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Differential *sthA* gene expression between filamentous and isolated forms of *Sphaerotilus natans*

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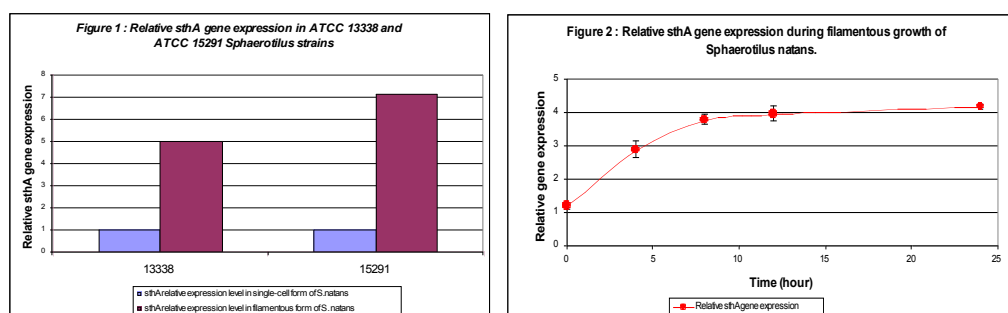
Background:

The activated sludge is the most commonly used technology for biological wastewater treatment. Filamentous bacteria are essential component of the activated sludge due to the important roles they play in sludge settleability. Excessive growth of filamentous bacteria, known as bulking, leads to a poor settlement of activated sludge. *Sphaerotilus natans* has been reported as the dominant filamentous organism in 12% of bulking sludge samples in United-States (Jenkins D., 1984). This bacterium is characterized by a sheathed structure in which long chains of rod-shaped cells are enclosed. *S. natans* has also been identified in single-cell form (Stokes, 1954) as few others filamentous bacteria species isolated from activated sludge. The growth morphology is determined by the environmental conditions. The molecular mechanisms that induce the filamentous growth from a single-cell population are still widely unknown. Nevertheless a gene essential for the filamentous growth and the sheath formation of *S. natans* ATCC 15291 has been identified and named *sthA* (Suzuki, et al., 2002). An inactivation of this gene results in sheathless single-cell form growth. In order to find more efficient treatments against bulking the molecular mechanisms of filamentation have to be better known.

Methods and results:

In this study, the presence of *sthA* gene in all the *S. natans* collection strains was demonstrated as its absence from *Leptothrix* genome, which is the closest phylogenetic neighbour of *S. natans*. This gene was sequenced.

To analyze the expression of *sthA* gene in filamentous and single-cell form of *S. natans*, *sthA* specific primers useable in RT-QPCR were designed. In opposition with Takeda and al. results, we determined that *sthA* is more expressed in filamentous form than in single cells form. The expression level is also depending of the *S. natans* strain studied (Fig.1). We finally determine that *sthA* expression increase during filamentous growth until it reaches a plateau (Fig.2).



Conclusions:

These findings indicate that *sthA* gene is highly specific to *S. natans* as it is not found in *Leptothrix* genome. This gene is directly implicated into the sheathed structure formation. As its expression vary in function of the morphology adopted and as it seems to be a very specific gene of *S. natans*, *sthA* may play a key role into the molecular mechanism of filamentation.

References:

Jenkins D., R. M. G., Daiggert G. T. (1984), *Manual of the Causes and Control of Activated Sludge Foaming and Bulking*, 1st ed., Lewis Publishers.

Stokes, J. L. (1954), Studies on the filamentous sheathed iron bacterium *Sphaerotilus natans*, *J. Bacteriol.*, *67*, 278-291.

Suzuki, T., et al. (2002), Identification of a gene essential for sheathed structure formation in *Sphaerotilus natans*, a filamentous sheathed bacterium, *Applied and Environmental Microbiology*, *68*, 365-371.