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Complete Genome Sequence Analysis of *Leuconostoc kimchii* IMSNU 11154[▽]

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***Leuconostoc kimchii* IMSNU 11154, isolated from kimchi, a traditional Korean fermented food, is known to be an important antimicrobial lactic acid bacterium with probiotic potential. Here we announce the complete genome sequence of *L. kimchii* IMSNU 11154 consisting of a 2,101,787-bp chromosome and five plasmids. The strain has genes for dextran formation from sucrose and for mannitol formation from fructose. Antimicrobial and antioxidative functions of *L. kimchii* IMSNU 11154 could be attributed to a leucosin B-like peptide and multiple enzymes to reduce hydrogen peroxide and oxidized thiols, respectively.**

Kimchi is a traditional Korean pickled vegetable dish with varied seasonings, and it is known to be an important source of vitamins, minerals, and dietary fiber as well as a good dietary source of lactic acid bacteria (LAB) for humans (2, 3). An exopolysaccharide (EPS)-producing LAB, designated IMSNU 11154, was isolated from kimchi made of cabbage and subsequently classified as a novel species, *Leuconostoc kimchii* (6). The strain and its culture broth showed antimicrobial activities against *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, *Bacillus cepacia*, *Candida albicans*, and *Aspergillus niger*. Here we report the genome sequence of *Leuconostoc kimchii* IMSNU 11154 using a whole-genome shotgun sequencing strategy (4). The complete sequences of one chromosome and five plasmids were obtained. The circular chromosome of strain IMSNU 11154 was 2,101,787 bp in length (37.9% G+C), and the five plasmids were LkipL48 (3,196 bp; 37.1% G+C), LkipL4701 (21,055 bp; 34.3% G+C), LkipL4704 (23,285 bp; 35.6% G+C), LkipL4719 (21,924 bp; 39.1% G+C), and LkipL4726 (29,616 bp; 35.5% G+C). The number of predicted open reading frames (ORFs) is 2,205, covering 89.5% (1,880,952 bp) of the genome. Non-coding RNA regions were identified as 68 tRNAs and 4 copies of rRNA operons. A small gene encoding a leucosin B-like peptide was identified.

Strain IMSNU 11154 was missing the fructose 1,6-bisphosphatase enzyme of the Embden-Meyerhof-Parnas pathway and transaldolase of the 6-phosphogluconate/phosphoketolase pathway. Tricarboxylic cycle enzymes were also absent, except for cytochrome oxidase bd-I subunits. The strain metabolized sucrose by invertase, sucrose phosphorylase, and dextransucrase. Formation of EPS and fructose from sucrose by dextransucrase could enhance the probiotic function as well as

improve the taste and flavor of kimchi. Strain IMSNU 11154 had a mannitol dehydrogenase gene (*mdh*) identical to *mdh* of *Leuconostoc mesenteroides* (1). By producing mannitol, it maintains its turgor and stabilizes membrane lipids and proteins at low water activity as well as scavenges free reactive oxygen radicals as previously observed for mannitol fermenters (10). Like other *Leuconostoc* spp., strain IMSNU 11154 does not bear any catalase or superoxide dismutase (SOD) enzymes but has six thioredoxins and four thioredoxin reductases that were shown to be important in coping with acid and oxidative stress (9, 11). Harboring thioredoxin systems on plasmids is a common feature for both *L. kimchii* IMSNU 11154 and *Leuconostoc citreum* KM20 (7). Glutathione protected some lactic acid bacteria against oxidative stress (8), but gamma-glutamylcysteine (γ -GC) is the major low-molecular-weight thiol in *Leuconostoc* spp., including IMSNU 11154 (5). Genes for γ -GC synthesis and reduction are present in strain IMSNU 11154 (5), and there are genes for putative peroxiredoxins that can reduce hydrogen peroxide via small thiols or thioredoxins. Thus, multiple antioxidative systems reduce thiols in strain IMSNU 11154.

In conclusion, the genome of *Leuconostoc kimchii* IMSNU 11154 revealed that its carbohydrate metabolism has adapted to the formation of dextran, fructose, and mannitol from sucrose. The antimicrobial activity of strain IMSNU 11154 could be due to a leucosin B-like peptide, and it contains multiple antioxidative systems to manage acid and oxidative stresses independent of SOD and catalase.

Nucleotide sequence accession numbers. The genome information for the chromosome of *Leuconostoc kimchii* strain IMSNU 11154 was deposited in NCBI under GenBank accession number CP001758. The five plasmids of strain IMSNU 11154 are available in GenBank under accession numbers CP001753 (LkipL4701), CP001754 (LkipL4704), CP001755 (LkipL4719), CP001756 (LkipL4726), and CP001757 (LkipL48).

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