Metabolic engineering of *E. coli* for the enhanced production of L-valine based on comparative transcriptome analysis

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Escherichia coli L-valine production strain was constructed by rational design. L-valine production strain was constructed by releasing two regulatory mechanisms, feedback inhibition and attenuation. Two amino acids alterations were introduced into *ilvH* which is subject to feedback inhibition by using site-directed mutagenesis. The leader region of *ilvGMEDA* and *ilvBN* operon which is involved in attenuation was changed with the strong tac promoter by homologous recombination. Further improvement of the L-valine production strain was achieved by knocking out *ilvA, leuA* and *panB* genes thus making more substrate available for L-valine biosynthesis. Transcriptome analysis was used to identify the physiology at mRNA level during the biosynthesis of L-valine. And we also achieved improvement of L-valine production strain based on transcriptome profiling.[This work was supported by the Korea Science and Engineering Foundation (KOSEF) grant funded by the Korea government (MOST) (No. M10309020000-03B5002-00000). Further supports by LG Chem Chair Professorship, Microsoft and IBM SUR program are appreciated.]