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Genome Sequence of *Pediococcus pentosaceus* Strain IE-3

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We report the 1.8-Mb genome sequence of *Pediococcus pentosaceus* strain IE-3, isolated from a dairy effluent sample. The whole-genome sequence of this strain will aid in comparative genomics of *Pediococcus pentosaceus* strains of diverse ecological origins and their biotechnological applications.

The genus *Pediococcus* is composed of Gram-positive, nonmotile and spherical bacteria. They are largely found in fermented foods that are rich in sugar content and ferment glucose to produce lactic acid (1). They are homolactic acid fermentative and are frequently used in the food industry as nutritional enhancers and also used in dairy products (3, 7). The strain IE-3 was isolated from a dairy industry effluent sample during a screen for lactic acid bacilli (LAB) with biotechnological properties. The ability to produce lactic acid and its spherical shape assigned strain IE-3 to the family *Lactobacillaceae*, and 16S rRNA gene sequence analysis (GenBank accession no. HE716958) confirmed strain IE-3 as a member of the genus *Pediococcus*. Although it showed 99.7% identity with *Pediococcus pentosaceus* strain DSM 20336^{T} (8), it exhibited significant phenotypic differences, such as the inability to grow above 6% NaCl or below pH 5.0 and no acid production from sucrose and xylose. Interestingly, unlike other species, strains of *P. pentosaceus* have been found to be catalase positive, and thus anaerobic incubation was not necessary to grow them. However, the present study found that strain IE-3 is catalase negative and therefore requires anaerobic conditions for optimal growth.

To understand its phylogeny and taxonomy in detail, we sequenced the genome of IE-3 using the Roche 454 GS (FLX Titanium) pyrosequencing platform (Macrogen, Republic of Korea). The shotgun sequencing yielded 301,793 reads amounting to 170,437,620 bases and ~85-fold coverage. The GS De Novo assembler (v. 2.6) yielded 91 contigs (>500 bp) with an average contig size of 19.806 kb and a largest contig of 183.723 kb. The proportion of Q40+ bases was 99.35%. The genome of strain IE-3 has a G+C content of 37.2%, and annotation using the RAST (Rapid Annotation using Subsystem Technology) pipeline (5) and RNAmmer 1.2 (2) with further manual inspection revealed 1,733 predicted coding regions, 49 tRNA genes, and 3 rRNA genes.

Different strains of *Pediococcus* have been isolated from fermented food and reported to produce bacteriocins active against Gram-positive bacteria, including *Listeria*. However, their isolation from milk has not been reported, and this may be due to the absence of other growth factors in milk or an inability of these strains to utilize lactose as a carbon source. In our study, we isolated a strain from dairy waste that produces a bacteriocin which selectively inhibits the growth of *L. monocytogenes*. The genome of IE-3, along with that of another strain of *P. pentosaceus* (ATCC 25745) of plant origin (4, 6), will help in molecular evolutionary and ecological studies of these organisms and their systematic exploitation as probiotics.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at EMBL under accession numbers CAHU01000001 to CAHU01000091.

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