

Whole-transcriptome analysis of aerobic stress response gene in *Enterococcus gilvus* was performed using RNA-sequencing to identify carotenoid-based stress response genes in lactic acid bacteria. The expression of gene responsible for pyruvate dehydrogenase complex synthesis was highly upregulated after aerobic treatment. In addition, the expression of transcriptional regulator *spx* and genes encoding UvrABC system protein was also upregulated.