

Marta JASKULAK

Częstochowa University of Technology, Faculty of Infrastructure and Environment
Institute of Environmental Engineering
ul. Brzeźnicka 60A, 42-201 Częstochowa
Université Lille Nord de France, LGCgE-Lille 1, Ecologie Numérique et Ecotoxicologie
F-59650 Villeneuve d'Ascq, France
e-mail: m.jaskulak@is.pcz.pl

Implementation of Omics Research to Enhance Phytoremediation Efficiency - a Review

Wdrożenie badań omicznych w celu zwiększenia efektywności fitoremediacji - przegląd

Phytoremediation is recognized as a cost-effective and widely acceptable alternative to chemical and physical technologies of soil remediation but requires an overall longer time to achieve success. In the last decade, the vast progress in omics research had led to improvements in our understanding of plants metabolism under exposure to toxic substances and the interactions between microbial communities and plants. Omics research includes a number of disciplines aimed at explaining the biological and chemical principles of functioning a particular organism exposed to selected factors using modern methods of molecular biology (example: rt-qPCR - Quantitative polymerase chain reaction in real time). The names of individual branches of omics studies arise from a group of studied substances, example: transcriptomic refers to research related to changes occurring in the organism at the level of its transcriptome, and proteomics deals with the determination of complete information on the proteomic composition of a given sample. By merging available omics tools with new bioinformatic approaches, it is possible to understand and determinate the specific patterns of plants response to various stress factors. In this review, we provide an overview of how omics research including transcriptomic, proteomic, genomic and metagenomic approaches might be used to reduce the negative impact of toxic elements to plants growth and development in order to ultimately enhance the phytoremediation efficiency.

Keywords: phytoremediation, heavy metals, phytotoxicity, omics, transcriptomics, genomics

Introduction

Rapid industrial development in past two centuries has caused a significant contribution to soil and water contamination, primarily with heavy metals and organic pollutants [1]. Strategies for environmental clean-up technologies require not only reliable tools but also precise approaches and procedures that are cost-efficient and possible to use during large scale remediation programs subjected to continually changing conditions [2]. The technologies of phytoremediation which involves the use of plants to treat polluted areas have been extensively examined in the past

studies. By definition, phytoremediation takes advantage of plants natural ability to extract various substances including contaminants from soil and water [3]. The primary benefit of this process is its low cost - it has been shown to be at least 10 times less expensive in comparison to chemical and physical methods of environmental clean-up. Moreover, it is also considered as a safe practice since plants can also stabilize the contaminated area minimizing erosion and the amount of contaminated dust that could potentially move to another remote areas [4]. In comparison to bioremediation with bacteria and fungi, phytoremediation is visible and thus can be monitored and continuously controlled. Besides, plants can provide nutrients and stimulate rhizosphere bacteria which can also improve soil quality and aid the whole remediation process [5]. Finally, phytoremediation of degraded sites, especially after large-scale industrial activities, can provide a new habitat for wildlife including insects, birds and small mammals [6].

In the past, phytoremediation has been used to treat multiple kinds of pollutants including heavy metals, polycyclic aromatic hydrocarbons (PAHs), petroleum, solvents, and other toxic organic substances [4]. Depending on the type of substance, phytoremediation can involve different processes and approaches. For example, phytoremediation of metals has a unique challenge due to the fact that, they cannot be metabolized and therefore have to be translocated into the above-ground parts of plants which are easily removable by conventional harvesting. This approach is often referred to as "phytoextraction". It is an effective method of site remediation which reduces the total mass of contaminant [7]. Moreover, in comparison to physical methods which in this case would remove the top, most fertile layer of soil, phytoremediation does not reduce the fertility of the land [8]. Yet, after years of extensive research and successful laboratory trials, phytoremediation still lack large-scale application [9]. The primary drawback of such actions in comparison to classic chemical and physical methods is that it is too slow. In many countries, the regulatory agencies require significant effects in site decontamination to be obtained after just a few years which can make the use of phytoremediation impossible. Due to that, recent research on the ways to enhance the efficiency of phytoremediation has gained a lot of interest [10].

In the past, technologies aimed for developing specific approaches to use plants as bioindicators and then to use such species for remediation were strictly focused on using standard toxicity tests in order to evaluate the level of phytotoxicity and the level of persistence of selected contaminant in plants tissues [11]. For future improvement and optimization of any phytoremediation activities, the precise identification of metabolic mechanisms involved in contaminant tolerance, uptake and detoxification is required [1]. These consist of extremely complex cellular systems and pathways controlled by large families of genes. Thus, to precisely identify such traits for chosen species of plants and their symbiotic microbes, the application of new omics approaches can be a promising idea [12]. To tackle that issues, the next-generation sequencing (NGS) technologies have started to appear around the year of 2005 and since were vastly used in plants research including environmental studies, broadening our understanding of plants metabolism and interactions

between plants and symbiotic microbes [13]. In the beginning, large omics data was translated into applicable technologies mostly exclusively in medicine and health sector, due to its extremely high costs at the time. However, the total cost of NGS techniques is rapidly decreasing in recent years and therefore it is being applied to all kinds of life sciences including the problems of soil and water contamination [14, 15].

This review explores recent advances in application of omics in research involved in remediation of contaminated soils. Study mostly focuses on the applicability of transcriptomic and proteomics studies that allow for the identification of genes related to specific pathways of detoxification after exposure to heavy metals and organic pollutants. Moreover, the study presents recent advances of using omics studies to design new, genetically engineered plants for phytoremediation. We describe and discuss how the NGS approaches can be used to advance plants research and how it can be used in new phytoremediation strategies. Overall, we focused on phytoremediation; however, the high-throughput approaches are also massively studied for other environmental purposes such as managing plants pathogens and invasive species or optimizing the production of crops.

1. Standard approaches for phytoremediation of contaminated sites

The cost of chemical and physical treatments of contaminated sites is exceptionally high and involves transport, soil washing, excavation, extraction, pumping and chemical treatments including the addition of potassium permanganate, hydrogen peroxide and finally incineration. Therefore, due to the high cost, contaminated lands owned by private companies are more often abandoned and not properly cleaned up [7]. Hence, the implementation of more cost-efficient methods of soil remediation, such as phytoextraction of metals or phytodegradation of organic pollutants could potentially be a promising solution, especially in large areas contaminated in the past via various range of anthropogenic sources [16]. In order to achieve satisfactory results, investigation of the specific, best suitable plant species for given process is a necessity [17].

Plant species that are the most useful for phytoextraction are termed as metal hyperaccumulators - meaning that they are able to concentrate high level of metals in its biomass [18]. For example, in recent years *Petris vittata* had been used to remove arsenic by its hyperaccumulation. Arsenic is an acute and lethal poison, and *P. vittata* can extract it from a soil concentration of 97 ppm up to 894 µg per gram of its biomass. Moreover, approximately 95% of arsenic was translocated to plants shoots which were easily harvested [13]. Another example of successfully field-tested hyperaccumulator is *Thlaspi caerulescens* which is able to accumulate toxic cadmium in its shoots in a concentration exceeding the phytotoxic threshold by over a 1000 times [19]. The mechanisms of cadmium uptake in the whole *Brassicaceae* family have been studied and were shown to involve metal transporters

which are extensively expressed during such exposure. At the same time, since *Brassicaceae* are quite small and light-weight plants, high-biomass species including poplar and willow trees are also vastly studied for phytoremediation purposes [20].

For degradation of organic pollutants, phytodegradation seems to be an optimal solution which involves degradation of such contaminants by specific plants [17]. During this approach, plants metabolism breaks down the organic substance through internal or secreted enzymes. This process is currently mostly used for breaking down polycyclic aromatic hydrocarbons (PAHs), chlorinated hydrocarbons and multiple explosives [4]. As an example, hybrid poplars had been used to take up and degrade trichloroethylene (TCE), which is a common pollutant of groundwater that is both hepatotoxic and carcinogenic for humans [21]. Other example of victorious application of phytodegradation includes the use of multiple plant species to degrade carbon tetrachloride (CT) and perchloroethylene [22]. Phytodegradation also had been shown to be successful for polycyclic aromatic hydrocarbons (PAHs) and explosives including trinitrotoluene (TNT) [21, 23]. Through recent decades, the amount of PAHs in the environment is constantly increasing. One example of plant efficiency in PAHs degradation is *Populus nigra* which was shown to reduce the range of PAHs such as pyrene, benzopyrene, anthracene, phenanthrene, and chrysene [16].

Another alternative for contaminant clean-up is augmented bioremediation with specific bacterial species and strains that are able to transform or degrade particular contaminants [2]. On the other hand, this technology faces major drawback involving high sensitivity of microbial communities and thus, for successive remediation strict conditions must be kept on an optimal level. The primary conditions affecting the efficiency of such activities include the bioavailability and accessibility of specific microorganisms, the ability of selected microorganisms to survive and grow on a given environment, the presence and persistence of other dominant species, the presence of carbon as well as access to the source of all required micro and macronutrients [12].

2. Metagenomic approach to enhance phytoremediation efficiency

Introduction of plants to highly degraded and contaminated soils may augment both the quantity and quality of microbial populations occurring in bulk soil [24]. Although plant-microbe interactions are incredibly complex and sensitive to different environmental conditions, plants can favour certain species that promote its growth or inhibit the activity of pathogens. Moreover, microorganisms can also impact the potential uptake of pollutants including the uptake and translocation of heavy metals from roots to shoots of plants [23]. Overall, microbial communities that are able to create associations with plants can influence plants growth and development both positively and negatively which as a consequence will alter plants ability to remediate the soil [22]. Contaminants such as heavy metals can be

also either transformed by specific microorganisms in rhizosphere or be taken up and translocated by plants. Stimulation of microbial activities can be increased due to plants through the release of root exudate [12]. In order to test such complex interactions, metagenomic research can be extremely useful. In a brief, metagenomics is the study of the whole genetic material recovered directly from the environmental samples. Therefore, the metagenome refers to all of the genetic material that is present in the selected environmental sample, and consist of the genomes of many individual organisms [23].

A couple of recent studies in phytoremediation research including actual field trials used targeted amplicon sequencing in order to show, that the bacterial and fungi communities are shaped by two main factors: the concentration of the contaminant in the soil and the plant phylogeny [21, 25]. Other studies also noticed that the composition of arbuscular mycorrhizal depends on the concentration of metal [6]. Thus, studies suggest that plants abiotic stress can determinate the stimulation of microbial bioremediation. For example, experiment from 2012 showed, that exudate produced by wild rye exposed to hydrocarbons were not as repressive as exudate from wild rye grown on an uncontaminated medium, which overall demonstrated that plants might alter the extent to which they will promote total rhizosphere biodegradation [25]. Thus, it has to be taken into consideration that the overall degree to which plants can exert control over bacterial and fungi communities strictly depends on the concentration of given contaminant and its overall severity of toxic effects [26].

It is well established, that soil microorganisms play the crucial role in mineralization of organic matter in soils and also can transform specific contaminants to its different chemical forms including more stable and less toxic ones [27]. At the same time, one of the most frequent problems with research on soil microbial communities is that in many cases more than 99% of obtained microbial taxa are not yet cultured. Therefore, using NGS technologies can allow for significantly more thorough analysis of microbial composition and their activity while preserving environmental factors (both abiotic and biotic) that once shaped these microbial communities *in situ* [5]. In addition, to adequately probe the plant-associated microbial communities and examine plant-dependent habitats including plants rhizosphere, phyllosphere and endosphere, shotgun sequencing and amplicon-targeting of genes can be also used as a promising tool [20]. During the process of shotgun sequencing, the isolated DNA is broken up randomly into small segments, which are later sequenced using the chain termination method [7]. Bioinformatic tools are then used, and the overlapping ends of different reads are being assembled into one continuous sequence. Therefore, the novel advances in bioinformatics, had greatly aided the analysis of DNA sequences obtained from complex environmental samples, which allows the adaptation of shotgun sequencing to metagenomic samples. Such approach can be used to sequence many cultured microorganisms. Overall, the shotgun sequencing reveals all genes present in environmental samples [22]. In the study by Hao et al. shotgun high throughput metagenomic sequencing was used in order to capture the PAHs degrading features of *Taxus*

rhizosphere microbiome. Study showed numerous functional genes associated with biodegradation and metabolism of xenobiotics as well as multiple genes involved in a range of defence mechanisms against organic pollutants [26].

Simultaneously, in recent years of phytoremediation research, a lot of interest has also been given to plasmid DNA since contaminated soils, and plants rhizosphere is known to be a hotspot for rapid exchange of plasmids [6]. During the abiotic stress, plasmids can be used as a reservoir for genomic innovation which can enable the symbiotic bacteria and fungi to adapt to stress conditions. During one research, metagenomic sequencing of plasmid DNA from municipal wastewater-treatment plants displayed, that genes involved in heavy metal resistance are disproportionately abundant in plasmid DNA in comparison to the entire genome. The same study showed, that genes involved in the transformation and degradation of organic pollutants are also mostly present in plasmids [24]. Such knowledge has already been applied, and plasmids with genes responsible for toluene degradation were successfully transferred to aerial plant endophytes and increased the total degradation of contaminant that would have been volatilized [26]. Besides, metagenomic research performed in changing environmental conditions showed that the microbial communities in terms of its genetic and taxonomic composition could be linked to its activity to metabolize carbon. Also, the analysis of metagenomic DNA showed specific taxa which are involved in the suppression of plants diseases in soils [21]. Experiments by Balcom et al. displayed the potential of microorganisms to metabolise micropollutants such as xenobiotics during the process of wastewater treatment [24]. Metagenomic analysis revealed microorganisms and specific genes involved in degradation of benzoate. Collectively, study showed the abundance of xenobiotic metabolism genes present in biofilm of created wastewater treatment plant. In another study, metagenomic approach was applied to investigate the response of rhizosphere microorganisms of rice after exposure to PAHs. Results revealed that the total distance from the surface of roots and PAHs concentration affected the microbial communities in rice rhizosphere. Moreover, the abundance of genes related to PAHs degradation including dioxygenase genes mirrored the potential to PAHs degradation in rice rhizosphere [22]. A 2019 study applied molecular metagenomic approaches as well as compound-specific isotope analysis in order to check the efficiency and mechanisms of toluene biodegradation in the unsaturated zone where poplars were used to remediate the soil. Experiments revealed spatially-variable numbers of toluene degraders were in roots of hybrid poplars as well as other evidence for toluene biodegradation in the unsaturated zone [21]. Table 1 demonstrates the variability of environmental applications of metagenomic studies from the past five years. To summarize, metagenomic analyses can be used in environmental studies in various ways including: (i) to indicate some functional attributes to selected microbial assemblages; (ii) to identify and determinate the function of microbial genes associated to vast range of functions including the promotion of plants growth or biodegradation of hydrocarbons; (iii) to determinate the distinct environmental conditions that will favour our target symbiotic microorganisms [21, 23]. Moreover, it is now possible to determi-

nate the potential of not yet cultured microorganisms in the promotion of plants growth or contaminant biodegradation by the use of single-cell isolation and sequencing technologies. Such methods can not only precisely determine the full genome of selected uncultured strains but also identify new targets to be used in the field tests [22].

Table 1. **Major metagenomic studies applied for remediation of environmental contamination since 2014**

Goal of metagenomic research	Contaminant	Year	Reference
Analysis of an wastewater treatment plants microbial communities and their potential to metabolize pharmaceuticals	pharmaceuticals	2016	[24]
Understanding the mechanism and function of plant growth-promoting rhizobacteria (PGPR)	none	2017	[12]
Analysis of the response of microbial metagenome to polycyclic aromatic hydrocarbons (PAHs) degradation in the rice rhizosphere	PAHs	2015	[22]
Perspectives of lindane (γ -hexachlorocyclohexane) biodegradation	lindane	2018	[23]
Identification of the potential for toluene biodegradation in the vadose zone of a poplar	toluene	2019	[21]
Analysis of the influence of cadmium contamination on bioenergy cropping and microbial composition of cadmium contaminated soil	cadmium	2017	[6]
Analysis of the potential of <i>Taxus</i> rhizosphere microbiome for bioremediation and phytoremediation	none	2018	[26]
Analysis of rhizosphere microorganisms of PAHs contaminated soil planted with barley and alfalfa	PAHs	2018	[23]
Identification of the influence of microbial community on the efficiency of metal phytoremediation by <i>Sedum plumbizincicola</i>	cadmium and zinc	2017	[27]

3. Plants genomic and transcriptomic studies in the aspects of environmental contamination

3.1. Genomic

The incorporation of genomic approaches into environmental sciences has led to the identification of multiple genes involved in phytoremediation and plant tolerance to abiotic stress, including several contaminants [28]. It is well established, that the high-throughput techniques are especially useful in order to identify plants traits that depend on the specific combination of several genes. As an example, the mapping of quantitative trait loci between hybrids of zinc-tolerant *Arabidopsis helleri* and *Arabidopsis lyrata* which is zinc-intolerant had identified a couple of genomic regions that when combined explained more than 42% of plants tolerance

to zinc [10]. Quantitative trait locus analysis is a statistical method that links two types of information - the phenotypic data (selected trait measurements) and the genotypic data (usually selected molecular markers), in order to explain the genetic basis of variation in complex traits [11]. Similarly, quantitative trait loci for the accumulation of arsenic were successfully identified in leaves and stems of maize. Moreover, this study showed that only one of the quantitative trait loci was present in both tissues which suggested that for arsenic accumulation different genes are responsible in different tissues of the plant [4]. It also has to be noticed, that the complexity of plants genomes, which often include extreme polyploidy required extensive genomic characterization across species suitable for phytoremediation in order to identify the specific mechanisms involved in the selected type of remediation of a given contaminant. Therefore, the activity-focused approaches including such technologies as transcriptomics and proteomics might permit the precise examination of the functionality of specific candidate plant species after exposure to distinct environmental conditions including the type and concentration of the given contaminant [19].

3.2. Transcriptomic

Currently, most research in plants omics analyses in the area of environmental contamination has been performed on plants exposed to various heavy metals (Table 2). There are numerous examples of using transcriptomics to identify genes involved in stress tolerance in plants (Table 2). For instance, the stress response of *Brassica chinensis* exposed to chromium had been described using these technologies [29]. Work of Yildirim et al. applied Genome-wide transcriptome profiling in *Populus nigra* grown under exposure to boron and found several candidate genes responsible in boron uptake, transport and detoxification. During that study, highest induction was recorded for genes encoding: tyrosine aminotransferase, ATP binding cassette transporters, glutathione S transferases and metallochaperones. All of those genes are involved in cell detoxification including transport of substances to vacuoles, binding metals and the antioxidative response. Moreover, many other genes were showed to be highly upregulated after exposure to boron including genes involved in antioxidative systems, and signalling [9]. Another study, from 2018 revealed in total 72 metabolism pathways, including photosynthesis, phenylalanine metabolism, ribosome, phenylpropanoid biosynthesis, flavonoid biosynthesis and carbon fixation in *Phytolacca americana* exposed to cadmium. In addition, numerous genes related to cadmium tolerance, absorption, transport and accumulation were also determined, including the total of 11 expansins, 8 nicotianamine synthases, 6 aquaporins, 4 ZRT/IRT-like proteins, 3 ABC transporters and 3 metallothioneins [6]. In study by Song et al. analysis of transcriptome led to the determination of functional genes upregulated by stress caused by herbicide - atrazine. Among these were genes encoding the zinc finger proteins, intracellular/extracellular enzymes, structural proteins, anti-stress/anti-disease proteins, and electron transport-related proteins [5]. The results of another researchers showed regulatory mechanisms induced after the exposure to petroleum hydrocarbon stress

in *Z. mays* [4]. Transcriptomic approach was also applied to investigate the effects of thorium on plants metabolism. Thorium is actinide metal with high potential in nuclear energetics. Contamination by thorium, is mostly caused by mining or spills, and poses a significant threat since it is radioactive. Study from 2018 investigated the transcriptomic response of tobacco roots exposed to thorium. Such exposure resulted in up-regulation of the total of 152 genes and down-regulation of 100 genes. The induced genes were mostly related to the production of jasmonic and salicylic acid signalling pathways and various abiotic and biotic stress responsive genes. In addition, up-regulation was noticed in phosphate starvation genes and down-regulation in genes encoding the synthesis of phytic acid which indicated that thorium disturbed phosphate uptake or its signalling. Moreover, the expression of iron responsive genes was also highly influenced by exposure. The down-regulation of some aquaporins showed a severe disturbance of water homeostasis [30].

Overall, transcriptomic analyses can also be performed in a comparative matter, and such a connection between different species suitable for phytoremediation can allow identifying genes responsible for differences in plants response. In one study, researchers compared two species exposed to cadmium - *Solanum torvum* which does not accumulate significant amounts of cadmium in its tissues and *Solanum nigrum* which is identified as hyperaccumulator of Cd. Transcriptomic analyses identified a higher expression of multiple genes in *S. nigrum* which were involved in the transportation of metals and were not expressed in *S. torvum* [31].

Table 2. Major transcriptomic studies since 2014 of plants exposed to environmental contamination

Species	Contaminant	Year	Reference
<i>Sedum alfredii</i>	cadmium	2016	[8]
<i>Populus nigra</i>	boron	2016	[9]
<i>Phytolacca americana</i>	cadmium	2018	[6]
<i>Medicago sativa</i>	atrazine	2016	[5]
<i>Landoltia punctata</i>	cadmium	2018	[34]
<i>Zea mays</i>	PAHs	2018	[4]
<i>Festuca arundinacea</i>	cadmium	2018	[15]
<i>Nicotiana tabacum</i>	thorium	2018	[30]
<i>Sorghum bicolor</i>	cadmium	2017	[14]

3.3. The use of omics for designing new transgenic species

Currently, there is a growing interest in research focused on improving plants capacity to stabilize, store or remove specific contaminants from water and soil environments [33]. Successfully identified genes from microbes and plants are being used to enhance plants ability to survive, tolerate, store and degrade toxic substances [7]. In the past five years, the use of transgenic plants with specific bacterial genes had been successfully used to decrease the phytotoxic effects of nitro-

aromatic contaminants which were then used for their removal from soil (Table 3). Moreover, the overexpression of cytochrome P450s genes had been shown to increase the metabolism of a vast variety of herbicides and environmental pollutants in plants [17]. Also, genes involved in detoxification of heavy metals are used to enhance the efficiency of metal phytoremediation in numerous recent studies [10, 28, 32]. One of the studies showed that transgenic plants with bacterial genes could convert herbicide simazine to different and nontoxic forms [17]. Nahar et al. cloned, and transformed the *AtACR2* gene (encoding arsenic reductase 2) of *Arabidopsis thaliana* into the genome of *Nicotiana tabacum*. The obtained results revealed that the transgenic tobacco was much more tolerant to arsenic exposure than the wild type. Overall, transgenic plants could grow on medium containing 200 μ M of arsenate, whereas the wild could not survive such exposure [10]. Study by Zhang et al. investigated contamination, from the explosives, including hexahydro-1, 3, 5-trinitro-1, 3, 5-triazine (RDX), and 2, 4, 6-trinitrotoluene (TNT), on real sites contaminated due to fire training, military ranges in the USA. Such pollution creates a significant threat for both the environment and human health. Phytoremediation and phytodegradation of such explosives is a promising idea but high phytotoxicity of TNT makes it impossible to use on most plants species. Hence, the bacterial genes *xplA* and *xplB*, encoding the ability to degrade RDX and a bacterial nitroreductase gene *nfsI* was cloned and transformed into *Pascopyrum smithii* in order to enhance the capacity of plants to survive and detoxify TNT. All previous studies have used model plant species to demonstrate the efficacy of this action, therefore this time Perennial western wheatgrass was used as it is a United States native species, broadly distributed across all North America and useful for phytoremediation. Study showed that transformed plants removed significantly more RDX when compared to wild-type plants. Furthermore, these plants were also more resistant to TNT toxicity, and detoxified more TNT than wild-type plants [34].

Table 3. Successful application of transgenic plants during phytoremediation of selected contaminant from past five years

Transgenic species	Donor species	Used gene	Contaminant	Year	Reference
<i>Nicotiana tabacum</i>	<i>Arabidopsis thaliana</i>	<i>AtACR2</i> (arsenic reductase 2)	arsenic	2017	[10]
<i>Nicotiana tabacum</i>	<i>Oryza sativa</i>	<i>OsMTP1</i> protein belonging to the cation diffusion facilitator (CDF) and metal tolerance/transport protein (MTP) family	cadmium	2016	[28]
<i>Arabidopsis thaliana</i>	<i>Homo sapiens</i>	P450 isozymes <i>CYP1A2</i>	simazine	2016	[17]
<i>Medicago sativa</i>	<i>Acinetobacter radioresistens</i>	bacteria 2, 3-dihydroxybiphenyl-1, 2-dioxygenase gene (<i>bphC. B</i>)	Polychlorinated biphenyls (PCBs)	2018	[7]
<i>Pascopyrum smithii</i>	Range of bacteria species	<i>xplA</i> and <i>xplB</i> , confer the ability to degrade RDX in plants, and a bacterial nitroreductase gene <i>nfsI</i>	RDX and TNT	2018	[34]

Conclusions

Phytoremediation can be a reliable, cost-efficient and vastly socially acceptable technology for dealing with contaminated lands. To increase its efficiency new omics approaches has gained a lot of interest in recent years [34]. Our review shows, that such large omics data sets have already identified specific environmental conditions that shape the quantity and quality of microbial communities in soil. The possibility to alter the microbial composition through the introduction of plants or to alter plants growth via manipulation of microbial communities has application not only directly for phytoremediation purposes but also for the management of invasive species the production of crops and biofuel. One of the most prominent advantages of using omics for such research is its continuously-growing sets of data and continuously-decreasing costs. Therefore, the translocation of obtained data and overall knowledge into useful technologies is depending on research that uses omics analyses with precise applicable goals.

Acknowledgements

Study supported by internal grants BS/PB-401-304/11 and BS/MN-401-303/18.

References

- [1] Chaâbene Z., Rorat A., Hakim IR., Bernard F., Douglas GC., Elleuch A., Vandembulcke F., Mejdoub H., Insight into the expression variation of metal-responsive genes in the seedling of date palm (*Phoenix dactylifera*), *Chemosphere* 2018, 197, 123-134.
- [2] Grobelak A., Świątek J., Murtaś A., Jaskulak M., Cadmium-induced oxidative stress in plants, cadmium toxicity, and tolerance in plants, from physiology to remediation, *Cadmium Toxicity and Tolerance in Plants* 2019, 213-231.
- [3] Anjum NA., Shahid U., Iqbal M., Assessment of cadmium accumulation, toxicity, and tolerance in Brassicaceae and Fabaceae plants-implications for phytoremediation, *Environmental Science and Pollution Research* 2014, 21(17), 10286-10293.
- [4] Cevher-Keskin B., Selçukcan-Erol Ç., Yüksel B., Ertekin Ö., Yıldızhan Y., Onarıcı S., Memon A.R., Comparative transcriptome analysis of *Zea mays* in response to petroleum hydrocarbon stress, *Environmental Science and Pollution Research* 2018, 25(32), 32660-32674.
- [5] Song F., Li J., Fan X., Zhang Q., Chang W., Yang F., Geng G., Transcriptome analysis of *Glomus mosseae*/*Medicago sativa* mycorrhiza on atrazine stress, *Scientific Reports* 2016, 6(1), 202-245.
- [6] Chen Y., Zhi J., Zhang H., Li J., Zhao Q., Transcriptome analysis of *Phytolacca americana* L. in response to cadmium stress, *PLoS One* 2018, 13(6), e0199721.
- [7] Ren H., Wan Y., Zhao Y., Phytoremediation of polychlorinated biphenyl-contaminated soil by transgenic alfalfa associated bioemulsifier A1nA, *Twenty Years of Research and Development on Soil Pollution and Remediation in China*, 2018, 645-653.
- [8] Han X., Yin H., Song X., Zhang Y., Liu M., Sang J., Zhuo R., Integration of small RNAs, degradome and transcriptome sequencing in hyperaccumulator *Sedum alfredii* uncovers a complex regulatory network and provides insights into cadmium phytoremediation, *Plant Biotechnology Journal* 2016, 14(6), 1470-1483.
- [9] Yıldırım K., Uylaş S., Genome-wide transcriptome profiling of black poplar (*Populus nigra* L.) under boron toxicity revealed candidate genes responsible in boron uptake, transport and detoxification, *Plant Physiology and Biochemistry* 2016, 109, 146-155.

- [10] Nahar N., Rahman A., Nawani N.N., Ghosh S., Mandal A., Phytoremediation of arsenic from the contaminated soil using transgenic tobacco plants expressing ACR2 gene of *Arabidopsis thaliana*, *Journal of Plant Physiology* 2017, 218, 121-126.
- [11] Cox A., Venkatachalam P., Sahi S., Sharma N., Silver and titanium dioxide nanoparticle toxicity in plants: A review of current research, *Plant Physiology Biochemistry* 2017, 107, 147-163.
- [12] Bramhachari P.V., Nagaraju G.P., Kariali E., Metagenomic approaches in understanding the mechanism and function of PGPRs: Perspectives for sustainable agriculture, *Agriculturally Important Microbes for Sustainable Agriculture*, 2017, 163-182.
- [13] Liu X., Fu J., Tang N., Silva E.D., Cao Y., Turner B.L., Ma L.Q., Phytate induced arsenic uptake and plant growth in arsenic-hyperaccumulator *Pteris vittata*, *Environmental Pollution* 2017, 226, 212-218.
- [14] Feng J., Jia W., Lv S., Bao H., Miao F., Zhang X., Li Y., Comparative transcriptome combined with morpho-physiological analyses revealed key factors for differential cadmium accumulation in two contrasting sweet sorghum genotypes, *Plant Biotechnology Journal* 2017, 16(2), 558-571.
- [15] Zhu H., Ai H., Cao L., Sui R., Ye H., Du D., Chen L., Transcriptome analysis providing novel insights for Cd-resistant tall fescue responses to Cd stress, *Ecotoxicology and Environmental Safety* 2018, 160, 349-356.
- [16] Marchand L., Sabaris C., Desjardins D., Oustrière N., Pesme E., Butin D., Mench M., Plant responses to a phytomanaged urban technosol contaminated by trace elements and polycyclic aromatic hydrocarbons, *Environmental Science and Pollution Research* 2015, 23(4), 3120-3135.
- [17] Azab E., Hegazy A.K., El-Sharnouby M.E., Elsalam H.E., Phytoremediation of the organic Xenobiotic simazine by p450-1a2 transgenic *Arabidopsis thaliana* plants, *International Journal of Phytoremediation* 2016, 18(7), 738-746.
- [18] Jaskulak M., Rorat A., Grobelak A., Kacprzak M., Antioxidative enzymes and expression of *rbcl* gene as tools to monitor heavy metal-related stress in plants, *Journal of Environmental Management* 2018, 218, 71-78.
- [19] Bayçu G., Gevrek-Kürüm N., Moustaka J., Csatári I., Rognes S.E., Moustakas M., Cadmium-zinc accumulation and photosystem II responses of *Noccea caerulea* to Cd and Zn exposure, *Environmental Science and Pollution Research* 2016, 24(3), 2840-2850.
- [20] Kumar D., Pannu R., Perspectives of lindane (γ -hexachlorocyclohexane) biodegradation from the environment: A review, *Bioresources and Bioprocessing* 2018, 5(1), 29.
- [21] Benisrael M., Wanner P., Aravena R., Parker B.L., Haack E.A., Tsao D.T., Dunfield K.E., Toluene biodegradation in the vadose zone of a poplar phytoremediation system identified using metagenomics and toluene-specific stable carbon isotope analysis, *International Journal of Phytoremediation* 2019, 1-10.
- [22] Ma B., Lyu X., Zha T., Gong J., He Y., Xu J., Reconstructed metagenomes reveal changes of microbial functional profiling during PAHs degradation along a rice (*Oryza sativa*) rhizosphere gradient, *Journal of Applied Microbiology* 2015, 118(4), 890-900.
- [23] Kumar V., Almomin S., Al-Aqeel H., Al-Salameen F., Nair S., Shajan A., Metagenomic analysis of rhizosphere microflora of oil-contaminated soil planted with barley and alfalfa, *Plos One* 2018, 13(8).
- [24] Balcom I.N., Driscoll H., Vincent J., Leduc M., Metagenomic analysis of an ecological wastewater treatment plant's microbial communities and their potential to metabolize pharmaceuticals, *F1000Research* 2018, 5, 1881.
- [25] Phillips L.A., Greer C.W., Farrell R.E., Germida J.J., Plant root exudates impact the hydrocarbon degradation potential of a weathered-hydrocarbon contaminated soil, *Applied Soil Ecology* 2012, 52, 56-64.
- [26] Hao D., Zhang C., Xiao P., The first *Taxus* rhizosphere microbiome revealed by shotgun metagenomic sequencing, *Journal of Basic Microbiology* 2018, 58(6), 501-512.

- [27] Hou J., Liu W., Wu L., Hu P., Ma T., Luo Y., Christie P., Modulation of the efficiency of trace metal phytoremediation by *Sedum plumbizincicola* by microbial community structure and function, *Plant and Soil* 2017, 421(1-2), 285-299.
- [28] Das N., Bhattacharya S., Maiti M.K., Enhanced cadmium accumulation and tolerance in transgenic tobacco overexpressing rice metal tolerance protein gene OsMTP1 is promising for phytoremediation, *Plant Physiology and Biochemistry* 2016, 105, 297-309.
- [29] Zhou Q., Guo J., He C., Shen C., Huang Y., Chen J., Yang Z., Comparative transcriptome analysis between low- and high-cadmium-accumulating genotypes of pakchoi (*Brassica chinensis* L.) in response to cadmium stress, *Environmental Science & Technology* 2016, 50(12), 6485-6494.
- [30] Mazari K., Landa P., Přerostová S., Müller K., Vaňková R., Soudek P., Vaněk T., Thorium impact on tobacco root transcriptome, *Journal of Hazardous Materials* 2017, 325, 163-169.
- [31] Wang S., Wei S., Ji D., Bai J., Co-planting cd contaminated field using hyperaccumulator *Solanum Nigrum* L. through interplant with low accumulation welsh onion, *International Journal of Phytoremediation* 2015, 17(9), 879-884.
- [32] Grobelak A., Kokot P., Świątek J., Jaskulak M., Rorat A., Bacterial ACC deaminase activity in promoting plant growth on areas contaminated with heavy metals, *Journal of Ecological Engineering* 2018, 19(5), 150-157.
- [33] Bernard F., Dumez S., Lemière S., Platel A., Nesslany F., Deram A., Vandebulcke F., Cuny D., Impact of cadmium on forage kale (*Brassica oleracea* var. *viridis* cv "Prover") after 3-,10- and 56-day exposure to a Cd-spiked field soil, *Environmental Science and Pollution Research* 2018, 1-9.
- [34] Zhang L., Rylott E.L., Bruce N. C., Strand S.E., Genetic modification of western wheatgrass (*Pascopyrum smithii*) for the phytoremediation of RDX and TNT, *Planta* 2018, 1-9.

Streszczenie

Fitoremediacja jest uznawana za opłacalną i powszechnie akceptowaną alternatywę dla chemicznych i fizycznych technologii remediacji gleby, ale wymaga dłuższego czasu, aby osiągnąć sukces. W ostatnim dziesięcioleciu ogromny postęp w badaniach omicznych doprowadził do poprawy zrozumienia metabolizmu roślin poddanych ekspozycji na substancje toksyczne oraz interakcji pomiędzy mikroorganizmami symbiotycznymi a roślinami. Badania omiczne obejmują szereg dyscyplin zmierzających do wyjaśniania biologiczno-chemicznych zasad funkcjonowania wybranego organizmu poddanego danym czynnikom za pomocą nowoczesnych metod biologii molekularnej (np. rt-qPCR - ilościowa reakcja łańcuchowa polimerazy w czasie rzeczywistym). Nazwy poszczególnych gałęzi badań omicznych powstają od grupy badanych substancji, np. transkryptomika dotyczy badań związanych ze zmianami zachodzącymi w organizmie na poziomie jego transkryptomu, a proteomika zajmuje się określeniem pełnej informacji o składzie proteomicznym danej próbki. Łącząc dostępne narzędzia omiczne z nowymi technikami bioinformatycznymi, możliwe jest zrozumienie i określenie specyficznych wzorców reakcji komórek roślin na różne czynniki stresowe. W pracy przedstawiono przegląd najnowszych badań omicznych, w tym transkryptomicznych, proteomicznych, genomicznych i metagenomicznych, stosowanych w badaniach nad zmniejszeniem negatywnego wpływu toksycznych substancji na wzrost i rozwój roślin w celu zwiększenia skuteczności procesu fitoremediacji.

Słowa kluczowe: fitoremediacja, metale ciężkie, fitotoksyczność, badania omiczne, transkryptomika, genomika