

## Balancing redox cofactor generation and ATP synthesis: key microaerobic responses in thermophilic fermentations

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### Abstract

*Geobacillus thermoglucosidasius* is a Gram-positive, thermophilic bacterium capable of ethanologenic fermentation of both C<sub>5</sub> and C<sub>6</sub> sugars and may have possible use for commercial bioethanol production [Tang et al., 2009; Taylor et al. (2009) *Trends Biotechnol* 27(7): 398–405]. Little is known about the physiological changes that accompany a switch from aerobic (high redox) to microaerobic/fermentative (low redox) conditions in thermophilic organisms. The changes in the central metabolic pathways in response to a switch in redox potential were analyzed using quantitative real-time PCR and proteomics. During low redox (fermentative) states, results indicated that glycolysis was uniformly up-regulated, the Krebs (tricarboxylic acid or TCA) cycle non-uniformly down-regulated and that there was little to no change in the pentose phosphate pathway. Acetate accumulation was accounted for by strong down-regulation of the acetate CoA ligase gene (*acs*) in addition to up-regulation of the *pta* and *ackA* genes (involved in acetate production), thus conserving ATP while reducing flux through the TCA cycle. Substitution of an NADH dehydrogenase (down-regulated) by an up-regulated NADH:FAD oxidoreductase and up-regulation of an ATP synthase subunit, alongside the observed shifts in the TCA cycle, suggested that an oxygen-scavenging electron transport chain likely remained active during low redox conditions. Together with the observed up-regulation of a glyoxalase and down-regulation of superoxide dismutase, thought to provide protection against the accumulation of toxic phosphorylated glycolytic intermediates and reactive oxygen species, respectively, the changes observed in *G. thermoglucosidasius* NCIMB 11955 under conditions of aerobic-to-microaerobic switching were consistent with responses to low pO<sub>2</sub> stress.

### Introduction

Commercial production of ethanol for use as a fuel additive relies principally on the fermentation of starch or sucrose derived glucose by *Saccharomyces cerevisiae* (Hahn-Hagerdal et al., 2006). An understandable objection to the large scale production of ethanol via such methods is that the fermentative substrates generally originate from foodstuffs such as maize and sugarcane. The use of alternative non-food grade carbon feedstocks, principally lignocellulose, has received considerable attention over the last decade. It is now widely recognized that for efficient ethanol production from lignocellulosic feedstocks via



























- Samland AK, Sprenger GA. 2009. Transaldolase: From biochemistry to human disease. *Int J Biochem Cell Biol* 41(7):1482–1494.
- Shaw AJ, Podkaminer KK, Desai SG, Bardsley JS, Rogers SR, Thorne PG, Hogsett DA, Lynd LR. 2008. Metabolic engineering of a thermophilic bacterium to produce ethanol at high yield. *Proc Natl Acad Sci USA* 105(37):13769–13774.
- Shinar G, Rabinowitz JD, Alon U. 2009. Robustness in glyoxylate bypass regulation. *PLoS Comput Biol* 5(3):e1000297.
- Tang YJ, Sapra R, Joyner D, Hazen TC, Myers S, Reichmuth D, Blanch H, Keasling JD. 2009. Analysis of metabolic pathways and fluxes in a newly discovered thermophilic and ethanol-tolerant *Geobacillus* strain. *Biotechnol Bioeng* 102(5):1377–1386.
- Taylor MP, Eley KL, Martin S, Tuffin MI, Burton SG, Cowan DA. 2009. Thermophilic ethanologenes: Future prospects for second-generation bioethanol production. *Trends Biotechnol* 27(7):398–405.
- Trotter EW, Rolfe MD, Hounslow AM, Craven CJ, Williamson MP, Sanguinetti G, Poole RK, Green J. 2011. Reprogramming of *Escherichia coli* K-12 metabolism during the initial phase of transition from an anaerobic to a micro-aerobic environment. *PLoS ONE* 6(9): e25501.
- Wang Z, Chen M, Xu Y, Li S, Lu W, Ping S, Zhang W, Lin M. 2008. An ethanol-tolerant recombinant *Escherichia coli* expressing *Zymomonas mobilis* *pdc* and *adhB* genes for enhanced ethanol production from xylose. *Biotechnol Lett* 30(4):657–663.
- Yu W, Gao S, Yin C, Zhou Y, Ye B. 2011. Comparative transcriptome analysis of *Bacillus subtilis* responding to dissolved oxygen in adenosine fermentation. *PLoS ONE* 6(5):e20092.
- Zhang J, Sprung R, Pei J, Tan X, Kim S, Zhu H, Liu CF, Grishin NV, Zhao Y. 2009. Lysine acetylation is a highly abundant and evolutionarily conserved modification in *Escherichia coli*. *Mol Cell Proteomics* 8(2):215–225.
- Zhou B, Martin GJ, Pamment NB. 2008. Increased phenotypic stability and ethanol tolerance of recombinant *Escherichia coli* KO11 when immobilized in continuous fluidized bed culture. *Biotechnol Bioeng* 100(4):627–633.