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Biotechnology of absorption and remove of heavy metals by microorganism and plant

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ABSTRACT

Heavy metals are a dangerous and widespread contaminant in the world because of the difficulty of disposal. Heavy elements affect the life of organisms and cause many serious diseases in humans and lead to the deposition of heavy elements in the soil to the weakness of the growth of plants and its yield. There are many techniques to remove the deposits of heavy elements, including bioremediation. Many factors are used in the process of phytoremediation, such as microorganisms such as bacteria, fungi, yeasts, algae and different plants. Microbiology can absorb heavy elements through multiple mechanisms and specialized vectors. Molecular genetics techniques have been used to increase the tolerance of plant contaminants and to develop mechanisms to transfer isolated genes from bacteria to plants and to produce genetically modified plants that can grow in soils contaminated with high concentrations of heavy elements. The following review is a review of studies on phytoremediation to clean the environment from heavy element deposits.

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INTRODUCTION

Contaminants include minerals such as arsenic (As), cadmium (Cd), copper (Cu), Hg, manganese (Mn), selenium (Se), zinc (Zn) and Radionuclides such as Cesium (Cs), Phosphorus (P), U add to plant fertilizer like nitrate and phosphate (Singh *et al.,* 2011). These minerals are available in the form of positive or negative shipments. Inorganic contaminants can be exchanged by oxidation and Reduction and can be transported into cells and in other cases evaporate into the atmosphere such as mercury and selenium but unfortunately cannot be destroyed (Priyalaxmi *et al.,* 2014). A range of bioremediation methods for inorganic compounds, including restriction of their movement (immobilization), so-called phytostabilization, are available, withdrawn to the vegetative and seeds total harvested (phytoextraction or rhizofiltration) and in exceptional cases volatile (phytovolatilization) (Naik *et al.,* 2012; Mirlahiji and Eisazadeh, 2014). The methods of biotechnologies have focused on the production of tolerant plants or the accumulation of contaminants by focusing on metal-carrying genes and on genes that facilitate the production of a mixture (Mohsenzadeh and Rad, 2012). In the case of elements that can volatilize, then the emphasis is placed on the genes responsible for turning the contaminants into volatile**.**

Mechanism of removal and absorption of As by microorganism and plants

Arsenic detoxification is manifested in bacteria and yeasts, as the similarity between AsV and phosphates enables the yeasts cells to pull the contaminant from the phosphate vectors. In this context, the ability of microorganisms to reduce AsV to Aslll as a mechanism for these organisms to tolerant the contaminant (Kristanti *et al.,* 2011). It does not stop at this point but excludes those organisms Aslll oxyanions from their cells by vectors being used for this purpose (Bogacka, 2011). For example, it was found that bacteria (*Escherichia coli*) is reduced AsV to Aslll by an enzyme Arsenate reductase (ARSC) than Aslll is transported outside the

cell by an export pump Aslll and the mechanism thus acts as a contaminant resistance (Deeb and Altalhi, 2009). Proto organisms show another method course of detoxification Arsenic by the metabolism of inorganic arsenic into volatile organic compounds such as Trimethyl arsine after a series of methylation reactions and s-adenosylmethionine enzymes are used as a cofactor (Dobson and Burgess, 2007).

Studies of plant capacity in arsenic detoxification or absorption of various mechanisms have been identified, the most important of which is that, as long as AsV is a peer-to-P, it is absorbed by the plant system by the phosphate carrier (PHT1) (Garbisu and Alkorta, 2001), which has been demonstrated in a study on *A. thaliana*. It has also been found that AsV is inhibiting gene reactions to the plant's need for FPC, leading to the conclusion that ASV overlaps in the presence of phosphate from its absence to ensure a change in Phosphate signalling mechanism (Kim *et al.,* 2007). There were nine phosphates (PHT) carriers with high portability in (*A. thaliana*). There is certainly a need for further studies to diagnose the attractions of the different phosphate of the AsV and phosphate Paranthaman SR, (Karthikeyan, 2015). Several studies have suggested that AsV reduced to Aslll within plant cells by endogenous arsenate reductases, that identified in rice, *Holcus lanatus*, *Pteris vittata (Salido et al., 2003)*. It was found that the gene insulated from *A. thaliana* (ACR2) completes the function of zirconium down sampling in the strains of *E. coli (Rensing and Grass, 2003).* Recent studies have shown that the possession of aquaporins compounds MIP (Major intrinsic protein superfamily) and their function is to transport Aslll in rice (Tabak *et al.,* 2005). MIPs plant proteins are divided into four subfamilies, which include; proteins Plasma membrane intrinsic proteins (PIPs); tonoplast intrinsic proteins and abbreviation (TIPs); The Nodulin 26-like intrinsic proteins (NIPs) and finally small group proteins (small and basic intrinsic proteins SIPs) (Zaidi *et al.,* 2009).

Phytoremediation of arsenic (As)

Nature provides large-scale genetic material (germplasm), which can be considered as a gene bank at the request of the person at will. For example, *Pteris vittata* are estimated to accumulate large amounts of arsenic and grow profusely in tropical and under tropical areas. This plant can be a strong candidate for the bioremediation of arsenic-contaminated soils in Those areas. In contrast to other land plants, the plant Accumulates arsenic in the form of a Aslll (Chaney *et al.,* 2000). It was found that the gene PvACR3 which encodes the protein is slightly similar to the ACR3 available in the yeasts and is responsible for the flow of the As, and the Aslll flow to the gap for isolation (Li and Li. 2011). Although studies have shown that the fern holds high levels of arsenic in the soil under the conditions of the Glasshouse. The most important is the lack of full knowledge of the molecular mechanism to detoxify as by this fern (Machado *et al.,* 2008). Besides, its permanent growth is limited to tropical and subtropical areas and may be considered Invasive when transported to new areas, adversely affecting the new ecosystem**.**

Alternative strategies have been developed for the use of *P. vittata* in the search for genetic foundations and mechanisms for the creation of alternative plants at a lower cost. The basis for the work of these strategies is built on genetic manipulation of the inherited material to the desired capacity, such as increasing the endurance of the new plant to resist living under the conditions of the arsenic-contaminated environment, increasing the plant's susceptibility to remove the contaminant and transport it to the harvested parts of the plant (Marques *et al.,* 2014). Many of the research successes in development of genetically modified plants in the capacity of increased endurance and accumulation to include a high gene expression in the manufacture or PCs of the GSH, which has increased plant endurance for high levels of As but unfortunately failed to accumulate the contaminant in its tissues (Olatunji *et al.,* 2009).

Scientists developed genetically modified plants tolerance accumulation of the contaminant As in the vegetative by collecting expression of the gene isolated from bacteria. The expression of the isolated gene from the *E. coli* reductionist (arsC) in the leaves and Stimulate from the soybean plant-mediated by a small unit of the Roesco enzyme system (RuBisCO small subunit 1) (Lors *et al.,*2004). An expression of gene Synthetaseglutamylcysteine $^{\gamma}$ (ECS-$^{\gamma}$) isolated from *E. coli* bacteria in the vegetative and root groups was obtained through a strong synthetic catalyst named Actin2. Thus, the plants were genetically altered twice and showed a high tolerance compared to those of Ecs$^{\gamma}$ units (Peña-Montenegro *et al.,* 2015). What is interesting about this scientific achievement is that the plants that were genetically modified twice (double transgenic plants) formed a 17-fold greater biomass than the wild plant and accumulated the arsenic in the vegetative total 3 times more than wild plant after its development in media containing 125 micromoles of sodium arsenic (Velásquez and Dussan, 2009).

Absorption of AS by crops

The absorption and accumulation of as in crops like rice and vegetables is a very serious health problem to health and environment of living organisms, especially human beings (Borma *et al.,*

2003). The first is to reduce as in the vegetable parts of the harvest, as most crops are eaten by their green, pink, or seeds This is done by downsampling AsV to aslll in roots, with increased Aslll-thiol complexity by increasing the genetic expression of the encrypted genes of the cholinesterase reduction enzyme and the bio-manufacturing of protein-root pathways that are only carried out with the use of promoters that specialize in roots (Davis *et al.,* 2003). To increase AC production at the root, It can refrain from moving as to the green growth after the formation of ASLLL-PC and sending it to the root vascular tissue. Second, AsV absorption can be stopped by the roots when manipulating phts-inclined compounds to AsV phosphate allowance. Thirdly, the accumulation of aslll in crops, especially the rice, can be minimized and reduced by the genetic expression of gene Lsil, which is mediated by the absorption of the roots of both aslll and Lsi2 responsible for moving aslll from roots to green growth. Fourthly, the non-organic transformation into forms of methylated organic as, which reduces the toxicity as well as the occurrence of the As-MMA and DMA types to a gaseous state of the trimethylarsine (TMA) compound, which is augmented by the gene expression of the genome lll-S-adenosyl Methyltransferase (ArsM) of bacteria, algae or coded plant genes for the AS-methyltransferases enzyme diagnosed. However, TMA toxicity in the submerged fields is still needed for further studies (Gawali *et al.,*2014)**.**

Pollution and toxicity of Mercury (Hg)

Mercury is highly toxic and its spread in soil and water is a major threat to human health and the environment. Mercury is usually released to the environment in non-organic forms, either as a metal element [Hg (0)] or as [Hg (11)]. The ionic body is inclined to strongly link to the soil components, thereby reducing their availability and absorption (Gomes *et al.,* 2013). Organic forms are Hg and, specifically, Methylmercury, Dimethylmercury and Phenylmercury highly toxic and accumulate in membrane membranes. These compounds discourage the dynamic pathways of oxidation and optical manufacturing. The instance specializes Mercury (CH3HG) is the most toxic and poses the greatest risk to humans and the environment because it accumulates in large quantities in the food chain (Infante *et al.,*2014). The world felt the extreme severity of the mercury in 1950 after a major disaster in Japan as a result of mercury poisoning. The risk lies in contaminated sites where mercury cannot be removed forever because of the different forms that are not shattered by the biological activities of soil revival and its strong association with organic matter, which poses a permanent risk to the environment (Lozano and Dussán, 2013). Radiation from natural mercury has spread to all areas of the globe

Removal of Mercury (Hg) by plant and bacteria

Bacteria resistant to organic and inorganic mercury salts mediate their metabolic pathway to the non-toxic Mercury element Hg (0). Mercury-resistant bacteria genes are organized in the genes of *mer* operon and the latter varies from one type of bacteria to another in their composition (Ruiz *et al.,* 2011). In the case of bacterial resistance in its narrow conception of mercury, *mer* operon is made up of genes that encrypt functional proteins to regulate *merR*, transport (*mer*T, *mer*P, *mer*C, *mer*F) and chemoelectric reduction. While widely resistant bacteria carry an extra gene that encrypts *mer*B and which holds resistance to many types of elemental mercury. The organic Mercury Analyst (*mer*B) helps to convert R-Hg to Hg and reduces r-h when R represents a wide range of organic aggregates as an instance or vinyl totals. The reduced enzyme of mercury ion (*mer*A) assists the Hg (11) to Hg (0) (Wu *et al.,* 2015). The latter is less toxic than the Ionic Hg body or membership. Metallic mercury is relatively inert and very low and gaseous under normal temperature conditions allowing Its spread of bacteria produced. Mercury evaporates rapidly from bacteria and reduces in the atmosphere to concentrations with harmless levels (Villegas-Torres *et al.,* 2011).

Biotechnology in a plant of phytoremediation of Hg

Many plant species have been tested and unfortunately, none of the plants tested in the detoxification or conversion of the highly toxic mercury compound has succeeded to less toxic organic forms. As mentioned earlier, coded bacterial genes for shifting mercury from one form to another have been identified, laying a foundation on which molecular genetics specialists can increase plant tolerance for mercury (Gomes *et al.,* 2013). Richard Meagher developed a strategy for this purpose and his colleagues in the early 1990s, benefiting from the gene, isolated from genes *mer* operon bacteria, namely *mer*A and bacterial Organomercury lyase gene and transported them to the plants (Infante *et al.,* 2014). The efforts made by genetically engineered plant engineers have resulted in the transfer of Gengans to different plant varieties, most importantly, tobacco, cotton wool trees and rice. The genetically engineered expression of the genetically modified plants (Hg) has increased by ten times the lethal concentrations of non-genetically modified plants. After being altered, plants showed high susceptibility to high levels of Hg (0) compared to no Modified plants. Yellow Populus and

(Cottonwood) have been characterized by additional benefit because they are deep-rooted in the soil and growing in moist soils, absorbing the form of Mercury Hg (11) from the wide-area root total and dragging it to the vegetative total to fly into the atmosphere, providing a great opportunity To get rid of this contaminant in wet soils (Villegas-Torres *et al.,* 2011).

To increase plant efficiency in order to eliminate the toxicity of the mercury, *merA* and *merB* plants have been modified. It was found that the genetically modified plants of both genes carried a two-step conversion mercury to a volatile of Hg (0) and was 50 times the same As the lethal concentration of the plants of comparison and endured five times the concentration that kills plants modified by *merB* gene only (Wu *et al.,* 2015). When applying the results of the study to trees after the transfer of both gene to this plant, they showed a high tolerance of organic mercury. Previous results have enhanced the potential for the genetic engineering of a wide range of plants to include trees, shrubs and grasses and their use in the detoxification of widely available images of ionic and organic mercury in sites contaminated by Mercury.

The scientists went further when they noted that the plastids and the Endoplasmic reticular (ER) were the target of mercury poisoning, and concluded that the protection of these two parts of the cell was very important after the engineering of the detoxification systems in both components of the cell and would provide high protection of the vegetation from Mercury (Lozano and Dussán, 2013). The beginning was with plastids, genetically engineered by transporting both the gene *merA* and *merB* to the chloroplast. Genetic engineering was employed in bioreclamation after the transfer of gene *merA* and *merB* from bacteria to a group of plants. Modified plants have shown high susceptibility in disposing of the toxicity of a mercury instance and converting it into a Hg0 volatile (less toxic) (Ruiz *et al.,* 2011).

Selenium

Selenium is an essential nutrient for many organisms, including humans, and its gravity dangers in its increase or decrease concentration. Although the plant's need for Salonium is not certified, the plant absorbs it and represents it inside its tissues as it is similar to sulphur and is transported by sulphur carriers (Wang and Chen, 2009). Se is accumulated in all of the plant parts, including seeds and can be flown into the atmosphere, knowing that some items can accumulate high concentrations of Se up to 1% of their dry weight. Many of the plant species estimated in the accumulation and volatilization of Se, and can be invested in bioreclamation (KCR Sunil *et al.,* 2015).

It is believed that the toxicity of Se due to a non-specialized relationship between the two SeCys and SeMet with protein. To prevent plant poisoning, the latter will break seCys into a safe metallic Se (Se0) or represent it to a relatively non-toxic methyl-seCys compound which may accumulate to dimethyl diselenide (DMDSe) compound. Sulphur-loving plants such as mustard, latex, onion and garlic accumulate in normal conditions 0.01-0.1% of their dry weight Se and yet they are called ordinary accumulation types of Se (Jain *et al.,* 2012) (Wathah, and Marhoon, 2018). The accumulation of large amounts of se possesses a unique characteristic regarding its preference for the accumulation of Se instead of S and it could carry 1% of its dry weight under the conditions of the field as well as its accumulation of Methyl-SeCys compounds (Fan *et al.,* 2007).

Biotechnology of Selenium metabolism in plant

The first idea began to deal with the endurance, accumulation and volatility of Se when the gene expression of the genes included in the representation and volatilization of sulphur and selenium was increased. Indian mustard Plant *Brassica juncea* showed a high expression of the ATP sulfurylase (APS) that converts of Selenium from form to others and the plant has been able to increase the downsampling of salite (KCR Sunil *et al.,* 2015). The test results indicated an increase in the expression Cystathionine gamma-synthase (CGS), the first enzyme to convert SeCys to SeMet in the Indian mustard plant, which increased the volatility of Se by 2 to 3 times after genetically engineered with the gene crossing the enzyme (Lozano and Dussán, 2013).

Phytoremediation of Selenium

An experiment was carried out inside a glass house using natural soil containers contaminated with Selenium and others contaminated with sediment were used. Plants planted in the soil contaminated with Selenium and modified with gene APS Accumulated of Selenium triple compared to non- modified Indian mustard plants, and decrease contamination rate was 40% in the plants to transported gene CgS and the results were identical to laboratory research (Gawali *et al.,*2014). When plants are planted at a site contaminated with Selenium sediments, the plants with gene-APS have accumulated more than four times than the wild plant species (Mirlahiji and Eisazadeh, 2014). In a second field experiment, in which soil containing sediment from the element was used, the genetically modified plants of SL and SMT showed an increase in the accumulation of the component by two times, and the results were identical to the results of the research carried out under laboratory conditions

(Marhoon *et al.,* 2018). This follows from the importance of the use of biotechnologies in the area of plant Phytoremediation (Fan *et al.,* 2007).

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