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Characterization of the anaerobic metabolism of *Sphingopyxis macrogoltabida* TFA strain

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ABSTRACT

Motivation: *Sphingopyxis macrogoltabida* TFA strain is an alphaproteobacteria which is able to degrade the contaminant compound tetralin, found in multiple substances such as coal tar and petroleum (1). Tetralin biodegradation has been characterized under aerobic conditions, however no anaerobic growth has ever been observed in *Sphingomonadaceae* family. Many nitrate-respiring bacteria are able to transform nitrate to nitrite using *nar* genes, and eventually to gas nitrogen in a process called denitrification (2). Computer analysis of the genome sequence of TFA has shown different genes whose encoded proteins might be involved in anaerobic respiration pathways in TFA: three *fixLJ* pairs of genes, an *fnrL* gene and a *fixK* gene. It would be interesting to determine whether TFA is able to grow with no oxygen and to characterize this growth. Therefore, the objectives of this project are the characterization of the anaerobic metabolism of TFA and to determine growth rate under anaerobic conditions.

Aims: In order to determine whether TFA is able to grow under anaerobic conditions we will use nitrate, nitrite, fumarate and DMSO as final electron acceptors at different concentrations. We will design two insertion mutants in *fnrL* and *fixK* genes in order to test their anaerobic growth. The phenotype of some *fixLJ* mutants will be determined.

Results: We have successfully observed anaerobic growth of TFA reaching OD_{600} of 0.9 with some terminal electron acceptors. No anaerobic growth was observed using nitrite, fumarate or DMSO as sole electron acceptors. None of the mutants in *fixLJ1* and *fixLJ2* showed significant differences in their growth compared to the wild type strain.

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