**Study of differential gene expression profile of *E. coli* growing in glucose and acetate.**

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**Highlights**

* The gene expression profile exhibited great differences between both conditions.
* An increment in gene expression under acetate growth was observed.
* EutD and PrcP could be part of the underground metabolism through alternative enzymatic activities.

**1. Introduction**

*Escherichia coli* (*E. coli*) metabolism carbon fluxes are an important factor to take into account, since this bacteria is widely employed as a model organism in industrial and biotechnological processes. In this sense, *E. coli* can metabolize diverse carbon sources such as acetate, which is a poor carbon source, or glucose. Under glucose limitation conditions, *E. coli* develops carbon stress responses [1], so this bacteria exhibits an expansion in gene expression [2], the emergence of new pathways and alternative enzymatic activities. Thereby, diverse activities and new pathways could be part of underground reactions which may be connected to the existing network, increasing the potential of employing diverse and new carbon sources [3].

**2. Methods**

In this work, a gene expression study through a streptavidin-biotin-based microarray assay has been carried out to know the differences between the genetic global expression in *E. coli* K12 MG1655 growing in minimal medium M9 supplemented with glucose or acetate as carbon source. High density arrays "GeneChip E. coli Genome 2.0 Arrays" (P / N 900550, Affymetrix, Incorporated) were used

**3. Results and discussion**

The transcription profiles of *E. coli* K12 MG1655 growing in acetate supplemented medium exhibited great differences in gene expression respect to the strain growing in glucose supplemented medium. This behavior may be attributable to the increase in the number of genes expressed which allow a large scale carbon-scavenging to metabolize “low quality” carbon source [2]. The adaptation process may involve a refined regulatory response to only activate genes of acetate metabolism (*acs*, *ackA*, *actP*), but we observed an increment in the expression of genes, which belong to other pathways, such as the glyoxylate shunt, methylglyoxylate shunt, TCA cycle, and gluconeogenic flux, suggesting that these pathways are at least partially controlled at the transcriptional level. Furthermore, *eutD* and *prcP* genes were overexpressed in acetate growing. These two genes belong to the ethanolamine and propionate metabolism, respectively, so in acetate growingEutD and PrcP must present other alternative enzymatic activities and could be part of the underground metabolism reactions.

**4. Conclusions**

The gene expression change in acetate compared to glucose was used to assess the metabolic flux distribution in key pathways. Furthermore, the results suggest difficulties to identify adaptive mechanisms only through examination of expression changes, since there are other mechanisms that regulate metabolism, such as post-translational regulation, enzyme kinetics and allosteric control.

**References [Calibri 10]**

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