

Review

### Aerobic and anaerobic fungal metabolism and Omics insights for increasing polycyclic aromatic hydrocarbons biodegradation



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#### ABSTRACT

During the 19th century, increasing human activity followed by great use of fossil fuels and the production of manifold aromatics including polycyclic aromatic hydrocarbons (PAHs) induced the generation of aromatic end-products. PAH are toxic to human health since they have been classified as pollutants and may reduce the biodiversity of natural ecosystems. They may form extensive global contaminants which pose a threat to entire world. This study focuses on summarizes recent information of PAHs biodegradation by aerobic and anaerobic fungi. Such information develops a new point of view on how organic molecules including PAHs are metabolically degraded in a complicated ecosystem and assists the foundation of new decontamination strategies due to the microbial interactions between fungi and their associates. Emerging integrative approaches including metagenomics, metatranscriptomics, metabolomics, and metaproteomics are studied in order to understand how these approaches give insight into decipher the molecular mechanisms of degradation of PAHs by fungi at the single species and community levels.

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#### 1. Introduction

When the waste which is produced through industrial processes and operations is treated partly and discharged into soil-water environment it runs into water bodies such as lakes, streams, ponds and oceans. The pollutants may get dissolved or float in water or accumulate in soil sediments which lead to terrestrial and aquatic pollution. These pollution have toxic effects on ecosystem which damage living creatures and biota (Vila *et al.* 2015). Hazardous waste consisted of organic and inorganic constituents are generated by the industries such as petrochemical, pharmaceutical, pesticides and fertilizers (Mahmoudi *et al.* 2013). Polycyclic aromatic hydrocarbons (PAHs) are formed by organic compounds and they carry a risk to the environment as a pollutant. The incomplete incineration of organic constituents throughout industrial processes and further human activities cause the release of PAHs at a great extent (Li *et al.* 2015). PAHs pose a threat to human health

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due to their carcinogenic and mutagenic effects (Gupta *et al.* 2015). The rings of carbon and hydrogen atoms in PAHs are combined in linear and angular arrangements. In consequence of the resonance energy that balances their aromatic ring systems and requiring high energy for electron transfer reactions, PAHs are recalcitrant molecules which means aromatic rings are only cleaved by specific enzymes (Das and Chandran 2011; Fernández-Luqueño *et al.* 2011).

The microbial community of the environment consists of a diverse range of microorganisms. Several metabolic activities of microorganisms that are able to degrade pollutants are used in a technique named bioremediation. If the metabolic activities of microorganisms are effective as natural degradation, secondary environmental pollution is not occurred. Bioremediation is also known as a cost-effective technique. Regarding to PAH pollution, despite its advantages, bioremediation has some downsides, for instance: 1) the availability to access PAHs to microorganisms, 2) to control and maintain the growth of the microorganism in the polluted areas, and 3) affection of other utilizable nutrients present in the polluted site on the bioremediation capacity of the microbe (Isaac et al. 2015, Shahi et al. 2016a). In conclusion, basic information about the intrinsic microorganism takes an important place when considering the potential of bioremediation. In order to reach an effective level of degradation in bioremediation, understanding the microbial network is crucial. Degradation can be performed by both culturable and non-culturable microorganisms. Molecular biological methods e.g. (meta-) genomics, (meta-) transcriptomics, (meta-) metabolomics, and (meta-) proteomics can be used to understand the microbial network in an effective way. These "omics" approaches play

an important role on understanding the molecular mechanism of PAH degradation due to its ability to bring new perspectives to it and have been discussed both at the single species and community levels (El Amrani *et al.* 2015, Shahi *et al.* 2016b,c).

The molecular mechanism of PAH degradation in bacteria has been well investigated while despite the significance of aerobic and anaerobic fungi in the bioremediation of PAHs, the information of similar mechanism in fungi remained restricted. PAHs can be degraded by a variable group of lignolytic and non-lignolytic fungi. P-450 monooxygenase and the lignin degrading enzymatic systems are two major group of fungal enzymes participating in the first attack on PAHs which both are slightly non-specific for the PAHs that they degrade, as seen in Fig. 1 (Aranda, 2016). The collaboration (i.e. synergistic effects) has also been reported between fungi and bacteria over bioremediation process. For instance, alongside their direct ability of degrading hydrocarbons, fungal mycelia enhance the surface area for biodegradation and bacterial attack by penetrating in PAHs contaminated environment. It has been noted that although the initial degradation of petroleum was held by bacteria, the biodegradation rate was enhanced two times when both bacteria and fungi were used together due to their synchronous activity (Fernández-Luqueño et al. 2011).

This review paper covers polycyclic aromatic hydrocarbons and role of aerobic and anaerobic fungi including the characterization of specific enzymatic activity and gene expression during degradation of polycyclic aromatic hydrocarbons through molecular approaches. This review also examines the functions of next-generation sequencing and

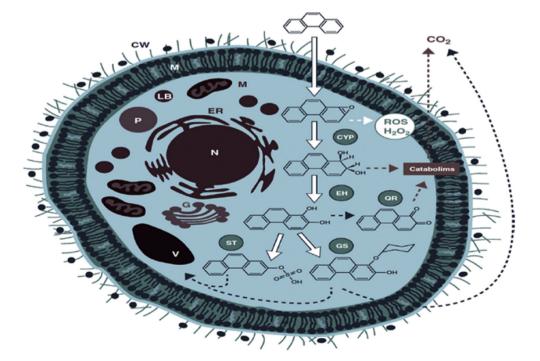


Fig. 1 – Simplified integrated model of the intracellular mechanism for conversion of polycyclic aromatic hydrocarbon in fungi (Aranda, 2016). M (membrane), WC (wall cell), V (vacuoles), G (Golgi apparatus), ER (endoplasmic reticulum), LB (lipid body), P (peroxisomes), N (nucleus), CYP (cytochrome P450 system), EH (epoxide hydrolase), ST (sulfotransferase), QR (quinone reductase).

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