

## Genome Analysis of *Leuconostoc kimchii*

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*Leuconostoc kimchii* is a Gram-positive, facultatively anaerobic, coccus-shaped bacterium isolated from kimchi, Korean traditional fermented food (Kim *et al.*, 2000). In this study, we present draft genome structure of *L. kimchii* KCTC 2386<sup>T</sup>.

The size of *Leuconostoc kimchii* genome was estimated to be 2.1Mb by pulsed-field gel electrophoresis of rare-cutting restriction digests. Small insert library for shot-gun sequencing was generated using TOPO shot-gun cloning kit (Invitrogen). Sequencing was done up to 7.4 fold coverage. Base-calling was achieved using phred program and assembly was carried out using phrap program. Open reading frames were searched and genes were identified using glimmer2 program (Delcher *et al.*, 1999). A total of 2,267 genes were identified and annotated using BLAST search to clusters of orthologous group (COG) database. Sixty-six percent (1,507 ORFs) were annotated according to COG nomenclature. *Leuconostoc kimchii* has 37% G+C chromosome containing 24 tRNA's, with no missing aminoacyl-tRNA synthetases. Key enzymes in Embden-Meyerhoff-Parnas, Entner-Douduroff, and Pentose phosphate pathway are deficient. Only phosphoketolase pathway is fully functional in this organism, and its consequence of heterofermentative feature is the production of lactate, ethanol, and CO<sub>2</sub>, which will enhance the taste and flavor of kimchi. Like other *Leuconostoc* spp., *L. kimchii* has a dextransucrase and related enzymes for dextran synthesis from sucrose.

*Leuconostoc kimchii* has impaired TCA cycle and oxidative respiratory system. Only alpha-ketoglutarate and oxaloacetate can be synthesized as building blocks for several amino acids and nucleotides. Glyoxalate pathway enzymes are deficient and methylglyoxal synthase is missing in *L. kimchii*. Even though major glycolytic pathways and TCA cycle are partially functional and anapleurotic pathways are missing, *L. kimchii* utilizes acetyl-CoA for precursor for fatty acid and amino acid catabolism, but not for generating ATP or NADH/H<sup>+</sup>.

In conclusion, *L. kimchii*, an aerotolerant fermentative anaerobe, has many key enzymes missing and has impaired biochemical metabolisms, and it requires limiting factors or nutrient supplies for its optimal growth requirement. Completion of its genome and subsequent functional genomics studies will reveal its role in kimchi fermentation process and in probiotic properties.

**Keywords:** *Leuconostoc kimchii*, genome sequencing, shot-gun sequencing

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