Investigation of the expression of glycolysis, pentose phosphate and fatty acid biosynthesis genes in aerobic and anaerobic conditions in *E. coli*

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Abstract:

In order to produce recombinant proteins, various expression systems are used such as prokaryotic expression systems. Escherichia coli is one of the most famous hosts in the production of recombinant proteins. In addition to its simplicity, safety, and its well-known genetic characteristic, another important criterion is the ease of transfection of *E. coli* with external DNA and its ability to grow very rapidly compared to mammalian cells.

In this study, we examined the expression of basic metabolic genes including glycolysis, pentose phosphate and fatty acid biosynthesis genes in aerobic and anaerobic conditions. In order to achieve this goal, bioinformatics databases such as Uniport, NCBI and KEGG were used to find the genes in these pathways and then were analyzed by applying GEO2R repository based on the calculated Log FC. We concluded that the pykA and gapC genes involving in glycolysis and pentose phosphate cycles are at the highest level of expression and the gpmA gene involving in glycolysis cycle is at the lowest level. These results have potential application in genetic engineering.

Keywords: *E. coli*; gene expression; aerobic and anaerobic

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