

Genome Sequence of *Weissella thailandensis* fsh4-2

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***Weissella thailandensis* fsh4-2 is a heterofermentative lactic acid bacterium isolated from the Korean fermented seafood condiment jeotkal. Here we report the draft genome sequence of *W. thailandensis* fsh4-2 (1,651 genes, 1,436 encoding known proteins, 183 encoding unknown proteins, 32 RNA genes), which consists of 50 large contigs of >100 bp.**

Weissella thailandensis, originally isolated from fermented fish (4), was reported to be able to grow at 10% NaCl. *W. thailandensis* strain fsh4-2 was isolated from jeotkal, a Korean fermented fish condiment which is based on fish, shrimp, and shellfish and contains up to 20% salt. *W. thailandensis* fsh4-2 grew at 10% NaCl *in vitro* using de Man, Rogosa, and Sharpe broth at 30°C. The only other fermented food product from which this species has also been isolated was Mexican Cotija cheese. These isolates grew in medium containing 7% NaCl (3). *W. thailandensis* thus appears to be a particularly salt-tolerant lactic acid bacterial species associated with high-salt and protein-rich food fermentations.

The genomic DNA of *W. thailandensis* fsh4-2 was isolated using the High Pure PCR template preparation kit (Roche). The genome was sequenced by a whole-genome shotgun strategy using Roche 454 GS FLX Titanium pyrosequencing (Lifesequencing S.L.) (386,107 reads totaling 1,968,992 bp [~1.97 Mbp], 76.11-fold coverage of the genome). Quality filtered reads were assembled *in silico* using 454 Life Science Newbler Assembler 2.3, giving 50 contigs (>100 bp in size). Annotation transfer was performed based on open reading frame (ORF) prediction and BlastN gene searching of public databases (UniProt and GenBank). Functional annotation of predicted protein-coding sequences was done using Gene Ontology terms (1) and InterPro motifs compared to the different *Weissella* and *Leuconostoc* proteomes.

The GC content was 40.0 mol%. There were 1,651 possible ORFs in 50 contigs, with sizes ranging from 64 to 1,711 bp. Most were under 1,000 bp, and only a few ORFs ($n = 10$) were >1,000 bp. Predicted copies of the 5S, 16S, and 23S rRNA genes (5 genes); 24 putative tRNA genes; and 3 genes encoding other RNA molecules were also detected. ORFs encoding the enzymes associated with obligately heterofermentative sugar metabolism via the phosphogluconate/phosphoketolase

pathway (2) were present, as well as genes for polysaccharide breakdown and transport and 9 aminopeptidases.

In accordance with the association of *W. thailandensis* with high-salt fermented foods, stress response genes encoding resilience to osmotic stress and changing redox and oxygen levels were identified. In addition to GroES and GroEL chaperonin, HrcA-GrpE-DnaK-DnaJ heat shock protein and an HSP33 heat shock protein were present. *W. thailandensis* also encodes a CspA cold shock protein and two alkaline shock proteins, as well as 4 systems to cope with osmotic shock, including the proline/betaine transporter ProP6, two glycine-betaine/carnitine/choline ATP binding cassette transporters, and one ABC-type proline/glycine-betaine transporter system. Although the genome of *W. thailandensis* does not encode a superoxide dismutase or a catalase, other gene products thought to contribute to intracellular redox balance include three glutathione reductases, one glutathione peroxidase, one iron-dependent peroxidase, one organic hydroperoxide resistance protein, thioredoxin, a possible thioredoxin disulfide reductase, and a thioredoxin reductase.

Nucleotide sequence accession numbers. The draft genome sequence of *W. thailandensis* fsh4-2 is available in the EMBL nucleotide sequence database (project 68571) under accession numbers HE575133 to HE575182.

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