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New molecular techniques: A shift in bioremediation overview

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Bioremediation is a sustainable solution to clean up the organic pollutants from the contaminated sites. Success in bioremediation processes relies largely on the relative abundance, structure, catabolic versatility and biotic/abiotic interactions of the autochthonous, amended or stimulated microbial communities at contaminated sites.

The limitations of culture-dependent methods have resulted in the increased use of molecular methods to determine the ecological fate of microorganisms under natural environments. Recent advancements in sequencing technologies and molecular techniques have opened new frontiers in microbial community analysis by providing unprecedented levels of coverage and resolution of the environmental microbiomes.

This work presents and discusses the recent advances in molecular and omics technologies, which have become an integral tool for managing and controlling bioremediation processes.

High-throughput sequencing of PCR-amplified bacterial 16S rRNA gene fragments has emerged as the most powerful tool to study the changes in the composition of the soil bacterial community, as a result of contamination and different bioremediation strategies. The impact of bioaugmentation and surfactant-enhanced bioremediation on soil bacterial communities were analyzed using this technique.

Genomics, metagenomics and proteomics analyses are being used to predict microbial biodegradation pathways and their regulating mechanisms at strain, consortium or community levels. The use of these approaches for the study of physiological interaction into a polycyclic aromatic hydrocarbons degrading consortium is presented.

The new molecular methodologies give us the possibility of a look sharp on microbial communities, which will allow us to develop predictive models of degradation activity of the soil microbial community in function of biotic and abiotic parameters and set clear and specific criteria for the selection and evaluation of bioremediation strategies. This will have an enormous impact on our efforts to make bioremediation a more reliable and safe technology.

Keywords: Microbial Community, Degradation, Omics, High-throughput sequencing