Global Analyses of Transcriptome and Proteome between a Parent Strain and a L-Threonine-Overproducing Mutant Strain

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We compared the transcriptome, proteome, and nucleotide sequences between the parent strain *E coli* W3110 and the L-threonine-overproducing mutant *E. coli* TF5015. DNA macroarrays were used to measure mRNA levels for the all genes of *E. coli* and two-dimensional gel electrophoresis was employed to compare protein levels. It was observed that only 54 in 4290 genes (1.3%) exhibited differential expression profiles. Typically, genes such as *aceA*, *aceB*, *icdA*, *gltA*, *glnA*, *leu* operon, *proA*, *thrA*, *thrC*, and *yigJ*, which are involved in glyoxylate shunt, TCA cycle, and amino acids biosynthesis (L-glutamine, L-leucine, proline, and L-threonine), were significantly up-regulated, while the genes *dadAX*, *hdeA*, *hdeB*, *ompF*, *oppA*, *oppB*, *oppF*, *yfiD*, and many ribosomal protein genes were down-regulated in TF5015 compared to W3110. The differential expressionsuch as up-regulation of *thr* operon and expression of *yigJ* would result in an accumulation of L-threonine in TF5015. Furthermore, two significant mutations, *thrA345* and *ilvA97*, which are essential for overproduction of L-threonine, were identified in TF5015 through the sequence analysis. In particular, expression of the mutated *thrABC* (pATF92) in W3110 gave rise to a significant incremental effect on L-threonine production. Up-regulation of *aceBA* and down-regulation of b1795, *hdeAB*, *oppA*, and *yfiD* seem to be linked with a low accumulation of acetate in TF5015. Such comprehensive analyses provideinformation to understand the regulatory mechanism of L-threonine production and the physiological consequences in the mutant stain.

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