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Comparative transcriptional profiling of the bacterial stress response in temperature and chemically-induced recombinant *E. coli* processes

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Background

Production of heterologous proteins results in a number of metabolic and physiological changes in the host cells during the course of a production process, namely the induction of stress responses and corresponding alterations in gene expression profiles [1].

Results

This study focuses on quantitative monitoring of the adaptation of *E. coli* to recombinant protein production on the transcriptome level by a bead-based RNA sandwich hybridisation assay, a rapid novel method based on the detection of hybridisation events between specific oligonucleotide probes and the target nucleic acids [2,3].

The expression profiles of selected genes including the product gene, anabolic and stress responsive genes were quantitatively analyzed in cells producing the human basic fibroblast growth factor (hFGF-2), a protein that partially aggregates into inclusion bodies. Transcriptome profiles during temperature- and IPTG-induced synthesis of hFGF-2 using the K12 strain TG1 and BL21(DE3) as production hosts, respectively, were compared.

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