Metagenomic analysis reveals the prevalence of biodegradation genes for organic pollutants in activated sludge

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HIGHLIGHTS

▶ High prevalence of biodegradation genes was reported in activated sludge.
▶ The *p450* gene was determined as the most abundant biodegradation gene.
▶ The *pmo* (2-monoxygenase) gene was the most dominant phenol degradation gene.
▶ Approximately 11.5–40.0% of biodegradation genes were carried on plasmids.
▶ *Mycobacterium* was the dominant population for degrading organic pollutants.

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ABSTRACT

The abundance, diversity, and distribution of biodegradation genes (BDGs) and phenol degradation genes (PDGs) in activated sludge (AS) from two wastewater treatment plants (WWTPs) at different sampling times were assessed by metagenomic analysis using a total of 15 datasets derived from Illumina high-throughput sequencing and BLAST comparisons to BDGs and PDGs databases. The results showed that the abundance (0.015–0.030%) and diversity of BDGs in AS varied with the WWTP and the sampling times. The *p450* and *pmo* genes were the most abundant genes in the BDGs and PDGs subgroups, respectively. MG-RAST analysis revealed that 87 detected bacterial genera potentially capable of degrading pollutants were mostly affiliated with *Proteobacteria* (59.8%), *Bacteroidetes* (17.2%), and *Actinobacteria* (9.2%). *Mycobacterium*, belonging to *Actinobacteria*, was found to be the most abundant genus (23.4%). This method could be used to monitor an AS's biodegradation ability for organic pollutants and to evaluate its wastewater treatment efficiency.

1. Introduction

Wastewater and sludge are considered to be the most common environmental sink for organic pollutants from domestic and industrial sources, including 114 organic compounds which have been designated as priority pollutants by United States Environmental Protection Agency. Some of priority pollutants have been frequently and persistently detected in wastewater and sludge systems and pose a potential risk to natural environments and human health (Negreanu et al., 2012). A number of studies have reported that they could be removed by wastewater treatment processes (Sales et al., 2011). It is worth noting that complex microbial consortia containing various biodegradation genes (BDGs) in activated sludge (AS) play a key role in removing or detoxifying those priority chemical pollutants (Suenaga et al., 2007). Therefore, there is an

increasing interest in revealing the abundance, diversity, and distribution of BDGs and the corresponding species present in AS.

The priority pollutant biodegradation capability of microorganisms and related BDGs in AS are usually studied using traditional cultivation-dependent, conventional PCR or quantitative polymerase chain reaction (qPCR) techniques (Felfoldi et al., 2010). Microbial degradation involves many important chemical processes, including dehalogenation, dealkylation, hydrolysis, oxidation, reduction, ring cleavage, conjugation, and methylation, which are catalysed correspondingly by various enzymes (e.g., monooxygenase, laccase, dioxygenase, cytochrome P450, dehydrogenase, lignin peroxidase, esterase, and dehalogenase) encoded by BDGs of microorganisms in biological wastewater treatment systems (Jechalke et al., 2011). Bunge et al. (2003) reported that microbial populations could dechlorinate recalcitrant chlorinated benzenes and dioxins, utilising them as carbon sources for growth by dehalogenation. van Beilen and Funhoff (2007) reported that cytochrome P450 (CYP) enzyme systems were mainly involved in the

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