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# Genome Sequence of *Weissella confusa* LBAE C39-2, Isolated from a Wheat Sourdough

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***Weissella confusa* is a rod-shaped heterofermentative lactic acid bacterium from the family of *Leuconostocaceae*. Here we report the draft genome sequence of the strain *W. confusa* LBAE C39-2 isolated from a traditional French wheat sourdough.**

The genus *Weissella* is phylogenetically related to *Leuconostoc* and *Oenococcus* and arose from the reclassification of *Leuconostoc paramesenteroides* and some related atypical heterofermentative lactobacilli (3). *Weissella confusa* (formerly *Lactobacillus confusus*) has been isolated from a variety of sources: sugar cane, carrot juice, milk, fermented foods and beverages, and human and animal samples (2, 3, 6, 9). It is more particularly found in many fermented cereals and vegetables (2, 3, 6). Some metabolic traits other than lactic acid fermentation, such as exopolysaccharide production from sucrose (4, 10, 13) and antifungal activity (14), have been reported, highlighting that *W. confusa* could be attractive for diverse biotechnological applications. For instance, a *W. confusa* strain was found promising for efficient *in situ* production of dextrans and isomaltooligosaccharides in sourdoughs without strong acidification (7). *W. confusa* is also present in the normal microflora of human intestines (15) and has been described as a potential probiotic species (1, 11).

*W. confusa* strain LBAE C39-2 was isolated from a traditional wheat sourdough (12). The genomic DNA was extracted from the cultured bacteria (MRS Broth, 30°C) by using a DNeasy blood and tissue kit (Qiagen). The genome of *W. confusa* C39-2 was sequenced with a whole-genome shotgun strategy using Roche 454 GS (FLX titanium) pyrosequencing. A total of 86,967 filtered reads corresponding to ~33 Mb and ~14-fold coverage of the genome were obtained. Assembly performed using Newbler v.2.5 software generated 71 contigs (>100 bp in size) with 57 contigs larger than 1,000 bp. Genome annotation was performed using the AGMIAL annotation platform (5). The draft genome includes 2,284,024 bp with an overall G+C content of 45%. It includes 2,156 protein-coding genes, of which 72% (1,559) were annotated with known proteins with biological function and 28% (597) were annotated as hypothetical proteins. It also includes six copies of the 5S rRNA, one single copy of the large-subunit rRNA, one single copy of the small-subunit rRNA-encoding genes and 73 tRNA-encoding genes. Most protein-coding genes were related to metabolic traits. Transposable elements and phage-related genes were also detected.

This is the first genome sequence provided for the *W. confusa* species. Whereas phylogenetic analyses showed that this species is closely related to *Weissella cibaria* (2), BLAST analyses revealed that fewer than 30% of the *W. confusa* LBAE C39-2 contig sequences matched the genome of *W. cibaria* KACC11862 (8) with more than 80% identity and an e-value lower than 10<sup>-4</sup>.

**Nucleotide sequence accession number.** The draft genome sequence of *W. confusa* LBAE C39-2 is available in the EMBL nucleotide sequence database under accession number **CAGH00000000**.

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