Genetically engineered microorganisms for bioremediation and removing soil contaminants in agricultural environments

Nidhi Mishra iD

*Corresponding author. Assistant Professor, Department of CS & IT, Kalinga University, Raipur, India. E-mail address: ku.nidhimishra@kalingauniversity.ac.in

Ghorpade Bipin Shivaji iD

Research Scholar, Department of CS & IT, Kalinga University, Raipur, India. E-mail address: ghorpade.bipin@kalingauniversity.ac.in

Abstract

Objectives

Environmental contamination and its mitigation are significant global challenges. A wide range of contaminants (CM), including pesticides, hydrocarbons, heavy metals, and dyes, are the primary contributors to environmental contamination. Removal of these contaminants can pose significant problems because such efforts often lead to additional release of contaminants into the aqueous environment. Bioremediation (BR) is a very effective technology for reducing environmental CMs and restoring damaged sites to their original conditions. Only a limited amount of cultivable Genetically Engineered Microorganisms (GEMs) has been used, while a vast array of microbial diversity still needs to be explored.

Materials and methods

A range of BR techniques have been extensively employed to improve the ability of GEMs to metabolize substances and restore ecological balance by breaking down persistent CM. These include chemotaxis, bio-stimulation, bioaugmentation, biofilm formation, the application of GEMs, and sophisticated omics methods.

Results

There has been significant progress in understanding how bacteria effectively break down and clean up environmental contamination. GEMs aid in the remediation of polluted environments by

efficiently decomposing waste materials ecologically soundly and generating harmless by-products.

Conclusions

The understanding of the dangerous effects of various chemical CMs has led to an increase in research efforts to develop remediation technologies that can effectively eradicate these CMs. BR is a safe, cost-effective, and sustainable procedure that enhances the biological process of biological degradation to eliminate CMs. Thus, to expand the knowledge of the communities of bacteria and their response to environmental CMs, it is crucial to have a deeper comprehension of molecular genetics. This will enable the researchers to boost the CM degradation capabilities of the most successful species. BR is a process that creates a route towards a more sustainable and pollution-free earth.

Introduction

The demand for a healthy and safe workplace has progressively increased over time. Both inorganic and organic Contaminants (CM) contaminate the surroundings and pose significant health hazards to people and other organisms (Bharti & Sharma 2022). Heavy Metals (HMs) are notorious CMs due to their abundance, non-biodegradable nature, and persistent characteristics (Bharti & Sharma, 2022). They contaminate the soil and water, causing adverse effects in living

organisms including, congenital disabilities, genetic damage, and mutations. Even at low quantities, endocrine disrupters can cause neurological disorders (Khatun et al. 2022). This encompasses several naturally occurring elements, such as metals or metalloids, with an atomic number of 20 or more and a thickness of 5 grams per cubic centimeter or more. Cadmium (Cd), arsenic (As), mercury (Hg), and lead (Pb) are considered unnecessary substances as they do not have any biological function in the human body (Khatun et al, 2022). Environmental agencies worldwide have classified them as "priority CMs" due to their substantial threat to human health and ecosystems (Bobir et al. 2024). Removal of HMs from the contaminated material is essential to protect the ecosystem and human health (Kumar et al. 2021).

The use of genetic engineering techniques to modify micro-organisms (MOs) has emerged as a cost-effective and environmentally sustainable solution to the problem of heavy metal pollution (Surendar et al. 2024). Physico-chemical remediation techniques are expensive and difficult to apply. They can cause secondary contamination, damage soil fertility and damage the agricultural landscape (Lin et al. 2022). This approach is the optimal choice due to its elevated toxicity, intricate breakdown, and buildup of biological molecules. These factors pose a significant threat to human well-being and the surroundings and provide a substantial challenge to the long-term viability of the ecosystem. To preserve a robust ecosystem, it is imperative to break down and halt the dissemination of detrimental pollutants (Veerasamy & Fredrik 2023). A wide range of methods has been studied to address contamination of the environment problems, including reduction and oxidation (evaporate), electrochemical therapy (physiochemical therapy), solidification (combustion), lagoons (landfill deposits), processing of biological molecules (using innovative enzyme structures), and reversible osmosis (landfill accumulation) (Lin et al. 2022). Phytoremediation is a technique where green plants and helpful MOs in the soil break down and remove harmful substances from contaminated soil, water, and sewage (Kafle et al. 2022). This environmentally friendly and non-intrusive remediation technology removes unwanted metals from degraded surfaces (Gladkov & Gladkova 2021). Phyto mining is the extraction of commercially valuable metals from contaminated areas, with the recovered metals sold for profit (Dang & Li 2021). Plant biomass is used to generate electricity as a fuel source through combustion. Land can be rehabilitated to promote and preserve sustainable agriculture (Pržulj & Tunguz 2022).

The degrading capacity of MOs is influenced by two main factors: dietary needs and environmental conditions. Bioremediation (BR) is classified into two forms, in situ and ex-situ, according to the removal of harmful substances and the techniques used for their transportation (Patel et al. 2022). The current procedures involve using Genetically Engineered Microorganisms (GEMs) to break down CMs effectively (Hanlon & Sewalt 2021). GEMs have proven effective

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in remedying various CMs in specific settings due to their superior genetic composition for pollution management. The inefficient breakdown by culturable GEMs makes it challenging for environmental biotechnology researchers to remove numerous hazardous and refractory CMs. Ecological considerations and legal limitations are the primary obstacles to using GEMs in field situations (Rafeeq et al. 2023). Although GEMs are highly effective in BR, their application in the environment is limited due to uncontrolled growth and horizontal transmission of genes. It is necessary to manage their lifespans carefully to reduce the spread of GEMs and mitigate their impact on the existing population of creatures (Stuhr & Curran 2020).

Bio-augmentation has evolved as a solution to the issue of slow and inefficient degradation of CMs and trash by employing genetically modified microbes to break them down. Due to these genetic modifications, domesticated crops and animals can be genetically engineered to achieve specific outcomes, such as combinations, substitutes, and induced mutations (Veerasamy & Fredrik 2023). In addition to bacterial engineering, alternative techniques for changing the genetic code of plants, animals, or MOs are all driven by unique objectives (Dessy et al. 2023). GEMs have been altered using in-vitro molecular biology processes. GEM mainly describes MOs such as fungi, bacteria, and yeast that have undergone this transformation by humans. The introduction of genes results in the transformation of a single microbe into many MOs (Rafeeq et al. 2023). BR uses MOs or their enzymes to break down and remove pollutants from surroundings. GEMs are additionally acceptable for that reason, as seen in Figure 1 (Hamza Rafeeq et al. 2023).

Genetically engineered microorganisms (GMEs) for environmental remediation
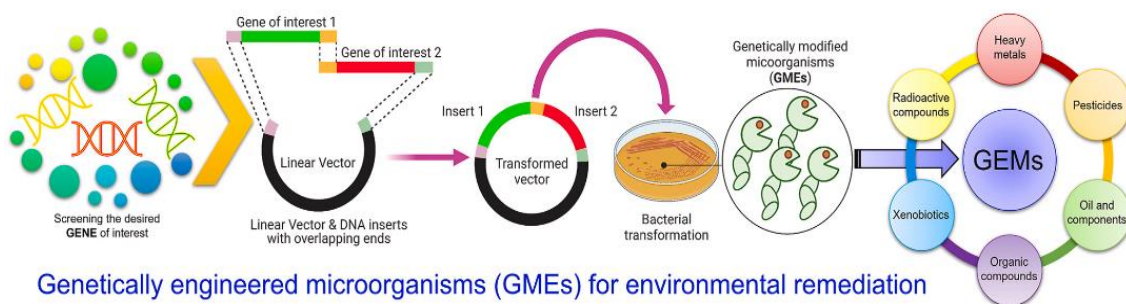
Figure 1. GEMS for environmental Remediation

Bacteria have a robust capacity to break down and decompose environmental CMs (Kumar et al. 2021). Bacterial strains that can break down various CMs, such as nitro-aromatics, chlor-aromatics, and polycyclic aromatic substances, have been found (Dessy et al. 2023). These strains can be used to bioremediate polluted areas by utilizing their metabolic capabilities. Certain MOs cannot break down some of the most resistant and hazardous xenobiotic substances, such as highly nitrated or halogenated aromatic substances, pesticides, and explosives (Rafeeq et al. 2023).

These molecules are chemically inactive in natural conditions and do not degrade effectively. The combination of CMs and their toxicity to existing populations of microbes creates challenges for efficient microbial biological degradation. Novel bacterial strains with enhanced metabolism have been engineered to surpass existing MOs' limitations, increasing their potential for biological remediation. Composting is electro-BR, microbe-assisted phyto-BR, and other BR techniques are all bio-stimulation and bioaugmentation. The popularity of utilizing genetic engineering to enhance the innate remediation capacities of MOs is increasing in light of current scientific discoveries (Kumar et al. 2021). The significance of several scientific fields in the effective use of genetically modified microorganisms (GEMs) for in-place biological remediation (BR). Here is a quick summary of the reasons why each region is essential:

Ecology: To determine how GEMs will interact with the current flora and fauna, it is essential to comprehend the local ecology. This information ensures that the cleaning procedure promotes the general health of the environment and aids in predicting any effects.

Biological Sciences: Understanding the behavior and workings of GEMs requires a solid basis in biological concepts. This entails comprehending microbial ecology, metabolic processes, and inter-microorganism interactions (Mohammadabadi et al. 2024).

Field Biochemical Procedures: The ability to monitor and evaluate GEM activity and environment effectively is made possible by a proficiency in field biochemical procedures. Samples, biochemical tests, and data gathering techniques that are essential for assessing the efficacy of remediation initiatives may fall under this category.

Genetic Engineering: The ability to construct GEMs with certain characteristics appropriate for remedial activities requires expertise in genetic engineering. This involves choosing the right genes for environmental adaptation, stress resistance, or degradation processes (Mohammadabadi et al. 2024).

Combining these domains makes it possible for GEMs to be effectively integrated into the environment, meet their remedial objectives, and reduce risks. Figure 2 illustrates several methods of BR (Patel et al. 2022).
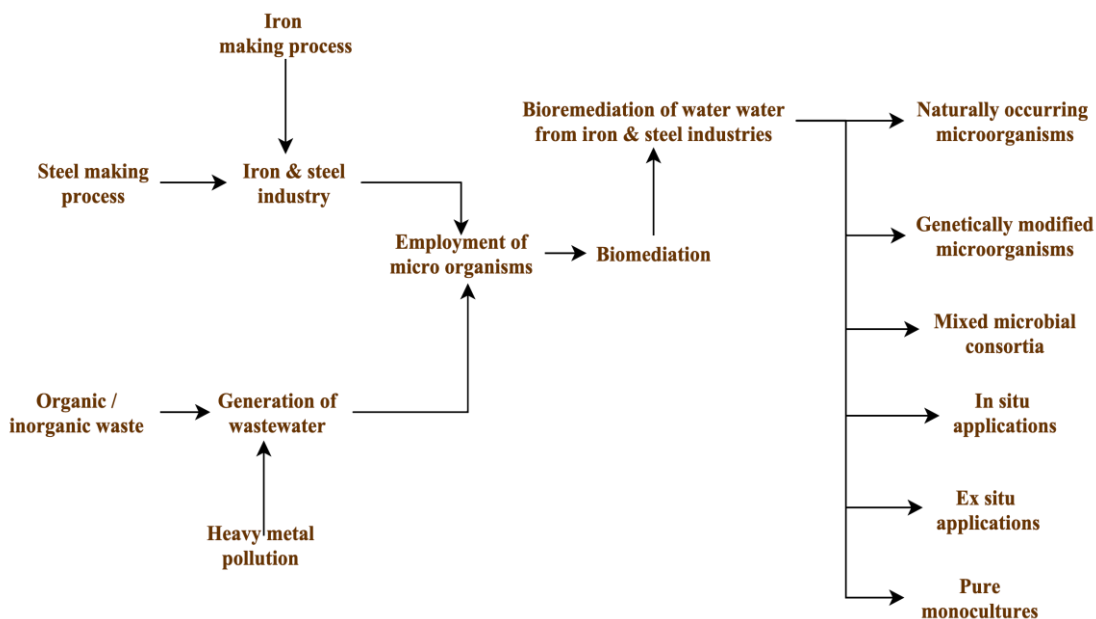
Figure 2. BR flow of the model

There is a complex relationship between microbes and other species within the highest level of the ecosystem. It is improbable that a single MO can directly harness the energy produced by its metabolic processes. Therefore, co-metabolism is the primary method by which CMs are broken down. The phenomenon of MOs collaborating and working together to degrade CMs is ubiquitous and commonly observed. The metabolites of one organism enable the survival of another organism, leading to mutual nutritional dependencies between both. The community of MOs executes this operation (Patel et al. 2022). To precisely assess the rates at which environmental contamination is deteriorating, it is necessary to consider all facets of a particular activity. While degradation bacteria exist in the environment, CMs will not undergo regular breakdown in competitive conditions. It describes a situation in which specific bacteria outcompete others and thrive in particular environments, especially when it comes to breaking down germs. This may often happen in settings with little resources or under certain circumstances. The beneficial microbes in these situations may be those that can take advantage of the nutrients that are readily accessible or those can withstand certain circumstances, such as very high or low pH. Their quick development may cause them to overtake other species as the dominant species in that ecosystem, which would have a negative effect on the environment's general health and nutrient cycling. If their environment is changed or there is a lot of competition, degrading bacteria—which often have important functions in recycling nutrients and breaking down organic matter—may find it difficult to survive. This method effects may result in nutrient imbalances or even a breakdown of the ecosystem. This is the primary clarification for this

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phenomenon. Comprehending the arrangement of microbial population facilitates the anticipation of the final destination for CMs in the surroundings, the development of tailored BR strategies for different kinds of CMs, and the breeding of certain specific degrading microbial populations.

Materials and Methods

Principles of Biological Method: Soil culture is the most effective BR technology because of its simplicity, low resource requirements, and rapid results. This phenomenon is more prevalent in ex-situ BR. It does sometimes occur during in-situ BR. BR involves placing the contaminated soil above the surface, where it may be subjected to air, and undergoing nutritional treatment to accelerate the metabolic activity of bacteria. In-situ biological monitoring by natural elimination, also known as "inherent BR," is a method of remediation that involves cleaning up contaminated regions without needing external intervention. Using genetically altered materials can enhance biodegradable properties. Biosparging is a technique that injects air into the top layer of soil to enhance the activity of MOs and accelerate the degradation of CMs in contaminated areas. The bio-slurping system employs a vacuum-enhanced pump, soil gas, the extraction process, and venting to efficiently remediate contaminated soil by indirectly delivering oxygen and accelerating the organic biodegradation of CMs. BR refers to using living organisms to degrade waste containing potentially hazardous substances. Due to their substantial toxicity and limited capacity to break down naturally, several xenobiotic substances have a detrimental effect on the ecosystem. MOs can break down substances due to the involvement of genes, digestive enzymes, and degrading processes in biological breakdown. MOs can utilize xenobiotic CMs as substitutes for carbon or nitrogen to facilitate their growth and metabolic activities. Various microbial communities can flourish in challenging and contaminated environments, exhibiting a significant ability for biodegradation, enabling them to decompose and transform CMs. Advanced molecular methods offer a comprehensive comprehension of many microbial populations' structure and function traits.

Enzymatic Degradation Method: Multiple enzymes have been utilized to degrade environmental CMs, each with a distinct method. Enzymes from one organism are often preferred over enzymes from diverse species due to their superior catalytic performance.

Bacterial enzymes: Deoxygenation can also act as a catalyst for thiol oxidation and the breakdown of C-C and C-S bonds. The bacterially produced dioxygenase enzyme contributes to the breakdown of several other enzymes produced by bacteria by converting hydrophobic substances into hydrophilic molecules. BR is a promising and ecologically acceptable technology for restoration that utilizes bacteria's enzymes to clear up colors and heavy metals. Bacterial enzymes convert organic and inorganic pigments into non-toxic compounds, resulting in total

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demineralization. Azoreductase digestive enzymes, such as destruction and desulfonation, break down the azo linkages of refractory intermediary atoms, transforming them into harmless compounds. Microbial oxygenase proteins metabolize or degrade naphthalene into hydrophilic compounds after being derived via the desulfonation of naphthalene-1,5-disulfonic acidity. Bacteria synthesize diverse enzymes that degrade azo dyes, which constitute the vast majority of reactive colors. Laccase and oxidoreductase are two specific types of enzymes. In this case, Escherichia coli was employed to generate an excessive amount of a chemical that catalyzes the oxidation of polyunsaturated fatty acids, producing free radicals. These unpaired electrons react with triphenylmethane dyes through co-oxidation. Lysinibacillus phallus efficiently decomposed the azo dyes via laccase and azo reductase activities. These compounds are produced due to a non-specific chemical process involving the laccase enzymes and free radicals. The ping-pong process occurs due to the breakdown of the colors by azoreductase.

Degradation of heavy metals: Bacterial enzymes can convert heavy metals into innocuous molecules instead of undergoing chemical breakdown. The process of converting metal can only occur with the presence of oxidative and limiting proteins (Figure 3). Streptomyces utilizes copper reducer enzymes derived from bacteria to facilitate the process of copper elimination. The elements nickel, cobalt, cadmium, copper, and zinc were formed by the catalytic action of the urease enzyme that occurs in Sporosarcina pasteurii. Urease is a catalyst that decomposes urea into carbon dioxide and ammonium. The alteration in the equilibrium of water-based solutions facilitates the extraction or deposition of metallic elements. In the past few decades, a multitude of bacterial catalysts have been identified that have the potential to break down and eliminate harmful pesticides. These bacteria resulted in an estimated degradation of 81%.
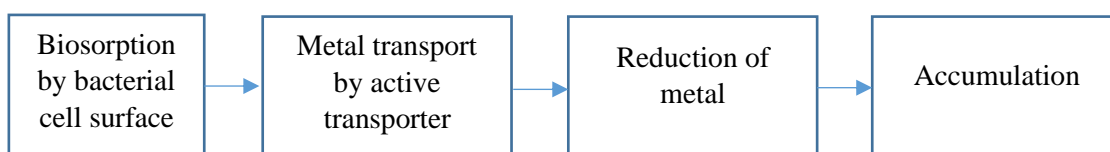
Figure 3. Four Faces of Heavy Metal Degradation by Bacteria

Degradation of plastic present: Most reduction or oxidation pathways are implicated in MOs' enzymatic degradation of plastics. Enzymes derived from both endogenous and exogenous sources are involved in this procedure. A depolymerase is a prevalent extracellular enzyme that catalyzes the breakdown of large polymeric monomers into smaller components. Recently identified Bacillus and Pseudomonas genera have been shown to secrete depolymerase enzymes that may degrade brominated polystyrene polymers. The enzymes facilitated the degradation of

Polyethylene Sulfonate (PES). Hydrolase proteins regulate a crucial stage in the polymeric cleavage cycle. They achieve this by initiating a nucleophilic assault on the carbon atomic particles, resulting in the cleavage of the bonds among ester compounds and the subsequent reduction or disintegration of the entire structure.

Modern Approaches: In recent years, there has been significant progress in the advancement of state-of-the-art techniques for microbial degradation. These methods employ molecular techniques, genetic manipulation, and biological computational tools. Gaining insight into the mechanisms by which germs interact with each other is of utmost importance.

Quorum sensing: The environment serves as an intricate habitat for MOs, whereby they engage in interactions that give rise to intricate chemical systems. Quorum detecting, in the setting of bacteria, refers to a chemical method of interaction between cells that regulates gene transcription at the population level in response to alterations in the surroundings. The chemical connection plays a significant role in the interplay between fungus, bacteria, and crops and is also evident in the interactions across other biological domains.

Antimicrobial compounds: Fungi interact with bacteria vulnerable to antibiotics and possess several Antibiotic-Resistance Genes (ARGs) inside their genetic makeup. Some species of fungus create substantial amounts of antimicrobial substances, including antibiotics, in their surroundings. Based on the metagenomic investigation, there is a direct correlation between the prevalence of the antibiotic-resistant bacteria species and the Ascomycota and Zygomycota phyla in soils. ARGs play a crucial role in maintaining resistance to antifungal agents. Notably, proteobacteria belonging to the Oidiodendron and Penicillium families have the highest average number of ARGs per chromosome.

Steady-Com model: Steady-Com, a mathematical model, has been created to establish a framework for predicting the distribution of metabolic flow suitable for steady needs. The Steady-Com was initially showcased using a group of four dual auxotrophic because mutant E. coli strains and nine different kinds of intestinal bacteria from the prominent phyla Proteobacteria, Actinobacteria, Firmicutes, and Bacteroidetes. This prototype provides a comprehensive understanding of the growth and abundance of microbes. Unlike Flux Balancing Assessment (FBA), it can forecast variations in species diversity when diets are altered within certain limitations. This is achieved by arbitrarily adjusting the rate at which bacteria absorb light. Steady-Com is a valuable tool for predicting the makeup of the air microbes in a specific location.

Microfluidics platform: Creating Syn-Com requires thorough screening of various combinations of MOs for assembly. This process is arduous, time-intensive, and expensive. Although microfluidics is not cost-effective, it enables fast and accurate strain screening and facilitates real-time interaction among the chosen MOs. Microfluidic instruments offer a confined

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space for conducting single-cell characterization, microbial communication, and population creation. These devices give enhanced visibility and record-keeping capabilities while allowing for precise control over dynamic processes.

Genetic Engineering Tools: Multiple experiments have been undertaken to enhance genetically modified crops and microbes. Gene-editing methods provide innovative and valuable system features. However, omics methods supply accurate genetic and translational information in the topic overview. Scientists must effectively collaborate with MOs to facilitate the degradation of hydrocarbon compounds and enhance the development of genetically modified plants under abiotic stress conditions. In addition, they require a substantial amount of genomic sequence information to utilize as a resource using Clustered Regularly Interspaced Short Palindromic Repetition (CRISPR).

Role of CRISPR: CRISPR can elucidate several conceptual aspects of bacterial physiology related to the breakdown of PAHs. The inhibition of the quorum sensing mechanism in Pseudomonas aeruginosa resulted in decreased degradation of Polycyclic Aromatic Hydrocarbons (PAHs) and catechol dioxygenase activity. The presence of the quorum sensing system and genes associated with antibiotic resistance can modify the communication among microbial communities. Scientists have endeavoured to develop an artificial strain or modify the genes responsible for hydrocarbon degradation for over ten years. To enhance the dioxygenase's capacity to detect Polychlorinated Biphenyls, 20 amino acid sequences were altered using site-specific mutagenesis. Replacing alanine with aspartic acid at location 375 might enhance the dioxygenase activities in breaking down various substrates.

Results and discussion

In summary up, the use of genetically modified microbes offers a novel and promising method for bioremediation, the process of eliminating pollutants from soil in agricultural settings. Researchers may create specialized solutions to break down certain contaminants, enhance soil health, and rehabilitate polluted places more successfully than with conventional procedures by boosting the inherent powers of these microbes. By using cutting-edge genetic approaches, these organisms may function more effectively, adapt more readily, and remain resilient under a variety of soil conditions.

The isolates shown promising potential for future studies and may become part of a team to clean up heavy metal polluted soils. The microorganisms were biocompatibility assessed before they could join the consortium (Table 1). Four separate consortiums were formed from the chosen microbes. In Consortium A, the ratio of Rhizobium radiobacter, Klebsiella oxytoca, and

Achromobacter denitrificans was 1:1:1, in Consortium B, it was 2:1:1, in Consortium C, it was 1:2:1, and in Consortium D, it was 1:1:2. Because cells (such as biosurfactants) produce active molecules and the binding area between heavy metals and cells becomes larger, increased biomass aids in the removal of these pollutants from the environment. Bacterial growth is also affected by temperature and pH. With careful selection, these factors enhance bioremediation while lowering production costs in industrial settings. Figures 4 and 5 show the ideal conditions for growing plants. Consortium D, which showed the greatest promise, had its ideal cultivation settings chosen. Regarding the isolation of Pb, Ni, As, and Cu pollutants, the collaboration stands far and wide above the competition. In addition to being the best in synthesizing indole-3-acetic and indole-3-butyric acids, the consortium is also the most effective when it comes to mixed heavy-metal pollution. Figures 4 and 5 demonstrate the ideal culture parameters used for Consortium D. Heat waves of 35 °C or higher reduced biomass output. Additionally, the microbial growth was suppressed at a temperature of 20 °C. Preferred growing conditions were temperatures between 25 and 30 degrees Celsius.

Table 1 Biocompatibility of the studied microorganism

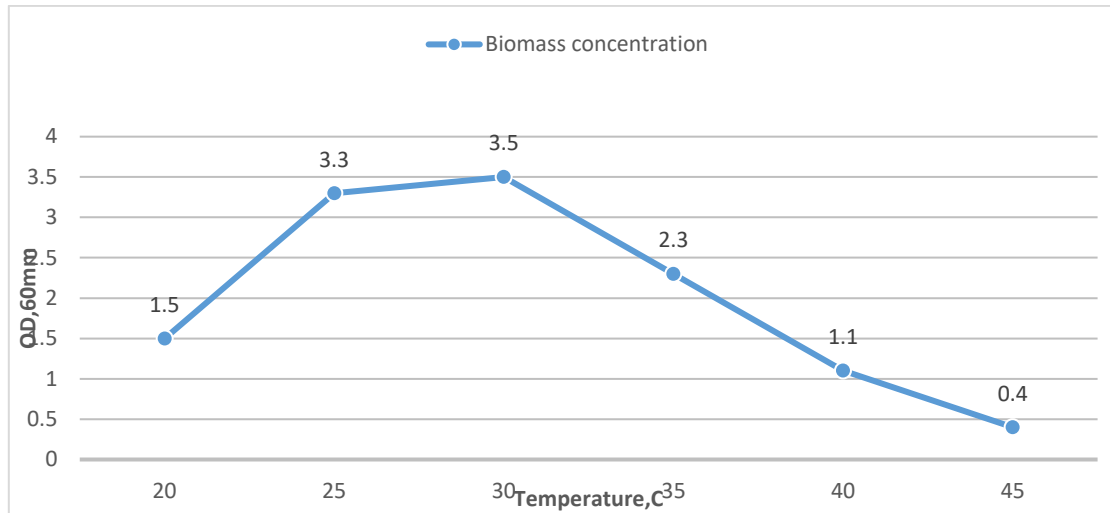| MICROORGANISM	PANTOEA SP.	ACHROMOBACTER DENITRIFICANS	KLEBSIELLA OXYTOCA	RHIZOBIUM RADIOBACTER	PSEUDOMONAS FLUORESCENS
PANTOEA **SP.**		-	+	-	+
ACHROMOBACTER DENITRIFICANS	-		+	+	-
KLEBSIELLA OXYTOCA	+	+		+	-
RHIZOBIUM RADIOBACTER	-	+	+		-
PSEUDOMONAS FLUORESCENS	+	-	-	-	

Figure 4. Impact of temperature on the development of biomass: Cooperation D
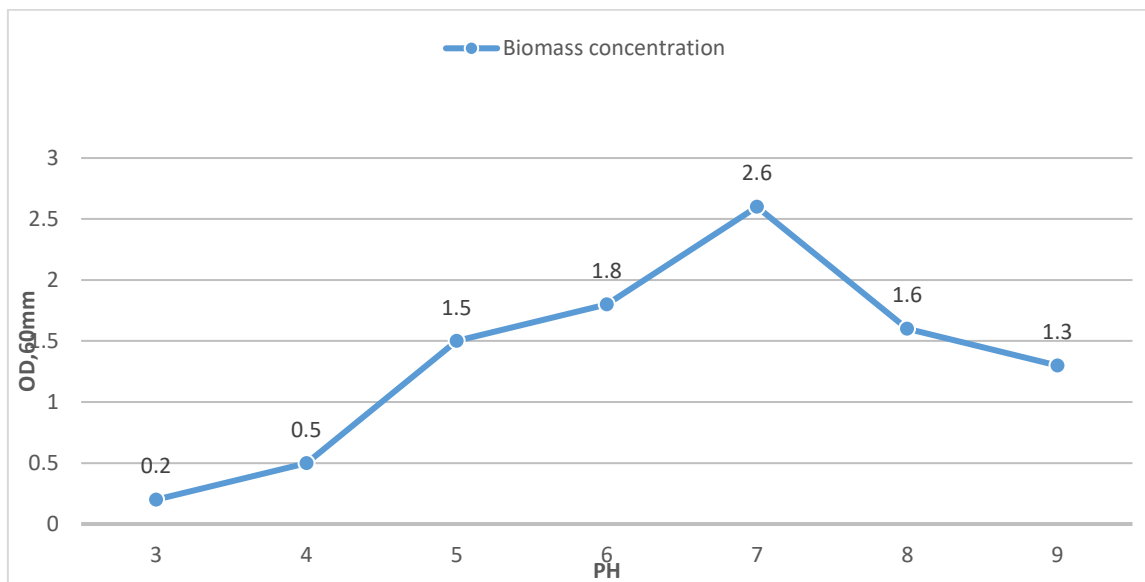

Figure 5. Consortium D's acidity effect on biomass accumulation

In very acidic and extremely alkaline conditions, Consortium D showed very little biomass accumulation. Bacterial growth was 1.21 OD (600 mm) at pH 9, but no biomass accumulation occurred at pH 3. According to Figure 5, the ideal response of the medium on the development of Consortium D was a pH of 7. Based on the results, Consortium D has limited usage; it is ineffective in very acidic soils (since excessive acidity kills cells), but it may have some success in slightly alkaline soils. Heavy metals' electrostatic attraction to bacterial surfaces was shown to be negatively affected by the alkaline reaction of the medium. It is most promising to employ

Consortium D in conjunction with phytoremediation approaches since it can eliminate heavy metals and also synthesizes phytohormones, which encourage plant growth and development.

Conclusions: The understanding of the dangerous effects of various chemical CMs has led to an increase in research efforts to develop remediation technologies that can effectively eradicate these CMs. BR is a safe, cost-effective, and sustainable procedure that enhances the biological process of biological degradation to eliminate CMs. Thus, to expand the knowledge of the communities of bacteria and their response to environmental CMs, it is crucial to have a deeper comprehension of molecular genetics. This will enable the researchers to boost the CM degradation capabilities of the most successful species. BR is a process that creates a route towards a more sustainable and pollution-free earth.

Conflict of Interest: There is no conflict of Interest.

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میکروارگانیسم های دستکاری شده ژنتیکی برای پاکسازی زیستی و حذف آلاینده‌های خاک در محیط‌های کشاورزی

نیضی میشرا iD

*نویسـنده مسـئول: اسـتادیار، گروه علوم کامپیوتر و فناوری اطلاعات، دانشـگاه کالینگا، رایپور، هند. آدرس پسـت الکترونیکی:
ku.nidhimishra@kalingauniversity.ac.in

قورپاده بی‌پین شیواجی iD

پژوهشـگر، گروه علوم کـامپیوتر و فنـاوری اطلاعـات، دانشـگاه کـالینگـا، رایپور، هنـد. آدرس پسـت للکترونیکی:
ghorpade.bipin@kalingauniversity.ac.in

چکیده

هدف: آلودگی محیط زیست و کاهش آن از چالش‌های مهم جهانی است. طیف گسترده‌ای از آلاینده‌ها، از جمله آفت کش‌ها،
هیدروکربن‌ها، فلزات سنگین و رنگ‌ها، عوامل اصلی آلودگی محیطی هستند. حذف این آلاینده‌ها می‌تواند مشکلات قابل توجهی
ایجاد کند زیرا چنین تلاش‌هایی اغلب منجر به انتشار بیشتر آلاینده‌ها در محیط آبی می‌شود. بایورمدیاسیون (Bioremediation)
یا BR یک فناوری بسیار موثر برای کاهش آلاینده‌های محیطی و بازگرداندن مکان‌های آسیب دیده به شرایط اولیه است. تنها مقدار
محدودی از میکروارگانیسم‌های دستکاری شده ژنتیکی قابل کشت (GEM) مورد استفاده قرار گرفته‌اند، در حالی که طیف گسترده‌ای
از تنوع میکروبی هنوز نیاز به بررسی دارد.

مواد و روش‌ها: طیف وسیعی از تکنیک‌های BR به طور گسترده برای بهبود توانایی GEMها در متابولیسم مواد و بازگرداندن
تعادل اکولوژیکی با شکستن آلاینده‌های پایدار به کار گرفته شده است. این‌ها شامل کموتاکسی، تحریک زیستی، افزایش زیستی،
تشکیل بیوفیلم، استفاده از GEMها و روش‌های پیچیده اومیکس می‌باشد.

نتایج: پیشـرفت قابل توجهی در درک چگونگی شکسـتن و پاکسـازی موثر باکتری‌ها از آلودگی‌های محیطی صورت گرفته است.
GEMها با تجزیه موثر مواد زائد از نظر زیسـت محیطی سـالم و تولید محصـولات جانبی بی ضـرر، به اصـلاح محیط‌های آلوده
کمک می‌کنند.

نتیجه گیری: درک اثرات خطرناک آلاینده‌های شیمیایی مختلف منجر به افزایش تلاش‌های تحقیقاتی برای توسعه فناوری‌های اصلاحی شده است که می‌توانند به طور موثر این آلاینده‌ها را ریشه کن کنند. BR یک روش ایمن، مقرون به صرفه و پایدار است که فرآیند تخریب بیولوژیکی را برای حذف آلاینده‌ها افزایش می‌دهد. بنابراین، برای گسترش دانش جوامع باکتریایی و پاسخ آنها به آلاینده‌های محیطی، داشتن درک عمیق‌تر از ژنتیک مولکولی بسیار مهم است. این امر محققین را قادر می سازد تا قابلیت های تخریب آلاینده‌ها موفق‌ترین گونه‌ها را تقویت کنند. BR فرآیندی است که مسیری را به سمت زمینی پایدارتر و عاری از آلودگی ایجاد می‌کند.

واژه‌های کلیدی: اصلاح محیطی، تخریب آنزیمی، روش بیولوژیکی، سنجش حد نصاب، کریسپر

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