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Water and soil contaminated by arsenic: the use of microorganisms and plants in bioremediation

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Abstract

Owing to their roles in the arsenic (As) biogeochemical cycle, microorganisms and plants offer significant potential for developing innovative biotechnological applications able to remediate As pollutions. This possible use in bioremediation processes and phytomanagement is based on their ability to catalyse various biotransformation reactions leading to, e.g. the precipitation, dissolution, and sequestration of As, stabilisation in the root zone and shoot As removal. On the one hand, genomic studies of microorganisms and their communities are useful in understanding their metabolic activities and their interaction with As. On the other hand, our knowledge of molecular mechanisms and fate of As in plants has been improved by laboratory and field experiments. Such studies pave new avenues for developing environmentally friendly bioprocessing options targeting As, which worldwide represents a major risk to many ecosystems and human health.

Keywords Arsenic · Bioremediation · Phytoremediation · Microbial genomics · Metabolism · Phytomanagement

Introduction

Arsenic (As), which is often considered a non-essential element except for some organisms (but would be in fact an ultratrace element) and classified as a carcinogen, is a common contaminant of water, soil and food, and a global danger to human health (Nordstrom 2002; Zhao et al. 2010; ATSDR 2017; Marchant et al. 2017; da Silva et al. 2018a). Drinking water being considered as the main source of As ingestion, WHO recommended $10 \mu\text{g L}^{-1}$ as the As drinking water guideline value (WHO 2017), which has been adopted

as the concentration limit in drinking water in most countries. Only a few guideline values for As concentrations in foodstuffs were defined. In Europe (EU 2015/1006), As concentration limits are given for some rice products (from 0.1 to 0.3 mg kg^{-1} wet weight). An acute or chronic exposure to As excess can cause many diseases, including various cancer forms. Its presence in water is one main source of contamination, but many studies have demonstrated its presence in fishes and crops from contaminated areas (Carlin et al. 2016; Jackson et al. 2012; Manjón and Ramírez-Andreotta 2020; Molin et al. 2015; WHO 2011; Zhao 2020). In several Chinese provinces, As-contaminated farmland impairs rice production (Li et al. 2019b). Irrigation of agricultural soils with As-rich water may contribute to As accumulation in soil and crops, and its entry into the food chain (Sandhi et al. 2018).

From natural or anthropogenic sources, As is present worldwide in the environment and many areas have a high As geochemical background suffering from soil and groundwater contamination, e.g. Chaco-Pampean plain in Argentina, West Bengal in India, Bangladesh, South-East Asia, and Limousin in France (Singh et al. 2015; Marchant et al. 2017; Antoni et al. 2019). Soil As contamination oftenly increases due to anthropogenic activities, e.g. As wood preservatives and treated wood washings, glassworks and crystal, mining and tailings, smelting, semiconductors,

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electronics and batteries, paints, toner, weapons, adhesives, disposal of industrial effluents, fossil fuel combustion, pesticides, and P fertilisers (Belon et al. 2012; Singh et al. 2015; Tóth et al. 2016; Reimann et al. 2017; Navazas et al. 2019). Mid-2018, 1355 out of 6808 French polluted sites (19.9%) display an As contamination, including 806 sites for soils and 317 ones for soils and groundwater (Antoni et al. 2019). More than 600 As-contaminated sites require remediation in the USA (da Silva et al. 2018a, 2019a). Reducing As accumulation in rice is a top priority in the management of Chinese contaminated soils (Zhao 2020).

Background values for total soil As (in mg kg^{-1}) usually range from 0.1 to 67 with an average value around 5 (Singh et al. 2015; da Silva et al. 2018a), e.g. frequent French values: 1–25 and geochemical outliers: 30–60, median and mean values for French topsoils: 12 and 18 (Baize 2016). French topsoils exceeding potential guideline values ($45\text{--}50 \text{ mg As kg}^{-1}$) occur in localised hot-spots primarily attributed to geology and mineralisation, mining, pesticides, and some anthropogenic activities (Marchant et al. 2017). Mean, median, minimum, maximum, and outlier values in English topsoils are respectively (mg As kg^{-1}): 16, 14.1, <0.5 , 1008, and 555–15,100 (Ander et al. 2013).

Major bioavailable As forms are arsenates (As(V), i.e. H_2AsO_4^- and HAsO_4^{2-}) and arsenites (As(III), i.e. H_3AsO_3 , and H_2AsO_3^-). Arsenical species depend on soil types, pH and their redox status, their toxicity ranking as $\text{As(III)} > \text{As(V)} > \text{organic forms}$: monomethylarsonic acid (MMA) $>$ dimethylarsinic acid (DMA) (Jain and Ali 2000). Inorganic As forms react with soil Al/Fe/Mn oxides, Ca/Mg carbonates, and clay minerals whereas dissolved organic matter can promote As desorption (Kumpiene et al. 2019). Arsenical species display contrasting properties for their sorption to Fe/Mn-containing minerals, depending on soil pH and other soil factors (Vega et al. 2017; Kumpiene et al. 2019). As(V) generally predominates in aerobic conditions, while As(III) prevails under anaerobic conditions being more (bio)available than As(V). Various organic arsenicals are reported (Singh et al. 2015). Soil flooding and aerobic-anaerobic transitions affect As speciation, sorption, and bioavailability in relation to the soil redox status and potential releases due to Fe oxyhydroxide dissolution (Li et al. 2019b; Zhao 2020). One option to reduce As exposure in contaminated soils and water is the use of Fe/Mn-based minerals and their derivatives in line with As speciation. However, bioremediation options for As-contaminated soils must generally address both metal(loid)s and xenobiotics, accounting for benefits and limits, including energy and C balance (Plewniak et al. 2018; Gonzalez-Martinez et al. 2019).

Maximum permitted concentrations are in force or guideline values proposed in several countries according to the use (e.g. for drinking water and soil, WHO $10 \mu\text{g As L}^{-1}$ and US EPA 24 mg As kg^{-1} , respectively), but this is hampered by

the bioavailable As fraction and the variability of soil types. Remediation costs, time frame, water and soil volumes to treat with physico-chemical technologies, and by-products/secondary contamination to manage are frequently not financially and technically sustainable. This leads most countries to adopt a risk-based management system to manage/remediate polluted sites and soils, e.g. France (Info Terre 2017), UK (Jiang et al. 2015). This review aims to inventory the current knowledge on the interactions between As, microbes and plants, supporting the development of promising methods based on microbiological processes or phytotechnologies that could therefore be useful to reduce the harmful effects on human health due to As contamination of soils and groundwater.

From microbial genomics to metagenomics

Throughout geological periods, microorganisms have occupied multiple ecological niches, including those whose physico-chemical conditions are deemed to be extreme. The diversity of their metabolic activities is pivotal in biogeochemical cycles, which can have a deep impact on water quality and soil productivity (Madsen 2011). In addition, they represent a huge gene reservoir, many of which are still of unknown function and which could present a strong potential for developing biotechnological applications (Yang and Ding 2014, Krüger et al. 2018).

The rise of molecular biology and the considerable advances in DNA sequencing methods have contributed to the emergence of genomics, whose methods aim to study the organisation and activity of living organisms based on the understanding of their genome (Bertin et al. 2015, Land et al. 2015). However, data on microbial diversity within ecosystems provided by conventional molecular methods have revealed that a large majority of microorganisms belong to taxa for which no representative has been isolated yet in pure culture (Rashid and Stingl 2015). Indeed, the culture of a majority of them can be extremely tedious and, therefore, accessing their genome and their metabolic potential could be facilitated by the use of environmental genomics methods. For example, the genome of a new uncultured betaproteobacterial species was assembled from metagenomic data obtained from a polymetallic mine. The physiology of this strain, i.e. ‘*Candidatus Gallionella acididurans*’, was investigated, in particular regarding Fe metabolism (Kadnikov et al. 2016). Likewise, the genome of a *Ferrovum* bacterial strain, able to oxidise Fe, was rebuilt using a mixed culture made from samples taken in a mining water treatment plant (Ullrich et al. 2016), and both metagenomic and metatranscriptomic data (Plewniak et al. 2020).

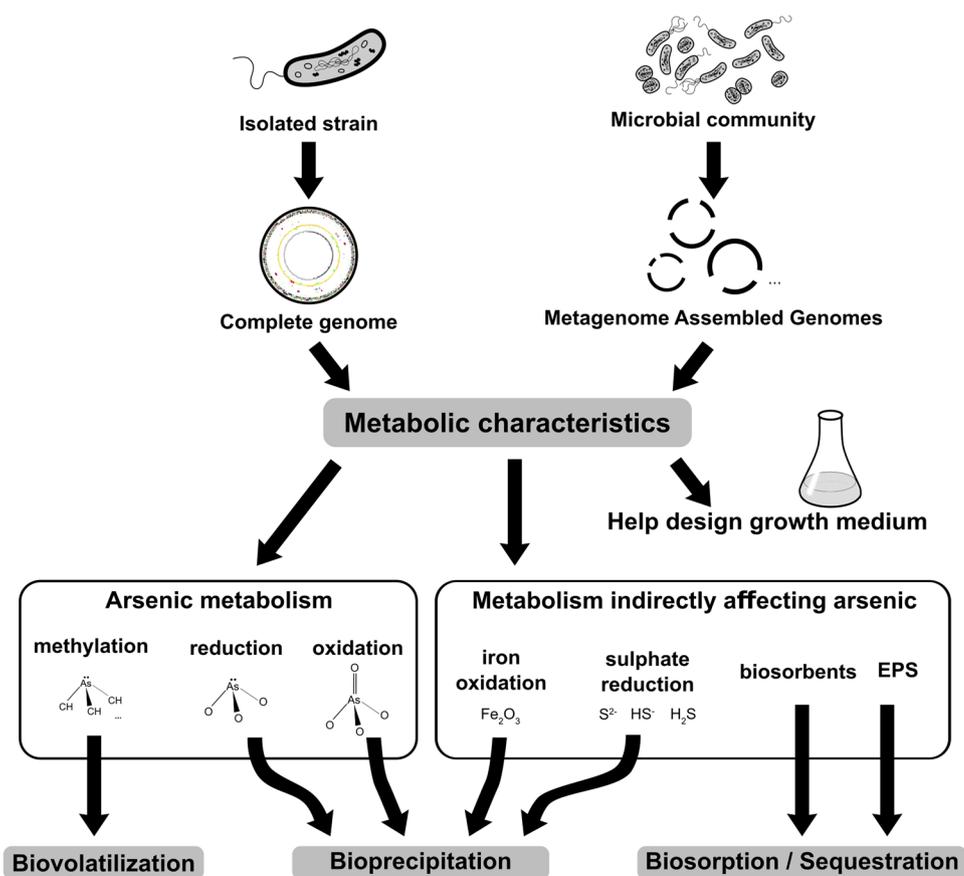
Combined with genome bioinformatic analysis, molecular techniques have proven to be valuable tools for deciphering

genomic data (Vallenet et al. 2017, Machado et al. 2017). Nevertheless, cultural approaches are still required in microbiology to broaden our knowledge of the microorganism physiology for exploiting their properties in bioremediation strategies (Overmann et al. 2017). Such approaches represent a significant challenge because microorganisms isolated from various environments can grow extremely slowly and may require specific nutrients and growth conditions. Consequently, the genome characterisation of an organism can be used to try to identify its metabolic characteristics and use them to attempt to cultivate it (Garza and Dutilh 2015). The isolation of *Leptospirillum ferrodiazotrophum*, an acidophilic Fe-oxidising bacterium is an example (Tyson et al. 2005). Similarly, from environmental DNA sequencing, non-cultured ‘*Candidatus Desulforudis audaxviator*’ was described as virtually the only species identified in a gold mine (Chivian et al. 2008), until another strain with a highly similar genome was isolated from a deep aquifer in Siberia and grown in laboratory conditions (Karnachuk et al. 2019).

The genome of several microorganisms metabolising As has been characterised from various ecosystems, as well as the genes involved in the various aspects of this metabolism (Fig. 1, Andres and Bertin 2016, Ben Fekih et al. 2018). The first described bacterium is *Herminiimonas arsenicoxydans*, a β -proteobacterium isolated from an industrial water

treatment plant. It is resistant to high As concentrations and able to oxidise As(III) to As(V) (Muller et al. 2007). Based on functional genomics, a biphasic response to the As presence occurs: *H. arsenicoxydans* firstly activates resistance mechanisms partly based on efflux pumps; then the metabolic processes driving to the As(III) oxidation are triggered (Cleiss-Arnold et al. 2010, Koechler et al. 2010). Based on electron microscopy, this strain synthesises an exopolysaccharide (extracellular polymeric substance: EPS) able to sequester As in its matrix (Muller et al. 2007). The strain *Thiomonas* sp. 3As, isolated from an abandoned mine in southern France, also produces significant EPS amounts when exposed to arsenite; it would be therefore a relevant candidate for developing bioremediation processes based on biofilm-based bioreactors (Arsène-Ploetze et al. 2010). Unlike the previous two, a *Rhizobium* strain isolated from a gold mine in Australia carries the genes involved in the resistance and detoxification of As on a plasmid. Such a genetic tool could be interesting from a phytoremediation perspective by transferring the As detoxification capacity to related plant-associated bacteria (Andres et al. 2013). Finally, we can mention the genome of two hyper-As(III)-tolerant strains able to oxidise arsenite: *Halomonas* A3H3 and *Pseudomonas xanthomarina* S11, respectively isolated from the Mediterranean Sea-contaminated sediments

Fig. 1 Genomic studies applied to isolated microorganisms and microbial communities can provide information about their metabolic capacities. Predictions of trophic and energy metabolism may thus help design or improve an efficient growing medium. Other metabolic activities involving arsenic (methylation, reduction, and oxidation) or whose products can interact with arsenic may be leveraged for As removal by either volatilisation, precipitation, or adsorption



(Koechler et al. 2013) and a French old gold mine (Koechler et al. 2015).

High-throughput sequencing techniques and the development of assembly software are continuously improved and facilitate to determine the genomic sequences of non-cultured microorganisms by direct sequencing of environmental DNA extracted from complex microbial communities (Fig. 1). Even though some problems remain concerning notably sampling, collating, and annotating (Thomas et al. 2012, Teeling and Glöckner 2012), in 2018 the Genomes Online database contained nearly 40,000 analysed metagenomes (Mukherjee et al. 2018). This number should further increase accounting for gigantic projects like the Earth Microbiome Project. Nearly 500,000 genomes would indeed be used to build a global genetic atlas of microbial communities (Gilbert et al. 2010; Thompson et al. 2017; Danko et al. 2019).

Currently, environmental descriptive and functional genomics can provide a comprehensive overview of microbial communities extending studies focusing on specific organisms. Such a global vision of both community structure and functioning would improve our understanding of natural remediation processes and help to find candidate species suitable for designing bioprocesses. In line, ecological questions related to the diversity and dynamics of microbial populations can be addressed using high-throughput sequencing methods. For example, bacterial, archaeal and fungal communities in rice paddy soils were inventoried by such approach, and shown to be strongly affected by irrigation with waters contaminated by metals such as Cu, Pb, and Zn (Wang et al. 2018b). Environmental DNA and RNA sequencing was also successfully used to analyse the response of bacteria belonging to a new deltaproteobacterial order, ‘*Candidatus acidulodesulfobacterales*’. Based on metabolic pathways reconstructed from metagenome-assembled genomes (MAG) and gene expression profiles, these microorganisms would be facultative anaerobic autotrophs possibly involved in Fe cycling (Tan et al. 2019).

Similarly, environmental genomics have been used on As-contaminated ecosystems (Andres and Bertin 2016; Huang et al. 2016). For example, seven microbial genomes present in an acid mine drainage (AMD) (Carnoulès, France) were almost completely reconstructed. The combination of the metabolic activities of the corresponding microorganisms, in particular the oxidation of arsenite and its coprecipitation with Fe and S, leads to a natural attenuation process, which greatly reduces the As concentration along the stream (Bertin et al. 2011). Recently, a metatranscriptomic study of Carnoulès AMD sediment samples shed light on how food webs may affect the structure and activities of microbial communities in such environments. In particular C:N and N:P ratios, influenced by the presence of metazoa and the riparian vegetation, may be pivotal, along

with predation patterns, in shaping microbial communities (Plewniak et al. 2021). Another study has compared sediments extracted from two ports in the Mediterranean Sea. The specific sequences belonging to bacteria metabolising S match with both the biotic reduction of sulfates and the abiotic production of thioarsenical compounds. These elements being highly soluble, this likely explains why the most contaminated site has higher As mobility (Plewniak et al. 2013). Moreover, 27 genomes of Micrarchaeota and 12 Parvarchaeota were assembled from 12 metagenomes from the Richmond mine, California. These organisms could participate in C and N cycles by degrading organic matter and be key players in Fe oxidation (Chen et al. 2017). Therefore, many microbial communities and their hosted organisms metabolising Fe, S, and As could be candidates for the development of novel bioremediation processes. In this regard, sulfate-reducing bacteria resistant to metal(loid)s and acidic conditions were used to remove As from an AMD (Serrano and Leiva 2017).

Arsenic microbial metabolisms and bioremediation

Conventional technologies for As removal from As-rich waters mainly include physico-chemical treatments like alum, Fe and Mn precipitation, enhanced lime softening, ion exchange, electro dialysis, reverse osmosis, coagulation/filtration, and adsorption (Ng et al. 2004; Nicomel et al. 2016). For reducing management costs and enhancing the water treatment capacity, several adsorption technologies have been developed (Mohan and Pittman 2007; Nicomel et al. 2016). Considering that these technologies are very effective in removing As(V), a pre-oxidation step allowing the conversion of As(III) to As(V) is often required. For this purpose, strong chemical oxidising agents are commonly utilised (Katsoyiannis et al. 2002; Simeonova et al. 2005).

Over the last years, the use of biological processes for As removal has been widely investigated and a large number of potential applications were proposed to remediate As-contaminated ecosystems due to their environmental compatibility and cost-effectiveness (Kruger et al. 2013; Plewniak et al. 2018; Sher and Rehman 2019; Upadhyay et al. 2018; Wang and Zhao 2009). Among the bacterial As-remediation processes, biosynthesis of adsorbent materials, biovolatilisation, bioprecipitation and biosorption are mostly applied (Fig. 1, Fazi et al. 2016a). The occurrence of sulfides and biogenic iron oxides in groundwater facilitates As bioprecipitation resulting in a low As concentration (Omeregic et al. 2013). Many bacteria, indeed, are able to reduce As-, Fe-, and Mn-bearing minerals and promote As sorption onto freshly formed hydrous ferric oxide (HFO) (Katsoyiannis and Zouboulis 2004; Omeregic et al. 2013). Many

microorganisms may also produce adsorbent materials, such as FeOOH nanoparticles within extracellular polymeric substance (EPS) hydrogel (Fe-EPS), used to treat As-rich drinking water (Casentini et al. 2015; Mandal et al. 2006). In addition, biosorption processes could be applied for removing metal(loid)s and other elements from diluted aqueous solutions even though few studies reported its application in drinking water treatment (Mohan and Pittman 2007; Hasan et al. 2010; Prasad et al. 2013).

Although with a limited impact on aquifer contamination, biovolatilisation may contribute to the As removal from soil and water (Jakob et al. 2010; Lloyd 2010; Liu et al. 2011). Arsenic methylation is considered a key player of the As cycle on Earth (Bhattacharjee and Rosen 2007). Volatile arsenic is formed through a consecutive transformation of inorganic As to methylated species (Rahman et al. 2014). In spite of this process being widely investigated, its exploitation for bioremediation purposes is still limited (Zhang et al. 2015a; Wang and Zhao 2009). Indeed, although many microbes may aerobically or anaerobically perform the methylation of As species, low rates of biological As volatilisation are reported in soil (< 10% of total As content) (Liu et al. 2011). The first described microorganism able to convert As(V) to volatile methylarsines is *Methanobacterium bryantii* (McBride and Wolfe 1971). *Achromobacter* sp. and *Enterobacter* sp. have the capability to convert As(V) to mono- and di-methylarsine, while *Aeromonas* sp. and *Nocardia* sp transform this element in mono-, di-, and trimethylarsine (Cullen and Reimer 1989). Although the volatilisation is considered a detoxification process, it produces highly toxic species whose availability in soils and groundwater can represent a serious threat (Bentley and Chasteen 2002; Wang and Mulligan 2006).

Arsenic oxidising microorganisms

Among the bioprocesses involved in the regulation of As biogeochemical cycle in aquifers, the capability of microorganisms to transform As through oxidation–reduction reactions are of great interest in As bioremediation applications. In recent years, the As(III) oxidation mediated by microorganisms has assumed increasing importance as a precursor step of commonly used iron-based treatment methods (Crognalet et al. 2017; Fazi et al. 2016a). Usually, chemical oxidising reagents (e.g. chlorine, potassium permanganate, manganese oxide, hydrogen peroxide, and ozone) are added to the water (Driehaus et al. 1995; Kim and Nriagu 2000). However, this chemical pre-oxidation may cause secondary problems due to the occurrence of residuals or by-products formation, and a significant increase in operational costs (Katsoyiannis and Zouboulis 2004). To circumvent these limitations, the microbiological As(III) oxidation has been proposed as an eco-friendly alternative to conventional chemical pre-treatment

methods (Bahar et al. 2013). Several As(III)-oxidising microorganisms have been recovered in various As-rich environments including geothermal sites, soils, sediments, mine, arsenical pesticides and smelter-impacted sites (Engel et al. 2013; Fazi et al. 2016b; Heinrich-Salmeron et al. 2011; Lami et al. 2013; Paul et al. 2018; Quéméneur et al. 2008, 2010; Satyapal et al. 2018; Sultana et al. 2012; Thul et al. 2019). The As(III) oxidation is a detoxification process in heterotrophic bacteria (Bahar et al. 2012; Muller et al. 2003; Vanden Hoven and Santini 2004), or an energetic metabolism in chemolithoautotrophic microorganisms, such as *Rhizobium* NT-26 and *T. arsenivorans* (Battaglia-Brunet et al. 2006; Garcia-Dominguez et al. 2008; Hoefft et al. 2007; Santini et al. 2000). The capability of microorganisms to anaerobically oxidize As(III) in combination with nitrate respiration or anoxygenic photosynthesis is reported in several studies (Cui et al. 2018; Hoefft et al. 2007; Kulp et al. 2008; Ospino et al. 2019; Zargar et al. 2012; Zhang et al. 2015b, 2017). Over the last years, lab-scale experiments have been performed on immobilised bacteria, biofilms, and planktonic cells to better elucidate the potential of the aerobic biological As(III) oxidation process in water treatment (Battaglia-Brunet et al. 2002; Dastidar and Wang 2012; Ito et al. 2012; Michel et al. 2007; Michon et al. 2010). The capability to oxidise As(III) is reported in several bacterial strains, e.g. *Aliihoeflea* sp. 2WW, *Bacillus* spp., *Bosea* sp. AS-1, *Delftia* spp. BAs29, *Ensifer adhaerens*, *Micrococcus* sp., *Pseudomonas chengduensis*, and *T. arsenivorans* (Biswas and Sarkar 2019; Biswas et al. 2019; Corsini et al. 2014; Ito et al. 2012; Jebelli et al. 2018; Lu et al. 2018; Roychowdhury et al. 2018; Wan et al. 2010).

A fixed bed up-flow filtration unit allowing for the simultaneous biotic oxidation and removal of As(III) and Fe(II)/Mn(II) has been developed and tested in several studies (Hassan et al. 2009; Katsoyiannis and Zouboulis 2004; Katsoyiannis et al. 2004; Tani et al. 2004). Few investigations have combined biological As(III) oxidation with the use of activated alumina and metallic Fe adsorbents to remove As (Ike et al. 2008; Wan et al. 2010). The use of a polarised electrode as terminal electron acceptor for the bioelectrochemical As(III) oxidation has been recently investigated (Pous et al. 2015; Nguyen et al. 2017). Additionally, the cathodic electroactivity of a new chemolithoautotrophic arsenite oxidising bacterium, *Ancylobacter* Ts-1 has been proved suggesting the potential application of bioelectrochemical process in bioremediation of natural and bio-engineered environments (Anguita et al. 2018).

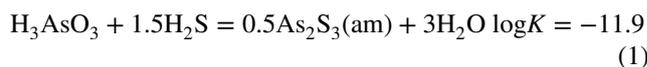
As(III) oxidising biofilms can play a key role in the design of simple passive bio-processes (Battaglia-Brunet et al. 2005). Initially, this approach has been investigated by using mixed microbial communities or populations recovered from As-rich extreme environments. For example, an autotrophic As(III) oxidising bacterial population, named CAsO1, has been tested at lab-scale in a fixed bed

column reactor revealing a high capability in oxidising As(III) at a rate of $166 \text{ mg L}^{-1} \text{ h}^{-1}$ (Battaglia-Brunet et al. 2002, 2005). Due to the formation of an EPS matrix, the biofilm may act as a physical barrier for several particles, cations, anions and apolar compounds occurring in the water (Flemming and Wingender 2010; Michel et al. 2007). The application of As(III) oxidising biofilms in combination with Fe- and Fe-/Mn-oxidation processes may increase the efficiency of simultaneous As-, Fe-, and Mn- removal from groundwater (Casiot et al. 2006; Hassan et al. 2009; Katsoyiannis and Zouboulis 2004; Katsoyiannis et al. 2004, 2007; Tani et al. 2004). Moreover, the As(III)-oxidising biofilters have high potentialities in the treatment of As-contaminated groundwater (Crognale et al. 2019; Gude et al. 2018; Li et al. 2016; Yang et al. 2014). Up to 150 mg As L^{-1} ($\approx 98.2\%$ of total As), 1.5 mg Fe L^{-1} and 1.2 mg Mn L^{-1} have been simultaneously removed from groundwater within 180 days by using quartz sand biofilter (Yang et al. 2014). Li et al. (2016) reported the capability of a lab-scale biofilter, inoculated with an As(III)-oxidising population to oxidise $1.1 \text{ mg As(III) L}^{-1}$ within 10 min. Gude et al. (2018) have tested the As(III) oxidising potentialities of a biofilter started up with a native As-rich groundwater microbial community showing the importance of initial acclimation to As(III)-rich groundwater. Indeed, up to 98% of 0.1 mg L^{-1} of As(III) has been oxidised in 38 days by using a not-acclimated biofilter and within three weeks with a biofilter previously exposed to As-contaminated groundwater (Gude et al. 2018). Crognale et al. (2019) have tested the biofilter potentialities using autochthonous As-rich groundwater microbial communities under experimental conditions mimicking those used in household-scale treatment system (Casentini et al. 2016). This study evidenced a high oxidation efficiency (up to 90% of $0.1 \text{ mg As(III) L}^{-1}$ in 3 h) in a biofilter filled with coarse sand.

The use of combined As(III) and Fe(II) bio-oxidising activities was developed for treating a neutral pH surface water containing 5 to 12 mg Fe L^{-1} and 0.2 to 2.0 mg As L^{-1} - with 50 to 100% As(III) - in an entirely passive system at the Loperec site (Finistère, France) (Battaglia-Brunet et al. 2006). Bacteria developed as a biofilm composed of a complex community, on pozzolana support, and promoted the precipitation of Fe hydroxides (ferrihydrite) as an efficient adsorbent for As(V) resulting from bacterial As(III) oxidation. This process implemented at real scale since 2017 is treating an average $15 \text{ m}^3 \text{ h}^{-1}$ flux of water flowing from an exploration gallery. The residence time optimised at the laboratory could be decreased to 0.5 h without affecting the treatment efficiency, the total As concentration being reduced below the $100 \text{ } \mu\text{g L}^{-1}$ limit for discharge in the environment.

Bioreduction mechanisms for As bio-precipitation

In low-pH conditions, characteristic of AMD, efficient Fe precipitation can be problematic. In other polluted waters, Fe concentration in the water to be treated is too low for the efficient co-precipitation of As with Fe. An alternative to oxidising processes can be the bio-precipitation of As sulfides with the help of bacteria able to perform the dissimilatory reduction of sulfate, sulfate-reducing bacteria (SRB), and bacteria able to reduce As(V) into As(III), either through dissimilatory As(V) reduction or As(V) reduction linked to the As resistance system. Arsenate respiration is based on the activity of the arsenate respiratory reductase (ARR, Afkar et al. 2003). This enzyme is a periplasmic dimethyl sulfoxide (DMSO)-type reductase that reduces As(V) to As(III) (Saltikov and Newman 2003). Arsenic, in the As(III) state, precipitates with sulfide to form the insoluble yellow amorphous orpiment As_2S_3 . Eary (1992) was the first to report solubility data for amorphous As_2S_3 , which suggested the following two equilibria:



When sulfide concentration exceeded 1 mg L^{-1} , soluble complex thioarsenate species would form at circa neutral and higher pH (Smieja and Wilkin 2003).

The first characterised sulfate-reducing organism able to use As(V) as terminal electron acceptor was isolated from surface sediments of the Upper Mystic Lake, Massachusetts, USA (Newman et al. 1997a, b). This bacterium described as *Desulfosporosinus auripigmenti* (Stackebrandt et al. 2003) is a freshwater, gram-positive, non-motile, strictly anaerobic chemoorganotroph. It oxidises H_2 , lactate, pyruvate, butyrate, ethanol, glycerol, and malate for its growth concomitantly with the reduction of either sulfate or arsenate. Macy et al. (2000) worked with two SRB able to reduce both As(V) and SO_4 concomitantly. One of them, *Desulfomicrobium* Ben-RB, used As(V) as terminal electron acceptor. The second SRB, *Desulfovibrio* Ben-RA, reduced As(V) through an As resistance system. Although *Desulfovibrio* Ben-RA did not perform dissimilatory As(V) reduction, it was able to promote As_2S_3 precipitation. Both *D. auripigmenti*, *Desulfomicrobium* Ben-RB and *Desulfovibrio* Ben-RA were grown in near-neutral pH conditions.

Another SRB related to *D. auripigmenti* was isolated from sediments of the polluted Onondaga Lake (Syracuse, NY, USA). This As(V) respiring isolate, named strain Y5, can utilise aromatic substrates (Liu et al. 2004). Both *D. auripigmenti* and strain Y5 are spore-forming rods. The lack of motility differentiates *D. auripigmenti* from the other *Desulfosporosinus* strains (*D. orientis*, *D. meridiei* and

strain Y5). In this group, only *D. auripigmenti* and strain Y5 are known to reduce As(V). Demergasso et al. (2007) obtained enrichments and isolates from boron deposits in Andean salt flats. Two strains isolated, CC-1 and Asc-3 grew using SO_4 or As(V) as electron acceptors. The nearest phylogenetic relatives (based on 16S rRNA sequences) of CC-1 and Asc-3 are *Pseudomonas* sp. PHLL and *Enterobacter* sp. BL2, respectively.

Bio-precipitation of As sulfide from synthetic acid solutions was performed in continuously fed laboratory column bioreactor (Battaglia-Brunet et al. 2012). In this system, the acid (pH 2.7 to 5) feeding solution contained 100 mg As(V) L^{-1} , and glycerol or H_2 were provided as energy sources. Bacteria embedded in As- and S-rich mineral phases were observed at the surface of the bioreactor filling material (Fig. 2). The removal rate reached 2.5 mg As $\text{L}^{-1} \text{h}^{-1}$. The diverse bacterial community developed in the bioreactor included *Desulfosporosinus*-like sulfate-reducing bacteria and fermenting ones. The retrieved *arrA* sequences were 100% identical to that of the As(V)-respiring SRB strain *Desulfosporosinus* Y5 (Liu et al. 2004); this suggested that a *Desulfosporosinus*-related bacteria contributed to As(V) reduction via a dissimilatory mechanism.

With a real As-rich AMD water containing 90 mg As L^{-1} (Carnoules site, Gard, France), growth of SRB inducing precipitation of the As sulfides orpiment and realgar, together with ZnS nanoparticles, has been proven in batch experiments (Le Pape et al. 2017). This bioprocess was then tested at laboratory scale in continuous feeding conditions (Battaglia-Brunet et al. 2021) and is currently up-scaled to be tested on site. Up to now, As removal in SRB systems was reported at real scale on a few sites, but with mine waters and effluents less acidic than that of the Carnoules site. One

is located at the Wood Cadillac mine, Northwestern Quebec, which features sulfide poor but As rich, tailings, laid down between 1939 and 1949 (Tassé et al. 2003). A biofilter (50 m \times 57 m, 1 m thick, vertical flow and residence time of 25 h) was implemented, with wood chips as low-rate delivered energy source, to treat mine water at pH 6–7 with relatively low As concentrations (0.1 to 1.2 mg L^{-1}). Another real scale application has been implemented near the city of Trail in British Columbia, Canada (Al et al. 2011). Anaerobic biofilters filled with a mixture of limestone, quartz sand and biosolids, a by-product of the pulp and paper industry, are treating effluent water from smelting operations at pH 5.9 containing around 50 mg As L^{-1} . The size of both bioreactors in series are 18 \times 30 m and 18 \times 25 m, and the residence time of the water in these two systems is 720 and 600 h, respectively.

Phytoremediation of As-contaminated soils

Phosphate transporters (Pht) mediate root uptake of As(V), which competes with phosphates (Farooq et al. 2016; Kofronova et al. 2018, Vromman et al. 2018, Zhao and Wang 2020). In *Pteris vittata* (As hyperaccumulator) three genes would collaborate, i.e. *PvPht1;3*, a phosphate (P) transporter gene; *PvACR2*, an As(V) reductase gene; and *PvACR3*, an As(III) transport gene, in sensitive As(V) absorption, constitutive As(V) reduction, and subsequent As(III) transportation (Wei et al. 2021). Several elements, i.e. Si, Se, Fe, P, and Mo, can challenge As uptake by roots (Mu et al. 2019). As(V) taken up is mostly reduced to As(III) through arsenate reductases in higher plant tissues (Triptahti et al. 2012; Kofronova et al. 2018). The protein high arsenic

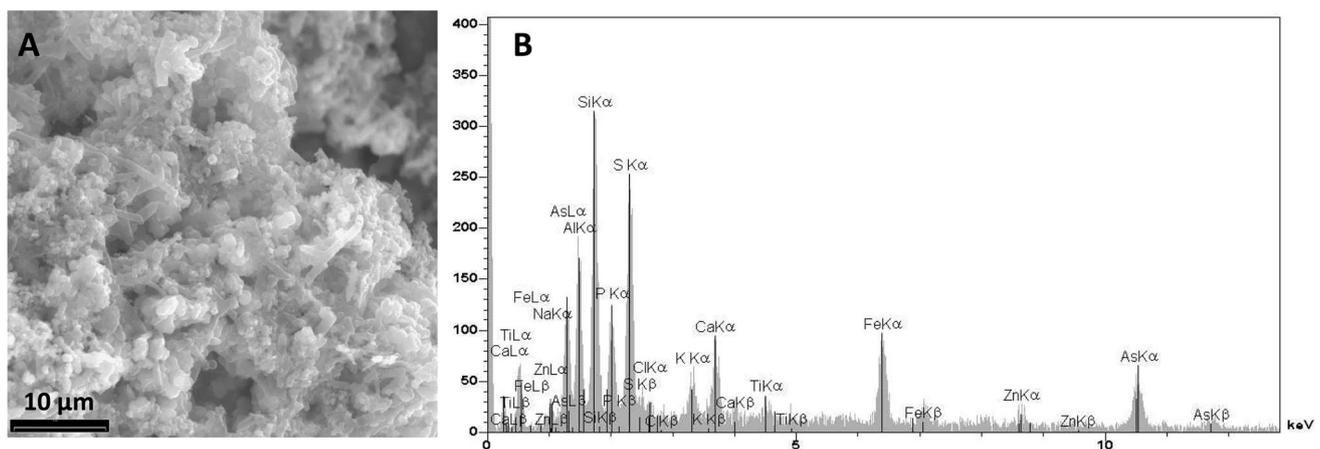


Fig. 2 SEM observation (A) of biofilm embedded in bioprecipitates in a sulfate-reducing column bioreactor fed with a 100-mg As L^{-1} solution (Battaglia-Brunet et al. 2012) and (B) corresponding EDS spectrum analysis. EDWARDS Auto 306 apparatus (EMS, Hat-

field, PA, USA), then observed using a JSM 6100 Scanning Electron Microscope (JEOL, Tokyo, Japan) coupled to an X-ray Energy Dispersive Spectrometer KEVEX Quantum (Thermo Electron Corp., Dreieich, Germany)

concentration 1 (HAC1) would drive As(V) reductase activity in the outer root layer (epidermis) and the inner one adjacent to the xylem (pericycle). Nodulin 26-like intrinsic protein (NIPs) aquaporine channel transports As(III) in the plants; the OsLsi1/NIP2;1 transporter, mediating transport of silicic acid into roots, is expressed in the zone of Casparian strips at plasma membrane and contributes to As(III) intake in rice and maize. The As methylated forms display generally a lower uptake rate than that of the inorganic ones. Monomethylarsonic acid (MMA) and dimethylarsinic acid (DMA) are detected in plant parts (Kofronova et al. 2018). Arabidopsis plants with mutated inositol transporter genes (i.e. AtINT2, AtINT4) exhibit lower As(III) concentrations in the phloem. As(III) binding to sulfhydryl groups can affect the function of several proteins; it can be chelated by phytochelatins (PCs) and then transported and sequestered in vacuoles (Zhao et al. 2010; Triptahti et al. 2012; Zhao and Wang 2020; Wei et al. 2021). Arsenic forms differ between root tissues. The translocation of As species from roots to shoots depends on plant species: As(III) predominates in the xylem sap of tomato, cucumber, rice, and the fern *Pteris vittata*; larger As(V) amounts occur in Indian mustard, wheat, and barley. Arsenic excess can be phytotoxic: it decreases plant growth, alters inorganic nutrition, impairs the plant water status, generates oxidative stress and may be a nitrosative one, restrains photosynthesis, and changes the hormonal content. This leads to physiological disruptions and finally the plants die (Farooq et al. 2016). As(III) inactivates many enzymes by disorganising their structure and damages the metabolism by impeding protein–protein interactions (Navazas et al. 2019). This impacts many cellular metabolic key processes, e.g. glucose uptake, glutathione production, and fatty acid metabolism. For reviews on plant responses to As excess, see, e.g. Clemens and Ma (2016), Kofronova et al. (2018), Zhang et al. (2018), Zhao (2020), and Wei et al. (2021).

Obvious ways to alleviate pollutant linkages due to As excess are to avoid sources leading to As contamination and exposure, to select plant species and associated microorganisms for minimising As concentration in edible plant parts, and to reduce As in exposure pathways (Kofronova et al. 2018; Zhao 2020). Physico-chemical technologies, e.g. oxidation, coagulation-flocculation, soil washing, adsorption, ion exchange, electrokinetics and membrane technologies, are reviewed elsewhere (Singh et al. 2015; Kumpiene et al. 2019). Development of efficient, less-invasive remediation (phyto)technologies is crucial for soils and water contaminated with both metal(loid)s and xenobiotics, notably to phytostabilise/exclude or phytoextract As, and large volume/area. Several shortcomings accompany As phytoextraction. One is the number of successive crops needed to extract bioavailable soil As (the remediation time should not be estimated on the basis of total soil As). The phytoextraction

option is also limited to the surface soil (~ 1 m). For all phytomanagement options, heatwaves, drought, late frost, pests, etc. and hydric conditions may hinder the plant development. Climate change must be considered, including storms to prevent flooding and erosion.

Arsenic is tolerated and accumulated in roots, with low translocation in shoots, by many plant species, so-called excluders. Some others retain As in their roots but also display high shoot As concentration, i.e. (hyper)accumulators. Use of these plant phenotypes leads to various phytotechnologies and phytomanagement options, from sequestration of labile As pools in the root zone (exclusion, phytostabilisation) to harvest of As accumulated in plant parts (phytoextraction) (Hettick et al. 2015; Wang et al. 2017). *Pteris vittata* (Chinese brake fern) is a notorious As hyperaccumulator, its fronds being able to amass up to 23 g As kg⁻¹ (da Silva et al. 2018a). These phytoremediation options influence physico-chemical and biological soil properties underlying ecosystem services, including gain in biodiversity and resilience to metal(loid) excess and climate changes (Mench et al. 2003a, b, 2010, 2014; Renella et al. 2008; Kidd et al. 2015).

Phytovolatilisation of arsenicals during phytomanagement is questionable. Dimethylchloroarsine (AsCl(CH₃)₂) and pentamethylarsine (As(CH₃)₅) were released by rabbitfoot grass (*Polypogon monspeliensis*) but not the more toxic organic As forms, i.e. arsine, MMA, DMA, and trimethylarsinic acid (TMA) (Ruppert et al. 2013). Phytovolatilisation of arsenicals from fronds of *P. vittata* grown in As-contaminated soil was claimed, but the method used is controversial and may just reflect evapotranspiration and As leaching from fronds (Sakakibara et al. 2010).

Phytomanagement concept

Phytomanagement options (POs) for remediating contaminated land are a set of long-term, risk management phytotechnologies, involving plants and associated microorganisms, that promote a profitable crop production or other beneficial land uses (e.g. recreational park) and also lead gradually to the reduction of pollutant linkages due to contaminant excess (e.g. As) and a net gain in soil ecological functions underlying ecosystem services (Cundy et al. 2016). POs can be customised along contaminant linkages related to site/contaminant specificity and time frame, and can provide a wide range of environmental, economic and societal profits during and after the polluted land phytomanagement (Kidd et al. 2015). POs encompass the former phytoremediation options, which are long treatment time, but the phytomanagement concept overtakes them. One main purpose is to assist low-and medium-level polluted sites to return to productive usage, including either urban design, landscape architecture, or community gardens/parkland, in

rural, urban, and suburban areas. The harvested biomass, produced by excluders or hyperaccumulators, is not a waste to dispose but a resource.

Where the marked lengthy time scales needed to achieve soil remediation, notably if based on total soil contaminants, has banned phytoremediation as a common technical option for urban polluted sites, phytomanagement, notably with either excluders or bioavailable contaminant stripping, is more considered by local and national authorities. (Aided) phytoextraction consists to (yearly) strip phytoavailable contaminants accumulate in harvestable plant parts (accounting for tissue concentration and biomass), eventually in combination with soil conditioners. It is mainly applicable to reduce pollutant linkages for large soil areas or water volume with low and medium exposure levels. However, phytoextraction using As-hyperaccumulators may be challenged, due to their specificity, at sites with multiple contaminants. Potential candidates for As-focused phytoremediation options are worldwide explored in hydroponics, pot experiments and field surveys (Table 1, Jiang et al. 2015). Only pot experiments with real As-contaminated soils (not spiked with salts), without dust exposure (for shoots collected on contaminated sites, dust trapped in stomatal chambers and wax cannot be simply washed) and giving information on plant growth and health (no necrotic plants), and thereafter confirm by field trials (accounting for climatic conditions and water supply), can validate such candidates (Table 1; Fig. 3). Among As-tolerant plant species, van der Ent et al. (2013) suggest 1000 mg As kg⁻¹ DW in shoots as hyperaccumulation threshold criteria (excluding shoots contaminated by dust particles, notably in stomatal chambers), however shoot As removal (and bioavailable As stripping) is also a matter of biomass. Hyperaccumulators frequently have a low biomass production, and tolerance to either one, two, or rarely more elements, which limits the metal(loid) phytoextraction. In addition, their resilience to xenobiotic exposure at site with mixed pollution is poorly explored. In contrast, root compartments and excluders are useful to sequester bioavailable As in the root zone, but As phytostabilization can be only claimed when decreases in bioavailable soil As and As-focused pollutant linkages are demonstrated.

Plant traits

Several model plants with potential use in phytoremediation are investigated for their biological responses to As excess and their As accumulation in plant parts (Table 1). Rice is of concern for grain As and one studied crop for the mechanisms of As uptake, distribution, and detoxification (Zhao 2020). As tolerance in As excluders is likely partly based on the suppression of high affinity phosphate/arsenate

co-transport systems (Karimi et al. 2009, Karimi and Souri 2016).

Brassicaceae

Isatis cappadocica metallicolous (M) and non-metallicolous (NM) populations (Iran, temperate Asia) are claimed As accumulators, with potentially constitutive As chelation by thiols and PCs, and tolerance not based through deletion of high-affinity P/As co-transport (Karimi et al. 2009). Both NM and M populations are more resistant than other commercial Brassicaceae (e.g. broccoli, cabbage, and cauliflower), M plants being more As-tolerant than NM ones over 1.3 mM As. At 1825 mg As kg⁻¹ (fading soil series with mine soil), *I. cappadocica* shoots displayed 350 mg As kg⁻¹. Potential mechanisms, e.g. detoxification of oxidative stress, are discussed in Souri et al. (2020). Indian mustard (*Brassica juncea*, Gupta et al. 2009) and Ethiopian mustard (*B. carinata*, Irtelli and Nacari-Izzo 2008) can display high shoot As concentration, but their phenotype is not well established (Karimi et al. 2009). In Indian mustard cultivars with shoot As concentration ranging from 16 to 1138 mg kg⁻¹ DW, 10,870 genes are differentially expressed mainly in reaction to stress, metabolic processes, transporter activity, and signal transduction (Thakur et al. 2019). Transcription regulator activity is up-modulated whereas many genes implied in photosynthesis, developmental processes, and cell growth are downregulated.

Arabidopsis thaliana was modified into an As accumulator by heterologously expressing PvACR3 in the athac1 background and knocking out the *HAC1* gene, AtHAC1 being an As reductase (Wang et al. 2018a). Muting the As reductase reduced As efflux into the medium (Zhang et al. 2018). For these transgenic plants, expression of the vacuolar As transporter ACR3 in the roots did not promote As(III) efflux into the medium, nor its vacuolar sequestration, but helped As loading into the vasculature and promoted translocation to the shoots. In transgenic *A. thaliana* and soybean, PvPht1;3 is expressed in stele cells and probably contributed to P/As translocation. Such PvPht1;3 expression raises As transfer and build-up in shoots, which may improve As phytoextraction in As-polluted soils.

Ferns

Several ferns (Pteridaceae), i.e. *Pteris vittata*, *P. cretica*, can tolerate and hyperaccumulate high As levels, without visible phytotoxicity symptoms. For sporophytes exposed to As(V), arsenate is absorbed by the roots, translocated via the xylem, and stored in the vacuoles of the leaf-like fronds as As(III) (Cai et al. 2019). *Pteris vittata* efficiently extracts As in low-P soils, increases in root growth and exudation helping to solubilise non-labile As and P from soils (da Silva

Table 1 Candidate plant species for As-focused phytoremediation in hydroponics, pot experiments, and field trials

Plant species	Exposure/growth period	Phenotype for As	Remediation option	Reference
Field experiments				
<i>Lolium</i> spp., <i>Eschscholzia californica</i>	6 years	Excluders	Phytostabilisation	Pardo et al. (2018)
<i>Pityrogramma calomelanos</i>	136–269 mg As kg ⁻¹ , 12 weeks	Hyperaccumulator	Phytoextraction	Jankong et al. (2007)
<i>Pityrogramma calomelanos</i> , <i>Pteris vittata</i>	324–909 mg As kg ⁻¹	Hyperaccumulators	Phytoextraction	Niazi et al. (2012)
<i>Dicranopteris linearis</i> , <i>Histiopteris incisa</i> , <i>Nephrolepis hirsutula</i> , <i>Pinus</i> sp., <i>Thy-sanolaena latifolia</i> , <i>Melastoma malabathricum</i> , <i>Pityrogramma calomelanos</i> , <i>Pteris vittata</i>	1091 mg As kg ⁻¹ mining site	Excluders; accumulators	Phytostabilisation; phytoextraction	Claveria et al. (2019)
<i>Agrostis castellana</i> , <i>Holcus lanatus</i>	1325 mg As kg ⁻¹ , 4 years	Excluders	(Aided) phytostabilisation	Bleeker et al. (2002)
<i>Triticum aestivum</i> (<i>Pteris vittata</i> , <i>Phragmites australis</i> , <i>Vetiveria zizanioides</i>)	50 mg As kg ⁻¹ , 2 years	Excluders	Phytostabilisation	Praveen et al. (2019)
<i>Lolium multiflorum</i> var. <i>italicum</i> , <i>Secale cereale</i> , <i>Vicia villosa</i> , and <i>Trifolium pratense</i>	642 mg As kg ⁻¹ , 3 months	Excluders	Phytostabilisation	Kim et al. (2018)
<i>Halogeton glomeratus</i>	3 mg kg ⁻¹ , 1 year	Accumulator	Phytoextraction	Li et al. (2019a)
<i>Pteris vittata</i>	190 mg As kg ⁻¹ , 2 years	Hyperaccumulator	Phytoextraction	Kertulis-Tartar et al. (2006)
<i>Pteris vittata</i>	26.7 and 129 mg As kg ⁻¹	Hyperaccumulator	Phytoextraction	da Silva et al. (2018a)
<i>Pteris vittata</i>		Hyperaccumulator	Phytoextraction	Gray et al. 2005; Shelmerdine et al. 2009 (cited in Jiang et al. 2015)
<i>Pteris vittata</i> intercropped with <i>Zea mays</i>	93 mg As kg ⁻¹	Hyperaccumulator + excluder	Phytoextraction; intercropping	Ma et al. (2018)
<i>Pteris ensiformis</i> , <i>Boehmeria nivea</i> , and 18 other species	125–6656 mg As kg ⁻¹		Phytoextraction; phytostabilisation	Pan et al. (2019)
<i>Oryza sativa</i>	72.7 mg As kg ⁻¹ , 5 months	Excluder	Phytostabilisation/in situ immobilisation	Li et al. (2019b)
Watercourse/stream				
<i>Sagittaria montevidensis</i>			Rhizofiltration	Demarco et al. (2019)
20 macrophytes	9.7–13.6 mg As kg ⁻¹	Excluders	Phytostabilisation	Bonanno et al. (2018)
Outdoor lysimeters/vats				
<i>Pinus pinaster</i>	1325 mg As kg ⁻¹ , 3 years	Excluders	Phytostabilisation	Mench et al. (2003a)
<i>Holcus lanatus</i>	1325 mg As kg ⁻¹ , 3 years	Excluders	Phytostabilisation	Mench et al. (2003a)
<i>Pteris vittata</i>	113 mg As kg ⁻¹ , 7 years	Hyperaccumulator	Phytoextraction	Mench et al. (2014)
Pot experiments				
<i>Dahlia pinnata</i>		Excluder	Phytostabilisation	Raza et al. (2019)
Aromatic plants for essential oils		Excluders	Phytoremediation	Pandey et al. (2019)

Table 1 (continued)

Plant species	Exposure/growth period	Phenotype for As	Remediation option	Reference
<i>Miscanthus sacchariflorus</i> A0104, <i>M. sinensis</i> C0424 and C0640	36–250 mg As kg ⁻¹ (spiked soils)	Excluders	Phytostabilisation	Jiang et al. (2018)
<i>Miscanthus x giganteus</i>	75–515 mg As kg ⁻¹ 2 years	Excluder	Phytostabilisation	Pidlisnyuk et al. (2019)
<i>Salix miyabeana</i> ‘SX67’	12 weeks CCA/PCDD/Fs	Excluder	Phytostabilisation	Fredette et al. (2019)
<i>Salix alba</i> , <i>Salix</i> sp.	Mine tailings	Excluders	Phytostabilisation	Vamerali et al. (2009)
<i>Salix viminalis</i> , <i>Salix purpurea</i>	Mine tailings	Excluders	Phytostabilisation	Bart et al. (2016)
<i>Populus</i>	Mine tailings	Excluder	Phytostabilisation	Vamerali et al. (2009)
<i>Populus nigra</i>	728 mg As kg ⁻¹ , 28 days	Excluder	Phytostabilisation	Nandillon et al. (2019)
<i>Acer platanoides</i>	90 days	Excluder	Phytostabilisation	Budzynska et al. (2019b)
<i>Acer pseudoplatanus</i>	90 days	Excluder	Phytostabilisation	Budzynska et al. (2019b)
<i>Betula pendula</i>	90 days	Excluder	Phytostabilisation	Budzynska et al. (2019b)
<i>Quercus robur</i>	90 days	Excluder	Phytostabilisation	Budzynska et al. (2019b)
<i>Tilia cordata</i>	90 days	Excluder	Phytostabilisation	Budzynska et al. (2019b)
<i>Ulmus laevis</i>	90 days	Excluder	Phytostabilisation	Budzynska et al. (2019b)
<i>Jatropha curcas</i>	60–120 days, 18–1121 mg As kg ⁻¹	Excluder	Phytostabilisation	Alvarez-Mateos et al. (2019)
<i>Brassica juncea</i>	30 days	Indicator + K ₂ HPO ₄ + PGPB	Aided phytoextraction	Franchi et al. (2019)
<i>Isatis cappadocica</i> cabbage (<i>Brassica oleracea</i> var. <i>sabauda</i>), broccoli (<i>B. oleracea</i> var. <i>italica</i>), cauliflower (<i>B. oleracea</i> var. <i>botrytis</i>)	145–6525/1825 mg As kg ⁻¹	Hyperaccumulators	Phytoextraction	Karimi et al. (2009)
<i>Zea mays</i>	30 days	Excluder + K ₂ HPO ₄ + PGPB	Aided phytoextraction	Franchi et al. (2019)
<i>Helianthus annuus</i>	30 days	Excluder + K ₂ HPO ₄ + PGPB	Aided phytoextraction	Franchi et al. (2019)
<i>Helianthus annuus</i> , <i>Lolium perenne</i>	15.9 g As kg ⁻¹	Excluders	Aided phytostabilisation	Vitkova et al. (2018)
<i>Lactuca sativa</i>	2 months		In situ immobilisation	Arco-Lázaro et al. (2018)
Barley; wheat	40–80 mg As kg ⁻¹ 4 months	Indicator; excluder	Phytoextraction; phytostabilisation	Gonzalez et al. (2019a)
<i>Brassica napus</i>	60 days	Excluder	Phytostabilisation	Gasco et al. (2019)
<i>Vetiveria zizanioides</i>	6 months	Excluder	Phytostabilisation	Mu et al. (2019)
<i>Oriza sativa</i>	0–100 mg kg ⁻¹	Excluder	Phytostabilisation	Irem et al. (2019)
<i>Arundo donax</i>	79.6 mg As kg ⁻¹ , 9 months	Excluder	Co-planting with <i>P. vittata</i>	Zeng et al. (2019a)
<i>Arundo donax</i> , <i>Phragmites australis</i>	371 to 22,661 mg As kg ⁻¹	Excluders	Phytostabilisation	Castaldi et al. (2018)
<i>Morus alba</i> , <i>Broussonetia papyrifera</i>	41 mg As kg ⁻¹ , 9 months	Excluders	Co-planting with <i>P. vittata</i>	Zeng et al. (2019a, b)
<i>Pteris cretica</i>	30 days, 200 mg As kg ⁻¹	Hyperaccumulator	Phytoextraction	Eze and Harvey (2018)
<i>Pteris vittata</i>		Hyperaccumulator	Phytoextraction	Yang et al. (2018)
<i>Pteris vittata</i>	251 mg As kg ⁻¹ , 4 months	Hyperaccumulator	Phytoextraction	Wu et al. (2018)
<i>Pteris vittata</i>	65.8 mg As kg ⁻¹ , 28 days	Hyperaccumulator	Phytoextraction	Wan et al. (2018)
<i>Pteris multifida</i>	0.5 mg As kg ⁻¹ (spiked soil), 3 months	Accumulator	Phytoextraction	Rahman et al. (2018)
<i>Holcus lanatus</i>	65.8 mg As kg ⁻¹ , 28 days	Excluder	Phytostabilisation	Wan et al. (2018)
<i>Rosmarinus officinalis</i>	4–2738 mg As kg ⁻¹	Excluder	Phytostabilisation	Affholder et al. (2014)

Table 1 (continued)

Plant species	Exposure/growth period	Phenotype for As	Remediation option	Reference
<i>Polypogon monspeliensis</i>	250 mg As kg ⁻¹ (spiked soil)		Phytovolatilisation	Ruppert et al. (2013)
<i>Eupatorium cannabinum</i>	11 mg As L ⁻¹ , 20 days	Excluder	Phytostabilisation	Gonzalez et al. (2019b)
Mesocosms/columns				
<i>Kosteletzkya pentacarpos</i>	75 mg As kg ⁻¹	Excluder	Rhizofiltration/phytostabilisation	Zhou et al. (2019)
<i>Tamarix gallica</i>		Excluder	Phytostabilisation	Sghaier et al. (2019)
<i>Phragmites australis</i>	8 months	Excluder	Phytoextraction	Cortes-Torres et al. (2019)
Constructed wetlands				
<i>Cyperus haspan</i>	85 µg L ⁻¹ , 419 days	Indicator	Rhizofiltration	Corroto et al. (2019)
<i>Juncus effusus</i>	85 µg L ⁻¹ , 419 days	Excluder	Rhizofiltration	Corroto et al. (2019)
<i>Colocasia esculenta</i>	0.48 mg L ⁻¹ , 122 days	Excluder	Rhizofiltration	Vanlop et al. (2019)
Hydroponics				
<i>Salix atrocinerea</i>	18 mg As L ⁻¹ , 30 days	Excluder	Phytostabilisation	Navazas et al. (2019)
<i>Salix</i> spp.		Excluder	Phytostabilisation	Purdy and Smart (2008)
<i>Salix purpurea</i> cv. 'Fish Creek'	0–100 mg As/L (0–1335 µM)	Excluder	Phytostabilisation	Yanitch et al. (2017)
<i>Pteris vittata</i>	2 mM As(III) or As(V), 24 h	Hyperaccumulator	Phytoextraction	Yang et al. (2018)
<i>Pteris multifida</i>	21 µg L ⁻¹ As(III) (NaAsO ₂), 5 days; 33 µg L ⁻¹ As(III) 24 days	Hyperaccumulator	Phytoextraction	Rahman et al. (2018)
<i>Acer pseudoplatanus</i>	1 month, 1 mM As; 3 months, 0.06–0.6 mM As(III), As(V), DMA	Excluder (sensitive)	Phytostabilisation	Budzynska et al. (2019a); Budzynska et al. (2018)
<i>Betula pendula</i>	1 month, 1 mM As	Excluder	Phytostabilisation	Budzynska et al. (2019b)
<i>Quercus robur</i>	1 month, 1 mM As	Excluder (sensitive)	Phytostabilisation	Budzynska et al. (2019b)
<i>Ulmus laevis</i>	1 month, 1 mM As	Excluder (sensitive)	Phytostabilisation	Budzynska et al. (2019b)
<i>Atriplex atacamensis</i>	2 weeks, 50 µM As(III) or As(V)	Excluder	Phytostabilisation/rhizofiltration	Vromman et al. (2018)
<i>Lemna valdiviana</i>	0.5 mg L ⁻¹ As(V), 7 days	Accumulator	Rhizofiltration	Souza et al. (2019)
<i>Pistia stratiotes</i>	1–4 days, 5–20 µM As(III)	Excluder	Rhizofiltration	de Campos et al. (2019)
<i>Pistia stratiotes</i> , <i>Spirodela polyrhiza</i> , <i>Eichhornia crassipes</i>	15 days	Accumulators	Phytofiltration	Rai (2019)
<i>Eichhornia crassipes</i>	3 days, 7 µM As	Accumulator	Rhizofiltration	de Souza Reis et al. (2020)
<i>Elodea canadensis</i>	15–250 µg As L ⁻¹ 72 h	Excluder	Rhizofiltration	Picco et al. (2019)
<i>Vallisneria spiralis</i>	14 days	Excluder	Rhizofiltration	Li et al. (2018b)
<i>Salvinia molesta</i>	0–20 µM As(III), 96 h	Accumulator	Phytofiltration	da Silva et al. (2018b)
<i>Eupatorium cannabinum</i> , <i>Dittrichia viscosa</i> , <i>Melilotus alba</i> , <i>Betula pubescens</i> , <i>Populus nigra</i>	11 mg L ⁻¹ As(V)	Excluders	Phytostabilisation	Gonzalez et al. (2019b)
<i>Dahlia pinnata</i> Cav	0–120 µM	Excluder	Potential phytostabilisation	Raza et al. (2019)

et al. 2018a, Fig. 3). The *P. vittata* roots absorb arsenate via a PO₄ transporter (PvPht1;3), while the aquaporin tonoplast intrinsic protein 4 (PvTIP4) eases the arsenite absorption. The PvACR2 As(V) reductase, the PvGRX5 glutaredoxin, and maybe other reductases are then converting arsenate

to As(III) (Cai et al. 2019). The As(III) loading into the vacuoles of *P. vittata* gametophytes is facilitated by the PvACR3 As(III) transporter. Three genes, i.e. glyceraldehyde 3-phosphate dehydrogenase (PvGAPC1), glutathione S-transferase (PvGSTF1), and organic cation transporter



Fig. 3 Clockwise: *Pteris vittata* growing on the As-contaminated Reppel soil placed in large mesocosms at the INRAE research center, Villenave d’Ornon, France (Phytorehab and Greenland EU projects); focus on passive samplers of soil pore water (Rhizon) inserted for monitoring changes in As exposure in the *P. vittata* rhizosphere; year 2 of the phytostabilisation field trial implemented at the Jales tail-

ings, Portugal (EU Phytorehab project, FP5): (left) untreated topsoil; (right) topsoil amended with compost, coal fly ashes (beringite), and iron grit and colonised by As-tolerant populations of *Agrostis castelana*, *Holcus lanatus*, and *Cytisus striatus*. Photo © Dr. M. Mench (in collaboration with Pr. J. Vangronsveld, Hasselt Universiteit, Dr. P. Bleeker and Dr T. De Koe, Bleeker et al. 2002)

4 (PvOCT4), As-upregulated, are needed for As tolerance (Cai et al. 2019). The PvGAPC1 protein includes an uncommon active site having a lower affinity for phosphate than arsenate; PvOCT4 is present as puncta in the cytoplasm and PvGSTF1 displays As(V)-reductase activity. Arsenate, PvGSTF1, and PvGAPC1 are co-located. Once As(V) enters the cell, it would be converted into 1-arseno-3-phosphoglycerate by PvGAPC1. This one would be pumped into As-metabolising vesicles by the PvOCT4 protein and then hydrolysed to release As(V); this allows thereafter its reduction by PvGSTF1 to As(III) and vacuolar compartmentation. While phosphate limits As root uptake, phytate increases As absorption and development of *P. vittata* by regulating phosphate transporters, i.e. PvPht1;3 increased while PvPht1;1 decreased (Liu et al. 2018). The P and Si transporters mainly facilitate As absorption and its excess damages plant metabolism at various levels, e.g. impacts through oxidative stress, carbohydrate metabolism tightly connected to photosynthesis, and metabolic pathways coping with As-induced oxidative and nitrosative stresses. The PvPht1;3 gene from *P. vittata* complements a yeast P-uptake mutant and has a greater affinity and carriage capacity to As(V) than PvPht1;2 (Cao et al. 2019).

Vacuolar sequestration is one main mechanisms for plants to control excessive exposure to metal(oid)s. Angiosperms sequester PC–As(III) or GSH (glutathione)–As(III) conjugates in their root vacuoles (Zhao et al. 2010). PvACR3 occurs in the genomes of all the main plant lines but not in angiosperms, possibly explaining why they cannot accumulate or tolerate high As levels. Arsenic transporters are identified in *P. vittata*: a MIP (major intrinsic protein), PvTIP4;1, is mediating As(III) inflow into cells, whereas PvACR3 and PvACR3;1 intervene As(III) efflux into vacuoles (Yang et al. 2018). 824 transcripts are differentially expressed in As-stressed *P. vittata* ferns (Potdukhe et al. 2018). These genes are transcription factors and metal transporters, or are involved in chelator biosynthesis in line with absorption and accumulation mechanisms: e.g. cysteine-rich RLK, and ABC transporter G family member 26. Yan et al. (2019) have proposed a network consisting of six major transporter families, i.e. arsenical resistance protein Acr3 (ACR3), the major facilitator superfamily (MFS), the ABC superfamily, P-type ATPase, MIP, and nitrate transporter 3.1 (NRT3.1), two resistance pathways (i.e. GSH metabolism, notably Glutathione S-transferase (GST) and endoplasmic reticulum-associated protein degradation (ERAD) in roots, and a regulatory system for As

hyperaccumulation—regulation mechanisms in *P. vittata* tissues following high acute As(III) and As(V) exposure.

As-(hyper)tolerant grasses and dicots

Cultivation of forage crops and perennial grasses may either reduce the human exposure to As while increasing the farmer incomes or promote the vegetation cover reducing the contaminant dispersion by natural agents. As-hypertolerant populations of *Holcus lanatus* are identified and assessed at several contaminated sites (Hartley-Whitaker et al. 2002; Mench et al. 2003a, b, 2010; Karczewska et al. 2013). At the acidic metal/As-polluted Jales mine tailings, the combined addition of Beringite (a fly ash containing modified aluminosilicates), iron grit and compost was most effective to change As phytoavailability and soil pH and, after 4 years, to sustainably improve the revegetation by As-excluder colonists, notably *Agrostis castellana* and *H. lanatus* (Bleeker et al. 2002, Fig. 3). *Rosmarinus officinalis* has a potential to phytostabilise As and metals in Mediterranean area (Affholder et al. 2014).

Lolium multiflorum var. *italicum*, *Secale cereale*, *Vicia villosa*, and *Trifolium pratense* were cultivated in an agricultural soil adjacent to a mining area after amendment with either pig manure or AMD sludge (AMDS) (Kim et al. 2018). Bioavailable soil As increased in pig manure-treated soil, due to desorption by dissolved organic matter, in both non-cultivated and cultivated soils, apart for *T. pratense*; in contrast, it fell down in all AMDS-treatments. To cultivate such excluders resulted in safe crops. Water stable aggregation was enhanced by these plants, but As phytostabilisation did not occur. In situ soil flushing (8 days, with monopotassium phosphate (KH_2PO_4) solutions) combined with cultivating *P. vittata* and *L. multiflorum* facilitated As removal from the rhizosphere soil, reaching 35% and 53%, respectively, which exceed the 9% removal rate from soil flushing alone (Yan et al. 2018). Some As excluders, aromatic plants from the Poaceae (e.g. Vetiver (*Chrysopogon zizanioides*), Lemon grass (*Cymbopogon flexuosus*), Palmarosa (*Cymbopogon martinii*), and Citronella (*Cymbopogon winterianus*), Lamiaceae (Ocimum, Mentha, Lavender, Salvia, and Rosemary), Asteraceae (Chamomile), and Geraniaceae (*Pelargonium* sp.) families, used for producing essential oils, can give financial returns and have a potential for phytomanaging As-contaminated soils as these non-food crops are reducing the hazard of food chain contamination (Pandey et al. 2019).

Miscanthus x giganteus was growing well during 2-year in potted soils collected at former military sites, i.e. Sliac, Slovakia and Kamenetz-Podilsky, Ukraine (Pidlisnyuk et al. 2019). Major part of the metal(loid)s remained in the roots, notably in year 2, and rather limited amounts moved to the shoots, foliar As concentrations being below detection

limit. Both *Miscanthus sacchariflorus* A0104, and *M. sinensis* C0424 and C0640 exposed to As-spiked soil display As-excluder phenotype (Jiang et al. 2018). The biomass of *Phragmites australis* and *Arundo donax*, both being As excluders, increased in amended, As/metal-contaminated soils and soil amendments promoted aided phytostabilisation in the decreasing order: municipal solid waste compost (MSW-C) > Fe-rich water treatment residue (Fe-WTR) + MSW-C > Fe-WTR (Castaldi et al. 2018). At acidic soil pH (3.8), the highest As accumulation was recorded for plants grown on untreated soil. At neutral and alkaline soil pH, root As concentrations increased for compost-amended soils.

Macrophytes

Macrophytes are potentially useful for filtering As-contaminated effluents and water through their rhizosphere and root mats. In *Eichhornia crassipes* 3-day-exposed to 7 μM As, defense mechanisms against oxidative stress, enzyme activities related to S metabolism, and chelating substances are stimulated: the ATP sulphurylase (ATPS) activity increases in roots (de Souza Reis et al. 2020). Glutathione reductase (GR) activity in leaves and glutathione peroxidase (GSH-Px) in roots decrease. Glutathione sulphotransferase (GST) activity is enhanced in roots, suggesting increased GSH conjugation to As, and limited in leaves, and γ -glutamylcysteine synthetase (γ -ECS) activity is higher in leaves, suggesting PCs synthesis.

The aquatic moss *Warnstorfia fluitans* can filtrate As(V) and As(III) from As-contaminated-water (Sandhi et al. 2018). Arsenic removal was faster in arsenite than arsenate solutions, optimum (80–90% within 2 h) being at pH 6.5 and 9.5 and at 20 and 30 °C, and at low oxygenation levels. No As net efflux process occurred in the water system except after 48 h in As(V)-treated medium at 30 °C. Most internal As, i.e. 95% in the As(V) and 85% in the As(III) treatments, was bound to the tissue.

Rhizofiltration of As by macrophytes is also documented for *Sagittaria montevidensis* (Demarco et al. 2019); water hyacinth (*E. crassipes*), water ferns (*Azolla* spp.), duckweeds (*Lemna* sp., *Spirodela* sp. and *Wolffia* sp.), hydrilla (*Hydrilla verticillata*), and water cresses (*Nasturtium officinale*, *N. microphyllum*) have a potential for phytofiltration (Rahman and Hasegawa 2011). Twenty macrophytes from an Italian wetland area affected by urban and industrial pollutants display high tolerance to metal(loid) excess and capacity for phytostabilisation (Bonanno et al. 2018). Bioconcentration factor (BCF) values (from sediment to roots) for As ranged from 0.02 (*N. officinale*, *Paspalum paspaloides*) to 0.25 (*E. crassipes*, *P. australis*); leaf/ root transfer factor (TF) values varied from 0.12 (*Cyperus longus*) to 1.32 (*Lemna gibba*). *Lemna* sp. can uptake high amounts of metal(loid)

s with a relatively high biomass yield. Efficiency of *Lemna valdiviana* for As removal peaked between pH 6.3 and 7.0, with available phosphorus of 0.049 mmol P-PO₄ L⁻¹ and 7.9 mmol N-NO₃ L⁻¹, accumulating up to 1190 mg As kg⁻¹ DW (Souza et al. 2019). *Eichhornia crassipes* (60%) was more efficient for As removal than *Pistia stratiotes* (water lettuce, 49%) and *Spirodela polyrhiza* (a duckweed, 37%) in a microcosm experiment (Rai 2019).

In *Elodea canadensis* plants exposed to 15 µg and 250 µg As L⁻¹, foliar As concentration reached 0.34 and 0.4 mg As kg⁻¹, and roots 0.34 and 4.3 mg As kg⁻¹, as an excluder (Picco et al. 2019). These plants can filtrate As from tap water of an Argentine city located in an As-endemic area from 36 µg As L⁻¹ to undetectable levels (10 ng As L⁻¹). The submerged macrophyte *Vallisneria spiralis* was exposed to the binary As(III)/As(V) system (Li et al. 2018b). Total As and As(III) in water dropped within 3 days, while As(V) first increased slightly and then gradually decreased. About 1.2% DMA was detected at day 14. Both As(III) and As(V) were higher in roots than in leaves. In leaves, As(III) increased with the elapsed exposure time. The proportions of As(V) (28–40%) were lower than those of As(III) and arsenobetaine (AsB) was detected (0.5–1.9 mg kg⁻¹) after day 7, suggesting As(V) reduction and As(III) methylation to AsB. In *Salvinia molesta* (an aquatic fern) exposed to 20 µM As(III) for 4 days at pH 6.5 floating leaves reached 103 mg As kg⁻¹ (da Silva et al. 2018b).

In constructed wetlands (CW), high As removal is obtained with *Zantedeschia aethiopica* and *Anemopsis californica*, *Eleocharis macrostachya*, *Schoenoplectus americanus*, *Juncus effusus*, *Phragmites australis*, and *Echinodorus cordifolius* (Corroto et al. 2019). *Pistia stratiotes* plants were exposed in the 0–20-µM As(III) range for 4 days (de Campos et al. 2019). Root and shoot As concentrations peaked at 10 µM As(III) (i.e. 1120 and 31 mg kg⁻¹ DW), displaying an excluder phenotype. At the lower As exposure, the biomass production was not affected; at 20 µM As(III), it decreased by 77%. Chlorosis, darkening, and reduction of the root system were mirrored by increased membrane damages and the contents of reactive oxygen species. Rhizofiltration using *Cyperus haspan* (A), *Juncus effusus* (B), and a mix of laterite and gravel (substrate as a control, (C)) in subsurface horizontal-flow constructed wetlands (CW) was assessed to decrease As concentration in the reverse osmosis residues in Buenos Aires province, Argentina, because As concentrations in drinking water for c.a. 10% of the population exceed the WHO threshold value (10 µg L⁻¹) (Corroto et al. 2019). Arsenic removal ranged from 30 to 80% in the *J. effusus*-planted CW and between 10 and 40% using the *C. haspan*-planted CW. Arsenic concentration along CW was similar in the C and A treatments. The cumulative As mass was 62%, 34%, and 27% for A, B, and C treatments, respectively. During the elapsed time, *C. haspan* and *J.*

effusus contributed between 12 and 67% and 22 and 87%, respectively. For *J. effusus*, the accumulation is higher than the translocation process (BCF 1.6 and TF 0.2), whereas for *C. haspan* both factors were analogous (1.1 and 1.0, respectively). In a pilot-scale CW filled with laterite soil (20–28% Fe by weight) and planted with *Colocasia esculenta*, water As concentration decreased by 89% in the planted CW as compared to 52% in the unplanted one (Vanlop et al. 2019). Arsenic was mostly located within the root zone, because of rhizo-stabilisation and the Fe-adsorbing process within the laterite soil. Its sorption increased with the elapsed time. CWs planted with *P. australis* (Mexico) displayed high As removal rate (73–83%), and metal(loid) amounts removed from the substrates were in decreasing order: Fe > Cu > As (Cortes-Torres et al. 2019).

Trees

Tree root systems are an advantage to colonise and remediate deep contaminated soil layers. Salicaceae, i.e. willows, poplars, is one option for biomass production on As-contaminated soils (Purdy and Smart 2008; Vamerali et al. 2009; Janssen et al. 2015; Jiang et al. 2015, Bart et al. 2016). Their high biomass may compensate for their moderate shoot metal(loid)-concentrations. In hydroponics, *S. viminalis* x *S. miyabeana* and *S. sachalinensis* x *S. miyabeana* hybrids were most tolerant to As excess (Purdy and Smart 2008). Mechanisms involved in As root uptake, storage in vacuole, potential transport through the plant, and As tolerance of *Salix purpurea* and *S. atrocinerea* are described in transcriptomic analyses (Yanitch et al. 2017; Navazas et al. 2019). In As-stressed *S. purpurea*, biosynthesis of phenylpropanoids is induced, with the increased production of tannins. In hydroponics (18 mg As L⁻¹), a *S. atrocinerea* clone, from an As-contaminated brownfield, concentrates up to 2400 mg As kg⁻¹ DW in roots and 25 mg As kg⁻¹ DW in leaves. Roots reducing As(V) to As(III), As(III) predominates in roots and As(V) in leaves (Navazas et al. 2019). Since day 1, leaves and roots display de novo synthesis and increased non-protein thiols. To cultivate fast-growing willow shrubs, either in CWs or soils, can be a flexible and inexpensive solution to treat wood leaching containing metal(loid)s or polychlorinated dibenzo-dioxin/furan congeners (PCDD/Fs) generated at wood preservation sites (Fredette et al. 2019). *Salix miyabeana* 'SX67' was grown in three substrates irrigated with leachates containing increasing concentration of pentachlorophenol (PCP) and chromated chromium arsenate (CCA) over 12 weeks. The growing substrate affected willow ecophysiological responses and overall performance, leaf area being decreased with rising leachate concentration. Contaminants were stored in willow roots, but PCDD/Fs and Cu were also allocated to shoots.

Populus nigra seeds collected in the Loire Valley, France, were short-term cultivated on a potted soil from As/Pb mine tailings with three amendments, i.e. garden soil, compost and biochar, either alone or combined (Nandillon et al. 2019). The As concentration in the soil pore water (SPW) increased in all amended soils (18 to 416 times) notably with the compost treatment, which may promote As leaching. Seed germinated and plant grew only on amended soils, but adding biochar was less efficient. Poplar plantlets were As excluders, but the sustainable colonisation of such tailings by poplar populations remain to prove. Arsenic phytoextraction by four tree species, i.e. *Acer pseudoplatanus*, *Quercus robur*, *Betula pendula*, and *Ulmus laevis*, was evaluated in hydroponics (1 mM As(V), Budzynska et al. 2019a). The As accumulation peaked in *B. pendula* (BCF=0.87) and *Q. robur* (BCF=0.5). *Betula pendula* retained about 80% of As in its roots (excluder, TF=0.2) whereas *Q. robur* allocated more than 60% of As in its shoots (TF=1.6), which can be in hydroponics a sensitive behavior due to As excess as well as for *U. laevis* and *A. pseudoplatanus*. As(V) phytoextraction decreased root P and S concentrations in these tree species. The absorption of inorganic (As(III), As(V)) and organic arsenic (As-org) forms was then assessed with these tree species and two others, i.e. *Acer platanoides*, and *Tilia cordata*, in a pot experiment with As-contaminated mining sludge (Budzynska et al. 2019b). Total As was mainly stored in the roots of all these tree species, which were generally thinner, shorter and/or black after the experiment. The As(III) and As(V) concentrations peaked in the *A. pseudoplatanus* and *A. platanoides* roots (174 and 420 mg kg⁻¹, respectively). Relatively high As(III) concentrations (in mg kg⁻¹) were recorded in the *B. pendula* shoots (12) and As(V) in the shoots of *U. laevis* and *A. pseudoplatanus* (77 and 70). With some exceptions, As-org (present in mining sludge in low concentration) predominated in the tree organs. Influence of As forms, i.e. As(III), As(V), and DMA was assessed with *A. platanoides* in hydroponics (Budzynska et al. 2018). The exposure to particular As forms in single, double, and triple experimental systems decreased the seedling biomass. Negative symptoms depended on arsenicals and their concentration in solution, ranging from slight visible changes (inorganic compounds separately or jointly), through smaller and discolored leaves (DMA exposure), and finally to their withering (high DMA excess). Changes in color and shape for root systems exposed to arsenical combination occurred, despite seedling biomass were not affected. Root, stem, and foliar concentrations plateaued at 590, 70, and 140 mg As kg⁻¹ DW, respectively, under different combinations, showing an excluder phenotype. The highest BCF values reached 10.8 for root systems exposed to 0.06 mM of As(V) and DMA, while the highest TF value (1.0) was for 0.6 As(V) plus 0.06 mM DMA.

Halophytes

Phytomanagement of contaminated soils is of concern also in area affected by salinity (Sghaier et al. 2019). *Atriplex atacamensis*, a perennial shrub from Northern Chile occurring on As-contaminated area, may experience transient flooding conditions. This As excluder was exposed to either 50 μM As(III) or As(V) (Vromman et al. 2018). As(III) decreased plant development, stomatal conductance, and photosystem II efficiency while As(V) did not. Root As concentration peaked in reaction to As(III) excess in contrast to As(V). As(III) oxidation may occur because As forms are detected in roots for each treatment. Over 40% of As was sorbed to the cell wall in the As(V)-exposed roots whereas this rate decreased in the As(III)-exposed ones. Total As and its cell wall-bound fraction in leaves were similar after As(V) and As(III) exposure. Non-protein thiols peaked in response to As(V) excess in comparison to As(III), whilst ethylene synthesis was only enhanced in As(III)-exposed plants. *Kosteletzkya pentacarpos* was cultivated on a column device allowing leachate harvest, on a metal(loid)-spiked soil (i.e. 6.5 mg Cd, 75 mg As, 200 mg Zn, and 300 mg Pb kg⁻¹ DW) and irrigated with salt water (final soil electrical conductivity 5.0 mS cm⁻¹) (Zhou et al. 2019). Salinity decreased bioavailable soil As and shoot As concentration (0.7–1 mg As kg⁻¹, excluder).

Halogeton glomeratus seeds, from arid regions in Northwest China, were sown in metal(loid)-contaminated saline soil plots (Li et al. 2019a). In year 1, total salt yield extracted from plants was 2105 kg ha⁻¹, and salt concentration was 1.61 g As kg⁻¹. Seeds contained 0.26 mg As kg⁻¹ and their oil content was 19% with 91% of unsaturated fatty acids.

Field survey and case studies

Out of 20 native species from the Baoshan mining area (China, total soil As: 125–6656 mg kg⁻¹), *Pteris ensiformis* accumulated 1091 mg As kg⁻¹ in its shoots, with potential use for As phytoextraction (Pan et al. 2019); *Boehmeria nivea* shoots, usable for textile fibers, reached 701 mg As kg⁻¹. In both cases, high root-to-shoot transfer factor and unexpected high shoot Pb concentrations however may mirror foliar exposure. Several As excluders, i.e. *Dicranopteris linearis*, *Histiopteris incisa*, *Nephrolepis hirsutula*, *Pinus* sp., *Thysanolaena latifolia*, and *Melastoma malabathricum*, and As-accumulators, i.e. *Pityrogramma calomelanos* (210 mg As kg⁻¹) and *P. vittata*, were identified nearby the Lepanto As–Cu–Au mine in the Philippines, being options to post-mining rehabilitation (Claveria et al. 2019). Many herbaceous plant species growing in mining area, e.g. *Agrostis castellana*, *Rumex acetosella*, can display high root As concentration (> 200 mg kg⁻¹), being candidates for phyto-stabilisation (Otones et al. 2011).

One option to phytoextract As from contaminated soils is to use As-hyperaccumulating ferns from the *Pteris* genus, e.g. *P. vittata*, *P. cretica*, *P. longifolia*, and *P. umbrosa*, and other ones, e.g. *Pityrogramma calomelanos* var. *austroramericana* (gold dust fern) and *P. calomelanos* (silver fern) (Francesconi et al. 2002; Niazi et al. 2012). *Pteris vittata* prefers to grow in alkaline soils, shady area and in warm, humid climates. However, it can be grown outside in mild-Atlantic climate (SW France), and protect from strong frost under cold greenhouse or by mulching.

As hyperaccumulation is a constitutive trait for *P. vittata*, but M populations from As-contaminated soils differ from NM ones for As accumulation (Wu et al. 2018). Fern NM populations were collected from two Chinese uncontaminated sites, i.e. ZD and NN, and M ones in As and Pb/Zn mining and/or smelting sites, i.e. SG and GY. Both NM populations display higher As(V) and As(III) uptake than the M ones. Arsenate reductase activities in roots peaked in the NM populations. Root exudates from the NN and GY populations contained similar organic acid patterns, dominated by oxalic acid (> 67%) plus malic and succinic acids. For oxalate, the NN population released 4.2 times more than the SG one. The NN root exudates mobilised more As from polluted soils than the SG ones, oxalate being the most efficient to extract As.

In hydroponics (24 days) and in the presence of Pb and Cd, the temperate zone fern *P. multifida* (able to tolerate low temperatures from 5 to -4.6 °C) removed 50% of As(III) (Rahman et al. 2018). Frond As concentration was higher than in other plant parts whereas Cd and Pb concentrations peaked in roots and rhizome. In potted spiked soils, As concentration reached 1200 and roughly 250 mg kg⁻¹ in the rhizome and fronds of *P. multifida*, whereas the frond As concentration of the tropical zone fern *P. vittata* was 2100 mg kg⁻¹. Co-accumulation of metal(loid)s by *P. vittata* is questionable. Two Chinese *P. vittata* populations, one from a Sb smelting area (total soil As: 147) and one from a Pb–Zn mining area (total soil As: 572), and one As-excluder *Holcus lanatus* population were cultivated on a Sb/As-polluted soil (Wan et al. 2018). The fern displayed high As- but limited Sb-accumulating capacity: shoot As and Sb concentrations culminated at 455 and 26 mg kg⁻¹, respectively. At day 28, the Sb and As concentrations in the soil solution were respectively decreased by 22% and 36% in the fern treatments. In contrast, the Sb and As accumulation by *H. lanatus* shoots was limited. In *P. vittata*, As(V) was converted to As(III), which dominated in shoots, but reduction of antimonate to antimonite was limited (with > 90% of shoot Sb existing as antimonate). The fern M population showed 35% higher As uptake than the NM one. Both populations did not differ for Sb accumulation. In contaminated soils dominated by Cu excess from a wood preservation site, *P. vittata* growth is affected and As-phytoextraction limited

(Mench unpublished). For *P. calomelanos* plants exposed at 1 mM As, 90% of the As absorbed was accumulated in shoots, and no As stress symptoms were visible on plant parts (Campos et al. 2018). At higher exposure (10 and 30 mM As), As uptake by roots was mainly translocated into the shoots (81–74%), with marginal and apical necroses on pinnae, damages being mainly in the secondary veins and adjacent cells. In the As-stressed roots, tenuous alterations were identified, i.e. separation of border-like cells and presence of granular substances in cortical cells.

Several field trials are cited by Jiang et al. (2015): *P. vittata* and *P. cretica* in southwest England (Gray et al. 2005), low shoot DW yield (*P. vittata*, 0.76 t DW ha⁻¹) being the main drawback; *P. vittata* assessment at 21 As-contaminated sites in England (Shelmerdine et al. 2009) demonstrating that the As amount phytoextracted generally fell down as total soil As expanded and pointing out the low fern yield; and a Chinese trial (2t DW ha⁻¹, Chen et al. 2006). At a former CCA-contaminated site in Florida, total topsoil As was decreased from 190 to 140 mg kg⁻¹ following a 2 year-cultivation of *P. vittata*. (Kertulis-Tartar et al. 2006). Using this fern, 8 years would be required to decrease the acid-extractable soil As from 80 to 40 mg kg⁻¹ (US-EPA limit) at an EPA Superfund site (Salido et al. 2003). The *P. vittata* capacity to phytoextract As decreases after several consecutive frond harvests and this fern species did not well regrow in the plots due to competition with weeds (Reichmann et al. 2004 cited in Niazi et al. 2012; Mench et al. 2014).

Silverback fern, *P. calomelanos*, is able to better prosper on tropical As-polluted soils than *Pteris* sp. (Clemens and Ma 2016). It was cultivated in both greenhouse and field trials in an As-polluted area of the Ron Phibun District, Thailand (Jankong et al. 2007). Rhizosphere bacteria and fungi were isolated from the fern roots. P fertiliser and rhizobacteria increased plant biomass and As accumulation, thus As phytoextraction. Rhizofungi decreased plant As concentration but enhanced plant biomass. Gold dust fern and Chinese brake fern were compared at a disused As-contaminated cattle-dip site for their As-phytoextraction capacities over 27 months (Wollongbar, NSW, Australia; Niazi et al. 2012). The frond DW yield, As concentration and As uptake were higher in the Gold dust fern than in *P. vittata*, at all harvests (i.e. 10, 22, and 27 months). Gold dust fern phytoextracted 25.4 kg As ha⁻¹ (cumulative over three harvests), 2.65 times more than *P. vittata* (9.7 kg As ha⁻¹), corresponding to 1.7–3.9% and 0.53–1.5% of total topsoil As. To assess P/As interaction, *P. vittata* was cultivated in two sandy polluted soils (C soil from an As-treated wood facility and D soil from a cattle-dipping vat, 129 and 26.7 mg As kg⁻¹) over 5 years and during 10 harvests, under P-sufficient (P-fertiliser) and P-limiting (phosphate rock) conditions (da Silva et al. 2018a). Frond biomass production and As removal peaked for the 9th (62–64 and 35–63 g As plant⁻¹) and 10th

harvests (58–60 and 52–57 g As plant⁻¹) for C and D soils, even though As concentration in fronds dropped. Soil As phytoextracted averaged 7–10% per harvest during the 1–6th harvests; it decreased to 0–3% during the 7–10th harvests for D and C soils. All soil As fractions, except the residual one, were concerned by plant uptake. Highest decrease occurred in the amorphous fraction of the C soil (64–66%) and in the crystalline fraction of the D soil (50–86%). Soil As concentrations decreased respectively by 37–47% from 26.7 and 129 to 16 and 69 mg kg⁻¹ for the D and C soils. Non-labile As was efficiently mobilised by *P. vittata* under P-limiting conditions without affecting its As depletion.

Soil pH is one major driving force for As phytoextraction. In a field survey, *P. vittata* and *P. calomelanos* only occurred in As-polluted areas with soil pH 7.2–8.8 and 2.3–4.2, respectively (Anh et al. 2018). Both fern species were further grown in potted soils spiked with 300 mg As kg⁻¹ with soil pH set at 5.1, 7.2, and 9. Silverback fern subsisted at these three soil pH and showed the highest frond As concentration and soil As phytoextraction at soil pH 5.1. In contrast, all *P. vittata* plants perished at this soil pH. At soil pH of 7.2 and 9, *P. vittata* displayed higher frond As concentration, shoot biomass, and shoot As removal than *P. calomelanos*. For alkaline soil (pH 7.8) spiked with increasing As levels, *P. vittata* exhibited higher life time, shoot biomass, As tolerance, and phytoextraction than *P. calomelanos*.

Conclusions and perspectives

The evidences so far available indicate the exploitation of the microbial As(III) oxidation as the most promising application for water treatment and bioremediation purposes. To date, the As transformation processes and the associated high microbial and functional diversity have been broadly studied and described. Only few investigations have however tested the biological As(III) oxidation process under exploratory settings mimicking real situations (e.g. long-term experiments managed at large scale and/or in water treatment plant) and this has strongly impacted on the further development of bio-based technologies. Consequently thereof, the field applicability of As microbiological remediation processes in combination with conventional methods was not fully exploited and evaluated so far. Overall, to employ autotrophic As(III) oxidisers may be favoured as the process does not require the addition of any organic carbon sources. However, this metabolism has been till now exclusively found in microorganisms isolated from extreme environments. Nevertheless, several bench scale studies showed the efficient exploitation of heterotrophic As(III) oxidation in bioremediation strategies. This potential deserves to be further investigated and assessed in systems at higher scale. Reductive microbial bio-processes also present interesting

potential in terms of As removal from water, in particular for mine and industrial polluted streams. The anaerobic bioreactors could be judiciously combined with downstream aerobic oxidative and/or phytoremediation steps, for removing the residual dissolved As and organic carbon, as shown in the example of Trail site (Al et al. 2011). As observed with other pollutant classes, the use of native bacteria is surely a feasible option for bioremediation purpose due to their high compatibility with the environment and tolerance to toxicity. Diversely, bioaugmentation with specialised bacteria implies the analysis of additional constraints that may be costly (e.g. the pre-cultivation and addition of highly concentrated microbial cultures) and may negatively impact the As transformation rate (e.g. the limited adaptation and persistence of the added microorganisms in the highly competitive environment).

Recent methods of genomics, such as DNA sequencing and transcriptome analysis, are at the interface between molecular biology and ecology. When they are applied to environmental issues, they go beyond the simple description of organisms present in ecosystems. They make indeed possible to characterise microbial communities, which are sometimes complex and which can shelter organisms recalcitrant to conventional cultural methods. Combined with functional approaches such as metaproteomics, metabolomics, and stable isotope probing (Fischer et al. 2016; Musat et al. 2016; Vogt et al. 2016; Zuñiga et al. 2017), these various methods can provide an overall vision of the ecosystem structure and functioning. Moreover, with the sequencing depth that these recent technologies are able to do, access to the less-depicted species, the so-called rare biosphere, becomes possible. Such an opportunity to characterise microbial communities quickly and cost-effectively could be particularly useful in monitoring bioremediation processes in As-contaminated environments, thus avoiding changes in parameters that would compromise the efficacy of bioremediation (Lovley 2003; Stenuit et al. 2008; Techtmann and Hazen 2016). Nevertheless, these approaches must be combined with laboratory and field experiments. In addition, they often require the development and optimisation of reproducible and efficient biological sampling and extraction methods. Finally, storing, exchanging and analysing the massive data amounts generated by high-throughput sequencing methods require the implementation of robust new computing methods, much more complex than those required by conventional statistical analyses (Pasolli et al. 2016; Li et al. 2017). The resulting studies must also include a set of complementary data, called metadata. Collected for each genome or metagenome studied, they must allow appropriate data exploitation (Satinsky et al. 2013), as specified by the Genomic Standard Consortium (Yilmaz et al. 2011).

Several practices are developed to enhance or reduce As (phyto)availability depending on the (bio)remediation

purposes and pollutant linkages. Use of chelating agents in combination with plants can promote either As phytostabilisation in excluder roots or bioavailable As stripping by accumulators, but it is controversial as metal(loid)-chelates may be leached and contaminate the groundwater. Soil amendments, e.g. Fe/Mn bearing phases, alkaline silicon slags, are investigated to regulate root As exposure (Kumpiene et al. 2019, 2021). Effectiveness of composts and biochars in reducing As bioavailability depends on many factors including the release of dissolved organic matter, Fe/Mn oxide content, dosage rate, etc. (O'Connor et al. 2018). Si-based fertiliser can mitigate As accumulation in rice (Zhao et al. 2010; Zhao 2020). Soil fertilisation (e.g. N, calcium phosphate) and inoculation with arbuscular mycorrhizal fungi (e.g. *Funneliformis mosseae*, *Glomus mosseae*) can increase fern biomass but with few or no effect on frond As removal (due to dilution in the biomass), whereas soluble P addition may desorb As from the soil bearing phases and promote its leaching (Matzen et al. 2020). The selection of plant species and genotypes can be used to produce safe crops regarding As (Allevato et al. 2019). The genetic engineering is also explored to improve As excluders or (hyper)accumulators (Clemens and Ma 2016; Zhang et al. 2018; Allevato et al. 2019; Zhao 2020). Bioaugmentation with Plant Growth Promoting Bacteria (PGPB) and endophytic bacteria can promote root As uptake and plant growth, and thus As phytoextraction. Intercropping and co-cropping of As-excluder cash crops with As-(hyper)accumulator ones is an option for maintaining agricultural production and harvesting valuable biomass during the phytoextraction of labile fraction of soil As in excess. Phytomanagement-borne biomass is a resource and not a waste. Combustion is becoming a past option (Nzihou and Stanmore 2013). Research trends focus on optimising the processing of such biomass in various ways. It can be converted into valuable platform-chemical compounds, bio-active products, biogas/syngas, bio-oils and biofuels (Carrier et al. 2012; Cai et al. 2021, Wang et al. 2021). (Hyper)accumulator biomass can be converted into biocatalysts. Ethanol extraction with anaerobic digestion is an option mobilising As from *P. vittata* biomass and producing methane (da Silva et al. 2019a, b). Solid residues can be processed by pyrolysis, producing biochars, and other technologies. Thermochemical processes, e.g. gasification and pyrolysis, can provide syngas and bio-oil products useable for heat and electricity generation and biosourced chemistry (He et al. 2019). Cai et al. (2021) extracted phenolic compounds from *P. vittata* biomass. Vegetal fibers and powders to reinforce bio-sourced plastics and cements are other processes to be explored.

Depending on the type of As-contaminated site and future land use, the science front (in a holistic approach) includes: to continue to identify relevant plant species and microorganisms regarding soil As phytomanagement, to

focus on molecular mechanisms of As phytomanagement (Thakur et al. 2020), promotion of mesofauna and bacterial communities through agricultural practices such as the permaculture (especially to facilitate rooting, water and nutrient uptake), (phyto)management of other contaminants combined with the soil As contamination (notably the case-studies of soil As/Cd co-contamination (Zhao 2020) and As/persistent organic pollutants), use of agro-ecology for As-contaminated agricultural areas, biomonitoring of the food chain transfer (Grignet et al. 2020), use of nanoparticles to reduce As exposure, and development of the (phyto-borne)-biomass-processing technologies.

Some phytomanagement gaps can be complemented by bioremediation (Roy et al. 2015), as microbes can: carry out the bioremediation out of the root zone and for groundwater; reduce bioavailable soil As, allowing plant colonists to cover the soil and to initiate a complementary phytoremediation; enhance contaminant removal (or xenobiotic dissipation) by promoting plant growth (e.g. atmospheric N fixation, mineral solubilisation and release of nutrients, production of plant growth regulators such as auxins, gibberellins and cytokinins, decrease of ethylene synthesis by 1-aminocyclopropane-1-carboxylate (ACC) deaminase, and challenging of pathogenic bacteria) and changing arsenical speciation; processing of plant biomass by anaerobic digestion etc. The use of transgenic plants and microbes is not addressed here but discussed elsewhere (Roy et al. 2015; Thakur et al. 2020; Zhao and Wang 2020) and currently not applicable in remediation strategies in Europe.

Public access to thousands of metagenomic samples, for example, from sites such as EBI metagenomics (Mitchell et al. 2017), associated with large data mining and analysis algorithms, and metabolic modeling methods is a real opportunity to better comprise how the various constituents of an ecosystem can work together in response to the biotic and abiotic factors of the environment. Rather than a simple inventory of biological objects, such a descriptive analysis can allow to answer questions such as: how do the concerned organisms work, what is their spatial and temporal distribution, what are the adaptive and even evolutionary processes involved and what are the metabolic interactions they may develop. In particular, such an integrated frame of the metabolic functions exerted by microbial communities should provide a better knowledge of the microbial processes at work in the biological treatment of As-contaminated water. Combined with the use of appropriate predictive models, this understanding should allow an optimal use of microorganisms and their properties for developing new biotechnological applications in the bioremediation field of As-contaminated soils and waters. They could also contribute to improve the functioning of existing bio-treatment processes and to better control and stabilise their long-term efficiency. The proof of the stability of biological activities in

continuously fed treatment plants would help to increase the applicability of As bioremediation options and their acceptance as robust low-cost technologies by the economic sector. The biological data generated by metagenomics approaches could also be a source of information to propose and test the validity of bioindicators, potentially useful for monitoring the bioremediation processes or to assess the As bioavailability. Moreover, extended microbial metagenomic analyses of the different environmental compartments, i.e. soil, water, and rhizosphere soil, and the different plant parts will contribute to the development of As bioremediation processes involving cooperation between bacteria, fungi, and plants.

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Declarations

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References

- Affholder MC, Pricop AD, Laffont-Schwob I, Coulomb B, Rabier J, Borla A, Demelas C, Prudent P (2014) As, Pb, Sb, and Zn transfer from soil to root of wild rosemary: do native symbionts matter? *Plant Soil* 382:219–236
- Afkar E, Lisak J, Saltikov C, Basu P, Oremland RS, Stolz JF (2003) The respiratory arsenate reductase from *Bacillus selenitireducens* strain MLS10. *FEMS Microbiol Lett* 226:107–112
- Al M, Evans LJ, Gould WD, Duncan WFA, Glasauer S (2011) The long term operation of a biologically based treatment system that removes As, S and Zn from industrial (smelter operation) landfill seepage. *Appl Geochem* 26:1886–1896
- Allevato E, Stazi SR, Marabottini R, D'Annibale A (2019) Mechanisms of arsenic assimilation by plants and countermeasures to attenuate its accumulation in crops other than rice. *Ecotoxicol Environ Saf* 185:109701
- Alvarez-Mateos P, Ales-Alvarez FJ, Garcia-Martin JF (2019) Phytoremediation of highly contaminated mining soils by *Jatropha curcas* L. and production of catalytic carbons from the generated biomass. *J Environ Manage* 231:886–895
- Ander EL, Johnson CC, Cave MR, Palumbo-Roe B, Nathanail CP, Lark RM (2013) Methodology for the determination of normal background concentrations of contaminants in English soil. *Sci Total Environ* 454–455:604–618
- Andres J, Bertin P (2016) The microbial genomics of arsenic. *FEMS Microbiol* 40:299–322
- Andres J, Arsène-Ploetze F, Barbe V, Brochier-Armanet C, Cleiss-Arnold J et al (2013) Life in an arsenic-containing gold mine: genome and physiology of the autotrophic arsenite-oxidizing bacterium *Rhizobium* sp. NT-26. *Genome Biol Evol* 5:934–953
- Anguita JM, Vera MA, Vargas I (2018) The electrochemically active arsenic oxidising bacterium *Ancylobacter* sp. TS-1. *ChemElectroChem* 5:3633–3638
- Anh BTK, Minh NN, Ha NTH, Kim DD, Kien NT, Trung NQ, Cuong TT, Danh LT (2018) Field survey and comparative study of *Pteris vittata* and *Pityrogramma calomelanos* grown on arsenic contaminated lands with different soil pH. *Bull Environ Contam Toxicol* 100:720–726
- Antoni V, Saby N, Arrouays D, Jolivet C, Boulonne L, Ratie C, Bispo A, Eglin T, Pierart A, Gay A, Perrin JL, Joassard I (2019) Arsenic et mercure dans les sols français: pollutions diffuses et ponctuelles. Quatrième Rencontres nationales de la Recherche sur les sites et sols pollués, 26 et 27 novembre, Le Beffroi de Montrouge. Available at https://www.researchgate.net/publication/331648803_Arsenic_et_mercure_dans_les_sols_francais_pollutions_diffuses_et_ponctuelles. Accessed 1 December 2021
- Arco-Lázaro E, Pardo T, Clemente R, Bernal MP (2018) Arsenic adsorption and plant availability in an agricultural soil irrigated with As-rich water: effects of Fe-rich amendments and organic and inorganic fertilisers. *J Environ Manage* 209:262–272
- Arsène-Ploetze F, Koechler S, Marchal M, Coppée JY, Chandler M, Bonnefoy V et al (2010) Structure, function, and evolution of the *Thiomonas* spp. Genome. *PLoS Genet* 6:e1000859
- ATSDR (Agency for Toxic Substances and Disease Registry) (2017). The ATSDR 2017 Substance Priority List. Available at <https://www.atsdr.cdc.gov/SPL/>. Accessed 13 Oct 2019
- Bahar MM, Megharaj M, Naidu R (2012) Arsenic bioremediation potential of a new arsenite-oxidizing bacterium *Stenotrophomonas* sp. MM-7 isolated from soil. *Biodegradation* 23:803–812
- Bahar MM, Megharaj M, Naidu R (2013) Bioremediation of arsenic-contaminated water: recent advances and future prospects. *Water Air Soil Pollut* 224:1–20
- Baize D (2016). Teneurs totales en éléments traces dans les sols (France). Gammes de valeurs "ordinaires" et d'anomalies naturelles. Available at https://www.denis-baize.fr/etm/gamme_s3.html. Accessed 13 Oct 2019
- Bart S, Motelica-Heino M, Miard F, Joussein E, Soubrand M, Bourgerie S, Morabito D (2016) Phytostabilization of As, Sb and Pb by two willow species (*S. viminalis* and *S. purpurea*) on former mine technosols. *CATENA* 136:44–52
- Battaglia-Brunet F, Dictor M, Garrido F, Cruzet C, Morin D (2002) An arsenic(III)-oxidizing bacterial population: selection, characterization, and performance in reactors. *J Appl Microbiol* 93:656–667

- Battaglia-Brunet F, Jouliau C, Garrido F, Dictor M, Morin D, Coupland K, Johnson DB, Hallberg KB, Baranger P (2006) Oxidation of arsenite by *Thiomonas* strains and characterization of *Thiomonas arsenivorans* sp. nov. *Antonie Van Leeuwenhoek* 89:99–108
- Battaglia-Brunet F, Crouzet C, Burnol A, Coulon S, Morin D, Jouliau C (2012) Precipitation of arsenic sulphide from acidic water in a fixed-film bioreactor. *Wat Res* 46:3923–3933
- Battaglia-Brunet F, Casiot C, Fernandez-Rojo L, Hery M, Le Pape P, Tris H, Morin G, Touzé S, Jouliau C (2021) Laboratory-scale bio-treatment of real arsenic-rich acid mine drainage. *Water Air Soil Pollut* 232:330
- Battaglia-Brunet F, Dictor MC, Garrido F, Michel C, Jouliau C, Bourgeois F, Baranger P, Itard Y, Morin D (2005) Remediation processes using biological As(III) oxidation. In: Proceedings of the 16th international bihydrometallurgy symposium, Cape Town, South Africa, pp 343–350
- Belon E, Boisson M, Deportes IZ, Eglin TK, Feix I, Bispo AO, Galsomies L, Leblond S, Gueiller CR (2012) An inventory of trace element inputs to French agricultural soils. *Sci Total Environ* 439:87–95
- Ben Fekih I, Zhang C, Li YP, Zhao Y, Alwathnani HA, Saquib Q, Rensing C, Cervantes C (2018) Distribution of arsenic resistance genes in prokaryotes. *Front Microbiol* 9:2473
- Bentley R, Chasteen TG (2002) Microbial methylation of metalloids: arsenic, antimony, and bismuth. *Microbiol Mol Biol Rev* 66:250–271
- Bertin PN, Heinrich-Salmeron A, Pelletier E, Goulhen-Chollet F, Arsène-Ploet F et al (2011) Metabolic diversity among main microorganisms inside an arsenic-rich ecosystem revealed by meta- and proteo-genomics. *ISME J* 5:1735–1747
- Bertin P, Michotey V, Normand P (2015) Contributions of descriptive and functional genomics to microbial ecology. In: Bertrand JC et al (eds) *Environmental microbiology: fundamentals and applications: microbial ecology*. Springer, pp 831–846
- Bhattacharjee H, Rosen BP (2007) Arsenic metabolism in prokaryotic and eukaryotic microbes. *Mol Microbiol Heavy Met, Microbiol Monogr* 6:371–406
- Biswas R, Sarkar A (2019) Characterization of arsenite oxidizing bacteria to decipher their role in arsenic bioremediation. *Prep Biochem Biotechnol* 49(1):30–37
- Biswas R, Vivekanand V, Saha A, Ghosh A, Sarkar A (2019) Arsenite oxidation by a facultative chemolithotrophic *Delftia* spp. BA529 for its potential application in groundwater arsenic bioremediation. *Int Biodeter Biodegr* 136:55–62
- Bleeker PM, Assunção AGL, Teiga PM, de Koe T, Verkleij JAC (2002) Revegetation of the acidic, As contaminated Jales mine spoil tips using a combination of spoil amendments and tolerant grasses. *Sci Total Environ* 300:1–13
- Bonanno G, Vymazal J, Cirelli GL (2018) Translocation, accumulation and bioindication of trace elements in wetland plants. *Sci Total Environ* 631–632:252–261
- Budzynska S, Magdziak Z, Golinski P, Niedzielski P, Mleczek M (2018) Arsenic forms in phytoextraction of this metalloid in organs of 2-year-old *Acer platanoides* seedlings. *Environ Sci Pollut Res* 25:27260–27273
- Budzynska S, Krzeslowska M, Niedzielski P, Goliński P, Mleczek M (2019a) Arsenate phytoextraction abilities of one-year-old tree species and its effects on the nutritional element content in plant organs. *Int J Phytorem* 21:1019–1031
- Budzynska S, Mleczek P, Szostek M, Goliński P, Niedzielski P, Kaniuczak J (2019b) Phytoextraction of arsenic forms in selected tree species growing in As-polluted mining sludge. *J Environ Sci Health, Part A* 54:933–942
- Cai C, Lanman NA, Withers KA, DeLeon AM, Wu Q, Gribskov M, Salt DE, Banks JA (2019) Three genes define a bacterial-like arsenic tolerance mechanism in the arsenic hyperaccumulating fern *Pteris vittata*. *Curr Biol* 29:1625–1633
- Cai W, Chen TB, Lei M, Wan XM (2021) Effective strategy to recycle arsenic-accumulated biomass of *Pteris vittata* with high benefits. *Sci Total Environ* 756:143890
- Campos NV, Arcanjo-Silva S, Freitas-Silva L, Oliveira de Araújo T, Souza-Fernandes DP, Azevedo AA (2018) Arsenic hyperaccumulation in *Pityrogramma calomelanos* L. (Link): adaptive traits to deal with high metalloid concentrations. *Environ Sci Pollut Res* 25:10720–10729
- Cao Y, Feng H, Sun D, Xu G, Rathinasabapathi B, Chen Y, Ma LQ (2019) Heterologous expression of *Pteris vittata* phosphate transporter PvPht1;3 enhances arsenic translocation to and accumulation in tobacco shoots. *Environ Sci Technol* 53:10636–10644
- Carlin DJ, Naujokas MF, Bradham KD, Cowden J, Heacock M et al (2016) Arsenic and environmental health: state of the science and future research opportunities. *Environ Health Perspect* 124:890–899
- Carrier M, Loppinet-Serani A, Absalon C, Aymonier C, Mench M (2012) Degradation pathways of holocellulose, lignin and α -cellulose from *Pteris vittata* fronds in sub- and super critical conditions. *Biomass Bioenergy* 43:65–71
- Casentini B, Falcione FT, Amalfitano S, Fazi S, Rossetti S (2016) Arsenic removal by discontinuous ZVI two steps system for drinking water production at household scale. *Water Res* 106:135–145
- Casentini B, Rossetti S, Gallo M, Baldi F (2015) Potentialities of biogenerated iron hydroxides nanoparticles in arsenic water treatment. In Conference proceeding 6th European bioremediation conference, Chania, Crete, Greece, June 29–July 2
- Casiot C, Pedron V, Bruneel O, Duran R, Personné JC, Grapin G, Drakidès C, Elbaz-Poulichet F (2006) A new bacterial strain mediating As oxidation in the Fe-rich biofilm naturally growing in a groundwater Fe treatment pilot unit. *Chemosphere* 64:492–496
- Castaldi P, Silvetti M, Manzano R, Brundu G, Roggero PP, Garau G (2018) Mutual effect of *Phragmites australis*, *Arundo donax* and immobilization agents on arsenic and trace metals phytostabilization in polluted soils. *Geoderma* 314:63–72
- Chen LX, Méndez-García C, Dombrowski N, Servín-Garcidueñas LE, Elae-Fadros EA, Fang BZ et al (2017) Metabolic versatility of small archaea Micrarchaeota and Parvarchaeota. *ISME J* 12:756–775
- Chen TB, Yong LX, Chun HZ, Mei L, Xue LW, Yu ML, et al (2006) Phytoremediation of arsenic-contaminated soil in China. In: NW (ed) *Methods Biotechnol, Phytoremediation Methods Rev*, vol 13. Humana Press Inc., Totawa (NJ), USA, pp 393–404
- Chivian D, Brodie EL, Alm EJ, Culley DE, Dehal PS et al (2008) Environmental genomics reveals a single-species ecosystem deep within earth. *Science* 322:275–278
- Claveria RJR, Perez TR, Perez REC, Algo JLC, Robles PQ (2019) The identification of indigenous Cu and As metallophytes in the Lepanto Cu-Au Mine, Luzon, Philippines. *Environ Monit Assess* 191:185
- Cleiss-Arnold J, Koechler S, Proux C, Fardeau ML, Dillies MA, Coppée JY, Bertin PN (2010) Temporal transcriptomic response during arsenic stress in *Herminiimonas arsenicoxydans*. *BMC Genomics* 11:709
- Clemens S, Ma JF (2016) Toxic heavy metal and metalloid accumulation in crop plants and foods. *Annu Rev Plant Biol* 67:489–512
- Corroto C, Iriel A, Fernandez Cirelli A, Perez Carrera AL (2019) Constructed wetlands as an alternative for arsenic removal from reverse osmosis effluent. *Sci Total Environ* 691:1242–1250
- Corsini A, Zaccaro P, Muzer G, Andreoni V, Cavalca L (2014) Arsenic transforming abilities of groundwater bacteria and the

- combined use of *Aliihoeflea* sp. strain 2WW and goethite in metalloid removal. *J Hazard Mater* 269:89–97
- Cortes-Torres C, Barrientos-Lozano L, Almaguer-Sierra P, Rosas-Mejia M, Rocandio-Rodriguez M, Alarcon A, Mora-Ravelo SG (2019) Removing arsenic, copper and iron from sewage sludge with reed (*Phragmites australis*). *Appl Ecol Environ Res* 17:5603–5617
- Crognale S, Amalfitano S, Casentini B, Fazi S, Petruccioli M, Rossetti S (2017) Arsenic-related microorganisms in groundwater: a review on distribution, metabolic activities and potential use in arsenic removal processes. *Rev Environ Sci Bio/Technology* 16:647–665
- Crognale S, Casentini B, Amalfitano S, Fazi S, Petruccioli M, Rossetti S (2019) Biological As(III) oxidation in biofilters by using native groundwater microorganisms. *Sci Total Environ* 651:93–102
- Cui J, Du J, Tian H, Chan T, Jing C (2018) Rethinking anaerobic As(III) oxidation in filters: effect of indigenous nitrate respirers. *Chemosphere* 196:223–230
- Cullen WR, Reimer KJ (1989) Arsenic-speciation in the environment. *Chem Rev* 89:713–763
- Cundy A, Bardos P, Puschenreiter M, Mench M, Bert V, Friesl-Hanl W, Müller I, Li X, Weyens N, Witters N, Vangronsveld J (2016) Brownfields to green fields: realising wider benefits from practical contaminant phytomanagement strategies. *J Environ Manage* 184:67–77
- da Silva EB, Less JT, Wilkie AC, Liu X, Liu YG, Ma LNQ (2018a) Arsenic removal by As-hyperaccumulator *Pteris vittata* from two contaminated soils: a 5-year study. *Chemosphere* 206:736–741
- da Silva AA, de Oliveira JA, de Campos FV, Ribeiro C, dos Santos FF, Costa AC (2018b) Phytoremediation potential of *Salvinia molesta* for arsenite contaminated water: role of antioxidant enzymes. *Theor Exper Plant Physiol* 30:275–286
- da Silva EB, Mussoline WA, Wilkie AC, Ma LQ (2019a) Anaerobic digestion to reduce biomass and remove arsenic from As-hyperaccumulator *Pteris vittata*. *Environ Pollut* 250:23–28
- da Silva EB, Mussoline WA, Wilkie AC, Ma LQ (2019b) Arsenic removal and biomass reduction of As-hyperaccumulator *Pteris vittata*: coupling ethanol extraction with anaerobic digestion. *Sci Total Environ* 666:205–211
- Danko DC, Bezdán D, Afshinnekoo E, Ahsanuddin S, Alicea J et al (2019) Global genetic cartography of urban metagenomes and anti-microbial resistance. *BioRxiv*. <https://doi.org/10.1101/724526>
- Dastidar A, Wang YT (2012) Modeling arsenite oxidation by chemo-autotrophic *Thiomonas arsenivorans* strain b6 in a packed-bed bioreactor. *Sci Total Environ* 432:113–121
- de Campos FV, de Oliveira JA, da Silva AA, Ribeiro C, dos Santos FF (2019) Phytoremediation of arsenite-contaminated environments: is *Pistia stratiotes* L. a useful tool? *Ecol Indic* 104:794–801
- de Souza Reis INR, Alves de Oliveira J, Ventrella MC, Otoni WC, Marinato CS, Paiva de Matos L (2020) Involvement of glutathione metabolism in *Eichhornia crassipes* tolerance to arsenic. *Plant Biol (Stuttgart, Germany)* 22(2):346–350
- Demarco CF, Afonso TF, Pieniz S, Quadro MS, de Oliveira Camargo FA, Andrezza R (2019) Phytoremediation of heavy metals and nutrients by the *Sagittaria montevidensis* into an anthropogenic contaminated site at Southern of Brazil. *Int J Phytorem* 21:1145–1152
- Demergasso CS, Chong GD, Escudero LG, Pueyo Mur JJ, Pedros-Alio C (2007) Microbial precipitation of arsenic sulfides in Andean salt flats. *Geomicrobiol J* 24:111–123
- Driehaus W, Seith R, Jekel M (1995) Oxidation of arsenate (III) with manganese oxides in water treatment. *Water Res* 29:297–305
- Eary LE (1992) The solubility of amorphous As₂S₃ from 25 to 90°C. *Geochim Cosmochim Acta* 56:2267–2280
- Engel AS, Johnson LR, Porter ML (2013) Arsenite oxidase gene diversity among Chloroflexi and Proteobacteria from El Tatio Geysers Field, Chile. *FEMS Microbiol Ecol* 83:745–756
- EU Commission regulation (EU) 2015/1006 of 25 June 2015 amending Regulation (EC) No 1881/2006 as regards maximum levels of inorganic arsenic in foodstuffs
- Eze VC, Harvey AP (2018) Extractive recovery and valorisation of arsenic from contaminated soil through phytoremediation using *Pteris cretica*. *Chemosphere* 208:484–492
- Farooq MA, Islam F, Ali B, Najeeb U, Mao B, Gill RA, Yan G, Siddique KHM, Zhou W (2016) Arsenic toxicity in plants: cellular and molecular mechanisms of its transport and metabolism. *Environ Exp Bot* 132:42–52
- Fazi S, Amalfitano S, Casentini B, Davolos D, Pietrangeli B, Crognale S et al (2016a) Arsenic removal from naturally contaminated waters: a review of methods combining chemical and biological treatments. *Rend Fis Acc Lincei* 27:51–58
- Fazi S, Crognale S, Casentini B, Amalfitano S, Lotti F, Rossetti S (2016b) The arsenite oxidation potential of native microbial communities from arsenic-rich freshwaters. *Microb Ecol* 72:25–35
- Fischer A, Manefield M, Bombach P (2016) Application of stable isotope tools for evaluating natural and stimulated biodegradation of organic pollutants in field studies. *Curr Opin Biotechnol* 41:99–107
- Flemming HC, Wingender J (2010) The biofilm matrix. *Nat Rev Microbiol* 8(9):623–633
- Francesconi K, Visoottiviseth P, Sridokchan W, Goessler W (2002) Arsenic species in an arsenic hyperaccumulating fern, *Pityrogramma calomelanos*: a potential phytoremediator of arsenic contaminated soils. *Sci Total Environ* 284:27–35
- Franchi E, Cosmina P, Pedron F, Rosellini I, Barbaferri M, Petruzzelli G, Vocciante M (2019) Improved arsenic phytoextraction by combined use of mobilizing chemicals and autochthonous soil bacteria. *Sci Total Environ* 655:328–336
- Fredette C, Comeau Y, Brisson J (2019) Ecophysiological responses of a willow cultivar (*Salix miyabeana* ‘SX67’) irrigated with treated wood leachate. *Water, Air, Soil, Pollut* 230(8):205
- Fu ZJ, Li WH, Xing XL, Xu MM, Liu XY, Li HC, Xue YD, Liu ZH, Tang JH (2016) Genetic analysis of arsenic accumulation in maize using QTL mapping. *Sci Rep* 6:21292
- Garcia-Dominguez E, Mumford A, Rhine ED, Paschal A, Young LY (2008) Novel autotrophic arsenite-oxidizing bacteria isolated from soil and sediments. *FEMS Microbiol Ecol* 66:401–410
- Garza DR, Dutilh BE (2015) From cultured to uncultured genome sequences: metagenomics and modeling microbial ecosystems. *Cell Mol Life Sci* 72:4287–4308
- Gasco G, Alvarez ML, Paz-Ferreiro J, Mendez A (2019) Combining phytoextraction by *Brassica napus* and biochar amendment for the remediation of a mining soil in Rio Tinto (Spain). *Chemosphere* 231:562–570
- Gilbert JA, Meyer F, Antonopoulos D, Balaji P, Brown CT, Brown CT et al (2010) Meeting report: The Terabase Metagenomics Workshop and the Vision of an Earth Microbiome Project. *Stand Genomic Sci* 3:243–248
- Gonzalez A, Garcia-Gonzalo P, Mar Gil-Diaz M, Alonso J, Lobo MC (2019a) Compost-assisted phytoremediation of As-polluted soil. *J Soil Sediment* 19:2971–2983
- Gonzalez H, Fernandez-Fuego D, Bertrand A, González A (2019b) Effect of pH and citric acid on the growth, arsenic accumulation, and phytochelatin synthesis in *Eupatorium cannabinum* L., a promising plant for phytostabilization. *Environ Sci Pollut R* 26:26242–26253
- Gonzalez-Martinez A, de Simon-Martin M, Lopez R, Táboas-Fernández R, Bernardo-Sánchez A (2019) Remediation of potential toxic elements from wastes and soils: analysis and energy prospects. *Sustainability* 11:3307

- Gray C, McGrath SP, Sweeney R (2005) Phytoextraction of metals: investigation of hyperaccumulation and field testing. CL: AIRE Research Project Report: RP6
- Grignet A, de Vauffleury A, Papin A, Bert V (2020) Urban soil phytomanagement for Zn and Cd in situ removal, greening, and Zn-rich biomass production taking care of snail exposure. *Environ Sci Pollut Res* 27:3187–3201
- Gude JCJ, Rietveld LC, van Halem D (2018) Biological As(III) oxidation in rapid sand filters. *J Water Process Eng* 21:107–115
- Gupta M, Sharma P, Sarin NB, Sinha AK (2009) Differential response of arsenic stress in two varieties of *Brassica juncea* L. *Chemosphere* 74:1201–1208
- Hartley-Whitaker J, Woods C, Meharg AA (2002) Is differential phytochelatin production related to decreased arsenate influx in arsenate tolerant *Holcus lanatus*? *New Phytol* 155:219–225
- Hasan HA, Abdullah SRS, Kofli NT, Kamaruddin SK (2010) Biosorption of manganese in drinking water by isolated bacteria. *J Appl Sci* 10:2653–2657
- Hassan KM, Fukuhara T, Hai FI, Bari QH, Islam KMS (2009) Development of a biophysicochemical technique for arsenic removal from groundwater. *Desalination* 249:224–229
- He J, Strezov V, Kan T, Weldekidan H, Kumar R (2019) Slow pyrolysis of metal(loid)-rich biomass from phytoextraction: characterisation of biomass, biochar and bio-oil. *Energy Procedia* 160:178–185
- Heinrich-Salmeron A, Cordi A, Halter D, Pagnout C, Abbaszadeh-fard E, Montaut D, Seby F, Bertin PN, Bauda P, Arsène-Ploetze F (2011) Unsuspected diversity of arsenite-oxidizing bacteria as revealed by widespread distribution of the *aoxB* Gene in Prokaryotes. *Appl Environ Microbiol* 77(13):4685–4692
- Hettick BE, Cañas-Carrell JE, French AD, Klein DM (2015) Arsenic: a review of the element's toxicity, plant interactions and potential methods of remediation. *J Agric Food Chem* 63:7097–7107
- Hoefst SE, Blum JS, Stolz JF, Tabita FR, Witte B, King GM, Santini JM, Oremland RS (2007) *Alkalilimnicola ehrlichii* sp. nov., a novel, arsenite-oxidizing haloalkaliphilic gammaproteobacterium capable of chemoautotrophic or heterotrophic growth with nitrate or oxygen as the electron acceptor. *Int J Syst Evol Microbiol* 57:504–512
- Huang LN, Kuang JL, Shu WS (2016) Microbial ecology and evolution in the acid mine drainage model system. *Trends Microbiol* 24:581–593
- Ike M, Miyazaki T, Yamamoto N, Sei K, Soda S (2008) Removal of arsenic from groundwater by arsenite-oxidizing bacteria. *Water Sci Technol* 58:1095–1100
- Info Terre (2017). Méthodologie nationale de gestion des sites et sols pollués. Available at <http://ssp-infoterre.brgm.fr/methodologie-nationale-gestion-sites-sols-pollues>. Accessed 24 Oct 2019
- Irem S, Islam E, Maathuis FJM, Niazi NK, Li T (2019) Assessment of potential dietary toxicity and arsenic accumulation in two contrasting rice genotypes: effect of soil amendments. *Chemosphere* 225:104–114
- Irtelli B, Nacari-Izzo F (2008) Uptake kinetics of different arsenic species by *Brassica carinata*. *Plant Soil* 303:105–113
- Ito A, Miura JI, Ishikawa N, Umita T (2012) Biological oxidation of arsenite in synthetic groundwater using immobilised bacteria. *Water Res* 46:4825–4831
- Jackson BP, Taylor VF, Karagas MR, Punshon T, Cottingham KL (2012) Arsenic, organic foods, and brown rice syrup. *Environ Health Perspect* 12:623–626
- Jain CK, Ali I (2000) Arsenic: occurrence, toxicity and speciation techniques. *Wat Res* 34:4304–4312
- Jakob R, Roth A, Haas K, Krupp EM, Raab A, Smichowski P, Gomez D, Feldmann J (2010) Atmospheric stability of arsines and the determination of their oxidative products in atmospheric aerosols (PM10): evidence of the widespread phenomena of biovolatilization of arsenic. *J Environ Monit* 12:409–416
- Jankong P, Visoottiviseth P, Khokiattiwong S (2007) Enhanced phytoremediation of arsenic contaminated land. *Chemosphere* 68:1906–1912
- Janssen J, Weyens N, Croes S, Beckers B, Meiresonne L, Van Peteghem P, Carleer R, Vangronsveld J (2015) Phytoremediation of metal contaminated soil using willow: exploiting plant-associated bacteria to improve biomass production and metal uptake. *Int J Phytorem* 17:1123–1136
- Jebelli MA, Maleki A, Amoozegar MA, Kalantar E, Gharibi F, Darvish N, Tashayoe H (2018) Isolation and identification of the native population bacteria for bioremediation of high levels of arsenic from water resources. *J Environ Manage* 212:39–45
- Jiang Y, Lei M, Duan L, Longhurst P (2015) Integrating phytoremediation with biomass valorisation and critical element recovery: a UK contaminated land perspective. *Biomass Bioenergy* 83:328–339
- Jiang H, Zhao X, Fang J, Xiao Y (2018) Physiological responses and metal uptake of *Miscanthus* under cadmium/arsenic stress. *Environ Sci Pollut Res* 25:28275–28284
- Kadnikov VV, Ivashenko DA, Beletsky AV, Mardanov AV, Danilova EV, Pimenov NV, Karnachuk OV, Ravin NV (2016) A novel uncultured bacterium of the family Gallionellaceae: Description and genome reconstruction based on the metagenomic analysis of microbial community in acid mine drainage. *Mikrobiologiya* 85(4):421–435
- Kamei-Ishikawa N, Segawa N, Yamazaki D, Ito A, Umita T (2017) Arsenic removal from arsenic-contaminated water by biological arsenite oxidation and chemical ferrous iron oxidation using a down-flow hanging sponge reactor. *Water Sci Technol* 17:1249–1259
- Karczewska A, Lewińska K, Gałka B (2013) Arsenic extractability and uptake by velvet grass *Holcus lanatus* and ryegrass *Lolium perenne* in variously treated soils polluted by tailing spills. *J Hazard Mater* 262:1014–1021
- Karimi N, Soury Z (2016) Antioxidant enzymes and compounds complement each other during arsenic detoxification in shoots of *Isatis cappadocica* Desv. *Chem Ecol* 32:937–951
- Karimi N, Ghaderian SM, Raab A, Feldmann J, Meharg AA (2009) An arsenic accumulating, hyper-tolerant brassica, *Isatis cappadocica* Desv. *New Phytol* 184:41–47
- Karnachuk OV, Frank YA, Lukina AP, Kadnikov VV, Beletsky AV, Mardanov AV, Ravin NV (2019) Domestication of previously uncultivated *Candidatus Desulfurudis audaxviator* from a deep aquifer in Siberia sheds light on its physiology and evolution. *ISME J* 13(8):1947–1959
- Katsoyiannis IA, Zouboulis AI (2004) Application of biological processes for the removal of arsenic from groundwaters. *Water Res* 38:17–26
- Katsoyiannis IA, Zouboulis AI, Althoff H, Bartel H (2002) As(III) removal from groundwater using fixed-bed upflow bioreactors. *Chemosphere* 47(3):325–332
- Katsoyiannis IA, Zouboulis AI, Jekel M (2004) Kinetics of bacterial As(III) oxidation and subsequent As(V) removal by sorption onto biogenic manganese oxides during groundwater treatment. *Ind Eng Chem Res* 43:486–493
- Katsoyiannis IA, Hug SJ, Amman A, Zikoudi A, Hatziliontos C (2007) Arsenic speciation and uranium concentrations in drinking water supply wells in Northern Greece: correlations with redox indicative parameters and implications for groundwater treatment. *Sci Total Environ* 383:128–140
- Kertulis-Tartar GM, Ma LQ, Tu C, Chirenje T (2006) Phytoremediation of an arsenic-contaminated site using *Pteris vittata* L.: a two year study. *Int J Phytorem* 8:311–322

- Kidd P, Mench M, Álvarez-López V, Bert V, Dimitriou I, Friesl-Hanl W, Herzig R, Janssen JO, Kolbas A, Müller I, Neu S, Renella G, Ruttens A, Vangronsveld J, Puschenreiter M (2015) Agronomic practices for improving gentle remediation of trace-element-contaminated soils. *Int J Phytorem* 17:1005–1037
- Kim MJ, Nriangu J (2000) Oxidation of arsenite in groundwater using ozone and oxygen. *Sci Total Environ* 247:71–79
- Kim MS, Min HG, Lee SH, Kim JG (2018) A Comparative study on Poaceae and Leguminosae forage crops for aided phytostabilization in trace-element-contaminated soil. *Agronomy-Basel* 8:105
- Koehler S, Cleiss J, Proux C, Sismeiro O, Dillies MA, Goulhen-Chollet F, Hommais F, Lièvreumont D, Arsène-Ploetze F, Coppée JY, Bertin PN (2010) Multiple controls affect arsenite oxidase gene expression in *Herminiimonas arsenicoxydans*. *BMC Microbiol* 10:53
- Koehler S, Plewniak F, Barbe V, Battaglia-Brunet F, Jost B, Joulain C, Philipps M, Vicaire S, Vincent S, Ye T, Bertin PN (2013) Genome sequence of *Halomonas* sp. strain A3H3, isolated from arsenic-rich marine sediments. *Genome Announc* 1(5):e00819-13
- Koehler S, Arsène-Ploetze F, Brochier C, Cholet F, Jost B, Lièvreumont D, Plewniak F, Philipps M, Salmeron A, Bertin PN, Lett MC (2015) Constitutive arsenite oxidase expression detected in the arsenic hypertolerant *Pseudomonas xanthomarina* S11. *Res Microbiol* 166:205–214
- Kofronova M, Maskova P, Lipavska H (2018) Two facets of world arsenic problem solution: crop poisoning restriction and enforcement of phytoremediation. *Planta* 248:19–35
- Kruger MC, Bertin PN, Heipieper HJ, Arsène-Ploetze F (2013) Bacterial metabolism of environmental arsenic—mechanisms and biotechnological applications. *Appl Microbiol Biotechnol* 97:3827–3841
- Krüger A, Schäfers C, Schröder C, Antranikian G (2018) Towards a sustainable biobased industry – highlighting the impact of extremophiles. *New Biotechnol* 40:144–153
- Kulp TR, Hoefft SE, Asao M, Madigan TM, Hollibaugh JT, Fisher JC, Stolz JF, Culbertson CW, Miller LG, Oremland SR (2008) Arsenic(III) fuels anoxygenic photosynthesis in hot spring biofilms from Mono Lake, California. *Science* 321:967–970
- Kumpiene J, Antelo J, Brännvall E, Carabante I, Ek K, Komárek M, Söderberg C, Wårell L (2019) In situ chemical stabilization of trace element-contaminated soil - field demonstrations and barriers to transition from laboratory to the field - A review. *Appl Geochem* 100:335–351
- Kumpiene J, Carabante I, Kasiuliene A, Austruy A, Mench M (2021) Long-term stability of arsenic in iron-amended contaminated soils. *Environ Pollut* 269:116017
- Lami R, Jones LC, Cottrell MT, Lafferty BJ, Ginder-Vogel M, Sparks DL, Kirchman DL (2013) Arsenite modifies structure of soil microbial communities and arsenite oxidation potential. *FEMS Microbiol Ecol* 84:270–279
- Land M, Hauser L, Jun SR, Nookaew I, Leuze MR, Ahn TH et al (2015) Insights from 20 years of bacterial genome sequencing. *Funct Integr Genomics* 15:141–161
- Le Pape P, Battaglia-Brunet F, Parmentier M, Joulain C, Gassaud C, Fernandez-Rojo L, Guigner JM, Ikogou M, Stetten L, Olivi L, Casiot C, Morin G (2017) Complete removal of arsenic and zinc from a heavily contaminated acid mine drainage via an indigenous SRB consortium. *J Hazard Mater* 321:764–772
- Li H, Zeng XC, He Z, Chen X, Guoji E, Han Y et al (2016) Long-term performance of rapid oxidation of arsenite in simulated groundwater using a population of arsenite-oxidizing microorganisms in a bioreactor. *Water Res* 101:393–401
- Li CI, Samuels DC, Zhao YY, Shyr Y, Guo Y (2017) Power and sample size calculations for high-throughput sequencing-based experiments. *Brief Bioinform* 5:1752–1779
- Li JX, Chen JB, Chen S (2018a) Supercritical water treatment of heavy metal and arsenic metalloids-bioaccumulating-biomass. *Ecotox Environ Safe* 157:102–110
- Li B, Gu B, Yang ZG (2018b) The role of submerged macrophytes in phytoremediation of arsenic from contaminated water: a case study on *Vallisneria natans* (Lour.) Hara. *Ecotox Environ Safe* 165:224–231
- Li B, Wang JC, Yao LR, Meng Y, Ma X, Si E, Ren P, Yang K, Shang X, Wang H (2019a) Halophyte *Halogeton glomeratus*, a promising candidate for phytoremediation of heavy metal-contaminated saline soils. *Plant Soil* 442:323–331
- Li B, Zhou S, Wei DN, Long JM, Peng L, Tie BQ, Williams PN, Lei M (2019b) Mitigating arsenic accumulation in rice (*Oryza sativa* L.) from typical arsenic contaminated paddy soil of southern China using nanostructured α -MnO₂: pot experiment and field application. *Sci Total Environ* 650:546–556
- Liu A, Garcia-Dominguez E, Rhine ED, Young LY (2004) A novel arsenate respiring isolate that can utilize aromatic substrates. *FEMS Microbiol Ecol* 48:323–332
- Liu S, Zhang F, Chen J, Sun G (2011) Arsenic removal from contaminated soil via biovolatilization by genetically engineered bacteria under laboratory conditions. *J Environ Sci* 23:1544–1550
- Liu X, Feng HY, Fu JW, Sun D, Cao Y, Chen YS, Xiang P, Liu Y, Ma LQ (2018) Phytate promoted arsenic uptake and growth in arsenic-hyperaccumulator *Pteris vittata* by upregulating phosphorus transporters. *Environ Pollut* 241:240–246
- Lloyd JR (2010) Microbial transformations of arsenic in aquifers. In: Sun H (ed) *Biological chemistry of arsenic, antimony and bismuth*, vol 6. Wiley, Chichester, pp 135–143
- Lovley DR (2003) Cleaning up with genomics: applying molecular biology to bioremediation. *Nat Rev Microbiol* 1:35–44
- Lu X, Zhang Y, Liu C, Wu M, Wang H (2018) Characterization of the antimoniite- and arsenite-oxidizing bacterium *Bosea* sp. AS-1 and its potential application in arsenic removal. *J Hazard Mater* 359:527–534
- Ma J, Lei E, Lei M, Liu YH, Chen TB (2018) Remediation of arsenic contaminated soil using malposed intercropping of *Pteris vittata* L. and maize. *Chemosphere* 194:737–744
- Machado H, Tuttle RN, Jensen PR (2017) Omics-based natural product discovery and the lexicon of genome mining. *Curr Op Microbiol* 39:136–142
- Macy JM, Santini JM, Pauling BV, O'Neill AH, Sly LI (2000) Two new arsenate/sulfate-reducing bacteria: mechanisms of arsenate reduction. *Arch Microbiol* 173:49–57
- Madsen EL (2011) Microorganisms and their roles in fundamental biogeochemical cycles. *Curr Op Biotechnol* 22:456–464
- Mandal D, Bolander ME, Mukhopadhyay D, Sarkar G, Mukherjee P (2006) The use of microorganisms for the formation of metal nanoparticles and their application. *Appl Microbiol Biotechnol* 69:485–492
- Manjón I, Ramírez-Andreotta MA (2020) A dietary assessment tool to estimate arsenic and cadmium exposures from locally grown foods. *Environ Geochem Health* 42:2121–2135
- Marchant BP, Saby NPA, Arrouays D (2017) A survey of topsoil arsenic and mercury concentrations across France. *Chemosphere* 181:635–644
- Matzen S, Fakra S, Nico P, Pallud C (2020) *Pteris vittata* arsenic accumulation only partially explains soil arsenic depletion during field-scale phytoextraction. *Soil Syst* 4:71
- McBride BC, Wolfe RS (1971) Biosynthesis of dimethylarsine by a methanobacterium. *Biochemistry* 10:4312–4317
- Mench M, Bussièr S, Boisson J, Castaing E, Vangronsveld J, Ruttens A, De Koe T, Bleeker P, Assunção A, Manceau A (2003a) Progress in remediation and revegetation of the barren Jales gold mine spoil after in situ treatments. *Plant Soil* 249:187–202

- Mench M, Bert V, Schwitzguébel JP, Lepp N, Schröder P, Gawronski S, Vangronsveld J (2010) Successes and limitations of phytotechnologies at field scale: outcomes, assessment and outlook from COST Action 859. *J Soil Sediment* 10:1039–1070
- Mench M, Galende M, Marchand L, Kechit F, Carrier M, Loppinet-Serani A, Caille N, Zhao FJ, Vangronsveld J (2014) Arsenic phytoextraction by *Pteris vittata* L. and frond conversion by solvolysis: an integrated gentle remediation option for restoring ecosystem services in line with the biorefinery and the bio-economy. In: Litter, Nicolli, Meichtry, Quici, Bundschuh, Bhattacharya, Naidu (eds) One century of the discovery of Arsenicosis in Latin America (1914–2014). Taylor & Francis Group, London, pp 836–838
- Mench M, Guinberteau J, Recalde N (2003b) Ectomycorrhizal fungi in the contaminated Jales soil after in situ treatment and phytostabilisation. pp. 180–181 In Conf. Proc. 7th ICOBTE, G.R. Gobran and N. Lepp (eds.), Vol. 1, Scientific programs II, SLU, Uppsala, Sweden. ISBN 91–576–6582–6
- Michel C, Jean M, Coulon S, Dictor MC, Delorme F, Morin D et al (2007) Biofilms of As(III)-oxidising bacteria: formation and activity studies for bioremediation process development. *Appl Microbiol Biotechnol* 77:457–467
- Michon J, Dagot C, Deluchat V, Dictor MC, Battaglia-Brunet F, Baudu M (2010) As(III) biological oxidation by CAsO1 consortium in fixed-bed reactors. *Process Biochem* 45:171–178
- Mitchell AL, Scheremetjew M, Denise H, Potter S, Tarkowska A, Qureshi M et al (2017) EBI Metagenomics in 2017: enriching the analysis of microbial communities, from sequence reads to assemblies. *Nucleic Acids Res* 46(D1):D726–D735
- Mohan D, Pittman CU (2007) Arsenic removal from water/wastewater using adsorbents—a critical review. *J Hazard Mater* 142:1–53
- Molin M, Ulven SM, Meltzer HM, Alexander J (2015) Arsenic in the human food chain, biotransformation and toxicology—review focusing on seafood arsenic. *J Trace Elem Med Biol* 31:249–259
- Mu J, Hu Z, Huang L, Tang S, Holm PE (2019) Influence of alkaline silicon-based amendment and incorporated with biochar on the growth and heavy metal translocation and accumulation of vetiver grass (*Vetiveria zizanioides*) grown in multi-metal-contaminated soils. *J Soil Sediment* 19:2277–2289
- Mukherjee S, Stamatis D, Bertsch J, Ovchinnikova G, Katta HY, Mojica A, Chen IA, Kyripides NC, Reddy TBK (2018) Genomes OnLine Database (GOLD) vol 7: updates and new features. *Nucl Acids Res* 47:D649–D659
- Muller D, Lièvremon D, Simeonova DD, Hubert JC, Lett M (2003) Arsenite oxidase *aox* genes from a metal-resistant β -proteobacterium. *J Bacteriol* 185:135–141
- Muller D, Médigue C, Koechler S, Barbe V, Barakat M, Talla E et al (2007) A tale of two oxidation states : bacterial colonization of arsenic-rich environments. *PLoS Genet* 3:e53
- Musat N, Musat F, Weber PK, Pett-Ridge J (2016) Tracking microbial interactions with NanoSIMS. *Curr Opin Biotechnol* 41:114–121
- Nandillon R, Lebrun M, Miard F, Gaillard M, Sabatier S, Villar M, Bourgerie S, Morabito D (2019) Capability of amendments (biochar, compost and garden soil) added to a mining technosol contaminated by Pb and As to allow poplar seed (*Populus nigra* L.) germination. *Environ Monit Assess* 191:465
- Navazas A, Hendrix S, Cuyper A, Gonzalez A (2019) Integrative response of arsenic uptake, speciation and detoxification by *Salix atrocinerea*. *Sci Total Environ* 689:422–433
- Newman DK, Kennedy EK, Coates JD, Ahmann D, Ellis DJ, Lovley DR, Morel FMM (1997a) Dissimilatory arsenate and sulphate reduction in *Desulfotomaculum auripigmentum* sp. nov. *Arch Microbiol* 168:380–388
- Newman DK, Beveridge TJ, Morel FMM (1997b) Precipitation of arsenic trisulfide by *Desulfotomaculum auripigmentum*. *Appl Environ Microbiol* 63:2022–2028
- Ng KS, Ujang Z, Le-Clech P (2004) Arsenic removal technologies for drinking water treatment. *Rev Environ Sci Biotechnol* 3:43–53
- Nguyen VK, Tran HT, Park Y, Yu J, Lee T (2017) Microbial arsenite oxidation with oxygen, nitrate, or an electrode as the sole electron acceptor. *J Ind Microbiol Biotechnol* 44:857–868
- Niazi NK, Singh B, Van Zwieten L, Kachenko AG (2012) Phytoremediation of an arsenic-contaminated site using *Pteris vittata* L. and *Pityrogramma calomelanos* var. *austroamericana*: a long-term study. *Environ Sci Pollut R* 19:3506–3515
- Nicomel NR, Leus K, Folens K, Van Der Voort P, Du Laing G (2016) Technologies for arsenic removal from water: current status and future perspectives. *Int J Environ Res Public Health* 13:1–24
- Nordstrom DK (2002) Public health—worldwide occurrences of arsenic in groundwater. *Science* 296:2143–2145
- Nzihou A, Stanmore B (2013) The fate of heavy metals during combustion and gasification of contaminated biomass—A brief review. *J Hazard Mater* 256:56–66
- O'Connor D, Peng T, Zhang J, Tsang DCW, Alessi DS, Shen Z, Bolan NS, Houa D (2018) Biochar application for the remediation of heavy metal polluted land: a review of in situ field trials. *Sci Total Environ* 619–620:815–826
- Omeregbe EO, Couture R, Van Cappellen P, Corkhill CL, Charnock JM, Polya DA et al (2013) Arsenic bioremediation by biogenic iron oxides and sulfides. *Appl Environ Microbiol* 79:4325–4335
- Ospino MC, Kojima H, Fukui M (2019) Arsenite oxidation by a newly isolated Betaproteobacterium possessing *ars* genes and diversity of the *ars* gene cluster in bacterial genomes. *Front Microbiol* 10:1210
- Otones V, Álvarez-Ayuso E, García-Sánchez A, Santa Regina I, Murciego A (2011) Mobility and phytoavailability of arsenic in an abandoned mining area. *Geoderma* 166:153–161
- Overmann J, Abt B, Sikorski J (2017) Present and future of culturing bacteria. *Annu Rev Microbiol* 71:711–730
- Pan P, Lei M, Qiao P, Zhou G, Wan XM, Chen TB (2019) Potential of indigenous plant species for phytoremediation of metal(loid)-contaminated soil in the Baoshan mining area, China. *Environ Sci Pollut Res* 26:23583–23592
- Pandey J, Verma RK, Singh S (2019) Suitability of aromatic plants for phytoremediation of heavy metal contaminated areas: a review. *Int J Phytorem* 21:405–418
- Pardo J, Mondaca P, Celis-Diez JL, Ginocchio R, Navarro-Villarroel C, Neaman A (2018) Assessment of revegetation of an acidic metal(loid)-polluted soils six years after the incorporation of lime with and without compost. *Geoderma* 331:81–86
- Pasolli E, Truong DT, Malik F, Waldron L, Segata N (2016) Machine learning meta-analysis of large metagenomic datasets: tools and biological insights. *PLoS Comput Biol* 12:e1004977
- Paul T, Chakraborty A, Islam E, Mukherjee SK (2018) Arsenic bioremediation potential of arsenite-oxidizing *Micrococcus* sp. KUMAs15 isolated from contaminated soil. *Pedosphere* 28(2):299–310
- Picco P, Hasuoka P, Verni E, Savio M, Pacheco P (2019) Arsenic species uptake and translocation in *Elodea canadensis*. *Int J Phytorem* 21:693–698
- Pidlisnyuk V, Erickson L, Stefanovska T, Popelka J, Hettiarachchi G, Davis L, Trögl J (2019) Potential phytomanagement of military polluted sites and biomass production using biofuel crop *Miscanthus x giganteus*. *Environ Pollut* 249:330–337
- Plewniak F, Koechler S, Navet B, Dugat-Bony E, Bouchez O et al (2013) Metagenomic insights into microbial metabolism affecting arsenic dispersion in Mediterranean marine sediments. *Mol Ecol* 22:4870–4883

- Plewniak F, Crognale S, Rossetti S, Bertin PN (2018) A genomic outlook on bioremediation: the case of arsenic removal. *Front Microbiol* 9:820
- Plewniak F, Koechler S, Le Paslier D, Héry M, Bruneel O, Bertin PN (2020) In situ metabolic activities of uncultivated *Ferrovum* sp. CARN8 evidenced by metatranscriptomic analysis. *Res Microbiol* 171:37–43
- Plewniak F, Crognale S, Bruneel O, Sismeiro O, Coppée J-Y, Rossetti S, Bertin P (2021) Metatranscriptomic outlook on green and brown food webs in acid mine drainage. *Environ Microbiol Rep* 13(5):606–615
- Potdukhe RM, Bedi P, Sarangi BK, Pandey RA, Thul ST (2018) Root transcripts associated with arsenic accumulation in hyperaccumulator *Pteris vittata*. *J Biosciences* 43:105–115
- Pous N, Casentini B, Rossetti S, Fazi S, Pug S, Aulenta F (2015) Anaerobic arsenite oxidation with an electrode serving as the sole electron acceptor: a novel approach to the bioremediation of arsenic-polluted groundwater. *J Hazard Mater* 283:617–622
- Prasad KS, Ramanathan AL, Paul J, Subramanian V, Prasad R (2013) Biosorption of arsenite (As(3)) and arsenate (As(5)) from aqueous solution by *Arthrobacter* sp. *Biomass Environ Technol* 34(17–20):2701–2708
- Praveen A, Mehrotra S, Singh N (2019) Mixed plantation of wheat and accumulators in arsenic contaminated plots: a novel way to reduce the uptake of arsenic in wheat and load on antioxidative defence of plant. *Ecotox Environ Safe* 182:109462
- Purdy JJ, Smart LB (2008) Hydroponic screening of shrub willow (*Salix* spp.) for arsenic tolerance and uptake. *Int J Phytorem* 10:515–528
- Quéménéur M, Heinrich-Salmeron A, Muller D, Lièvremon D, Jauzein M, Bertin PN, Garrido F, Joulain C (2008) Diversity surveys and evolutionary relationships of *aoxB* genes in aerobic arsenite-oxidizing bacteria. *Appl Environ Microbiol* 74:4567–4573
- Quéménéur M, Cébron A, Billard P, Battaglia-Brunet F, Garrido F, Leyval C, Joulain C (2010) Population structure and abundance of arsenite-oxidizing bacteria along an arsenic pollution gradient in waters of the upper isle river basin, France. *Appl Environ Microbiol* 76:4566–4570
- Rahman MA, Hasegawa H (2011) Aquatic arsenic: phytoremediation using floating macrophytes. *Chemosphere* 83:633–646
- Rahman S, Kim KH, Saha SK, Swaraz AM, Paul DK (2014) Review of remediation techniques for arsenic (As) contamination: a novel approach utilizing bio-organisms. *J Environ Manag* 134:175–185
- Rahman F, Sugawara K, Huang Y, Chien MF, Inoue C (2018) Arsenic, lead and cadmium removal potential of *Pteris multifida* from contaminated water and soil. *Int J Phytorem* 20:1187–1193
- Rai PK (2019) Heavy metals/metalloids remediation from wastewater using free floating macrophytes of a natural wetland. *Environ Technol Inno* 15:100393
- Rashid M, Stingl U (2015) Contemporary molecular tools in microbial ecology and their application to advancing biotechnology. *Biotechnol Adv* 33:1755–1773
- Raza A, Khan AHA, Nawaz I, Qu Z, Yousaf S, Ali MA, Sayal AU, Iqbal M (2019) Evaluation of arsenic-induced stress in *Dahlia pinnata* Cav.: morphological and physiological response. *Soil Sediment Contam* 28:716–728
- Reichmann KG, Gravel MR, Burren BG, Mayer DG, Wright CL (2004) Bioremediation of soil arsenic at a contaminated site using *Pteris vittata*. In: Proceedings of the 25th Biennial Conference of the Australian Society of Animal Production, vol 25. University of Melbourne, Collingwood, pp 305
- Reimann C, Négrel P, Ladenberger A, Birke M, Filzmoser P, O'Connor P, Demetriades A (2017) Comment on “Maps of heavy metals in the soils of the European Union and proposed priority areas for detailed assessment” by Tóth, G., Hermann, T., Sztatmári, G., Pásztor, L. *Sci Total Environ* 578:236–241
- Renella G, Landi L, Ascher J, Ceccherini MT, Pietramellara G, Mench M (2008) Long-term effects of aided phytostabilisation of trace elements on microbial biomass and activity, enzyme activities, and composition of microbial community in the Jales contaminated mine spoils. *Environ Pollut* 152:702–712
- Roman-Ponce B, Ramos-Garza J, Arroyo-Herrera I, Maldonado-Hernandez J, Bahena-Osorio Y, Vasquez-Murrieta MS, Wang ET (2018) Mechanism of arsenic resistance in endophytic bacteria isolated from endemic plant of mine tailings and their arsenophore production. *Arch Microbiol* 200:883–895
- Roy M, Giri AK, Dutta S, Mukherjee P (2015) Integrated phytobial remediation for sustainable management of arsenic in soil and water. *Environ Int* 75:180–198
- Roychowdhury R, Roy M, Rakshit A, Sarkar S, Mukherjee P (2018) Arsenic bioremediation by indigenous heavy metal resistant bacteria of fly ash pond. *Bull Environ Contam Toxicol* 101:527–535
- Ruppert L, Lin ZQ, Dixon RP, Johnson KA (2013) Assessment of solid phase microfiber extraction fibers for the monitoring of volatile organoarsinicals emitted from a plant–soil system. *J Hazard Mater* 262:1230–1236
- Sakakibara M, Watanabe A, Inoue M, Sano S, Kaise T (2010) Phytoextraction and phytovolatilization of arsenic from As-contaminated soils by *Pteris vittata*. Proceedings of the Annual International Conference on Soils, Sediments, Water and Energy 12, Article 26
- Salido A, Hasty KL, Lim J, Butcher DJ (2003) Phytoremediation of arsenic and lead in contaminated soil using Chinese brake fern (*Pteris vittata*) and Indian mustard (*Brassica juncea*). *Int J Phytorem* 5:89–103
- Saltikov CW, Newman DK (2003) Genetic identification of a respiratory arsenate reductase. *Proc Natl Acad Sci USA* 100:10983–10988
- Sandhi A, Landberg T, Greger M (2018) Effect of pH, temperature, and oxygenation on arsenic phytofiltration by aquatic moss (*Warnstorfia fluitans*). *J Environ Chem Eng* 6:3918–3925
- Santini JM, Sly LI, Schnagl RD, Macy JM (2000) A new chemolithoautotrophic arsenite-oxidizing bacterium isolated from a gold mine: phylogenetic, physiological, and preliminary biochemical studies. *Appl Environ Microbiol* 66:1–7
- Satinsky BM, Gifford SM, Crump BC, Moran MA (2013) Use of internal standards for quantitative metatranscriptome and metagenome analysis. *Methods Enzymol* 531:237–250
- Satyapal GK, Mishra SK, Srivastava A, Ranjan RK, Prakash K, Haque R, Kumar N (2018) Possible bioremediation of arsenic toxicity by isolating indigenous bacteria from the middle Gangetic plain of Bihar, India. *Biotechnol Rep* 17:117–125
- Serrano J, Leiva E (2017) Removal of arsenic using acid/metal-tolerant sulfate reducing bacteria: a new approach for bioremediation of high-arsenic acid minewaters. *Water* 9:994
- Sghaier DB, Pedro S, Duarte B, Caçador I, Sleimi N (2019) Arsenic tolerance mechanisms in halophytes: the case of *Tamarix gallice*. In: Hasanuzzaman M, Shabala S, Fujita M (eds) Halophytes and climate change: adaptive mechanisms and potential uses. CABI publisher, pp 255–265
- Shelmerdine PA, Black CR, McGrath SP, Young SD (2009) Modelling phytoremediation by the hyperaccumulating fern, *Pteris vittata*, of soils historically contaminated with arsenic. *Environ Pollut* 157:1589–1596
- Sher S, Rehman A (2019) Use of heavy metals resistant bacteria—a strategy for arsenic bioremediation. *Appl Microbiol Biotechnol* 103:6007–6021
- Simeonova DD, Micheva K, Muller DAE, Lagarde F, Lett MC, Groudeva VI et al (2005) Arsenite oxidation in batch reactors with alginate-immobilized ULPAs1 strain. *Biotechnol Bioeng* 91(4):441–446

- Singh R, Singh S, Parihar P, Singh VP, Prasad SM (2015) Arsenic contamination, consequences and remediation techniques: a review. *Ecotox Environ Safe* 112:247–270
- Smiedja JA, Wilkin R (2003) Preservation of sulfidic waters containing dissolved As(III). *J Environ Monit* 5:913–916
- Souri Z, Karimi N, Farooq MA, Sandalio LM (2020) Nitric oxide improves tolerance to arsenic stress in *Isatis cappadocica* desv. shoots by enhancing antioxidant defenses. *Chemosphere* 239:124523
- Souza TD, Borges AC, Braga AF, Veloso RW, Teixeira de Matos A (2019) Phytoremediation of arsenic-contaminated water by *Lemna valdiviana*: An optimization study. *Chemosphere* 23:402–408
- Stackebrandt E, Schumann P, Schüler E, Hippe H (2003) Reclassification of *Desulfotomaculum auripigmentum* as *Desulfosporosinus auripigmenti* corrig., comb. nov. *Int J Syst Evol Microbiol* 53:1439–1443
- Stenuit B, Eyers L, Schuler L, Agathos SN, George I (2008) Emerging high-throughput approaches to analyze bioremediation of sites contaminated with hazardous and/or recalcitrant wastes. *Biotechnol Adv* 26:561–575
- Sultana M, Vogler S, Zargar K, Schmidt AC, Saltikov C, Seifert J, Schlömann M (2012) New clusters of arsenite oxidase and unusual bacterial groups in enrichments from arsenic contaminated soil. *Arch Microbiol* 194:623–635
- Tan S, Liu J, Fang Y, Hedlund BP, Lian ZH, Huang LY, Li JT, Huang LN, Li WJ, Jiang HC, Dong HL, Shu WS (2019) Insights into ecological role of a new deltaproteobacterial order *Candidatus Acidulodesulfobacterales* by metagenomics and metatranscriptomics. *ISME J* 13:2044–2057
- Tani Y, Miyata N, Ohashi M, Ohnuki T, Seyama H, Iwahori K, Soma M (2004) Interaction of inorganic arsenic with biogenic manganese oxide produced by a Mn-oxidizing fungus, strain KR21-2. *Environ Sci Technol* 38(24):6618–6624
- Tassé N, Isabel D, Fontaine R (2003) Wood Cadillac Tailings: designing a biofilter for arsenic control. In “Proceedings of the Sudbury Mining and the Environment Conference”, Sudbury, ON, Canada
- Techtmann SM, Hazen TC (2016) Metagenomic applications in environmental monitoring and bioremediation. *J Ind Microbiol Biotechnol* 43:1345–1354
- Teeling H, Glöckner FO (2012) Current opportunities and challenges in microbial metagenome analysis - a bioinformatic perspective. *Brief Bioinform* 13:728–742
- Thakur S, Choudhary S, Dubey P, Bhardwaj P (2019) Comparative transcriptome profiling reveals the reprogramming of gene networks under arsenic stress in Indian mustard. *Genome* 62(12):833–847
- Thakur S, Choudhary S, Majeed A, Singh A, Bhardwaj P (2020) Insights into the molecular mechanism of arsenic phytoremediation. *J Plant Growth Regul* 39:532–543
- Thomas T, Gilbert J, Meyer F (2012) Metagenomics - a guide from sampling to data analysis. *Microb Infor Exper* 2:3
- Thompson LR, Sanders JG, McDonald D, Amir A, Ladau J, Locey KJ et al (2017) A communal catalogue reveals Earth’s multiscale microbial diversity. *Nature* 551:457
- Thul ST, Nigam B, Tiwari S, Pandey RA (2019) Arsenite-oxidation performance of microbes from abandoned iron ore mine. *Indian J Biotechnol* 18:34–41
- Tóth G, Hermann T, Da Silva MR, Montanarella L (2016) Heavy metals in agricultural soils of the European Union with implications for food safety. *Environ Int* 88:299–309
- Triptahti RD, Tripathi P, Dwiwedi S, Dubey S, Chatterjee S, Chakrabarty D, Trivedi PK (2012) Arsenomics: omics of arsenic metabolism in plants. *Front Physiol* 3:275
- Tyson GW, Lo I, Baker BJ, Allen EE, Hugenholtz P, Banfield JF (2005) Genome-directed isolation of the key nitrogen fixer *Leptospirillum ferrodiazotrophum* sp. nov. from an acidophilic microbial community. *Appl Environ Microbiol* 71:6319–6324
- Ullrich SR, Poehlein A, Tischler JS, González C, Ossandon FJ, Daniel R, Holmes DS, Schlömann M, Mühling M (2016) Genome analysis of the biotechnologically relevant acidophilic iron oxidising strain JA12 indicates phylogenetic and metabolic diversity within the novel genus “*Ferrofum*”. *PLoS ONE* 11(1):e0146832
- Upadhyay MK, Yadav P, Shukla A, Srivastava S (2018) Utilizing the potential of microorganisms for managing arsenic contamination: a feasible and sustainable approach. *Front Environ Sci* 6:24
- Vallenet D, Calteau A, Cruveiller S, Gachet M, Lajus A et al (2017) MicroScope in 2017: an expanding and evolving integrated resource for community expertise of microbial genomes. *Nucl Acids Res* 45:D517–D528
- Vamerali T, Bandiera M, Coletto L, Zanetti F, Dickinson NM, Mosca G (2009) Phytoremediation trials on metal- and arsenic-contaminated pyrite wastes (Torviscosa, Italy). *Environ Pollut* 157:887–894
- van den Ent A, Baker AJM, Reeves RD, Pollard AJ, Schat H (2013) Hyperaccumulators of metal and metalloid trace elements: facts and fiction. *Plant Soil* 362:319–334
- Vanden Hoven RN, Santini JM (2004) Arsenite oxidation by the heterotroph *Hydrogenophaga* sp. str. NT-14: the arsenite oxidase and its physiological electron acceptor. *Biochim Biophys Acta Bioenerg* 1656:148–155
- Vanlop T, Netnapid T, Chatpet Yossapol CHL, Wanpen W, Surapol P (2019) Role of *Colocasia esculenta* L. schott in arsenic removal by a pilot-scale constructed wetland filled with laterite soil. *Heliyon* 5:e01233
- Vega AS, Planer-Friedrich B, Pastén PA (2017) Arsenite and arsenate immobilization by preformed and concurrently formed disorder mackinawite (FeS). *Chem Geol* 475:62–75
- Vitkova M, Puschenreiter M, Komarek M (2018) Effect of nano zero-valent iron application on As, Cd, Pb, and Zn availability in the rhizosphere of metal(loid) contaminated soils. *Chemosphere* 200:217–226
- Vogt C, Dorer C, Musat F, Richnow HH (2016) Multi-element isotope fractionation concepts to characterize the biodegradation of hydrocarbons — from enzymes to the environment. *Curr Opin Biotechnol* 41:90–98
- Vromman D, Martinez JP, Kumar M, Šlejkovec Z, Lutts S (2018) Comparative effects of arsenite (As(III)) and arsenate (As(V)) on whole plants and cell lines of the arsenic-resistant halophyte plant species *Atriplex atacamensis*. *Environ Sci Pollut Res* 25:34473–34486
- Wan J, Klein J, Simon S, Joulain C, Dictor MC, Deluchat V et al (2010) As(III) oxidation by *Thiomonas arsenivorans* in up-flow fixed-bed reactors coupled to As sequestration onto zero-valent iron-coated sand. *Water Res* 44:5098–5108
- Wan XM, Yang JX, Lei M (2018) Speciation and uptake of antimony and arsenic by two populations of *Pteris vittata* L. and *Holcus lanatus* L. from co-contaminated soil. *Environ Sci Pollut Res* 25:32447–32457
- Wang S, Mulligan CN (2006) Effect of natural organic matter on arsenic release from soil and sediments into groundwater. *Environ Geochem Health* 28:197–214
- Wang S, Zhao X (2009) On the potential of biological treatment for arsenic contaminated soils and groundwater. *J Environ Manag* 90:2367–2376
- Wang L, Hu Y, Liu R, Sun W (2017) A review on in situ phytoremediation of mine tailings. *Chemosphere* 184:594–600
- Wang C, Na G, Bermejo ES, Chen Y, Banks JA, Salt DE, Zhao FJ (2018a) Dissecting the components controlling root-to-shoot arsenic translocation in *Arabidopsis thaliana*. *New Phytol* 217:206–218

- Wang H, Zeng Y, Guo C, Bao Y, Lu G, Reinfelder JR, Dang Z (2018b) Bacterial, archaeal, and fungal community responses to acid mine drainage-laden pollution in a rice paddy soil ecosystem. *Sci Tot Environ* 616–617:107–116
- Wang S, Wang J, Li JM, Hou Y, Shi L, Lian CL, Shen ZG, Chen Y (2021) Evaluation of biogas production potential of trace element-contaminated plants via anaerobic digestion. *Ecotoxicol Environ Saf* 208:111598
- Wei S, Kohda YHT, Inoue C, Chien MF (2021) Expression of *PvPht1;3*, *PvACR2* and *PvACR3* during arsenic processing in root of *Pteris vittata*. *Environ Exp Bot* 182:104312
- WHO (2011) Evaluation of certain contaminants in food. Seventy-second Report of the Joint FAO/WHO Expert Committee on Food Additives. WHO Technical Report Series no. 959
- WHO (2017) Guidelines for drinking water quality. 4th edition with 1st addendum. World Health Organisation, Geneva
- Wu F, Xu F, Ma X, Luo W, Lou L, Wong MH (2018) Do arsenate reductase activities and oxalate exudation contribute to variations of arsenic accumulation in populations of *Pteris vittata*? *J Soil Sediment* 18:3177–3185
- Yan X, Liu C, Zhong L, Liao X (2018) Combining phytoremediation with soil flushing for arsenic removal from contaminated soil. *Int J Phytorem* 20:1229–1235
- Yan H, Gao Y, Wu L, Wang LY, Zhang T, Dai CH, Xu WX, Feng L, Ma M, Zhu YG, He ZY (2019) Potential use of the *Pteris vittata* arsenic hyperaccumulation-regulation network for phytoremediation. *J Hazard Mater* 368:386–396
- Yang G, Ding Y (2014) Recent advances in biocatalyst discovery, development and applications. *Bioorg Med Chem* 22:5604–5612
- Yang L, Li X, Chu Z, Ren Y, Zhang J (2014) Distribution and genetic diversity of the microorganisms in the biofilter for the simultaneous removal of arsenic, iron and manganese from simulated groundwater. *Bioresour Technol* 156:384–388
- Yang J, Yang SS, Lei M, Yang JX, Wan XM, Chen TB, Wang XL, Guo GH, Guo JM, Liu SQ (2018) Comparison among soil additives for enhancing *Pteris vittata* L.: phytoremediation of As-contaminated soil. *Int J Phytorem* 20:1300–1306
- Yanitch A, Brereton NJB, Gonzalez E, Labrecque M, Joly S, Pitre FE (2017) Transcriptomic response of purple willow (*Salix purpurea*) to arsenic stress. *Front Plant Sci* 8:1115
- Yilmaz P, Kottmann R, Field D, Knight R et al (2011) Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. *Nat Biotechnol* 29:415–420
- Zargar K, Conrad A, Bernick DL, Lowe TM, Stolc V, Hoeft S, Oremland RS, Stolz J, Saltikov CW (2012) ArxA, a new clade of arsenite oxidase within the DMSO reductase family of molybdenum oxidoreductases. *Environ Microbiol* 14:1635–1645
- Zeng P, Guo Z, Xiao X, Peng C, Huang B, Feng WL (2019a) Complementarity of co-planting a hyperaccumulator with three metal(loid)-tolerant species for metal(loid)-contaminated soil remediation. *Ecotox Environ Safe* 169:306–315
- Zeng P, Guo ZH, Xiao XY, Peng C, Feng WL, Xin LQ, Xu Z (2019b) Phytoextraction potential of *Pteris vittata* L. co-planted with woody species for As, Cd, Pb and Zn in contaminated soil. *Sci Total Environ* 650:594–603
- Zhang J, Cao T, Tang Z, Shen Q, Rosen BP, Zhao FJ (2015a) Arsenic methylation and volatilization by arsenite *S*-adenosylmethionine methyltransferase in *Pseudomonas alcaligenes* NBRC14159. *Appl Environ Microbiol* 81:2852–2860
- Zhang J, Zhou W, Liu B, He J, Shen Q, Zhao FJ (2015b) Anaerobic arsenite oxidation by an autotrophic arsenite-oxidizing bacterium from an arsenic-contaminated paddy soil. *Environ Sci Technol* 49:5956–5964
- Zhang J, Zhao S, Xu Y, Zhou W, Huang K, Tang Z, Zhao FJ (2017) Nitrate stimulates anaerobic microbial arsenite oxidation in paddy soils. *Environ Sci Technol* 51:4377–4386
- Zhang J, Martinoia E, Lee Y (2018) Vacuolar transporters for cadmium and arsenic in plants and their applications in phytoremediation and crop development. *Plant Cell Physiol* 59:1317–1325
- Zhao FJ (2020) Strategies to manage the risk of heavy metal(loid) contamination in agricultural soils. *Front Agric Sci Eng* 7:333–338
- Zhao FJ, Wang P (2020) Arsenic and cadmium accumulation in rice and mitigation strategies. *Plant Soil* 446:1–21
- Zhao FJ, McGrath SP, Meharg AA (2010) Arsenic as a food chain contaminant: mechanism of plant uptake and metabolism and mitigation strategies. *Annu Rev Plant Biol* 61:535–559
- Zhou M, Engelmann T, Lutts S (2019) Salinity modifies heavy metals and arsenic absorption by the halophyte plant species *Kosteletzkya pentacarpos* and pollutant leaching from a polycontaminated substrate. *Ecotox Environ Safe* 182:109460
- Zuñiga C, Zaramela L, Zengler K (2017) Elucidation of complexity and prediction of interactions in microbial communities. *Microb Biotechnol* 10:1500–1522

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