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Whole genome sequencing of *Leuconostoc suionicum* and *L. pseudomesenteroides* isolates extracted from sugar beet roots

Shyam L. Kandel,[1] Carl A. Strausbaugh,[2] Malick Bill,[1,3] Bishwo N. Adhikari,[4] Xiaojun Hu[4]

AUTHOR AFFILIATIONS See affiliation list on p. 2.

ABSTRACT *Leuconostoc suionicum* and *Leuconostoc pseudomesenteroides* are important lactic acid bacteria identified in rotted tissues of roots in the field and stored sugar beets. Here, we announce the genomes of *L. suionicum* and *L. pseudomesenteroides*, isolated from post-harvest sugar beet roots from Idaho and Minnesota.

KEYWORDS sugar beet, *Leuconostoc*, root rot, storage

Leuconostoc species are often detected in deteriorated pre- and post-harvest sugar beet roots. They metabolize sucrose and interfere with the juice purification and crystallization procedure during factory processing (1, 2). Here, we report the genome sequences of three *Leuconostoc* isolates associated with sugar beet storage rot. *Leuconostoc* isolates, B322 (*Leuconostoc suionicum*; NRRL B-65327) and L12487 (*Leuconostoc pseudomesenteroides*), were isolated from sugar beet roots received from storage piles in Homedale and Golden Valley, ID, USA, respectively (2, 3). For the isolation of isolates, B322 and L12487, marginal areas between rotted and healthy-looking tissues of sugar beet roots were surface sterilized using 0.6% sodium hypochlorite for 60 s followed by rinsing with reverse osmosis water. Each 2 × 2-mm piece of disinfected tissue was macerated in sterile water and incubated on yeast extract-dextrose-calcium carbonate agar (YDC) or glucose-yeast extract-peptone agar (GYP) to recover individual bacterial colonies (2, 3). Individual colonies of each isolate were restreaked onto YDC or GYP and incubated at 30°C for 3–7 days to obtain a pure culture. Another isolate, L771 (*L. suionicum*), was isolated from rotted sugar beet roots collected from storage piles in Renville, MN, USA. A piece of infected tissue was rinsed two to three times with sterile nanopure water and plated on the potato dextrose (PD) agar (Difco, Sparks, MD, USA) for 3–5 days at 25°C and subsequently on nutrient agar for 3 days at 25°C to recover an isolated single colony (Sigma-Aldrich, St. Louis, MO, USA). Genomic DNA was extracted from freshly grown bacterial shake cultures (140 rpm) at 30°C for 48 h in the de Man, Rogosa, and Sharpe broth (EMD Chemicals Inc., Gibbstown, NJ, USA) or PD broth using the Norgen (Norgen Biotek, ON, Canada) or Zymo (Zymo Research, Irvine, CA, USA) DNA extraction kit. Additional clean-up was done with a sucrose buffer and proteinase K (Promega Corporation, Madison, MI, USA), and purified DNA samples were submitted to SeqCoast Genomics, Portsmouth, NH, USA for sequencing. Sequencing libraries were prepared using an Illumina DNA Tagmentation Kit (Illumina, San Diego, CA, USA) and sequenced in the Illumina NextSeq2000 platform with a 300-cycle flow cell kit (catalog nos. 20050264 and 20046813) to generate 2 × 150 bp paired sequence reads (Table 1).

Sequence reads were demultiplexed and trimmed using DRAGEN version 3.10.12 (4) and assembled by SPAdes genome assembler (version 3.15.4) (5). The assembled genomes were evaluated by QUAST (version 5.0.2) (6), and gene annotation was performed using Prokka (version 1.14.6) (7). Genome completeness and contamination percentage were determined using CheckM (version 12.2) (8). A digital DNA-DNA hybridization (dDDH) analysis (dDDH value, d_4 > 70% for the same species) using the

Editor Leighton Pritchard, University of Strathclyde, Glasgow, United Kingdom

Address correspondence to Shyam L. Kandel, shyam.kandel@usda.gov.

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TABLE 1 Summary of genome information of *Leuconostoc* isolates from sugar beet roots

Features	*Leuconostoc* isolates		
	B322 (NRRL B-65327)	L12487	L771
No. of reads after demultiplexing and trimming	4,607,222	4,757,550	5,259,322
Genome size (bp)	2,056,303	2,346,722	1,906,665
G + C content (%)	37.53	38.79	37.42
No. of contigs	490	137	23
N_{50} contig length (bp)	157,479	138,985	233,247
No. of protein-coding sequences	2,063	2,330	1,818
No. of rRNA	54	53	53
No. of tRNA	52	52	51
No. of tmRNA	1	1	1
Genome completeness (%)	99.26	98.66	99.26
Genome coverage	182.1×	153.3×	196.1×
Genome contamination (%)	4.95	1.47	0.18

Type Strain Genome Server (https://tygs.dsmz.de) (9) confirmed that isolates B322 and L771 are designated as *L. suionicum* with d_4 values of 83.5% and 83.7%, respectively, compared to *L. suionicum* DSM 20241 (CP015247.1). Moreover, an isolate L12487 was identified as *L. pseudomesenteroides* with a d_4 of 83.2% in comparison to *L. pseudomesenteroides* NCDO 768 (GCF_012396745.1).

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AUTHOR AFFILIATIONS

[1]USDA-ARS, Sugarbeet Research Unit, Edward T. Schafer Agricultural Research Center, Fargo, North Dakota, USA
[2]USDA-ARS, Northwest Irrigation and Soils Research Laboratory, Kimberely, Idaho, USA
[3]Department of Plant Pathology, North Dakota State University, Fargo, North Dakota, USA
[4]USDA-APHIS-Plant Germplasm Quarantine Program, Laurel, Maryland, USA

AUTHOR ORCIDs

Shyam L. Kandel http://orcid.org/0000-0002-3726-817X
Carl A. Strausbaugh http://orcid.org/0000-0001-6773-1375
Bishwo N. Adhikari http://orcid.org/0000-0003-4840-9609
Xiaojun Hu http://orcid.org/0000-0002-4464-206X

AUTHOR CONTRIBUTIONS

Shyam L. Kandel, Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Resources, Software, Supervision, Validation, Writing – original draft, Writing – review and editing | Carl A. Strausbaugh, Conceptualization, Investigation, Methodology, Resources, Supervision, Writing – review and editing | Malick Bill, Data curation, Formal analysis, Investigation, Methodology, Validation, Writing – review and editing | Bishwo N. Adhikari, Data curation, Formal analysis, Methodology, Software, Validation, Writing – review and editing | Xiaojun Hu, Data curation, Formal analysis, Software, Validation, Writing – review and editing

DATA AVAILABILITY

The raw reads of *Leuconostoc* isolates, L12487, B322, and L771, are publicly accessible through the NCBI SRA database under accession numbers SRR26421222, SRR26421223, and SRR26421224, respectively. Annotated genomes are available at FigShare repository as https://doi.org/10.6084/m9.figshare.25546129.v1 (L12487), https://doi.org/10.6084/m9.figshare.25540993.v1 (B322), and https://doi.org/10.6084/m9.figshare.25546093.v1 (L771). A summary of the genome sequencing and annotation statistics is shown in Table 1. The genomes were deposited in GenBank as BioProject no. PRJNA1028530 with accession nos. JBAGCU000000000.1 (*L. pseudomesenteroides*; L12487), JBAHVX000000000.1 (*L. suionicum*; B322), and JBAHVY000000000.1 (*L. suionicum*; L771).

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