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蛋白质组学方法分析不同苯酚浓度下菌株 *Acinetobacter* sp. EDP3 的应激机理

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收稿日期 2006-12-26 修回日期 网络版发布日期 接受日期 2007-7-18

摘要 Strain EDP3 was isolated from an industrial-activated sludge. It belonged to the gamma group of Proteobacteria with an identity of 97.0% to *Acinetobacter calcoaceticus* according to the 16S rRNA gene sequences. It can tolerate up to 1000mg/L phenol at room temperature with a much longer lag phase. This indicates that higher phenol concentration has induced some physiological and genotypic changes in the bacterium. The aim of this study is, therefore, to investigate these responses to phenol concentration variations in strain EDP3. Proteome analysis is conducted by means of a two-dimensional polyacrylamide gel electrophoresis (2D PAGE) and matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF-MS) was conducted to obtain a deeper insight into the adaptive responses inside the bacterium. Comparative analysis of the proteome profiles of strain EDP3 grown in 400mg/L and 1000mg/L phenol allowed us to identify that among all the proteins up-regulated under the higher phenol concentration, oxidative stress proteins were dominant. The synthesis of a heat shock protein, 60000 chaperonin GroEL, was also amplified. In addition, the expression of one membrane protein, adenosine 5'-triphosphate (ATP)-binding cassette (ABC) type sugar transporter, was found up-regulated. The inhibition of adenosine 5'-triphosphate (ATP) and RNA/protein synthesis was also observed.

关键词 [adaptation](#) [phenol-degrading bacteria](#) [Acinetobacter sp.](#) [proteome](#)

分类号

DOI:

Proteome analysis of the adaptation of a phenol-degrading bacterium *Acinetobacter* sp. EDP3 to the variation of phenol loadings

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Received 2006-12-26 Revised Online Accepted 2007-7-18

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Key words [adaptation](#); [phenol-degrading bacteria](#); [Acinetobacter sp.](#); [proteome](#)

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