

On the search for markers formed in the processes of microbiological metabolism of industrial waste on the example of lignin and oil sludge by gas chromatography-mass spectrometry (GC-MS)

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The natural environment is heavily polluted as a result of the extensive use of polyethylene, paints, petroleum products, industrial dyes, toxic chemicals and pesticides, and processed wood products. The indiscriminate use of these chemicals/polymers negatively affects humans and other living systems. One option for reducing the pressure of pollutants on the environment is their metabolic detoxification by microorganisms that use toxic compounds as a source of carbon and energy. In the course of evolution, microorganisms have developed a wide range of enzymes, pathways, and control mechanisms to degrade and recycle xenobiotics. Successful bioremediation requires efficient bacterial strains capable of degrading contaminants to minimal levels in the shortest possible time. Rapid and reliable identification of metabolites produced in the organism-substrate system and an understanding of the mechanisms of metabolic processes are a means of effective microbial selection.

Some of the most common industrial wastes are lignin from wood products and oil contaminants, which are complex hydrocarbon substrates.

In recent years, gas chromatography-mass spectrometry has been widely used for metabolomic studies of living organisms because it is ideal for the analysis of non-polar analytes. This method is highly sensitive and can therefore be used to analyze compounds formed in very small amounts. At the same time, in order to confirm the initiation/progress of oxidative transformation of a wide range of hydrocarbon compounds, it is important to detect substances corresponding to the structural elements of the substrates under study.

The aim of this study was to identify markers formed in the processes of microbiological metabolism of industrial waste on the example of lignin and oil sludge by gas chromatography-mass spectrometry.

When searching for markers of microbiological oxidation of lignin, transformation products of lignin structural elements were considered. Among the numerous compounds in the metabolic mixture, products containing G-fragments of lignin and products of their bacterial metabolism were identified: ferulic acid, guaiacol, vanillin, vanillic acid, succinic acid, malonic acid, oxalic acid; S-fragments of lignin and products

of their bacterial metabolism: sinapic acid, syringal and syringic acid; of the H-fragments of lignin, only p-hydroxybenzaldehyde was identified, indicating that the H-components in this lignin are negligible, or that the metabolic convection rate of these components into non-aromatic compounds is very high. The products identified in the metabolic mixture were found in existing descriptions of the KEGG PATHWAY microbial metabolic pathway maps; the possibility of reactions with these products was confirmed by separate experiments using model compounds that are G-, S-, and H-fragments of lignin as substrates.

Fluorenone and anthraquinone, which are present in the description of the KEGG PATHWAY microbial metabolic pathway maps, were identified and selected as markers of microbial oxidation of oil sludge components. The amounts of these compounds vary depending on the strain used. A possible oxidation product of PAHs is also dibenzfuran, the amount of which increases when microbial cultures are exposed to oil sludge and also varies depending on the strain used.

Thus, the work resulted in the identification and selection of markers that can be used to study the microbiological oxidation of products of industrial waste metabolism, using lignin and oil sludge as examples.

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