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Transcriptomic analysis of *Zymomonas mobilis* under SOS-induction

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Zymomonas mobilis is an ethanologenic α-proteobacterium considered for industrial bioethanol production. Its tolerance to mutagenic stress is of major interest in basic and applied directions. In studied proteobacteria, survival and genomic stability at severe mutagenic conditions depend on cellular functions elicited by the SOS response. The latter is manifested as a global induction of genes involved in DNA replication, repair and cell-cycle control – but not only, as has been lately shown.

In this work, the transcriptomes of *Z. mobilis* strains CP4 and UA1, a CP4 *recA*- mutant derivative constructed in our lab, were studied via RNAseq at various concentrations of the SOS-inducing agent MMS. Out of 1925 chromosomal and 157 plasmid ORFs predicted for strain CP4, 1660 and 142, respectively, were found to be normally transcribed. Upon MMS induction (0.05 mM to 15 mM), a gradual increase in differentially regulated genes was observed, along with an evident gene profile shift at around 1 mM MMS. Of well-characterized DNA repair genes, *lexA, ruvA* and *ruvC* were induced at lowest MMS concentrations, while *recA, uvrA, uvrB, uvrC, uvrD, ruvB, recR, recO, mutY* and *a ung* ortholog, at higher/st. A multitude of genes of other functions, including basic metabolism, transport, regulation, phage assembly and antimicrobial resistance, were differentially expressed, numbering from ca. 60 at lowest to two thirds of the genome at highest induction. α-proteobacterial SOS boxes preceded many of the induced genes, however not all genes bearing predicted SOS boxes where induced. Strain UA1 verified its SOS-null phenotype.

Biography

Giannis Savvakis, BSc in Biology, MSc in Bioinformatics (honors), is finishing his PhD in the Faculty of Biology, NKUA, Greece. He has been awarded the national Academy of Athens PhD Scholarship in Biology (2012-2016) and is recipient of the 'Siemens' Doctorate Fellowship of Excellence from the State Scholarship Foundation (2016-2017). He has participated in the *Zymomonas mobilis* DNA- and RNA-seq projects CSP_788284 and CSP_52 carried out jointly between the NKUA and the US DOE-Joint Genome Institute, as well as EU-cofunded research programs. His BSc and MSc dissertation work on Zymomonas has been hitherto presented and twice awarded in national and international conferences.

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