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DSM determines DNA sequence of *Aspergillus niger* genome

DSM has announced the successful completion of important research to determine the complete DNA sequence of a key production organism, the fungus *Aspergillus niger*. The project integrates a number of techniques, including high- throughput DNA sequencing, DNA microanalysis, proteomics, metabolomics and bioinformatics. The sequencing of the *A. niger* genome is the first step in one of the largest industrial genome projects in Europe, and has confirmed DSM's positioning as one of Europe's leading biotechnology companies.

Director of DSM Research and Development Life Sciences, Joop Roels, comments: "Since the DNA sequence of *A. niger* is almost 3 times larger than the bakers' yeast genome which is already known, the task for DSM and its partners was challenging. Ultimately, the sequencing of *A. niger* required the identification of over 13,000 genes encoded in approximately 34.5 million base pairs, and has been achieved in a remarkably short period."

When DSM initiated the project in July 2000, only 1–2 % of *A. niger* genes were known. Accuracy of the now-complete genetic sequence — critical to meaningful interpretation of such complex data — has been ensured by 8-fold coverage of the complete sequence and computer modeling. DNA arrays can now be designed to unravel the complex relationships between processes in living cells at a molecular level.

"By understanding the mechanisms of gene expression in certain enzyme production processes, it is possible to fine-tune individual enzyme activities — offering the possibility of tailoring products to customer's specific needs," continues Roels. "Our research and process development staff is confident of being able to replace current trial-and-error procedures with a rational, genomic-based approach. The result will be improved efficiency of a wide range of fermentation-based production processes — leading to lower costs and accelerated development of new and improved products. We forecast significant benefits for our customers in the bakery, fruit juice, beer, wine, dairy, nutraceutical and animal feed industries."

"Completion of the DNA sequencing phase of the *Aspergillus niger* genomics project will generate new opportunities to improve and protect DSM's technology base," adds

Wim de Boer, intellectual asset manager of DSM Life Science Products. "However, we understand that the genome could also be of significant interest to many other parties in industry and the academic world. DSM is therefore offering to make the results available to commercial partners within its existing licensing arrangements. In addition, a low-barrier access program will be made available to academic organizations from 1 January 2002."

DSM's partners in the *A. niger* genomics project include the German consortium Gene Alliance (high-throughput DNA sequencing) and its bioinformatics partner **Biomax Informatics AG**, the University of Amsterdam (DNA microarrays) and the University of Utrecht (proteomics).

About Biomax

Biomax Informatics AG (Martinsried, Germany), a leader in the development of customized bioinformatics solutions, was founded in 1997 as a spin-off of the GSF-MIPS academic research group, now the German Research Center for Environment and Health-Institute for Bioinformatics (GSF-IBI). Founded by Dr. D. Frishman, Dr. K. Heumann and Prof. Dr. H. W. Mewes, Biomax developed the well-known Pedant-Pro™ Sequence Analysis Suite, the HarvESTer™ EST Assembly and Clustering System, and other bioinformatics tools used in metabolic pathway, proteomics, and gene expression analyses. Additional information about Biomax can be found at the company's site on the World Wide Web at www.biomax.de.