

## **16S rRNA molecular profiling of heavy metal tolerant bacterial communities isolated from soil contaminated by electronic waste**

**Pankaj Kumar<sup>1</sup>, M H Fulekar<sup>2 3</sup>, R Y Hiranmai<sup>2</sup>, Ramesh Kumar<sup>4</sup>, Rajesh Kumar<sup>5</sup>**

<sup>1</sup>School of Environment and Sustainable Development, Central University of Gujarat, Gandhinagar, Gujarat, 382030, India. pankajb434@yahoo.com.

<sup>2</sup>School of Environment and Sustainable Development, Central University of Gujarat, Gandhinagar, Gujarat, 382030, India.

<sup>3</sup>Center of Research for Development, Parul University, Vadodara, Gujarat, 391760, India.

<sup>4</sup>Department of Environmental Sciences, School of Basic Sciences and Research, Sharda University, Greater Noida, 201310, Uttar Pradesh, India.

<sup>5</sup>Department of Environmental Science, School of Earth Sciences, Central University of Rajasthan, Ajmer, 305817, Rajasthan, India.

### **Abstract:**

Electronic waste is an evolving source of harmful pollutants in our surrounding environments and considered to be perilous as it contains toxic metals such as chromium, cadmium, lead, mercury, zinc, and nickel in huge quantities. Heavy metals are harmful contaminants and accumulated in the environment due to various anthropogenic activities. The present study was conducted to isolate and characterize different heavy metal tolerant bacterial species, based on molecular techniques from soil contaminated by electronic waste. The contaminated soil samples were analyzed for various physicochemical properties such as pH, electrical conductivity, soil moisture, water holding capacity, organic carbon, organic matter, available phosphorus, total nitrogen, and potassium using standard procedures. The soil samples were found to contain a higher amount of different heavy metals such as copper, chromium, lead, iron, cadmium, and nickel. Serial dilution and spread plate techniques have been used for bacterial isolation. The identification and molecular characterization of isolated bacterial species were done by biochemical tests and 16S rRNA gene sequencing technique. The 16S rRNA sequencing analysis confirmed the presence of different bacterial species as, *Micrococcus aloeverae*, *Kocuria turfanensis*, *Bacillus licheniformis*, *Bacillus jeotgali*, *Bacillus velezensis*, and *Bacillus haikouensis*. The findings indicated that the e-waste dumping sites are the storehouse of elite bacterial species. The present research study offers a platform for systematic analysis of e-waste sites by microbial profiling that may help in the innovation of novel microorganisms of scientific importance and better biotechnological potential.

### **Keywords:**

16S rRNA gene sequencing; Electronic waste; Heavy metals; Microbial diversity; Phylogenetic tree analysis.

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