

Abstract

Microbial diversity within uranium (U) mines at Jaduguda, Bagjata and Turamdih of Jharkhand, India was investigated to ascertain composition and structure of bacterial and archaeobacterial communities within metal and radionuclide contaminated mine tailings, mine water pit as well as sites without visible contamination of mine wastes. Physicochemical characterization indicated presence of several heavy metals including U across the samples. Small subunit ribosomal RNA (16S rRNA) gene clone library analysis revealed that non U-ore/ mine waste contaminated samples were mostly composed of bacterial phyla *Acidobacteria*, *Bacteroidetes*, *Firmicutes* and *Proteobacteria* along with less frequent *Nitrospira*, *Deferribacteres*, *Chloroflexi*. Samples obtained from highly contaminated locations, in contrast, showed distinct abundance of *Proteobacteria* along with *Acidobacteria*, *Bacteroidetes* and members of *Firmicutes*, *Chloroflexi*, Candidate division, *Planctomycete*, *Cyanobacteria* and *Actinobacteria* as minor groups. Distinct presence of *Crenarchaeota* and *Euryarchaeota*, respectively, was observed within tailings and mine water sediment. Distribution of dissimilatory sulfate reductase gene (*dsr*) studied within the samples showed its presence only within the vegetative tailings. Aerobic heterotrophic bacteria (119 numbers) were isolated from various samples and characterized for their heavy metal resistance capacity. Following an initial screening, 16 strains were selected for detail analysis. Taxonomic identity as ascertained by 16S rRNA gene analysis revealed dominance of genera *Bacillus* and *Staphylococcus*, followed by *Cronobacter*, *Acinetobacter*, *Pseudomonas*, *Burkholderia*, *Iodobacter* and *Flavobacterium*. *Staphylococcus* sp. strain 9–16, isolated from tailings sample selected for elaborate investigation showed high U resistance at low pH (pH 4.0) and rapid, concentration and pH dependent U accumulation with maximum loading of 90 mg U g⁻¹ dry wt. that remain insensitive to other co-ions (except Fe²⁺, Fe³⁺ and the multimetal mixture of Cd, Cr, Co, Cu, Ni, Fe²⁺, Fe³⁺ and Zn). Scanning electron microscopy coupled with energy dispersive X-ray analysis indicated increase in cell size following U uptake, while X-ray diffraction analysis suggested the formation of U-phosphate compounds within the metal accumulated cells. In order to exploit the potential of *Staphylococcus* sp. 9–16 in surviving and removing U and other metals from mine wastes, microcosm study was conducted using highly contaminated mine water effluent. The test bacterium showed high U removal capacity while maintaining its survival up to 30 days. A bacterial consortium developed by mixing this bacterium with two other strains (*Bacillus* sp. 12–21c and *P. aeruginosa* J007) also showed efficient removal of metals along with uranium.

Keywords: Uranium mine; Uranium tailings; Heavy metal; Microbial diversity; 16S rRNA gene; *Staphylococcus* sp.; Resistance; Accumulation; Microcosm; ARDRA; SEM; EDX; XRD; Bioremediation.