GENOME ANNOUNCEMENT

Draft Genome Sequence of Serratia marcescens Strain LCT-SM213

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Serratia marcescens is a species of Gram-negative, rod-shaped bacterium of the family Enterobacteriaceae. S. marcescens can cause nosocomial infections, particularly catheter-associated bacteremia, urinary tract infections, and wound infections. Here, we present the draft genome sequence of Serratia marcescens strain LCT-SM213, which was isolated from CGMCC 1.1857.

Serratia is a Gram-negative, facultative anaerobic, rod-shaped bacterium which, as a pathogen, has been reported to have a major impact on public health (14). The Serratia species of most concern, S. marcescens, is a human pathogen responsible for a large percentage of nosocomial infections involving the urinary tract, respiratory tract, wound infections, and bacteremia (1, 5, 7). Today, S. marcescens has attracted great attention due to its increasing number of cases, its virulence (7, 15), and its emerging resistance to antibiotics (13). However, in the genome database, only seven S. marcescens strains had been sequenced for the whole genome until now. Serratia marcescens strain LCT-SM213 originated from Serratia marcescens CGMCC 1.1857, obtained from the China General Microbiological Culture Collection Center (CGMCC). It displays 100% similarity with S. marcescens. A draft genome sequence of this strain is presented here.

The genome was sequenced using Illumina Hiseq 2000 at BGI-Shenzhen (BGI, Shenzhen, People’s Republic of China). A 90-bp sequence was used to search the 6,000-bp index library. The raw data were filtered before assembly, including those reads with low quality, high proportions of N, adapter contamination, and high numbers of duplications. In total, 1,864 Mbp clean reads were produced, providing about 350-fold coverage of the genome. The filtered high-quality reads were assembled into 36 contigs in 11 scaffolds with SOAPdenovo software (9).

Based on the assembled sequence, gene prediction was performed using Glimmer3.0 (4). rRNA and tRNA were predicted by using the software rRNAmmer (8) and tRNAscan-SE (11), respectively. Other noncoding RNAs, including microRNA (miRNA), small RNA (sRNA), and small nuclear RNA (snRNA), were analyzed by using the software Infernal (12) based on the Rfam database (6). Transposons were determined based on the Repbase transposable elements library or using RepeatMasker and RepeatProteinMasker (16). Tandem repeats were predicted using TRF software (2). The predicted genes were annotated through Blast searching based on the protein knowledge base Swiss-Prot and its computer-annotated supplement TrEMBL and the COG, KEGG, and NCBI-NR databases. Furthermore, we analyzed the antibiotic resistance and virulence of the strain by using BLASTP with databases ARDB (10) and VFDB (3), respectively.

The draft genome of Serratia marcescens LCT-SM213 has 5,067,328 bases with a G+C content of 59.72%, and there are 4,794 genes, with an average length of 924 bp. We found eight genes related to antibiotic resistance and eight virulence factors. There are 73 genes for tRNAs.

The red-pigmented prodigiosin is produced by Serratia marcescens. It attracts interest because of its immunosuppressive and anticancer activities (17). The prodigiosin biosynthetic genes (pigB-pigP) were found in Serratia marcescens strain LCT-SM213.

Nucleotide sequence accession number. The draft genome shotgun sequence of Serratia marcescens LCT-SM213 has been deposited at DDBJ/EMBL/GenBank under the accession number AJUV00000000.

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