Whole genome sequence of Enterobacter ludwigii type strain EN-119\textsuperscript{T}, isolated from clinical specimens

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ABSTRACT

Enterobacter ludwigii strain EN-119\textsuperscript{T} is the type strain of E. ludwigii, which belongs to the E. cloacae complex (Ecc). This strain was first reported and nominated in 2005 and later been found in many hospitals. In this paper, the whole genome sequencing of this strain was carried out. The total genome size of EN-119\textsuperscript{T} is 4952 770 bp with 4578 coding sequences, 88 tRNAs and 10 rRNAs. The genome sequence of EN-119\textsuperscript{T} is the first whole genome sequence of E. ludwigii, which will further our understanding of Ecc.

Keywords: PacBio; Enterobacter cloacae complex; PuuABCD
To understand the genetic difference between EN-119<sup>T</sup> and the <i>E. cloacae</i> subsp. <i>cloacae</i> type strain ATCC 13047<sup>T</sup> (Ren et al. 2010), we made a genome comparison between the two strains (Fig. 1) by using the Murasaki algorithm (Popendorf et al. 2010). We found a high sequence similarity between the two genomes as only 207 genes in EN-119<sup>T</sup> did not have homologs in ATCC 13047<sup>T</sup>. To further understand the difference of important pathways, we mapped the genome of EN-119<sup>T</sup> to KEGG database (Ogata et al. 1999). Not surprisingly, there is no difference in most of the important pathways including secretion system, flagellar assembly, bacterial chemotaxis, etc. However, two genes involved in environment processing, named <i>ompF</i> and <i>evgA</i>, were missing in EN-119<sup>T</sup>. Both genes have been reported to be involved in drug resistance (Cohen, McMurry and Levy 1988; Nishino and Yamaguchi 2002). This observation is in agreement with previous observations on the natural susceptibility to antimicrobial agents between members of Ecc (Stock, Gruger and Wiedemann 2001).

With regard to genes involved in metabolism, we also found a high level of similarity between EN-119<sup>T</sup> and ATCC 13047<sup>T</sup>, except the integrated gene cluster <i>puuABCD</i>, which was absent in EN-119<sup>T</sup>. These four genes are involved in putrescine degradation as reported before (Dong and Schellhorn 2009). Although there was no direct evidence about the role of this gene cluster in pathogenicity, previous global expression analysis based on the stress regulator RpoS found that the defect in rpoS resulted in impaired expression of <i>puuABCD</i> as well as several virulence genes (Dong and Schellhorn 2009). The result indicated that <i>PuuABCD</i> may be involved in pathogenicity or stress response.

This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the Accession Number JTLO00000000. The BioProject designation for this project is PRJNA268890.

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**REFERENCES**


