

## Phenol Degradation Potential of Bacteria Isolated From Extreme Habitats

Dezső-Róbert Fikó<sup>1,2</sup>, Erika Kovács<sup>2</sup>, Szabolcs Szilveszter<sup>2</sup>, Tamás Felföldi<sup>2,3</sup>, István Máthé<sup>2</sup>

<sup>1</sup>Faculty of Applied Chemistry and Material Sciences, University Politehnica of Bucharest  
RO-011061, Polizu 1-7 Bucharest, Romania  
fiko\_robi@yahoo.com

<sup>2</sup>Faculty of Economics, Socio-Human Sciences and Engineering, Sapientia Hungarian University of Transylvania  
RO-530104, Libertății Sq. nr. 1, Romania

kovacsrika@sapientia.siculatorum.ro; szilveszterszabolcs@sapientia.siculatorum.ro; matheistvan@sapientia.siculatorum.ro

<sup>3</sup>Department of Microbiology, Eötvös Loránd University  
Pázmány Péter sétány 1/C, Budapest, Hungary  
tamas.felfoldi@gmail.com

### Extended Abstract

Phenol is a pollutant that is usually found in many industrial wastewaters (pulp and paper manufacturing, pharmaceutical industries, coal processing plants, oil refineries) and represent a risk for the environment and human health, due to its toxic, carcinogenic and mutagenic properties [1,2]. Therefore, it is essential to remove phenolic compounds from polluted environments, for that, microbial degradation process is a cost effective solution [3].

The objective of our research was to investigate biological phenol degradation using different bacterial strains isolated from extreme habitats with the final aim to use them in bioremediation. One of the sampling sites was a municipal solid waste landfill leachate treatment bioreactor (near Odorheiu Secuiesc town, Romania) and the other was a contaminated salt mine lake (Ocna Mureș town, Romania).

Samples were inoculated into Mineral Medium culture broth containing phenol or bisphenol-A as sole carbon source. From the enrichment cultures, the surface of R2A medium was inoculated to isolate morphologically different bacterial colonies. For the taxonomic identification of isolated strains, the 16S rRNA gene sequencing method was used [4].

In total, 50 bacterial strains were isolated: 20 strains were obtained from Mineral Medium with bisphenol-A (representing 17 species) and 30 bacterial strains were obtained from phenol-containing Mineral Medium (representing 15 species). The most common genera were *Simplicispira*, *Paracoccus* and *Halomonas*. Due to its low 16S rRNA gene similarity, one *Simplicispira* strain represents potentially new species to science.

The biodegradation capacity of the identified strains was analyzed using various phenol concentrations. Some of the studied strains had high phenol degradation capacity (initial phenol concentration from 500 to 1000 mg/L in the growth medium), while other strains showed no growth and no degradation at lower (100 mg/L) initial phenol concentration.

### References

- [1] K. M. Basha, A. Rajendran and V. Thangavelu, "Recent advances in the Biodegradation of Phenol: A review," *Asian J. Exp. Biol. Sci.*, vol. 1, no. 2, pp. 219-234, 2010.
- [2] Y. F. Wang, X. L. Wang, H. Li, K. F. Lin, P. Wang, J. Yang, Y. D. Liu, Z. Y. Sun, L. H. Fan and Z. M. Wu, "Treatment of high salinity phenol-laden wastewater using a sequencing batch reactor containing halophilic bacterial community," *Int. Biodeter. Biodegr.*, vol. 93, pp. 138-144, 2014.
- [3] A. Haddadi and M. Shavandi, "Biodegradation of phenol in hypersaline conditions by *Halomonas* sp. strain PH2-2 isolated from saline soil," *Int. Biodeter. Biodegr.*, vol. 85, pp. 29-34, 2013.
- [4] B. J. Tindall, R. Rossello-Mora, H. J. Busse, W. Ludwig, and P. Kämpfer, "Notes on the characterization of prokaryote strains for taxonomic purposes," *Int. J. Syst. Evol. Microbiol.*, vol. 60, pp. 249-266, 2010.