



HAL
open science

Comparative analysis of proteomes expressed by single-cell or filamentous form of *sphaerotilus natans*

S. Lacroix, A. Guillot, T. Bouchez, C. Bureau, V. Monnet, J.J. Pernelle

► To cite this version:

S. Lacroix, A. Guillot, T. Bouchez, C. Bureau, V. Monnet, et al.. Comparative analysis of proteomes expressed by single-cell or filamentous form of *sphaerotilus natans*. 12th International Symposium on Microbial Ecology, Aug 2008, Cairns, Australia. 1 p. hal-00765907

HAL Id: hal-00765907

<https://hal.science/hal-00765907>

Submitted on 15 May 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

COMPARATIVE ANALYSIS OF PROTEOMES EXPRESSED BY SINGLE-CELL OR FILAMENTOUS FORM OF *SPHAEROTILUS NATANS*

Sébastien Lacroix¹, Alain Guillot², Théodore Bouchez¹, Chrystelle Bureau¹, Véronique Monnet², Jean-Jacques Pernelle¹.

¹ Cemagref, U.R. Hydrosystèmes et Bioprocédés, Parc de Tourvoie, BP 44, 92163 Antony, France.

² INRA PAPSS (Plateau d'Analyse Protéomique par Séquençage et Spectrométrie de masse), Domaine de Vilvert, F-78352 Jouy-en-Josas, France.

Background and aims:

Filamentous bulking is a widespread problem in activated sludge WWTP. The molecular mechanisms of bacteria filamentous growth are still widely unknown. *Sphaerotilus natans* is a sheathed bacteria sometimes responsible of this type of event, which can exist under single-cell or filamentous forms. The objective of this study is to identify proteins involved into the filamentation mechanism by proteome comparison of *S. natans* both morphologies by LC-MS-MS analyses, and characterization of proteins differently expressed, in order to improve the understanding of filamentous growth mechanisms.

Methods:

Proteins were extracted from pure cultures of single cells and filamentous form of *S. natans* ATCC 15291, and were separated by SDS-PAGE. Bands exhibiting differences in intensities between the two forms of *S. natans* were cut out, trypsin digested and analyzed by LC-MS-MS. Proteins were identified by using Bioworks 3.3 software, and their relative abundances in the two different forms were compared using spectra and peptide counting.

Results:

Among the 32 proteins identified, 13 are overexpressed in the single cell form. Most of them are proteins involved in cell division and enzymes of energetic metabolism. 19 proteins, belonging mainly to stress protein family and specific sheath amino acid synthesis, are overexpressed in the filamentous form of the bacteria

Conclusions:

The identification of proteins differently expressed between filamentous and single cell of *S. natans* will provide a better understanding of filamentous growth mechanisms. This will lead to the constitution of a model for the filamentation mechanisms of others bacteria species more frequently responsible of bulking events.