Cadmium (Cd) Resistant Bacteria

Ayan Ghorui[1], Subhajit Pal[1], Shovana Pal[1], Keshab Ghosh[1], Uparna Dutta[2], Bipasa Dey sutradhar[2], Deeti Das[2], Pritha Pal[1*], Aritri Laha[1*]

[1]Depertment of Microbiology, School of Life Sciences, Swami Vivekananda University
Barrackpore, 700121, West Bengal, India.
[2]Depertment of Biotechnology, School of Life Sciences, Swami Vivekananda University
Barrackpore, 700121, West Bengal, India.
[*]Corresponding Author. E-mail: *lahaaritri@gmail.com*, prithap@svu.ac.in

Abstract: - Anthropogenic sources of toxic cadmium (Cd) have significantly risen during the past few decades. Currently several physical and chemical techniques are used in the Cd decontamination methods. But these techniques are expensive and even causes secondary pollution. Therefore, it is crucial to investigate eco-friendly, effective, and affordable strategies that can eliminate the Cd threat from the environment. The biological methods are far suitable than other methods in recent years. A bunch of bacteria (*Bacillus cereus, Aeromonas caviae*) are able to tolerate this heavy metal. Cadmium tolarent bacteria (CdtB) are numerous and unrelated phylogenetically. They contain cadA and cadB gene systems which is responsible for their Cd-resistant capacity. The objective of this review is to demonstrate the importance, culturable diversity, metabolic purification mechanisms, and contemporary applications of CdtB bacteria in soil bioremediation processes.

Keywords: Cd, Bioremediation, Bacteria.

Introduction: -

Cadmium (Cd), a toxic heavy metal, is to blame for the pollution of the environment. From framing land soils to completed commodities in the food cycle for humans, this hazardous metal became a worry for human nutrition and health. The absolute maximum quantity of Cd that can be present in food crops in 2018 is 10 mg kg-1, according to the European Food Safety Authority FAO/WHO. The raw material cacao, which is used to manufacture chocolate, contains Cd, according to recent research, which shows that this is an issue. The importance of this issue has increased recently for the countries of Central and South America (Gramlich et al. , 2018). A considerable quantity of environmental Cd remains present in soils in unsuitable forms, such as Greenockite (CdS), Otavite (CdCO3), or less frequently, Monteponite (Cdo)(Traina,1999), which is an interesting observation given the widespread distribution of this metal content. The accessibility of Cd for plant consumption and accumulation in various crops, like lettuce and spinach, is influenced by the pH and Zn/Cd ratio (Tang et al. 2020). The soil bacteria that come into contact with the Cd forms that are present in soil solutions or that are taken in as solid-state phases experience the earliest direct and indirect effects of the existence of Cd in soils (Brookes, 1999). Cd-tolerant bacteria (CdtB) have evolved in agricultural soils with a high Cd content and are now essential for bioremediation (Bravo et al. 2018). The type of crop and any potential health problems throughout the entire food chain determines the maximum

Cd content that can be present in farming soils. The amount of Cd in rice and wheat can vary from 0.01 to 0.4 and 0.8 mg kg-1, respectively. The geoaccumulation index (Igeo), developed by Muller in 1969 and used to measure the impact of natural diagenesis, biogeochemical background values, and the degree of enrichment caused by anthropogenic contamination (Wang et al. 2015),

The Igeo index considers the topsoil Cd concentration (mainly rhizospheric soil) as well as the geochemical background values of Cd found at the same sampling points. Despite the index's importance, it is still unclear how Cd gets from agricultural areas' soil to food chains. To understand the movement of Cd in a particular crop, it is crucial to understand the geomicrobiology of the soil that was studied here.

Even though CdtB research started in the 1970s, it took significantly longer for agricultural research involving bacterial isolates from wheat and rice to begin (Babich and Stotzky 1977). Mobilization and immobilization of Cd are essential processes in bioremediation. While reducing leaching into groundwater and reducing the amount of Cd that plants absorb, immobilizing additives. Utilizing the mobilization activity will enhance Cd elimination through soil washing and plant uptake. It will be necessary to "mobilise" or "immobilise" the Cd content in farming soil depending on the crop system, the efficacy of the chosen biodegradation strategy, and the biogeochemical characteristics of the surrounding system (Bolan et al. 2014).

Mechanisms of cadmium remediation through Bacteria

Cd, as well as other harmful metals, are mostly removed by eukaryotic bacteria by associating with polythiols. Additionally, the microoraganism has developed a variety of defences against heavy metals. These tactics are crucial in cases where dangerous levels of heavy metals do not affect the ability of resistant microorganisms to divide their cells. The majority of the heavy metal resistance genes in bacteria are found on plasmids. . This plasmid enables bacteria to compete against heavy metalsPathogens that have been clinically isolated from people, such as Pseudomonas sp., Klebsiella sp., and Staphylococcus sp., typically carry the R plasmid. Genes that are involved in cadmium resistance can be found on chromosomes or plasmids. (Chen et al. 2014).

Efflux mechanisms

Efflux processes have been the subject of countless investigations. Incorporated proteins for ejection in the membrane or environmental bacteria-produced antibiotics, antimicrobials, toxic metals, or other hazardous compounds can form efflux pumps. There has been a lot of research done on S. aureus' efflux mechanism. plasmids or merely chromosomes, have been described in S. aureus to date, thanks to advancements in genome analysis and biological information technology. Heavy metal tolerance is also present in drug-resistant efflux pumps

The five membrane protein families into which the S. aureus efflux pumps are categorised are the RND superfamily, the ATP-binding domain superfamily, the MATE family, the small multidrug resistance (SMR) family, and the major facilitator superfamily (MFS). Gram-negative bacteria, notably the AcrAB-TolC complex of E. coli and the MexBA-OrpM combination of P. aeruginosa, have been found to contain a large number of RND transporters. These transporters have an uncommon tripartite structure composed of a periplasmic adaptor protein, a transmembrane pump, and an outer membrane channel. The drug resistance of gram-negative bacteria is brought on by RND transporters. Recently, a FarE homolog of the E. coli protein AcrB and a fragment of the RND tripartite efflux system was found in S. aureus. The four conserved domains of the ABC transporter are present. The MFS, which comprises the efflux pumps Nor A, Nor B, Nor C, Lmr S, Qac A, Qac B, Mde A, and Sdr M, has attracted the most research attention among staphylococcal efflux pumps. Staphylococcal MFS transporters are composed of 380–520 amino acids and have distinctive MFS folds. They often form huge cytoplasmic loops between helices 6 and 7 and 12 or 14 membrane-spanning helices (Bravo et al.,2022).

Cadmium resistant gene :-

An important technique for the purification of harmful metals is biological conversion, which is used by numerous species, such as bacteria and fungi. The valency of the organometallic elements or compounds is altered by biological action. This bioconversion frequently causes a change in the metal's valency, which produces less toxic and flammable molecules. Examples include the breakdown of Hg ions into silver ions and the chemical reaction of As (v) into As (III). How cadmium is physiologically transformed to CdO is yet unknown (Guo et al., 2016). When metals are transformed into organometallic compounds, methylation occurs, which is a crucial detoxifying mechanism. The only two metals that can go through methylation are mercury and lead. The hazardous properties of the free metal forms are lower than those of the methylated derivatives; for instance, methylmercury and dimethylmercury are more harmful than mercury. But only one study has demonstrated that cadmium and lead are biologically converted (Bravo et al.,2022).

Bacteria with cadmium resistance systems have an environmental advantage in terms of survival. With the ATP-dependent cadmium efflux transporters found in gram-positive microorganisms, the irrelevant chemiosmotic cation-proton antiporters noticed in gram-negative bacteria, and the metallothionein system used by cyanobacteria, cadmium tolerance appears to have evolved at least three times. In contrast, all of the bacteria studied have remarkably similar strategies for resisting arsenic and mercury.

The two genes' roles in *Staphylococcus aureus* are the only organisms whose functions have been completely studied. The two nearby genes cadA and cadC generate the cadmium resistance mechanism found in gram-positive bacteria. Since then, homologs of these genes have been discovered in a number of additional bacterial species, including *Bacillus firmus, Listeria monocytogenes*, *Lactococcus lactis*, *Listeria* *innocua*, *Stenotrophomonas maltophilia,* and *Geobacillus stearothermophilus*. It was only discovered that a few microbes, *including S. aureus, Listeria monocytogenes, and Lactobacillus lactis*, might actually confer cadmium resistance.

Two nearby genes, Cad A and Cad C, which are both required for cadmium resistance in vivo, define the cadmium resistance system of S. aureus. It has been established that the Cad A protein is a P-type cadmium efflux ATPase or a transport ATPase with a covalent phosphoprotein intermediate. Through in vitro tests, the trans-acting negative regulatory protein Cad C was discovered to have a reduced potential for DNA binding when cadmium was present.

Bindings of cadmium ions

Bacterial metallothioneins and metallochaperones are two intracellular binding proteins that cadmium-resistant bacteria have begun to use to bind Cd. Exopolysaccharides in the cell wall or surface components of some bacteria, such as *Arthobacter viscosus* and *Klebsiella aerogenosa* , cause cadmium to cling to the capsular surface, whereas in others, like mutant *Citrobacter,* cadmium combines to form unsolvable cell-obligated $CdHPO_4$ and is stored inside a cell(Coelho et al. 2016).

Cadmium-resistant bacteria

Microbial diversity has garnered a lot of interest in bioremediation due to its adaptability. However, because relatively few microbial strains in nature have been examined, it is still necessary to find fresh, capable strains. Microbial communities are frequently present in habitats that are polluted with metals and may resist harmful concentrations of heavy metals.

Cupriavidus taiwanensis KKU2500-3 and *P. aeruginosa* KKU2550-8, KKU2550-9, and KKU2550-20 that were isolated from Thai Jasmine rice (KaoHom Mali 105) were said to be resistant to cadmium up to 500 mM (Siripornadulsil ,2013). Additionally,(Stanbrough et al.,2013) discovered that the soil-isolated bacteria Achromobacter sp. strain AO22 was cadmium-resistant up to 100 mg L^{-1}.Four strains of bacteria obtained from Vietnamese coastal sediments, *Exiguobacterium aestuarii, Pseudomonas abietaniphila, Acinetobacter brisouii,* and *Planococcus rifietoensis*, all showed high resistance to cadmium at 100, 130, 60, and 400 mg L^{-1}, respectively.(Bhakta et al. 2014). Another mangrove sediment-isolated bacteria, *Bacillus safensis*, only displayed cadmium tolerance up to 20 mg L^{-1}(Bravo et al.,2022).

Cadmium uptakes by bacterial strains

Microorganisms frequently use biological absorption and biomagnification processes to remove heavy metals.Through biochemical reactions like chelate, complex, and ion exchange, microorganisms absorb metal ions during the biosorption process. *Halomonas BVR1*, a bacteria isolated from the effluent of the electrical sector, could absorb up to 12.023 mg g^{-1} of cadmium (Rajesh et al. 2014). *Citrobacter sp*. JH 11-2 was also discovered in soil mining areas near an abandoned electronic company, and it was able to successfully remove about 47.7% of the cadmium (Shim et al. 2019). In contrast to other bacterial strains like *S. typhi, Pseudomonas* luminescence, and *E. coli*, which showed the highest levels of cadmium elimination at about 92.4, 94.8, and 92.06%, respectively, the bacterial strain isolated from garment dye effluents, *Bacillus licheniformis,* showed cadmium removal ability up to 98.34%. Consequently, using such microbes in bioremediation may be a good choice (Bravo et al.,2022).

Conclusion and future scope

Based on interactions with other microorganisms as well as on its own biochemical characteristics and physiological reactions to pressures, bacteria may have evolved their unique cadmium resistance capacities. High salinity and heavy cadmium pollution present challenging conditions for soil bacteria to survive. Microorganisms possess unique traits that enable them to resist extreme Cd concentrations and high salinity. The application assessment of these microorganisms for the bioremediation of cadmium-polluted saline areas will be made possible by further study .

Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Author contributions:

Ayan Ghorui, Subhajit Pal, Shovana Pal, Keshab Ghosh, Uparna Dutta, Bipasa Dey sutradhar, Deeti Das - Data collection and Writing- Original draft preparation; Pritha Pal and Aritri Laha. Formal reviewing and Supervision

Acknowledgement:

The authors are grateful to the ICAR-Niche area of Excellence-Arsenic Research Laboratory, Bidhan Chandra Krishi Viswavidyalaya (BCKV), Kalyani, Nadia as well as Department of Genetics & Plant Breeding and Department of Agronomy, Bidhan Chandra Krishi Viswavidyalaya (BCKV), Mohanpur, Nadia, West Bengal, India for providing technical and all other necessary assistance during the study.

References: -

Babich, H., & Stotzky, G. (1977). Effect of cadmium on fungi and on interactions between fungi and bacteria in soil: influence of clay minerals and pH. *Applied and Environmental Microbiology*, *33*(5), 1059-1066.

Bravo, D., & Braissant, O. (2022). Cadmium-tolerant bacteria: current trends and applications in agriculture. *Letters in Applied Microbiology*, *74*(3), 311-333.

Bravo, D., Pardo-Díaz, S., Benavides-Erazo, J., Rengifo-Estrada, G., Braissant, O., & Leon-Moreno, C. (2018). Cadmium and cadmium-tolerant soil bacteria in cacao crops from northeastern Colombia. *Journal of applied microbiology*, *124*(5), 1175-1194.

Brookes, P. C. (1995). The use of microbial parameters in monitoring soil pollution by heavy metals. *Biology and Fertility of soils*, *19*, 269-279.

Chen, A., Zeng, G., Chen, G., Liu, L., Shang, C., Hu, X., ... & Zhang, Q. (2014). Plasma membrane behavior, oxidative damage, and defense mechanism in Phanerochaete chrysosporium under cadmium stress. *Process Biochemistry*, *49*(4), 589-598.

Choppala, G., Saifullah, Bolan, N., Bibi, S., Iqbal, M., Rengel, Z., ... & Ok, Y. S. (2014). Cellular mechanisms in higher plants governing tolerance to cadmium toxicity. *Critical reviews in plant sciences*, *33*(5), 374-391.

Codex Alimentarius Commission. (2018). Joint FAO/WHO food standards programme codex committee on contaminants in foods. *fifth session, The Hague, the netherlands*, 21-25.

Coelho, G. F., GonÇalves Jr, A. C., Nóvoa-Muñoz, J. C., Fernández-Calviño, D., Arias-Estévez, M., Fernández-Sanjurjo, M. J., ... & Núñez-Delgado, A. (2016). Competitive and non-competitive cadmium, copper and lead sorption/desorption on wheat straw affecting sustainability in vineyards. *Journal of Cleaner Production*, *139*, 1496-1503.

Gramlich, A., Tandy, S., Gauggel, C., López, M., Perla, D., Gonzalez, V., & Schulin, R. (2018). Soil cadmium uptake by cocoa in Honduras. *Science of The Total Environment*, *612*, 370-378.

Guo, H., Hong, C., Chen, X., Xu, Y., Liu, Y., Jiang, D., & Zheng, B. (2016). Different growth and physiological responses to cadmium of the three Miscanthus species. *PloS one*, *11*(4), e0153475.

Muller, O., White, W. B., & Roy, R. (1969). Infrared spectra of the chromates of magnesium, nickel and cadmium. *Spectrochimica Acta Part A: Molecular Spectroscopy*, *25*(8), 1491-1499.

Rajesh, V., Kumar, A. S. K., & Rajesh, N. (2014). Biosorption of cadmium using a novel bacterium isolated from an electronic industry effluent. *Chemical engineering journal*, *235*, 176-185.

Shim, J., Kumar, M., Mukherjee, S., & Goswami, R. (2019). Sustainable removal of pernicious arsenic and cadmium by a novel composite of MnO2 impregnated alginate beads: A cost-effective approach for wastewater treatment. *Journal of environmental management*, *234*, 8-20.

Tang, L., Hamid, Y., Zehra, A., Sahito, Z. A., He, Z., Khan, M. B., ... & Yang, X. (2020). Mechanisms of water regime effects on uptake of cadmium and nitrate by two ecotypes of water spinach (Ipomoea aquatica Forsk.) in contaminated soil. *Chemosphere*, *246*, 125798.

Traina, S. J. (1999). The environmental chemistry of cadmium. *Cadmium in soils and plants*, 11-37.

Wang, L., Cui, X., Cheng, H., Chen, F., Wang, J., Zhao, X., ... & Pu, X. (2015). A review of soil cadmium contamination in China including a health risk assessment. *Environmental Science and Pollution Research*, *22*, 16441-16452.

Zheng, J. L., Yuan, S. S., Wu, C. W., & Lv, Z. M. (2016). Acute exposure to waterborne cadmium induced oxidative stress and immunotoxicity in the brain, ovary and liver of zebrafish (Danio rerio). *Aquatic toxicology*, *180*, 36-44.

Schirawski, J., Hagens, W., Fitzgerald, G. F., & Van Sinderen, D. (2002). Molecular characterization of cadmium resistance in Streptococcus thermophilus strain 4134: an example of lateral gene transfer. *Applied and environmental microbiology*, *68*(11), 5508-5516.