Respiratory Versatility in *Desulfovibrio desulfuricans* ATCC 27774 – a proteomic approach

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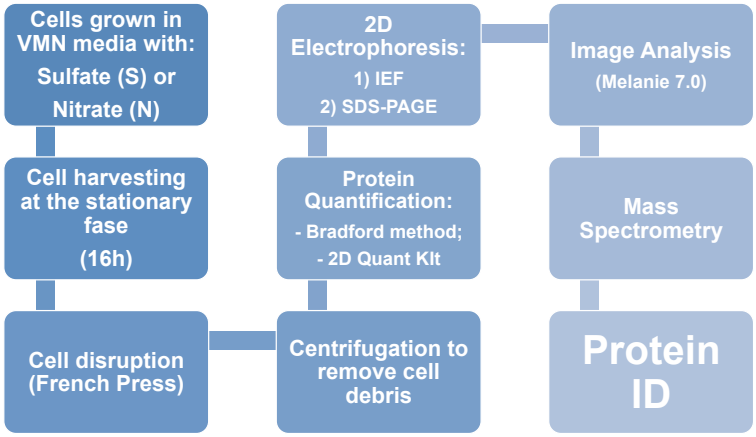
Introduction

Sulfate-reducing bacteria (SRB) are a diverse group of anaerobic microorganisms that obtain their energy from dissimilatory sulfate reduction[1]. Several studies demonstrated that some SRB species have high respiratory versatility due to the possible use of alternative electron acceptors. A good example is the bacterium *Desulfovibrio desulfuricans* (*Dd*) ATCC 27774 which grows in nitrate containing medium with rates and yields *ca*. 3 times superior to those observed in sulfate containing medium. Yet in the presence of both nutrients, *Dd* ATCC 27774 cells prefer the thermodynamically less favorable substrate, sulfate.[2] So far, little is known about the reasons behind this selection or how the bacterium is able to adapt to different sources of energy.

The main goal of this work is the identification of the metabolic tools involved in the respiratory flexibility of *Dd* ATCC 27774 cells induced by different electron acceptors (nitrate vs. sulfate).

Experimental



Results

Proteomes

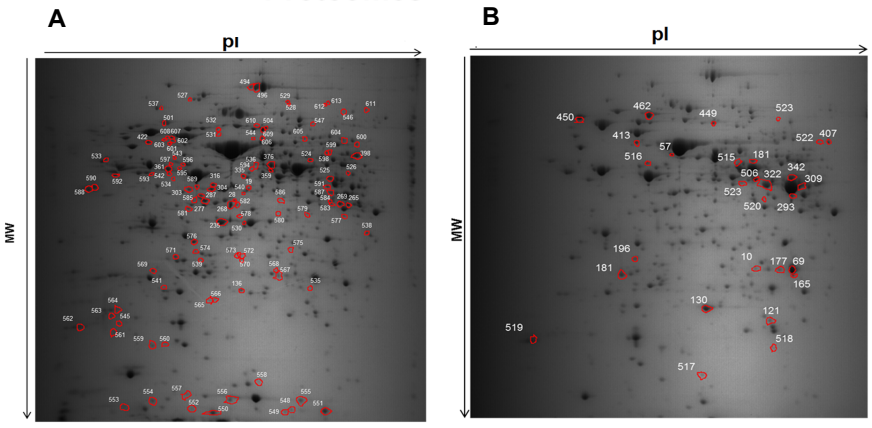


Fig.1: Overview of the 2D gel maps of total protein fractions from *D.d.* ATCC 27774 cells grown for 16h with nitrate (A) and sulfate (B) media. Circles indicate proteins up-regulated in both growths. Proteins (350 µg) were separated by 2D gel electrophoresis (12,5% acrylamide) in the pH gradient 4-7. Gels were stained with colloidal Coomassie blue. [images acquired from Melanie 7.0 software].

Statistical Analysis

Table 1: Statistical analysis of the total protein extracts from D.d. ATCC 27774 performed with Melanie 7.0 software. Proteins area considered overexpressed if there are two fold variations or more (>2), in relative spot volume.

Number of spots	Nitrate	Sulfate
Total	604	519
Overexpressed	22	20
Exclusive to one condition	90	9

Protein Identification

Table 2: Proteins from the nitrate and sulfate total protein fractions of *D. desulfuricans* cells identified by MS-TOF-TOF analysis of protein spots from 2D gels. *Theoretical values. N – nitrate, S - sulfate

Spot	Over-expression	Protein	MW*	pI*	Putative Function
196	2.6 S	Glutaminase	32.8	5.07	Glutaminase activity (glutamine > glutamate); NH_3 excretion
269	2.7 N	Glyceraldehyde-3-phosphate dehydrogenase	37.3	6.27	Glucose metabolism
303	2.3 N	2-hydroxyglutaryl dehydratase	47.3	5.05	Glutamate metabolism; NH_3 assimilation

Conclusions and Future Work

- ✓ 25% of differential spots;
- ✓ In the presence of nitrate, a greater number of proteins is produced; this may indicate that the metabolism shifting from sulfate to nitrate reduction has high biosynthetic costs, related with the need to express 90 new proteins.
- ❑ Validation with transcriptomic and metabolomic techniques.

References:

1. Muyzer G et al. (2008) *Nat Rev Microbiol* 6, 441-54; 2. Marietou A et al. (2009) *J Bacteriol* 191, 882-9

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