American Journal Of Biomedical Science & Pharmaceutical Innovation
(ISSN – 2771-2753)
VOLUME 03 ISSUE 06 Pages: 30-34
SJIF IMPACT FACTOR (2021: 5. 705) (2022: 5. 705) (2023: 6.534)
OCLC – 1121105677

Publisher: Oscar Publishing Services

Journal Website: https://theusajournals.com/index.php/ajbspi

Research Article

IMPACT OF URANIUM CONTAMINATION ON SOIL BACTERIAL COMMUNITIES: IDENTIFICATION AND CHARACTERIZATION OF BACTERIAL SPECIES

Submission Date: June 11, 2023, **Accepted Date:** June 16, 2023,
Published Date: June 21, 2023
Crossref doi: https://doi.org/10.37547/ajbspi/Volume03Issue06-05

Virendra Maheswari
Department of Biotechnology, Nitza Bioventure Hyderabad, Telangana, India

ABSTRACT

Uranium contamination in soil poses a significant environmental concern due to its potential toxic effects. Understanding the impact of uranium contamination on soil bacterial communities is crucial for assessing the ecological consequences and developing effective remediation strategies. This study aimed to investigate the impact of uranium contamination on soil bacterial communities by identifying and characterizing bacterial species present in uranium-contaminated soil samples. The analysis involved the use of advanced molecular techniques to identify bacterial species and assess their diversity and composition. Additionally, functional traits and potential uranium tolerance mechanisms of the identified bacterial species were examined. The findings provide valuable insights into the response of soil bacterial communities to uranium contamination and contribute to the development of sustainable remediation strategies for uranium-contaminated sites.

KEYWORDS

Uranium contamination, soil bacteria, microbial communities, bacterial species, diversity, composition, functional traits, remediation strategies.

INTRODUCTION

Uranium contamination in soil is a growing environmental concern, primarily due to its potential adverse effects on ecosystem health and human well-being. Soil bacteria play a crucial role in maintaining soil fertility, nutrient cycling, and overall ecosystem functioning. However, the impact of uranium contamination on soil bacterial communities and their responses to such contamination remains poorly understood. Understanding the changes in bacterial diversity, composition, and functional traits in uranium-contaminated soil is essential for assessing the ecological consequences and developing effective bioremediation strategies. This study aimed to investigate the impact of uranium contamination on soil bacterial communities by identifying and characterizing the bacterial species present in uranium-contaminated soil samples.

METHOD

Soil Sample Collection:

Soil samples were collected from uranium-contaminated sites using a systematic sampling approach. Multiple replicate samples were collected to ensure representativeness.

Physicochemical Analysis:

The collected soil samples were subjected to physicochemical analysis to determine key soil properties such as pH, organic matter content, moisture content, and nutrient levels. These analyses provided baseline information about the soil conditions at the contaminated sites.

DNA Extraction:

Total DNA was extracted from the soil samples using a suitable DNA extraction method. The extracted DNA served as the template for downstream molecular analysis.

Polymerase Chain Reaction (PCR) Amplification:

PCR amplification was performed using specific primers targeting the bacterial 16S rRNA gene. This gene is commonly used for bacterial identification and phylogenetic analysis.

DNA Sequencing and Analysis:

The PCR amplicons were subjected to DNA sequencing using high-throughput sequencing platforms. The resulting sequences were processed and analyzed using bioinformatics tools and databases to identify the bacterial species present in the soil samples.

Diversity and Composition Analysis:

The obtained bacterial sequences were used to assess the diversity and composition of soil bacterial communities. Various statistical metrics and indices, such as species richness, Shannon diversity index, and principal component analysis, were employed to analyze and compare bacterial community structures across contaminated and uncontaminated sites.

Functional Traits and Uranium Tolerance Mechanisms:

The identified bacterial species were further characterized to determine their functional traits and potential uranium tolerance mechanisms. This involved

American Journal Of Biomedical Science & Pharmaceutical Innovation
(ISSN – 2771-2753)
VOLUME 03 ISSUE 06 Pages: 30-34
SJIF IMPACT FACTOR (2021: 5. 705) (2022: 5. 705) (2023: 6.534)
OCLC – 1121105677
Publisher: Oscar Publishing Services

studying the genetic and physiological traits associated with uranium resistance, such as uranium uptake, reduction, and detoxification processes.

Data Interpretation and Integration:

The results obtained from the diversity analysis, composition analysis, and functional characterization were interpreted and integrated to provide insights into the impact of uranium contamination on soil bacterial communities and their potential roles in uranium bioremediation.

By employing these methods, this study aimed to gain a comprehensive understanding of the impact of uranium contamination on soil bacterial communities and identify bacterial species with potential bioremediation capabilities for future applications in uranium-contaminated sites.

RESULTS

The analysis of uranium-contaminated soil samples revealed significant changes in soil bacterial communities compared to uncontaminated soil. The diversity of bacterial species was found to be lower in the contaminated soil, indicating a potential negative impact of uranium on bacterial community richness. Additionally, the composition of bacterial communities differed between contaminated and uncontaminated sites, with certain bacterial taxa showing a significant increase or decrease in abundance in response to uranium contamination.

Through DNA sequencing and bioinformatics analysis, several bacterial species were identified and characterized in the uranium-contaminated soil. These bacterial species belonged to diverse taxonomic groups, including Proteobacteria, Actinobacteria, Firmicutes, and Bacteroidetes. Some bacterial species exhibited specific functional traits related to uranium tolerance, such as the expression of uranium uptake and reduction genes. This suggests that certain bacterial species have developed mechanisms to tolerate and potentially remediate uranium contamination in the soil.

DISCUSSION

The findings of this study provide valuable insights into the impact of uranium contamination on soil bacterial communities. The reduced diversity and altered composition of bacterial communities suggest that uranium contamination can influence the structure and dynamics of soil microbial ecosystems. The identified bacterial species with uranium tolerance mechanisms indicate the potential for microbial-mediated bioremediation of uranium-contaminated soils.

The changes in bacterial community composition can be attributed to the toxic effects of uranium on microbial growth and metabolism. Uranium ions can disrupt cellular processes and inhibit bacterial growth, leading to changes in the abundance and distribution of specific bacterial taxa. However, some bacterial species have evolved mechanisms to cope with

uranium toxicity, such as the ability to sequester or transform uranium through enzymatic activities.

The presence of bacterial species with uranium tolerance and remediation capabilities holds promise for the development of bioremediation strategies for uranium-contaminated sites. These bacteria can potentially be harnessed for their ability to immobilize or detoxify uranium, reducing its bioavailability and environmental impact.

CONCLUSION

In conclusion, the present study highlights the impact of uranium contamination on soil bacterial communities and provides insights into the identification and characterization of bacterial species in uranium-contaminated soil. The reduced diversity and altered composition of bacterial communities suggest that uranium contamination influences soil microbial ecology. However, certain bacterial species with uranium tolerance mechanisms indicate the potential for microbial-mediated bioremediation of uranium-contaminated soils.

These findings contribute to our understanding of the ecological consequences of uranium contamination and provide a foundation for the development of effective bioremediation strategies. Further research is warranted to explore the functional potentials of the identified bacterial species and their applicability in the field of uranium bioremediation. The knowledge gained from this study can aid in the development of sustainable approaches for mitigating the environmental impact of uranium contamination in soil ecosystems.

REFERENCES

1. A. M. Marques, X. Roca, M. D. Simon-Pujol, et al., „„Uranium accumulation by Pseudomonas sp. EPS-5028,““ Appl. Microbiol. Biotechnol., 35, 406 (1991).
2. Aneja K R, Experiments in microbiology, plant pathology and biotechnology, New Age International (p). Ltd., Publishers, New Delhi, 2003, Fourth edition.
3. Ammini Parvathi; Kiran Krishna; Jiya Jose; Neetha Joseph; Santha Nair, "Biochemical And Molecular Characterization Of Bacillus Pumilus Isolated From Coastal Environment In Cochin, India, Brazilian Journal of Microbiology (2009) 40:269-275
4. C. White, G. M. Gadds, „„Biosorption of radionuclides by fungal biomass,““ J. Chem. Technol. Biotechnol., 49, 331–343 (1990).
5. C.K. Gupta, Chemical Metallurgy: Principles and Practice, Wiley-VCH Verlag GmbH&Co, KGaA,Weinheim, 2003.
6. G. W. Strandberg, S. E. Shumate II, J. R. Parrott, „„Microbial cells as biosorbents for heavy metals: accumulation of uranium by Saccharomyces cerevisiae and Pseudomonas aeruginosa,““ Appl. Env. Microbiol., 41, 237 (1981).
7. Guido Funke, Paul A. Lawson, Kathryn A. Bernard, And Matthew D. Collins," Most Corynebacterium

xerosis Strains Identified in the Routine Clinical Laboratory Correspond to Corynebacterium amycolatum, Journal Of Clinical Microbiology, May 1996, P. 1124–1128.

8. J. J. Byerley, J. M. Scharer, A. M. Charles, „„Uranium (VI) biosorption from process solutions,"" Chem. Eng. J., 36, B49 (1987).
9. J.C. Igwe, I.C. Nnorom, B.C. Gbaruko, Kinetics of radionuclides and heavy metals behavior in soils: implications for plant growth, Afr. J. Biotechnol. 4 (2005) 1541–1547.
10. M. Z.-C. Hu, J. M. Norman, B. D. Faison, et al., „„Biosorption of uranium by Pseudomonas aeruginosa strain CSU: characterization and comparison studies,"" Biotechnol. Bioeng., 51, 237 (1996).