Exploring lowering the optimal growth temperature of *Escherichia coli* in biotechnology applications

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Abstract

Different microbes grow at different optimal growth temperature. But, what defines this metabolic adaptation at the molecular and genetic level? And, more importantly, how different metabolic and signalling networks interact to yield a cellular system able to achieve maximal growth rate at a specific temperature? Molecular knowledge of such interacting components could provide a template on which modifications could be made to help adapt a microbe to another optimal growth temperature. However, given the large number of genes, proteins and pathways involved, efforts to re-adapt a microbe to another optimal growth temperature is likely difficult through a rational design approach. On the other hand, laboratory evolution approach might do the trick, but significant efforts are needed to understand the biochemical and physiological logic of the re-adaption. Using the genetically tractable *Escherichia coli* as model organism, this work aims to explore the possibility of using a rational approach at lowering the optimal growth temperature of the bacterium from 37 ºC to 25 ºC to help reduce energy costs and carbon emissions of fermentation. To this end, population level RNA-seq would be used to understand the global transcriptome of *E. coli* cultivated at 25, 30 and 37 ºC in LB medium. Highly transcribed genes at 37 ºC would represent those that need to be activated during growth at 25 ºC. On the other hand, genes transcribed at a low level at 37 ºC should remain poorly expressed at 25 ºC. While modern genetic engineering tools such as use of promoters and terminators with differentiated strength would allow the targeted tuning of expression of specific genes, potential need for re-engineering the expression of large number of genes might present difficulties. Thus, answers to what tune a microbe to operate optimally at a specific temperature might come from the signalling and gene regulation level where genes and proteins occupying particular nodes in the biochemical network hold sway on the expression of large number of downstream genes. Knowledge such as these could accrue from the feeding of transcriptome data into genome-scale metabolic models able to help identify critical nodes in metabolic pathways whose modulation would change cellular physiology. Given the importance of regulons governed by specific sigma factors, their modulation through altering sigma factor expression might be critical to gaining more widespread control of global gene expression at particular temperature. Collectively, developing rational approaches for tuning the optimal growth temperature of *E. coli* present critical challenges compared to laboratory evolution methods. As gene expression is regulated at multiple levels using a variety of mechanisms, transposing expression levels of highly transcribed genes at 37 ºC to 25 ºC would require the simultaneous modulation of different regulatory nodes belonging to both metabolic and signalling pathways.

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Conflicts of interest

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