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COMPARATIVE PROTEOMIC ANALYSIS OF 2,6-DI-TERT-BUTYLPHENOL DEGRADATION BY *PSEUDOMONAS AERUGINOSE* SAN AI

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Due to a broad applications in plastics industry 2,6-di-tert-butylphenol (2,6-DTBP) became hazardous environmental pollutant. Ortho-disubstituted phenols are generally considered as substrates difficult for biodegradation. However, strain *Pseudomonas aeruginose* san ai, isolated from mineral cutting oil, can use 2,6-DTBP as a sole source of carbon and efficiently degrades it. The objective of this study was to analyzed differential protein expression in *P. aeruginose* san ai, during its exposure to 2,6-DTBP by proteomics approach based on liquid chromatography and tandem mass spectrometry (HPLC-MS/MS) coupled with bioinformatics to identify proteins. Prior HPLC-MS/MS proteins were separated by SDS-PAGE electrophoresis. Proteomes of *P. aeruginose* san ai grown on 2,6-DTBP and refined oil were compared.

Our results revealed a significant change in proteome during biodegradation of 2,6-DTBP. Proteomics analysis of *P. aeruginosa* san ai indicated that the core molecular response to 2,6-DTBP, comprised several up-regulated proteins belonging to six different functional categories including: energy metabolism, amino acid transport/metabolism, translation, post-translational modification and chaperone functions and inorganic ion transport/metabolism. In addition, a set of enzymes which neutralize reactive oxygen species was identified. To promote energy depletion key enzymes of the glyoxylate shunt were found. Remarkably, metabolism of non-polar amino acids was upregulated. Besides, the activities of enzymes from *P. aeruginosa* san ai involved in upper and lower biodegradation pathway of aromatic compounds were determined.

Proteomics approach applied in this study provided a deeper, more detailed understanding of the complex mechanisms of catabolism of 2,6-DTBP, its toxic effects and it also could serve for environmental biomonitoring.