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PROKARYOTES

Draft Genome Sequence of the Intimin-Positive Enteropathogenic *Escherichia albertii* Strain MBT-EA1, Isolated from Lettuce

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ABSTRACT The genome of the intimin (*eae*)-harboring *Escherichia albertii* strain MBT-EA1, isolated from lettuce in Germany, was sequenced. Sequence analysis showed the assembled draft genome size to be 4,560,948 bp, containing a predicted total of 4,414 protein-encoding genes, 11 rRNAs, and 82 tRNAs. Furthermore, three plasmid sequences were found.

Escherichia albertii is a zoonotic potential foodborne pathogen which has been isolated in various countries worldwide (1–4). In humans, *E. albertii* has the potential to cause severe infections (e.g., gastroenteritis), as it may integrate Shiga toxin-carrying bacteriophages into the chromosome (5, 6). The clinical significance and epidemiology of *E. albertii* infections are still unclear, as the microorganism was classified as a new *Escherichia* species in 2003 (1). Furthermore, the biochemical properties of this species are very similar to those of enteropathogenic *E. coli* (EPEC), which complicates their discrimination in routine diagnostics (2, 7).

We isolated an *eae*-positive *E. albertii* strain, MBT-EA1, from lettuce in the cold-storage area of a ready-to-eat salad-producing company. The colony showed white color on tryptone bile X-glucuronide (TBX) agar. The genomic DNA was extracted using the ZR-Fungal/Bacterial DNA-MiniPrep kit (Zymo Research, Freiburg, Germany) and quantified using a Qubit 3 fluorometer (Invitrogen, Darmstadt, Germany). The Nextera XT kit and Nextera mate-pair library prep kit were used to create libraries, and sequencing was performed as paired-end reads (2 × 251 bp) on an Illumina MiSeq platform (Illumina, Munich, Germany), according to the manufacturer's protocols. Adapter trimming of raw reads was done using the Illumina Pipeline. Furthermore, the reads of the Nextera mate-pair library were preprocessed by AdapterRemoval (8) to remove junction adapters. The results of both runs were *de novo* assembled using SPAdes 3.09.1 (9).

The draft genome assembly consisted of 10 contigs >1,000 bp, and the N_{50} value was 840,915 bp. Seven contigs mapped against reference strain *Escherichia albertii* strain KF1 (GenBank accession number CP007025) (10) using the Mauve plugin 1.1.1 (11). The draft genome size was 4,560,948 bp, with a mol% G+C content of 49.7%. Three contigs which did not map were identified as plasmid sequences and described here as pEA1 (116,103 bp, IncFIB), pEA2 (89,048 bp, IncFII, and colicins B and M), and pEA3 [circular 3,598 bp, Col(RNAi), similar to *Salmonella* plasmid (GenBank accession number CP006052)]. Genomic features were identified and annotated using the NCBI Prokaryotic Annotation Pipeline (PGAP) and Rapid Annotations using Subsystems Technology (RAST) (12). The assembled genome contained 4,414 predicted genes, 82 tRNA genes, 7 5S rRNA genes, 1 16S rRNA gene, and 3 23S rRNA genes.

The sequences were analyzed *in silico* for serotype (13), *fimH* type, virulence factors (14), plasmids (15), and antibiotic resistance genes (16) using the Center for Genomic

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Epidemiology online service (https://cge.cbs.dtu.dk/services/) (17). The strain was identified as belonging to serotype O144:H- with the *fimH* type 461. The virulence genes found included *eaeA* (intimin), *cdtB* (cytolethal distending toxin B), *cba* (colicin B), *cma* (colicin M), *espA* (type III secretion system), *espB* (secreted protein B), *espF* (type III secretion system), *gad* (glutamate decarboxylase), and *nleB* (non-locus of enterocyte effacement [non-LEE] encoded effector). No acquired antibiotic resistance genes were found. Thus, the genome data showed that the strain, which was isolated for the first time from raw produce, may be highly virulent. Therefore, *E. albertii* should also be taken into consideration in safety investigations of vegetable products (18).

Accession number(s). This draft genome sequence of *E. albertii* MBT-EA1 has been deposited at DDBJ/ENA/GenBank under the accession number PTLP00000000. The version described in this paper is version PTLP01000000.

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