Common reed (Phragmites australis) can invade and dominate in its natural habitat which is mainly wetlands. It can tolerate harsh environments as well as remEDIATE polluted and environmental degraded sites such as mine dumps and other polluted wastelands. For this reason, this can be a very critical reed to reclaim wastelands for agricultural use to ensure sustainability. The present review manuscript examined the microbial spectra of P. australis as recorded in various recent studies, its physiological response when growing under stress as well as complementation between rhizosphere microbes and physiological responses which result in plant growth promotion in the process of phytoremediation. Microbes associated with P. australis include Proteobacteria, Bacteriodetes, and Firmicutes, Fusobacteria, Actinobacteria, and Planctomycetes families of bacteria among others. Some of these microbes and arbuscular mycorrhizal fungi have facilitated plant growth and phytoremediation by P. australis. This is worthwhile considering that there are vast areas of polluted and wasted land which require reclamation for agricultural use. Common reed with its associated rhizosphere microbes can be utilized in these land reclamation efforts. This present study suggests further work to identify microbes which when administered to P. australis can stimulate its growth in polluted environments and help in land reclamations efforts for agricultural use.

Keywords: bioremediation, microbial spectra, physiological response, Phragmites australis, agricultural production

INTRODUCTION

Common reed (Phragmites australis) is an invasive helophytic grass which has great impact on the ecosystem. It is tall, slender with a bare stem and plume-like inflorescence. Phragmites australis is found in brackish and freshwater wetlands, temperate and tropical regions of the world (Den et al., 1989; Brix, 1999; Meyerson et al., 2000). The ability of this reed to proliferate and survive in diverse environmental conditions and invade the environment could be traced to its high productivity (Kettenring et al., 2012; Douhovnikoff and Hazelton, 2014; Eller et al., 2014; Saltonstall et al., 2014). The common reed can competitively displace indigenous vegetation; hence, it is referred to as an invasive plant. In places where it has become a nuisance, control measures are devised to limit its spread and its encroachment in the natural arena. Methods to curb its spread include cutting and burning, flooding, the use of natural enemies, and application of herbicides. Some of the methods are effective but some show very little success (Reimer, 1976; Thompson and Shay, 1985; Monterio et al., 1999; Ailstock et al., 2001; Gusewell, 2003; Relyea, 2005; Avers et al., 2007).
Despite the need to control its spread, *P. australis* has been found useful as a bioremediator of polluted environments due to its ability to survive under stress (Windham et al., 2003; Weis and Weis, 2004; Duman et al., 2007; Bragato et al., 2009; Cerne et al., 2011). The ability of *P. australis* to remediate the environment results from its various genetic and physiological characteristics and these include having the ability to create a rhizosphere environment which encourages the habituation and proliferation of certain rhizosphere microbes. The common reed exudes enzymes and other cell contents which make its rhizosphere conducive for habituation by a myriad of mutually beneficial microbes. Nejla et al. (2014) observed a significant positive correlation between soil dehydrogenase activity (DHA) and pentachlorophenol (PCP) removal in polluted soils with the aid of microorganisms present in the reed’s rhizosphere. This implied that microorganisms in the rhizosphere of *P. australis* and the enzyme activities promoted the biodegradation of PCP and the reclamation of the land. Work done by Cheema et al. (2009) and Yang et al. (2011) supported the findings of Nejla et al. (2014), whereby they observed both microbial and enzymatic activities as influenced by the root exudates promoted the remediation of the environment and freeing it of contaminants.

A plethora of the studies confirmed the findings that the rhizosphere of *P. australis* harbors diverse microorganisms that act as growth-promoting microbes which aid the growth of the reed and promote the remediation of the environment (Kadlec and Wallace, 2008; Jiang et al., 2013; Li et al., 2013; Zou et al., 2013; Bouali et al., 2014). This present review collated information on the microbial spectra associated with the rhizosphere of *P. australis* and the physiological response of the reed to environmental stress as well as the reed-microbes interaction that promotes the growth of the reed and enhance its bioremediation potential in the reclamation of land for agricultural use.

**DISTRIBUTION, IMPACT, AND USES OF *PHRAGMITES AUSTRALIS***

The common reed originates from Europe. However, traces of a North American origin exist (Saltonstall, 2002). Research involving molecular markers showed that the species that were not a native pedigree of the reed were introduced in North America, and these species are behind the sporadic increase of the reed in North America (Chambers et al., 1999; Saltonstall, 2002). Catling and Mitrow (2012) pointed out that the abundance of the reed in North America is an attribute of the sporadic, but similar-looking European subspecies of the reed. Pollution, eutrophication, and shoreline development are notable factors contributing to the distribution and abundance of the reed in North America for the past 150 years (Marks et al., 1994; Chambers et al., 1999). Chambers et al. (1999) further reported that the distribution and abundance of the reed increased across the continent.

Very little is known about this reed on the African continent. However, some work has been done in southern Africa where *P. australis* is considered native based on pollen fossil records which point to presence in the southern African region since the Late Quaternary period (Scott, 1982). Due to intense mining in South Africa and the need to rehabilitate mine dumps and acid mine wetlands, this reed has been very important as a primary remediator of many of these polluted sites. This led to the prevalence of the common reed in aquatic and semi-aquatic areas especially in riverbeds and wet places (Gibbs et al., 1990; Van Oudtshoorn, 1999; Leistner, 2000) as well as in various heavy metal polluted areas adjacent to the mines. The common reed displaces indigenous vegetation through its competitive ability hence reducing the biodiversity of native plants (Catling and Mitrow, 2012). It forms thickets of vegetation because of high biomass formed by the reed leading to the blockage of light rays needed for the growth of the native fauna. Consequently, native plants less competitive than *P. australis* receive less sunlight, photosynthesize poorly, and are eventually crowded out and displaced.

Physiologically, the reed produces gallic acid which is broken down in the presence of ultraviolet light rays to form mesoxalic acid, a toxic chemical that hinders the growth of susceptible plants and seedlings native in the area (Thimmamaraju et al., 2009). Controlling the growth of this common reed is a global concern and burning of the reed and its use as a forage for goats (Jolly, 2017) are believed to be the most effective methods for its control. The reed has some important uses despite its negative impact to the environment and biodiversity. The reed is used in weapon production like spears used for game hunting. It also provides shelter for birds and other kinds of animals. Some of its parts like the rootstocks are ground into flour or made into a thin liquid food of oatmeal and can be roasted in a moist state and eaten (Peterson, 2010). The reed is also known for its bioremediation role in most polluted environments because of its ability to thrive well in harsh conditions and the microbe-plant interaction that is predominant with reeds and promote their growth as well as enhance their remediation potential.

**MICROBIAL CONSORTIA ASSOCIATED WITH *PHRAGMITES AUSTRALIS* IN ENVIRONMENTAL REMEDIATION**

Plants are inhabited by microbes either as endophytes or as ectophytes or as pathogens. As colonizers of plants, microbes form either mutually beneficial relationships with plants playing crucial roles in recycling of nutrients and breaking down of pollutants (Srivastava et al., 2017; Lyu et al., 2020). Plant parts which are most likely inhabited by ectophytes are those which have high nutrient levels such as secretion organs. The rhizosphere is one of the environment-plant interfaces most colonized by ectophytic microbes and provides environment laden with oxygen and nutrients for microbes’ proliferation (Stottmeister et al., 2003). Microorganisms dominating the rhizosphere of macrophytes have been recorded to play important biological functions which include nutrient acquisition (Pii et al., 2015) that enhances growth and fitness, disease suppression (Mendes et al., 2011), and stress tolerance of the macrophytes (de Zelicourt et al., 2017).
which showed that adjusting plant-pointed out suggested that rhizosphere microbiome communities (2020) investigated the fungal and metabolome diversity of Gonzalez et al. (2018) found that the presence of denitrifying bacteria, in the root zone, guarantees high NO$_3^{-}$ removal efficiency from saturated soils. These established principles form the basis of constructing efficient wetlands for the removal of contaminants from soil. 

Constructed wetlands have been adopted for the past decades in the remediation of contaminated environments because the method is cost-effective and devoid of any environmental damage (Kadlec and Wallace, 2008; Li et al., 2013; Zou et al., 2013; Bouali et al., 2014). Chandra et al. (2012) pointed out that $P. australis$ has been employed in wetlands remediation of contaminated environment in both tropical and temperate part of the world. Ravit et al. (2003) stated that the plants’ high biomass, root depth, ability to thrive well and breakdown pollutants, and ability to adapt easily are the bases upon which the reed and other species of plants used in bioremediation are selected. However, the effectiveness of the constructed wetlands in the treatment of polluted environment is dependent on the microbial consortia present in the rhizosphere of plant species selected for the bioremediation (Tian et al., 2014). Some of these microbes enhance plants’ development (Jiang et al., 2013) and possibly promote the bioremediation process.

Shaw et al. (2006) views the rhizosphere as an exceptional zone around the root that is known for complex biological activities involving many microorganisms. Raaijmakers et al. (2009) pointed out that among the various microbes present in the rhizosphere, bacterial populations play a vital role in most activities in the rhizosphere because of their high level of host specificity. The various communities of bacteria present in the rhizosphere assist plants in the acquisition of inorganic nutrients, promote nitrogen uptake as well as protecting plants against attack by pathogenic fungi (Cocking, 2003; Berg et al., 2005; Uroz et al., 2007). Because of the importance of bacteria in natural ecosystems, it becomes necessary to unravel the bacterial diversity and possibly the bacteria-plant interactions in the habitats and how they aid in polluted land reclamation for crop production.

Microbial consortia of many wetland plants’ roots have been investigated via culture-dependent and molecular methods (Jiang et al., 2013; Li et al., 2013; Abed et al., 2018). The era of high-throughput genomic technologies accelerated the discovery of root zones microbes as well as their biological activities. The uncovering of the microbial consortia and microbial metabolic activity was through the new fields of metagenomics and meta-transcriptomics. Notably studies include Kumar et al. (2018) which uncovered the rhizobacteria population composition of barley and alfalfa in oil-contaminated soils. Another noteworthy study is that of Brereton et al. (2020) which cataloged the rhizosphere microbiome of $Festuca arundinacea$, $Salix miyabeana$ and $Medicago sativa$ in contaminated soil. In addition, Kalu et al. (2021) investigated the fungal and metabolome diversity of rhizosphere and endosphere of $P. australis$ in an acid mine-polluted environment. Furthermore, Mang and Ntushelo (2021) investigated the influence of acid mine water on the diversity and metabolite shift of microbial populations of the common reed. Obieze et al. (2020) investigated the functional attributes and response of bacterial communities to nature-based fertilization during hydrocarbon remediation. Bledsoe et al. (2020) observed increased bacterial diversity in bulk soils and plant rhizospheres in a long-term nutrient enriched oligotroph-dominated wetland. Hu et al. (2021) investigated the composition and co-occurrence patterns of $P. australis$ rhizosphere bacterial community and observed the characterization of the rhizosphere by $Arthrobacter$, $Pseudomonas$, $Trichococcus$, and $Rhambacter$ that also played a crucial role in the regulation of plant fitness and nutrient cycling. Lyu et al. (2020) observed that bacterial phyla enriched in the rhizosphere of $P. australis$ were found to be putative keystone taxa and might be involved in the regulation of bacterial interactions and plant growth. The investigation of the sediment microbiomes associated with the rhizosphere of emergent macrophytes in a shallow, subtropical lake by Huang et al. (2020) suggested that rhizosphere microbiome communities are influenced by the presence of macrophyte roots, with oxygenated rhizosphere and surface sediment communities being more diverse, and organized into more interconnected co-occurrence networks.

Metatranscriptomic studies which have accelerated our understanding of rhizosphere microbes in relation to phytoremediation include those by Yergeau et al. (2018) and Gonzalez et al. (2018) which both revealed the metatranscriptomics of the root zone in plants growing in contaminated soils with huge implications for phytoremediation. The exudates from the roots of plants are known to promote the growth and actions of rhizosphere associated microbes (Jiang et al., 2013; Zou et al., 2013). Most of the constructed wetlands are based on the principle of microbes-host plant interaction enhanced through the exudates from the plant. Abed et al. (2014) pointed out that there are very little wetlands built for bioremediation of oil polluted water. Few studies done fronted well-constructed wetlands as an effective bioremediation method for hydrocarbons contaminated water (Zou et al., 2013; Tian et al., 2014). One of the largest surface flows constructed wetland system in Oman, Arabian Gulf region, for oil-produced water remediation is predominated by $P. australis$ (Abed et al., 2014). However, the knowledge of the microbial consortia of the reed’s rhizosphere in oil-polluted wetlands is still minimal. Abed et al. (2018) reported bacterial communities in the rhizosphere of the reed from an oil-polluted wetland using molecular (Illumina MiSeq sequencing) and culture-based methods, and showed that
the dominant phyla belonged to *Proteobacteria*, *Bacteriodetes*, and *Firmicutes*.

Integration of constructed wetland into the landscape could provide an efficient remediation of organic pollutants (Lorah and Voytek, 2004). *Phragmites* sp. and *Typha angustifolia* known as wetland plants have been shown in various studies to possess the potential of remediating chlorinated pollutants (Ma and Burken, 2002; Miglioranza et al., 2004; Zhang et al., 2005; Gomez-Hermosillo et al., 2006; Monferran et al., 2007; Ma and Havelka, 2009; Faure et al., 2012; San et al., 2013). Furthermore, some studies done have shown that most mineralization of recalcitrant organic contaminants occur at the rhizosphere (Kuiper et al., 2004; Krutz et al., 2005; Kidd et al., 2008; Gerhardt et al., 2009). A study of San et al. (2014) used pyrosequencing approaches to show that the rhizosphere of the reed in organochlorine contaminated soil were dominated by the phyla *Proteobacteria*. Furthermore, they identified *Sphingomonas* sp., *Pseudomonas* sp., *Devosia* sp. and *Sphingobium* sp. to be persistent in the organochlorine’s environment indicating them as potential bioremediation microorganisms. Ding et al. (2021) identified the following genera *Rhodobacter*, *Cattellibacterium*, *Hydrogenophaga*, *Geothrix* and *Aeromonas* as colonizers of the rhizosphere of *P. australis* and these facilitate the removal NH$_4^+$-N and chemical oxygen demand from the constructed wetland.

The significance of microbes-plant interaction has prompted many studies to be focussed on the interactions between microbes and *P. australis*. In wetlands colonized by the reed, the endophytic bacteria clustered into phyla *Proteobacteria*, *Firmicutes*, *Bacteroidetes*, *Fusobacteria* and small portion of unidentified bacteria have the potential to promote phytoremediation (Li et al., 2010). However, Borsodi et al. (2007) observed less diverse periphyton bacterial communities that were clustered into phyla *Proteobacteria*, *Firmicutes* and *Actinobacteria* in the reed using culture-dependent methods. Vladár et al. (2008) identified *Desulfovibrio*, *Desulfotomaculum*, and *Desulfobulbus* as the reed rhizosphere’s sulfate-reducing bacteria. Work done by Zhang et al. (2013) on bacterial diversity of the rhizosphere of three ecotypes of the reed using the pyrosequencing approach showed the following phyla *Proteobacteria*, *Actinobacteria*, *Bacteroidetes*, *Chloroflexi*, *Gemmatimonadetes* and *Planctomycetes* to be the dominant bacterial cluster although differences in bacterial diversity existed in the different ecotypes.

A brief description of the roles of the bacterial communities colonizing the rhizosphere of *P. australis* provided an indication of their role in enhancing the growth of this reed, promoting their bioremediation ability necessary to reclaim polluted agricultural lands for expanded agricultural production. The genera *Methylophilales*, *Nitrosomonadales*, and *Desulfurimonadales* belonging to the phylum *Proteobacteria* have been reported to play a crucial role in nitrogen, sulfur, and global carbon recycling that enhances the growth of the reed and promote their phytoremediation ability (Ansola et al., 2014). *Bacteroidetes* has been reported to be actively involved in nitrogen fixation, a major component of the nitrogen cycle needed to enrich the soil and promote crop production in various species of halophytes (Alishahi et al., 2020). *Cyanobacteria* promote degradation of organic pollutants and enhance the process of the carbon cycle (Savage et al., 2010; Wang et al., 2016). *Betaproteobacteria* has varieties of ammonia oxidizing bacteria that enhance the removal of excess nitrogen that could constitute a major challenge to the growth of crops (Wang et al., 2013). Other denitrifying bacteria associated with the rhizosphere of *P. australis* include *Catellibacterium* (Kong et al., 2019), *Hydrogenophaga* (Xing et al., 2018), *Aeromonas* (Sun et al., 2019), and *Geothrix* (Zhang et al., 2010). *Sediminibacterium* was reported to play vital role in the biodegradation of vinyl chloride (Wilson et al., 2016). *Acidovorax* enhances the removal of heavy metals (Zhang et al., 2019). *Geobacter* promotes the removal of amino acids and organic acids in systems under suitable conditions (Lu et al., 2015). *Bacillus* biodegrades various organic compounds necessary for dissolved organic carbon reduction (Guan et al., 2015). *Nitrospira* ammonia oxidizing bacteria promote nitrogen cycling (Dong and Reddy, 2012). *Flavobacterium* promotes denitrification treatment nitrogenous contaminants (Pishgar et al., 2019). *Thauera* stimulate organic matter removal through enzyme secretion pathway that enhances chemical oxygen demand removal efficiency (Sanchez et al., 2018). The above alluded roles of these bacterial communities colonizing this rhizosphere of this reed contribute immensely to the growth of the reed while promoting the bioremediation potential as well as reclamation of contaminated agricultural land and enhancing agricultural production.

As previously mentioned in this review, the advancement in the sequencing technologies and computational analysis have unveiled knowledge on spectra of microorganisms which colonize the rhizosphere. Alegría et al. (2016) stated that the wetland plants microbiota could promote phytodepuration. Pietrangelo et al. (2018) showed composition and functional capability of bacteria microbiota of the rhizosphere of *P. australis* and *T. latifolia* using Illumina MiSeq sequencing techniques that the rhizosphere is dominated by *Actinobacteria*, *Firmicutes*, *Proteobacteria*, and *Planctomycetes*. However, the microbiota assemblage compositions and their potential contribution to phytodepuration needs further research. Table 1 provides a summary of the microbial spectra associated with *P. australis* in the remediation of polluted environments.

Aquatic macrophytes control their physiological activity to enhance their adaptation to changes in the environment. *P. australis* enhances its ability to survive under flooding conditions by increasing the rate of evapotranspiration to enhance its protection and uptake of nutrients (Zhao et al., 2012; Srivastava et al., 2014). Furthermore, these macrophytes, through plant residue decomposition, nutrients uptake, and root exudates, modify the physiochemical parameters of the soil to enable their proliferation and possibly the remediation of the environment (Luigimaria et al., 2014; Hallin et al., 2015; Packer et al., 2017). Hence, the next subsection of this review looked at the physiological response of *P. australis* to environmental stress.
**TABLE 1 |** Summary of the microbial spectra associated with *P. australis* in the remediation of polluted environment.

| Remediation sites                  | Source of microorganism | Methods of identification                      | Phylum/Family of organisms                                                                 | References        |
|-----------------------------------|-------------------------|------------------------------------------------|-------------------------------------------------------------------------------------------|-------------------|
| Oil-polluted wetlands             | Rhizosphere             | Molecular (Illumina MiSeq sequencing) and culture-based | Proteobacteria, Bacteroidetes, and Firmicutes                                             | Abed et al. (2018) |
| Organochlorines contaminated sites | Rhizosphere             | Molecular (Pyrosequencing approach)             | Proteobacteria                                                                           | San et al. (2014)  |
| Constructed wetland               | Endophytes              | Culture-independent method and                  | Proteobacteria, Firmicutes, Bacteroidetes, Fusobacteria                                   | Li et al. (2010)   |
| Lake                              | Periphyton Samples      | Culture-based method                            | Proteobacteria, Firmicutes and Actinobacteria                                             | Borsodi et al. (2007) |
| Lake                              | Rhizosphere             | Culture-based and molecular method              | Proteobacteria, Firmicutes                                                               | Vladár et al. (2008) |
| Natural wetland                   | Rhizosphere             | Molecular method (pyrosequencing)               | Proteobacteria, Actinobacteria, Bacteroidetes, Planctomycetes, Eusimicrobia, Aquificae, Caldiserica, Chlamydaceae, Chlorobi, Chloroflexi, Cyanobacteria, Deinococcus-Thermus, Eusimicrobia, Fibrobacteres, Lentisphaerae, Planctomycetes, Spirochaetes, Tenericutes, Verrucomicrobia | Zhang et al. (2013) |
| Natural wetland                   | Rhizosphere             | Illumina MiSeq sequencing techniques            | Actinobacteria, Firmicutes, Proteobacteria, and Planctomycetes                           | Pietrangelo et al. (2018) |
| Tailing dam of Mintails Mogale Gold Mine and Sibanye Gold Mine | Rhizosphere and endosphere | MiSeq high-throughput technology                | Ascomycota and Basidiomycota                                                             | Kalu et al. (2021) |
| Constructed wetland               | Rhizosphere             | Quantitative polymerase chain reaction (qPCR)   | Rhodobacter, Catellobacterium, Hydrogenophaga, Geothrix and Aeromonas                     | Ding et al. (2021b) |

**PHYSIOLOGICAL RESPONSE OF PHRAGMITES AUSTRALIS IN STRESSED ENVIRONMENT**

Response of plants to environmental stress is dynamic and it involves physiological, metabolic, and molecular responses which all constitute plant fitness. Some plants only survive stress but have their growth and reproduction retarded. However, some survive and still manage to grow and proliferate in the presence of stress. The focus of this section is the physiological response of *P. australis* to stress in polluted environments. The authors demonstrate the unique physiological response which enables *P. australis* dominance in polluted environments.

Physiological response of plants and microorganisms in a stressed environment varies with the types and levels of stress. The physiological response involves the production of metabolites that promotes their survival or remediation potential. In view of the ability of *P. australis* to thrive well in stressed environments, a myriad of studies investigated the physiological dynamics of this reed when growing under...
stressed environments as a factor that contributes to their survival. Majken et al. (2005) showed that P. australis responds physiologically to water deficit stress through the production of the metabolite proline. Proline is believed to enhance the plant survival in the water deficit environment. In a regime of drought and flooding Wen et al. (2017) found that P. australis net photosynthetic rate, stomatal conductance, intercellular CO₂, and transpiration rates decreased with prolonged drought stress and the delay in subsequent flooding after the drought. However, this reed is able to increase its physiological response even before it receives flooding under which it copes better. This shows a balance between water conversation and growth. This is probably a coping measure to conserve water to ensure water retention within the plant during water scarcity but on the other hand, maintain a foliage that allows the plant to undertake its various biological and ecological functions. In the saline-alkaline marsh in which the reed was growing, it accumulated more Na⁺ in the shoots after long-term drought stress showing a self-regulatory mechanism of ion balance in different organs with increasing drought stress. Most recently, Ding and Sun (2021) found that various depths of flooding of P. australis triggered varying physiologic responses with leaf blades maintaining high enzyme activity and proline content while leaf sheaths maintained the greatest amount of soluble protein again demonstrating an orchestrated physiological response to flooding characterized by tissue specialization.

Similarly, in an earlier study Ding et al. (2021a), in a more targeted P. australis study about the role of tissue in partitioning various metals found that leaf sheaths had the highest potential to store metals of all the organs observed. The highest translocation factor for Fe was observed from the stems to the leaf sheaths and a higher bio-concentration factor for Mn was found in the leaf blades and leaf sheaths with Cd and Zn higher bio-concentration factors observed in the stems. This demonstrated tissue specialization in P. australis in stress resistance. Investigating the enrichment characteristics and biological response of P. australis to sulfamethoxazole and ofloxacin residues, Lv et al. (2020) found that sulfamethoxazole and ofloxacin accumulated in the plant in the rank root > leaf > stem and accumulation and transport of ofloxacin was higher than that of sulfamethoxazole. Besides these few studies, other studies have uncovered the physiologic responses of P. australis to stress and found results which have implications for the use of this reed as a phytoremediator. This includes the study of Wu et al. (2020) who investigated the responses of P. australis to Cu stress using a combined approach which employed morphology, physiology, and proteomics. Dayou et al. (2021) investigated trait-based adaptability of P. australis to the effects of soil water and salinity in the Yellow River Delta. The authors observed reduction in the average height and stem diameter with increase in leaf water content and thickness as well as salinity stress tolerant strategy in P. australis that enables the reed to dominate the river. Wahman et al. (2021) evaluated the changes in the metabolome profiles of P. australis when exposed to stress caused by drugs using a serial coupling of reversed-phase liquid chromatography and hydrophilic interaction liquid chromatography combined with accurate high-resolution time-of-flight mass spectrometer (TOF-MS) and observed variation in the metabolites shift in respect to different drugs. Strikingly, an increase in the production of quercetin was observed by the authors in the plant after diclofenac incubation.

Plügmačer et al. (2001) observed the production of glutathione conjugate and cysteine conjugate in all cormus part of P. australis in the complete metabolism of cyanobacterial toxin microcystin and enzymes such as glutathione S-transferases (sGST) that enhances the complete breakdown of the toxins. Sauvêtre et al. (2018) observed the production of metabolites involving GSH conjugation and 2,3-dihydroxylation, as well as acride related compounds in Armoracia rusticana (hair root culture) treated with endophytic bacteria from P. australis in response to carbamazepine (CBZ) exposure. Carbamazepine is known as a recalcitrant pharmaceutical pollutant in the aquatic environment. In their work, higher removal rate of CBZ and metabolite production were observed when the endophytes were introduced. This implied that the endophytes could enhance the development of the plant and promote the breakdown of CBZ.

In addition, Luisa et al. (2004) reported increase production of phytochelatins, and antioxidant enzymes such as glutathione reductase, glutathione-S-transferase, catalase, ascorbate peroxidase, dehydroascorbate reductase, guaiacol peroxidase in P. australis when exposed to increased concentration of Cd. Sulaiman and Alfadul (2013) also observed increased production of metabolites such as malondialdehyde, aspartate, glutamate, serine, histidine, glycine, threonine, cysteine, valine, methionine, phenylalanine, isoleucine, leucine, lysine, proline, and the activities of antioxidant enzymes such as superoxide dismutase, catalase, ascorbate peroxidase, glutathione peroxidase and peroxidase in response to the increase concentration Cd, Zn, Cu, and Pb. P. australis’ increase production of metabolites and antioxidant enzymes are stress response of the plant to the increase concentrations of heavy metals which enhance its survival and sequestration of heavy metals by the plant. Table 2 provides a summary of metabolites produced as well as synthesized enzymes by P. australis in a stressed environment. The interaction between P. australis and associated rhizospheric microbes and endophytes is believed to initiate physiological response leading to the production of diverse metabolites either by the reed or associated microbes that have the tendency to promote growth and bioremediation potential of the reed.

INTERACTION OF THE STRESS INDUCED PHYSIOLOGICAL RESPONSES AND RHIZOSPHERE MICROBES OF PHRAGMITES AUSTRALIS AS FACILITATOR OF GROWTH AND BIOREMEDIATION POTENTIAL OF THE REED

The plant environment from the roots to the apex is a continuum of physiological and metabolic activity under various influences either internal such as genetic or external such
as the environment characterized by the climate, ecological interactions, and the condition of the soil. Given this proven fact, it is logical that rhizosphere microbes influence the response of the plant to environmental stress. This has been proven in many studies, but we limit our focus on the effect of rhizosphere microbes on the physiological responses of *P. australis* to stress, in particular stress related to soil pollution. We also look at the use of rhizosphere microbes to improve the bioremediation efforts of *P. australis*. These include the use of rhizosphere microbes to first degrade complex chains of pollutant compounds into their smaller subunits for easier adsorption by the reed.

For the reclamation of polluted land needed for the growth of crops and sustainability of agricultural production, there is a serious need to unravel various microbial communities in association with stress resistant plants which include macrophytes like *P. australis* and the physiological mechanisms adopted by the plants that could aid in the remediation of the contaminated land. Toyama et al. (2009) evaluated the biodegradation of bisphenol A (BPA) and bisphenol F (BPF) in rhizosphere sediment of *P. australis*. Bisphenols are endocrine disrupting chemicals with the potentials to cause adverse effect on human health and other animals when released on land and absorbed by crops (Chen et al., 2002; Crain et al., 2007). Consequent upon the adverse effect of bisphenols, there existed the need to remediate the environment contaminated with these chemicals. The authors observed a high rate of BPA and BPF removal and the presence of A BPA-degrading bacterium, *Novosphingobium* sp. strain TYA-1, and a BPF-degrading bacterium, *Sphingobium yanoikuyae* strain TYF-1. The results suggested that the interactions of *P. australis* and these bacteria can speed up the rate of removal of bisphenols from the sediment (Toyama et al., 2009).

Nejla et al. (2014) examined the phytoremediation potential of *P. australis* grown in pentachlorophenol and cadmium co-contaminated soils. They observed significant positive correlation between soil dehydrogenase activity (DHA) and pentachlorophenol (PCP) removal in planted soil implying that *P. australis* enhanced the biodegradation of PCP through the activities of enzymes and the microorganisms in the rhizosphere of the plant. The degradation of cyanobacteria toxin microcystin by *P. australis* (Pflugmacher et al., 2001) provided a good indication of the application of the reed in the bioremediation of polluted agricultural land and the reclamation of the land for agricultural practices. Physiology and rhizosphere microbiology

### Table 2: Summary of the metabolites produced, and enzymes synthesized by *P. australis* in response to stress.

| Causes of the stress | Metabolites produced | Enzymes secreted | Suggested purpose of metabolites and enzyme secretion | References |
|----------------------|----------------------|------------------|------------------------------------------------------|-------------|
| Water deficit        | Proline              | Glutathione S-transferases (sGST) | Maintaining the water level of the plant for its survival | Majken et al. (2005) |
| Cyanobacterial toxin microcystin (MC-LR) | Glutathione conjugate and cysteine conjugate |                | Breakdown of the toxin | Pflugmacher et al. (2001) |
| Carbamazepine (CBZ)  | GSH conjugation and 2,3-dihydroxylation, as well as acridine related compounds | Glutathione reductase, Glutathione-S-transferase, Catalase, Ascorbate peroxidase, Dehydroascorbate reductase, Guaiacol peroxidase | Breakdown of recalcitrant pharmaceutical pollutant (CBZ) | Sauvêtre et al. (2018) |
| Cadmium (Cd)         | Phytocelatins (PC)   |                | Removal of Cd | Luisa et al. (2004) |
| Cd, Zn, Cu, and Pb   | Malondialdehyde (MDA), Aspartate, Glutamate, Serine, Histidine, Glycine, Threonine, Cysteine, Valine, Methionine, Phenylalanine, Isoleucine, Leucine, Lysine, Proline | Superoxide dismutase, catalase, ascorbate peroxidase, glutathione peroxidase and peroxidase | Removal of the heavy metals | Sulaiman and Alfadul (2013) |
| Presence of drugs    | Quercetin            |                | Removal of the drugs from the environment | Wahman et al. (2021) |
TABLE 3 | Remediation ability of *P. australis* in diverse polluted environment.

| Nature of the environment                      | Bioremediation potential                                                                 | References                        |
|-----------------------------------------------|-----------------------------------------------------------------------------------------|-----------------------------------|
| Fe contaminated                               | 100% bioaccumulation of Fe                                                              | Batty (2003)                      |
| Cu, Cd, Ni, Pb, and Zn contaminated aqueous solution | Adsorption of Cu, Cd, Ni, Pb, and Zn                                                   | Soutichak et al. (2006)           |
| As and Sb contaminated                         | Removal of As and Sb                                                                      | Ghassasmezdah et al. (2008)        |
| Cu contaminated                               | High Cu tolerance                                                                        | Ali et al. (2002)                 |
| Zn and Mn contaminated                         | High root accumulation of Zn and Mn                                                      | Peiter et al. (2003)              |
| Cu, Cd, Cr, Ni, Fe, Pb and Zn contaminated     | Removal of Cu, Cd, Cr, Ni, Fe, Pb and Zn                                                 | Menka and Tripathi (2015)         |
| Cd, Cr, Hg, Mn, Ni, Pb, and Zn contaminated    | Cd, Cr, Hg, Mn, Ni, Pb, and Zn accumulation in the order root->rhizome->leaf->stem      | Bonanno and Lo Giudice (2010)      |
| As and trace metal contaminated                | Phytostabilization of As and trace metals                                               | Paola et al. (2018)               |
| Cd, Cu, Pb, and Zn contaminated sediments     | Bioaccumulation of Cd, Cu, Pb, and Zn                                                    | Fawazy et al. (2012)              |
| Trace elements (Ag, Al, As, B, Ba, Be, Co, Fe, Mo, Pd, Pt, Rh, Sb, Se, Sr, Ti, and V) contaminated | Removal of Ag, Al, As, B, Ba, Be, Co, Fe, Mo, Pd, Pt, Rh, Sb, Se, Sr, Ti, and V in the order root->rhizome->leaf->stem | Bonanno (2011)                     |
| Co, Cr, Cu, Fe, Cd, Ni, Mn, and Zn contaminated | High bioaccumulation of Co, Cr, Cu, Fe, Ni, Mn, and Zn in the roots and Cd, and Pb in the leaves | Rzymaki et al. (2014)             |
| Heavy metal (Co, Ni, Mo, Cd, Pb, Cr, Cu, Fe, Mn, Zn and Hg) and trace metal (As, Se, Ba) contaminated estuarine sediments | Decrease the metals in the order Fe > Mn > Zn > Pb > Ba > Cr > As > Cu > Ni > Co > Mo > Cd > Se > Hg | Cicero-Fernández et al. (2017)     |
| Bisphenol A (BPA) and bisphenol F (BPF) contaminated | High rate of BPA and BPF removal in the presence of A BPA-degrading bacterium, Novosphingobium sp. strain TYA-1, and a BPF-degrading bacterium, Sphingobium yanoikuyae strain TYF-1) in the rhizosphere sediment of *P. australis* | Toyama et al. (2009)              |
| pentachlorophenol and cadmium co-contaminated soils | Enhancement of the biodegradation of PCP through the activities of soil dehydrogenase (DHA) and the microorganisms in the rhizosphere of the plant | Nejla et al. (2014)               |
| Butachlor contaminated                         | Degradation of butachlor                                                                  | Yang et al. (2011)                |
| Urban runoff treatment                         | Reduction of biological oxygen demand (BOD), and remove large amount of nitrogen         | Byoung-Hwa and Miklas (2007)      |
| Cyanobacterial toxin microcystin (MC-LR) contaminated | Complete remediation of cyanobacterial toxin microcystin (MC-LR)                   | Pfugmarcher et al. (2001)         |
| Ni and Pb contamintated Lake Burullus, Egypt   | Phytoextraction of Ni and Pb                                                              | Eid et al. (2021)                 |

were also completed in the work of Fahid et al. (2020) who found that *P. australis* vegetated with three bacterial strains belonging to *Acinetobacter* and *Bacillus* had an improved capacity of hydrocarbon extraction from diesel contaminated water. Likewise, *P. australis* grew more rapidly in the presence of the bacteria which were also hydrocarbon degrading strains. This was more of a complementation exercise as the ability of the reed to adsorb hydrocarbons was probably because the long chain hydrocarbons had first been degraded by the bacteria to make them easier for adsorption by the reed. Plant growth promotion by rhizosphere microbes of the *P. australis* has been proven in several studies, and logically growth promotion can be seen to aid phytoremediation in places where this reed grows as a remediator of a polluted site. Riva et al. (2019) found that cultivable microbes isolated from the rhizosphere and the interior of *P. australis* in a constructed wetland in Morocco improved growth of *Juncus acutus*. Some of the strains improve the growth of *J. acutus* and its ability to remove azo-dyes. This indicates that the rhizosphere of *P. australis* is an enrichment niche for microbes which can be effectively used in phytoremediation even using a different plant species. Similarly, Saleem et al. (2019) investigated the feasibility of *P. australis* in combination with *Acinetobacter*, *Bacillus*, and *Pseudomonas* in phenol degradation. The authors observed the colonization of the reed’s rhizosphere by the microbes which aid in their growth and phenol degradation. You et al. (2021) investigated the effect of arbuscular mycorrhizal fungi on the growth and toxic element uptake by *P. australis* under Zn/Cd stress. The authors observed that the reduction of Zn and Cd toxicity in the reed as impacted by the actions of arbuscular mycorrhizal fungi via the increase of the reed biomass and regulatory patterns under different Zn/Cd concentrations. Wu et al. (2020) found that inoculation of *P. australis* with arbuscular mycorrhizal fungi can relieve this plant of photosynthesis inhibition caused by Cu stress as a result, promote the growth of the reed. This study proved the existence of a symbiotic relationship between the fungi and the plant, and this can be manipulated in several bioremediation efforts. Table 3 provided a summary of the remediation potentials of *P. australis*. The ability of *P. australis* to bioaccumulate heavy metals could be an attribute of the plant's growing periods and physiology (Windham et al., 2001). Furthermore, the...
bioremediation potential of *P. australis* could be attributed to the interaction between the reed and the associated microbes which is culminated with a lot of physiological response involving the production of metabolites and various enzymatic activities that can enhance the growth of the reed. The association between *P. australis* and its rhizosphere microbes has implications for phytoremediation of wastelands that can be claimed for agricultural use.

Proteobacteria, Bacteriodetes, and Firmicutes, Fusobacteria, Actinobacteria, and Planctomycetes are the major families of bacteria dominating the rhizosphere of *P. australis*. Some species belonging to this families as well as some arbuscular mycorrhizal fungi have been found to play major roles in the biological activities that promotes the growth of the reed and the reed’s remediation potential. However, further research is required to unveil other species of bacteria and other microbes that can promote the growth of *P. australis* in polluted environment and enhance the phytoremediation process necessary for the reclamation of agricultural land for sustainable agricultural production.

**AUTHOR CONTRIBUTIONS**

CK, MR, and KN drafted the manuscript. KN also provided oversight of the writing process. All authors have read and approved the manuscript.

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**REFERENCES**

Abed, R. M. M., Al-Kharusi, S., Gkorezis, P., Prigent, S., and Headley, T. (2018). Bacterial communities in the rhizosphere of *Phragmites australis* from an oil-polluted wetland. *Arch. Agron. Soil Sci.* 64, 360–370. doi: 10.1080/03630340.2017.1352087

Abed, R. M. M., Al-Kharusi, S., Prigent, S., and Headley, T. (2014). Diversity, distribution and hydrocarbon biodegradation capabilities of microbial communities in oil-contaminated cyanobacterial mats from a constructed wetland. *PloS ONE* 9:e114570. doi: 10.1371/journal.pone.0114570

Allstock, S. M., Norman, M. C., and Bushmann, P. J. (2001). Common reed *Phragmites australis*: control and effects upon biodiversity in freshwater non-tidal wetlands. *Restor. Ecol.* 9, 49–59. doi: 10.1046/j.1526-100x.2001.001049.x

Alegria, T. R., Giles, C., Paterson, E., Robertson-Albertyn, S., Cesco, S., Mimmo, T., et al. (2016). Plant-microbiota interactions as a driver of the mineral turnover in the rhizosphere. *Adv. Appl. Microbiol.* 95, 1–67. doi: 10.1016/j.1526-0340.2016.03.001

Ali, N. A., Bernal, M. P., and Ater, M. (2002). Tolerance and bioaccumulation of copper in *Phragmites australis* and *Zea mays*. *Plant Soil* 239, 103–111. doi: 10.1023/A:100498521560

Alishahi, F., Alikhani, H. A., Khoshkholgh-Sima, N. A., and Etesami, H. (2020). Seasonal variations of Cu, Zn, Ni and Cr concentration in *Phragmites australis* (Cav.) Trin ex steudel in a constructed wetland of North Italy. *Dsalination* 246, 35–44. doi: 10.1016/j.desal.2008.02.036

Beretron, N. J. B., Gonzalez, E., Desjardins, D., and Labrecque, M.,Pitre, F.E. (2020). Co-cropping with three phytoremediation crops influences rhizosphere microbiome community in contaminated soil. *Sci. Total Environ.* 711:135067. doi: 10.1016/j.scitotenv.2019.135067

Bouali, M., Feki, M., and Bakhrouf, A. (2014). Comparative study of two constructed wetlands for wastewater treatment. *J. Chem. Biol. Phys. Sci.* 45, 103–109. doi: 10.1016/j.jhazmat.2008.12.027

Bruzzi, H. (1999). Genetic diversity, ecophysiology, and growth dynamics of reed (*Phragmites australis*). *Aquat. Bot.* 64, 179–184. doi: 10.1016/S0304-3770(99)00050-9

Byoung-Hwa, L., and Miklas, S. (2007). What is the role of *Phragmites australis* in experimental constructed wetland filters treating urban runoff? *Ecol. Eng.* 29, 87–95. doi: 10.1016/j.ecolefin.2006.08.001

Catling, P. M. and Mitrow, G., (2012). Major invasive alien plants of natural habitats in Canada: Common buckthorn, European buckthorn. *Can. Bot. Assoc.* 45, 110–117.

Cerne, M., Smošik, B., and Štrok, M. (2011). Uptake of radionuclides by a common reed (*Phragmites australis*) and biomonitoring applications. *Bioresour. Technol.* 103, 78–86. doi: 10.1016/j.biortech.2011.09.132

Chandra, R., Bharagava, R. N., Kapley, A., and Purohit, H. J. (2012). Uptake of radionuclides by a common reed (*Phragmites communis*) periphyton bacterial communities in a Hungarian shallow soda lake. *Microb. Ecol.* 63, 612–620. doi: 10.1007/s00248-006-9133-x

Chambers, R. M., Meyerson, L. A., and Saltonstall, K. (1999). Expansion of *Phragmites australis* into tidal wetlands of North America. *Aquat. Bot.* 64, 261–273. doi: 10.1016/S0304-3770(99)00055-8

Chandra, R., Bharagava, R. N., Kapley, A., and Purohit, H. J. (2012). Characterization of *Phragmites communis* rhizosphere bacterial communities and metabolic products during the two-stage sequential treatment of post methanated distillery effluent by bacteria and wetland plants. *Bioresour. Technol.* 103, 78–86. doi: 10.1016/j.biortech.2011.09.132

Cheema, S. A., Khan, M. I., Tang, X., Zhang, C., Shen, C., Malik, Z., et al. (2009). Enhancement of phanethrene and pyrene degradation in rhizosphere of tall fescue (*Festuca arundinacea*). *J. Hazard. Mater.* 166, 1226–1231. doi: 10.1016/j.jhazmat.2008.12.027
Chen, M. Y., Ike, M., and Fujita, M. (2002). Acute toxicity, mutagenicity, and estrogenicity of bisphenol-A and other bisphenols. Environ. Toxicol. 17, 80–86. doi: 10.1002/tox.10035
Cicero-Fernández, D., Manuel, P., Jose, A. E., and Blanca, A. (2017). Long-term (two annual cycles) phytoremediation of heavy metal-contaminated estuarine sediments by Phragmites australis. New Biotechnol. 38, 56–64. doi: 10.1016/j.nbt.2017.06.011
Cocking, E. C. (2003). Endophytic colonization of plant roots by nitrogen fixing bacteria. Plant Soil 252, 169–175. doi: 10.1023/A:1024106058006
Crain, D. A., Erikson, M., Iguchi, T., Jolling, S., LaFuer, H., LeBlanc, G. A., et al. (2007). An ecological assessment of bisphenol-A: evidence from comparative biology. Reprod. Toxicol. 24, 225–239. doi: 10.1016/j.reprotox.2007.05.008
Dayou, Z., Yuehan, N., Xiaona, Y., et al. (2021). Trait-based Adaptability of Phragmites Australis to the Effects of Soil Water and Salinity in the Yellow River Delta. Authorea.
de Zalcourt, A., Al-Yousif, M., and Hirt, H. (2013). Rhizosphere microbes as essential partners for plant stress tolerance. Mol. Plant 6, 242-245. doi: 10.1093/mp/sts028
Den, H. C., Kvet, J., and Sukopp, H. (1989). Reed: a common species in decline. Environ. Contam. Toxicol. 40, 189–197. doi: 10.1016/j.ecoleng.2011.12.022
Ding, Z., and Sun, Q. (2021). Effects of flooding depth on metal (loid) absorption and physiological characteristics of Phragmites australis in acid mine drainage phytoremediation. Environ. Technol. Innov. 101512. doi: 10.1016/j.eti.2021.101512
Dong, X., and Reddy, G. B. (2012). Ammonia-oxidizing bacterial community and nitrification rates in constructed wetlands treating swine wastewater. Ecol. Eng. 40, 189-197. doi: 10.1016/j.ecoleng.2011.12.022
Douhovnikoff, V., and Hazeltin, E. L. (2014). Clonal growth: Invasion or stability? a comparative study of clonal architecture and diversity in native and introduced lineages of Phragmites australis (Poaceae). Am. J. Bot. 10, 1577–1584. doi: 10.1016/j.ajb.1400177
Duman, F., Cicek, M., and Sezen, G. (2007). Seasonal changes of metal accumulation and distribution in common club rush (Schoenoplectus lacustris) and common reed (Phragmites australis). Ecotoxicology 16, 457–463. doi: 10.1007/s10646-007-0150-4
Eid, E. M., Kamal, H. S., Yassin, M., Al-S, Soliman, A. H., Tarek, M. G., Hamdi, A., et al. (2021). Temporal Potential of Phragmites australis as a Phytoremediator to Remove Ni and Pb from Water and Sediment in Lake Burullus, Egypt. Bull. Environ. Contam. Toxicol. 106, 516–527. doi: 10.1007/s00120-021-03210-y
Eller, F., Lambertini, C., Nguyen, L. X., and Brix, H. (2014). Increased invasive potential of non-native Phragmites australis: elevated CO2 and temperature alleviate salinity effects on photosynthesis and growth. Glob. Change Biol. 20, 531–543. doi: 10.1111/gcb.12346
Fahid, M., Arslan, M., Shabir, G., Younus, S., Yaseen, T., Rizwan, M., et al. (2020). Phragmites australis in combination with hydrocarbons degrading bacteria is a suitable option for remediation of diesel-contaminated water in floating wetlands. Chemosphere 240,124899. doi: 10.1016/j.chemosphere.2019.124899
Faure, M., San, M. A., Ravelan, P., and Raveton, M. (2012). Concentration responses to organochlorines in Phragmites australis. Environ. Pollut. 164, 188–194. doi: 10.1016/j.envpol.2012.01.040
Fawazy, M. A., Badr, N. E. S., and Abo-El-Kassem, A. (2012). Heavy metal biomonitoring and phytoremediation potentials of aquatic macrophytes in River Nile. Environ. Monit. Assess. 184, 1753–1771. doi: 10.1007/s10661-011-1976-9
Gerhardt, K. D., Huang, X. D., Glick, B. R., and Greenberg, B. M. (2009). Phytoremediation and rhizoremediation of organic soil contamination: potential and challenges. Plant Sci. 176, 20–30. doi: 10.1016/j.plantsci.2008.09.014
Ghasemzadeh, F., Yousefzadeh, H., and Arbab-Zavar, M. H. (2008). Removing arsenic and antimony by Phragmites australis: rhizofiltration technology. J. Appl. Sci. 8, 1668–1675 doi: 10.3923/jas.2008.1668.1675
Gibbs, G. E., Watson, L., Koekemoer, M., Sooklo, L., Barker, N. P., Anderson, H. M., et al. (1990). “Grasses of Southern Africa,” in Memoirs of the Botanical Survey of South Africa No. 58.
Gomez-Hermosillo, C., Pardue, J. H., and Reible, D. D. (2006). Wetland plant uptake of desorption-resistant organic compounds from sediments. Environ. Sci. Technol. 40, 3229–3236. doi: 10.1021/es0513411
Gonzalez, E., Pite, F. E., Pagé, A. P., Marleau, J., Nissim, W. G., St-Arnaud, M., et al. (2018). Trees, fungi, and bacteria: tripartite metatranscriptomics of a root microbiome responding to soil contamination. Microbiome 6, 1–30. doi: 10.1186/s40168-018-0432-5
Guan, W., Yin, M., He, T., and Xie, S. (2015). Influence of substrate type on microbial community structure in vertical-flow constructed wetland treating polluted river water. Environ. Sci. Pollut. Res. 22, 16202–16209. doi: 10.1007/s11356-015-5160-9
Gusewell, S. (2003). Management of Phragmites australis in Swiss fen meadows by mowing in early summer. Wetl. Ecol. Manag. 11, 433–445. doi: 10.1023/B:WETL.0000007197.85070.58
Hallin, S., Hellman, M., Choudhury, M. I., and Ecke, F. (2015). Relative importance of plant uptake and plant associated denitrification for removal of nitrogen from mine drainage insub-arctic wetlands. Water Res. 85, 377–383. doi: 10.1016/j.watres.2015.08.060
Hu, S., He, R., Wang, W., Dayong, Z., Jin, Z., Rui, H., et al. (2021). Composition and co-occurrence patterns of Phragmites australis rhizosphere bacterial community. Aquatic Ecol. 49,855. doi: 10.1007/s10452-021-08955-4
Huang, R., Zeng, J., Zhao, D. Y., Cook, K. V., Hambright, K. D., and Yu, Z. B. (2020). Sediment microbiomes associated with the rhizosphere of emergent macrophytes in a shallow, subtropical lake. Limnol. Oceanogr. 65, S38–S48. doi: 10.1002/lno.11325
Jiang, X. T., Peng, X., Deng, G. H., Sheng, H. F., Wang, Y., Zhou, H. W., et al. (2013). Illumina sequencing of 16S rRNA Tag revealed spatial variations of bacterial communities in a Mangrove wetland. Environ. Microbiol. 66, 96–104. doi: 10.1111/j.1462-2920.2012.02383.x
Jolly, J. (2017). The Goats Fighting America’s Plant Invasion. Available online at: https://www.bbc.com/news/magazine-30583512
Kadlec, R. H., and Wallace, S. (2008). Treatment Wetlands. Boca Raton (FL): CRC Press. Available online at: http://colinmayfield.com/waterhealth/course3/Resources/treatment-wetlands--kadlec-and-wallace--part-iv
Kalu et al. Ecology of Trait-based Adaptability of Phragmites Australis to the Effects of Soil Water and Salinity in the Yellow River Delta. Authorea.
Zhang, X., He, R., Su, R., Zeng, J., Zhou, Q., Huang, R., et al. (2021). Composition and co-occurrence network of the rhizosphere bacterial community of two emergent macrophytes and implications for phytoremediation. Marine Freshwater Res. 9:1689. doi: 10.1071/MF20082

Zhang, X., Zhao, S., Gao, J., Lei, Y., Yuan, Y., Jiang, Y., et al. (2019). Microbial action and mechanisms for Cr(VI) removal performance by layered double hydroxide modified zeolite and quartz sand in constructed wetlands. J. Environ. Manage. 246, 636–646. doi: 10.1016/j.jenvman.2019.06.017

Zhao, Y., Yang, Z., Xia, X., and Wang, F. (2012). A shallow lake remediation regime with Phragmites australis: incorporating nutrient removal and water evapotranspiration. Water Res. 46, 5635–5644. doi: 10.1016/j.watres.2012.07.053

Zou, J., Liu, X., He, C., Zhang, X., Zhong, C., Wang, C., et al. (2013). Effect of Scripus triqueter of its rhizosphere and root exudates on microbial community structure of simulated diesel-spiked wetland. Int. Biodeterior. Biodegrad. 82, 110–116. doi: 10.1016/j.ibiod.2013.03.006

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