

Enhancement of dibenzothiophene biodesulfurization by *Gordonia alkanivorans* strain 1B using fructose rich culture media

L. Alves*, T.P. Silva, B.F. Arez, S.M. Paixão*

LNEG – U. Bioenergia, Estrada do Paço do Lumiar, 22, 1649-038 Lisboa, Portugal

*Corresponding author: luis.alves@lneg.pt; susana.alves@lneg.pt

Background – The removal of sulfur mediated by microorganisms or biodesulfurization (BDS) is already an extensively studied approach. The first studies were reported in the 50's and 60's, but only in the last 20 years have been successful breakthroughs. Through BDS it is possible to remove most of the recalcitrant sulfur compounds to the commonly physico-chemical process at mild operating conditions without molecular hydrogen, resorting to microorganisms. These microorganisms can remove sulfur from dibenzothiophene (DBT), a model compound, and other polycyclic aromatic using them as their sulfur source, making BDS an easy and environmental friendly process. *Gordonia alkanivorans* strain 1B [1] has been described as a desulphurizing bacterium, able to desulfurize DBT to 2-hydroxybiphenyl (2-HBP), the final product of the 4S pathway, using D-glucose as carbon source. However, both the cell growth and the desulphurization rate can be largely affected by the nutrient composition of the growth medium [2,3,4], due to cofactor requirements of many enzymes involved in BDS biochemical pathway.

Objectives – In this study, the main goal was to investigate the influence of several carbon sources on the growth and DBT desulfurization ability of *G. alkanivorans* strain 1B.

Methods – Growth patterns for different carbon sources and their effect on DBT desulfurization by *G. alkanivorans* were evaluated. Growth and desulfurization kinetics with the different carbon sources were also compared viewing a high DBT-biodesulfurization performance. The desulfurization rates were determined by GC analysis of DBT consumed and/or 2-HBP produced.

Conclusions – The results of desulfurization tests showed that the lowest values for the growth rate (0.025 h^{-1}) and for the overall 2-HBP production rate (1.80 mM/h) by the strain 1B were obtained in glucose. In sucrose, the increase of growth rate exhibited by strain 1B led to a higher biomass productivity, which induced a slightly increase in the 2-HBP production rate (1.91 mM/h), but in terms of 2-HBP specific production rate ($q_{2\text{-HBP}}$) the value obtained was significantly lower (0.718 mmol/g/h in sucrose versus 1.22 mmol/g/h in glucose). When a mixture of glucose and fructose was used as carbon source, strain 1B reached a value of $q_{2\text{-HBP}} = 1.90 \text{ mmol/g/h}$, close to that in fructose ($q_{2\text{-HBP}} = 2.12 \text{ mmol/g/h}$). The highest values for both cell growth ($\mu = 0.091 \text{ h}^{-1}$) and 2-HBP production (9.29 mM/h) were obtained when strain 1B was desulfurizing the DBT in the presence of fructose as the only carbon source, appointing towards a fructophilic behaviour by this bacterium. This fact is corroborated by the highest value of biomass productivity by strain 1B be in fructose, which permitted to have more effective cells fulfilling the DBT-desulfurization. The greater number of functional cells conducted to a more effectiveness BDS process by strain 1B, as they attained a $q_{2\text{-HBP}}$ about 74% higher than in glucose. Moreover, this significant BDS enhancement can better be observed in terms of the overall 2-HBP production rate, which increased over 5-fold, from 1.80 mM/h (in glucose) to 9.29 mM/h (in fructose). Moreover, the fructophilic behaviour exhibited by this bacterium opens a new focus of research to find cheaper alternative carbon sources rich in fructose, which will contribute for a BDS more cost-effective viewing its future industrial application.

Acknowledgments: The authors gratefully acknowledge the financial support of the project Carbon4Desulf - FCOMP-01-0124-FEDER-013932 by FCT (Fundação para a Ciência e a Tecnologia).

References

- [1] Alves L., et al., *App Biochem Biotech* **120** (2005), 199-208.
- [2] Alves L., et al., *Chemosphere* **70** (2008), 967-973.
- [3] Silva T.P., et al., *J Chem Technol Biot* (in press), DOI 10.1002/jctb.3921.
- [4] Paixão S.M., et al., *New Biotechnology* (in press), DOI 10.1016/j.nbt.2013.02.002.