteria* and *Acidobacteria*. *Gammaproteobacteria* members affiliated to *Acinetobacter*, *Marinobacter*, *Alcanivorax*, *Halovibrio* and *Halomonas* were predominated in host rocks along with members of α -*Proteobacteria* (*Sphingomonas*, *Bosea* and *Caulobacter*) and *Bacteroidetes*. Soil communities on the other hand were represented by *Acidobacteria* and γ -*Proteobacteria* (*Succinivibrio*, *Cellovibrio*, *Legionella*) followed by α -, β - and δ -*Proteobacteria* (*Methylocystis*, *Rhodocyclus* and *Desulfuromonas*, respectively); *Firmicutes* (*Bacillus*), *Bacteroidetes*, and *Actinobacteria*. Members of *Archaea* were detected only in one host rock sample from Jaduguda. Principal component analysis (PCA) of geochemical data and cluster analysis of DGGE profiles using unweighted pair group method with arithmetic average (UPGMA) algorithm showed characteristic relatedness of samples obtained from ores, host rocks or soils. Culturable bacterial community from the uranium ore was found to be predominated by γ -, β - and α -*Proteobacteria*, *Actinobacteria*, and *Firmicutes* with uranium and other metal resistance properties well distributed among diverse genera represented by *Microbacterium*, *Arthrobacter*, *Acinetobacter*, *Stenotrophomonas*, *Pigmentiphaga*, *Pseudomonas*, etc. Transmission electron microscopy and X-ray diffraction analysis revealed that U resistant *Stenotrophomonas* sp. U18 could precipitate U as crystalline deposits of uranium phosphate compounds. DGGE and real time PCR based analysis of 16S rRNA genes retrieved from microcosms indicated that U ore amendments exerted significant impact on metabolically active bacterial community in soil. This study enlightens diverse autochthonous microbial communities present in U mine environments and indicates that indigenous bacteria from U ore could resist toxicity of uranium and other heavy metals, and have U sequestration ability. This study also ascertains the effect of U ore contamination on agriculture soil bacterial diversity.

Keywords: Uranium mine; Uranium ore; Heavy metal; Microbial diversity; 16S rRNA gene; Resistance; Accumulation; Microcosm; ARDRA; DGGE; Real-time PCR; Bioremediation