Chapter 12
"Omics" Technologies in Biodegradation Processes

Sevcan Aydin and Mahmut Çalışkan

Abstract The considerable environmental impact of pollution due to human activities is driving the development of new decontamination and clean-up methods. Hereby, the interactions between the various microbial communities at polluted sites is receiving increased research attention, with the novel omics approaches, opening up new ways to study bioremediation pathways and their mechanisms. This has allowed innovation in the field of new bioremediation as an effective way to combat pollution. In particular, the omics approaches offer great potential to predict the metabolic processes of microbes in environments experiencing pollution. The high-performance analyses provided by these approaches can, amongst others, help track novel organisms for use in bioremediation and offer new, high-quality insights into those molecular pathways that are critical to biodegradation. In short, through multi-omics approaches, the field of bioremediation will benefit from the establishment of new theory-based methodologies to mitigate pollution.

Keywords Bioremediation · Biodegradation · Microorganisms · Metagenomics · Genetic analysis · Horizontal gene transfer

12.1 Introduction

Due to population growth and the accompanying increase in industrial activities, pollution is rising across the world. The growth of industrialization in particular has led to manufacturing processes that produce and incorporate various chemicals for use in high-tech products, including heavy metals, hydrocarbons, and xenobiotics. These substances are not only toxic but also persist in the environment, and thus have a significant adverse effect on ecosystems and organisms. However, there are

---

S. Aydin (✉) · M. Çalışkan
Division of Biotechnology, Biology Department, Faculty of Science, Istanbul University, Istanbul, Turkey
e-mail: sevcan.aydin@istanbul.edu.tr

T. Encarnação, A. Canelas Pais (eds.), *Marine Organisms: A Solution to Environmental Pollution?*, Environmental Challenges and Solutions,
https://doi.org/10.1007/978-3-031-17226-7_12

several natural methods that can address these imbalances, with microorganisms representing an effective natural tool with which to remove toxic compounds from contaminated sites. Microbial-mediated biodegradation therefore has considerable potential to naturally restore polluted ecosystems (Shahi et al. 2016a; Aydin et al. 2017; Nwankwo et al. 2021; Sales et al. 2021).

The microbial ecology of an environment, whether pristine or anthropogenically affected, can be assessed using culture-based methods. However, as many of the identified microorganisms of interest to research are not culturable in a laboratory, there remain several challenges in their study. The research trying to culture such microbial communities has so far only been successful with no more than 1% of any given sample of prokaryotes. Moreover, there remains a gap in the knowledge of which factors influence the microbial communities of polluted environments, e.g. their metabolism, growth, or dynamics. Of the abovementioned omics approaches, metagenomics offers a way to conduct genome-level studies of microbial communities, providing substantial insights into the so-called uncultured microbiota (Aydin et al. 2015). The other omics approaches, such as genomics, transcriptomics, proteomics, and metabolomics, have recently also begun to offer an array of advanced techniques designed to treat pollutants in a way that causes no further damage to the environment (Aydin et al. 2022; Malik et al. 2021; Wright et al. 2021).

This chapter sets out to explore to what extent omics techniques can be applied to monitor the processes of biodegradation. In this context, it proposes using a community systems biology approach, integrating the abovementioned multi-omics with bioinformatics as well as simulation tools. The aim hereby is to enhance the predictive ability of models regarding the persistence of toxic chemicals in environmental settings, which should be taken into account and integrated into a tiered assessment strategy regarding the persistence of toxic chemicals. The findings of the research should offer an enhanced understanding of how the composition of the microbial community relates to the catabolic potential and environmental conditions as well as the properties of the chemical under investigation.

12.2 Omics Approaches for Monitoring Biodegradation Processes

Pollution continues to be both a tenacious problem and a significant threat to the health of humans and the environment. While numerous strategies have been applied to address this issue, it is still a challenge, even in terms of simple monitoring, and environmental contamination continues on a global scale. The severity of the issue calls for novel pollution mitigation strategies to ensure environmental and human health, with bioremediation being one of the most promising to emerge in recent years. Bioremediation using microorganisms is receiving increasing research interest, with studies striving to identify ways to effectively restore environments affected by pollution (Shahi et al. 2016b). Microorganisms present themselves as particularly suitable as they can exist in a variety of environments, even degraded ones, by producing metabolites that have the ability to degrade or even transform contaminants, thereby allowing polluted sites to be naturally restored (Kour et al. 2021). The design of effective strategies hereby depends on modern omics technologies, including metagenomics, proteomics, and transcriptomics, which enable the microbiota's diversity and ecology to be studied to facilitate their implementation in the context of environmental monitoring as well as bioremediation (Aydin 2016).

Strategies based on bioremediation or biotransformation aim to exploit the natural diverse catabolic abilities of microorganisms regarding the degradation, accumulation, or transformation of multitudinous environmentally harmful compounds, such as pharmaceutical substances, heavy metals and polyaromatic hydrocarbons (PAHs). Recent developments in next-generation sequencing (NGS) have enabled key microorganisms to be genomically, metagenomically, and bioinformatically analyzed, allowing hitherto incomprehensible biodegradative pathways to be understood (Shahi et al. 2016c; Tancsics et al. 2021). Similarly, horizontal gene transfer (HGT) is crucial to the processes of microbial biodegradation in that it affects the activities of the microbiota. Specifically, bioremediation relies on functional genes to be transferred between key members of the microbial community. As the availability of macronutrients, among various other abiotic factors, influence HGT in polluted settings, the microbiota's capacity for biodegradation is dissimilar between sites. Hence, a thorough knowledge of which mobile elements and functional genes lead to HGT would further aid the potential for the bioremediation of a polluted area. In addition, as the biodegradation abilities of the microbial community dictate to what extent HGT can occur in a contaminated site, assessing HGT can be employed to monitor bioremediation to evaluate the biodegradation process (Shahi et al. 2017).

The prior research has evidenced a significant correlation between HGT and the existence of functional genes (French et al. 2020). For instance, in their investigation into the horizontal transfer of the alkB, nah, and phnAc genes in the biostimulation of soils contaminated by petroleum, Shahi et al. (2016b) found that the alkB and phnAc genes transferred when nutrients were highly available. They also demonstrated that HGT was positively linked to nutrient content, with an increase in the carbon to nitrogen ratio from 100:5 to 100:15 correlating with increased rates of HGT. Building on this, Shahi et al. (2016a, b, c) showed that the evaluation of the microbial population and the presence of functional genes could be used to assess the efficiency of existing bioremediation efforts. In this study, they were successful in showing that HGT could serve as a suitable monitoring approach to measure the effectiveness of bioremediation for soils that had been contaminated by petroleum. They also found that this method could further be utilized to assess contaminated sites' potential for biodegradation.

12.3 Conclusion

The combined effects of globalization leading to increased industrialization, population growth, and consumption-based lifestyles have caused non-degradable pollutants to persist in the environment, adversely affecting human health. Due to their environmentally and cost-effective characteristics, methods based on bioremediation are opening up new avenues to mitigate these pollutants beyond conventional physicochemical treatments. Almost all polluted environments contain microbial strains that are capable of degrading the contaminants specific to those environments, with the population density increasing with the increasing presence of such contaminants. As the metabolic effectiveness of the microbiota relies on HGT between microorganisms, choosing the right gene for the degradation process and then monitoring how this gene is horizontally transferred comprise a feasible strategy to assess the effectiveness of bioremediation. The bioremediation potential of specific sites can hereby also be assessed. The necessary information on the genes as well as their genomic structure, metabolic and biological pathways, functions, and evolution can be gathered through the omics approaches. Moreover, a functional characterization of the relevant genes, proteins, coding regions, and products of the metabolism should be conducted to quantify the relevant biological processes of the microbiota. Recent developments in the omics fields, especially genomics, proteomics, metabolomics, transcriptomics, and interactomics, thus provide an array of technical techniques and expertise in this respect.

Acknowledgement The authors are grateful for the financial support from TUBITAK (Turkish Association of Science and Technology) (No: 116Y096).

References

Aydin S (2016) Microbial sequencing methods for monitoring of anaerobic treatment of antibiotics to optimize performance and prevent system failure. Appl Microbiol Biotechnol 100(12): 5313–5321

Aydin S, Ince B, Ince O (2015) Development of antibiotic resistance genes in microbial communities during long-term operation of anaerobic reactors in the treatment of pharmaceutical wastewater. Water Res 83:337–344

Aydin S, Karaçay HA, Shahi A, Gökçe S, Ince B, Ince O (2017) Aerobic and anaerobic fungal metabolism and omics insights for increasing polycyclic aromatic hydrocarbons biodegradation. Fungal Biol Rev 31(2):61–72

Aydin S, Ünlü İD, Arabacı DN, Duru ÖA (2022) Evaluating the effect of microalga Haematococcus pluvialis bioaugmentation on aerobic membrane bioreactor in terms of performance, membrane fouling and microbial community structure. Sci Total Environ 807:149908

French KE, Zhou Z, Terry N (2020) Horizontal 'gene drives' harness indigenous bacteria for bioremediation. Sci Rep 10(1):1–11

Kour D, Kaur T, Devi R, Yadav A, Singh M, Joshi D et al (2021) Beneficial microbiomes for bioremediation of diverse contaminated environments for environmental sustainability: present status and future challenges. Environ Sci Pollut Res 28:1–23

Malik G, Arora R, Chaturvedi R, Paul MS (2021) Implementation of genetic engineering and novel omics approaches to enhance bioremediation: a focused review. Bull Environ Contam Toxicol 108:1–8

Nwankwo W, Adetunji CO, Ukhurebor KE, Panpatte DG, Makinde AS, Hefft DI (2021) Recent advances in application of microbial enzymes for biodegradation of waste and hazardous waste material. In: Microbial rejuvenation of polluted environment, pp 35–56

Sales JCS, Santos AG, de Castro AM, Coelho MAZ (2021) A critical view on the technology readiness level (TRL) of microbial plastics biodegradation. World J Microbiol Biotechnol 37(7): 1–15

Shahi A, Aydin S, Ince B, Ince O (2016a) The effects of white-rot fungi Trametes versicolor and Bjerkandera adusta on microbial community structure and functional genes during the bioaugmentation process following biostimulation practice of petroleum contaminated soil. Int Biodeterior Biodegradation 114:67–74

Shahi A, Aydin S, Ince B, Ince O (2016b) Evaluation of microbial population and functional genes during the bioremediation of petroleum-contaminated soil as an effective monitoring approach. Ecotoxicol Environ Saf 125:153–160

Shahi A, Aydin S, Ince B, Ince O (2016c) Reconstruction of bacterial community structure and variation for enhanced petroleum hydrocarbons degradation through biostimulation of oil contaminated soil. Chem Eng J 306:60–66

Shahi A, Ince B, Aydin S, Ince O (2017) Assessment of the horizontal transfer of functional genes as a suitable approach for evaluation of the bioremediation potential of petroleum-contaminated sites: a mini-review. Appl Microbiol Biotechnol 101(11):4341–4348

Tancsics A, Li M, Chrzanowski L (2021) New insights into the biodegradation of organic contaminants in subsurface ecosystems: approaches and achievements of the multiomics era. Front Microbiol 12:946

Wright RJ, Bosch R, Langille MG, Gibson MI, Christie-Oleza JA (2021) A multi-OMIC characterisation of biodegradation and microbial community succession within the PET plastisphere. Microbiome 9(1):1–22