Biodegradation of Phenol by Antarctic Strains of *Aspergillus fumigatus*

Maria Gerginova, Jordan Manasiev, Husein Yemendzhiev, Anna Terziyska, Nadejda Peneva, and Zlatka Alexieva*

Institute of Microbiology, Bulgarian Academy of Sciences, Acad. G. Bontchev Str., bl. 26, Sofia 1113, Bulgaria. Fax: +359 2 8700109. E-mail: zlatkama@yahoo.com

* Author for correspondence and reprint requests

Z. Naturforsch. **68 c**, 384–393 (2013); received June 22, 2012/June 25, 2013

Taxonomic identification of three newly isolated Antarctic fungal strains by their 18S rDNA sequences revealed their affiliation with *Aspergillus fumigatus*. Phenol (0.5 g/l) as the sole carbon source was completely degraded by all strains within less than two weeks. Intracellular activities of three key enzymes involved in the phenol catabolism were determined. Activities of phenol hydroxylase (EC 1.14.13.7), hydroquinone hydroxylase (EC 1.14.13.x), and catechol 1,2-dioxygenase (EC 1.13.11.1) varied significantly between strains. The rates of phenol degradation in the three strains correlated best with the activity of catechol 1,2-dioxygenase.

Six pairs of oligonucleotide primers were designed on the basis of the *Aspergillus fumigatus* Af293 genome sequence (NCBI Acc. No. XM_743491.1) and used to amplify phenol hydroxylase-related gene sequences. DNA sequences of about 1200 bp were amplified from all three strains and found to have a high degree of sequence identity with the corresponding gene of *Aspergillus fumigatus* Af293.

Key words: Phenol, *Aspergillus fumigatus*, Phenol Hydroxylase Gene