Draft Genome Sequence of Enterotoxigenic *Escherichia coli* Strain W25K

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Enterotoxigenic *Escherichia coli* (ETEC) is a major cause of diarrheal disease in humans and newly weaned pigs. Here, we report the draft genome sequence of ETEC strain W25K, which causes diarrhea in piglets.

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Enterotoxigenic *Escherichia coli* (ETEC) causes travelers' diarrhea and is a leading cause of infectious diarrhea in children from developing nations (1). ETEC is also a major cause of diarrhea in newly weaned pigs (2). The K88 (F4) fimbrial adhesin and heat-stable (ST) and heat-labile (LT) enterotoxins have been identified as important virulence factors leading to diarrheal diseases in piglets (3, 4). Although the complete genomes of three ETEC strains that infect humans, *E. coli* H10407 (5), E24377A (6), and B2C (7), have been published, no ETEC strain isolated from piglets with ETEC diarrhea has been completely sequenced. W25K is an O149:K88 serotype strain of ETEC that causes diarrhea in piglets (8).

Genomic DNA was extracted from W25K using a QIAamp DNA minikit (Qiagen), according to the manufacturer's protocol. One nanogram of genomic DNA was used to generate a library using the Nextera XT kit (Illumina). Micro-Seq Enterprises sequenced the libraries on a MiSeq sequencing system (Illumina). The sequencing generated approximately 4 million read pairs, constituting ~53-fold coverage of the genome. The read pairs were overlapped where possible and trimmed for quality using DNAStar software. A *de novo* assembly of the overlapped and quality-trimmed reads was generated using DNAStar.

The final assembly consists of 153 contigs. The genome size of ETEC W25K is estimated to be 5.6 Mb. The genome sequence was annotated using the RAST genome annotation servers (9). An analysis of the genome showed that ETEC W25K has 599 subsystems, 5,793 coding sequences, and 114 RNAs. Type II and type VI protein secretion systems were identified. Classical ETEC virulence genes, *eltA* and *eltB*, the genes encoding the two subunits of heat-labile enterotoxin, were also found.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. JNBX00000000. The version described in this paper is version JNBX01000000.

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REFERENCES

1. **Fleckenstein JM, Hardwidge PR, Munson GP, Rasko DA, Sommerfelt H, Steinsland H.** 2010. Molecular mechanisms of enterotoxigenic *Escherichia coli* infection. Microbes Infect. **12**:89–98. http://dx.doi.org/10.1016/j.micinf.2009.10.002.
2. **Frydendahl K.** 2002. Prevalence of serogroups and virulence genes in *Escherichia coli* associated with postweaning diarrhoea and edema disease in pigs and a comparison of diagnostic approaches. Vet. Microbiol. **85**:169–182. http://dx.doi.org/10.1016/S0378-1135(01)00504-1.
3. **Nagy B, Fekete PZ.** 2005. Enterotoxigenic *Escherichia coli* in veterinary medicine. Int. J. Med. Microbiol. **295**:443–454. http://dx.doi.org/10.1016/j.ijmm.2005.07.003.
4. **Nagy B, Wilson RA, Whittam TS.** 1999. Genetic diversity among *Escherichia coli* isolates carrying f18 genes from pigs with porcine postweaning diarrhea and edema disease. J. Clin. Microbiol. **37**:1642–1645.
5. **Crossman LC, Chaudhuri RR, Beatson SA, Wells TJ, Desvaux M, Cunningham AF, Petty NK, Mahon V, Brinkley C, Hobman JL, Savarino SJ, Turner SM, Pallen MJ, Penn CW, Parkhill J, Turner AK, Johnson TJ, Thomson NR, Smith SG, Henderson IR.** 2010. A commensal gone bad: complete genome sequence of the prototypical enterotoxigenic *Escherichia coli* strain H10407. J. Bacteriol. **192**:5822–5831. http://dx.doi.org/10.1128/JB.00710-10.
6. **Sahl JW, Rasko DA.** 2012. Analysis of global transcriptional profiles of enterotoxigenic *Escherichia coli* isolate E24377A. Infect. Immun. **80**:1232–1242. http://dx.doi.org/10.1128/IAI.06138-11.
7. **Madhavan TP, Steen JA, Hugenholtz P, Sakellaris H.** 2014. Genome sequence of enterotoxigenic *Escherichia coli* strain. Genome Announc. **2**(2):e00247-14. http://dx.doi.org/10.1128/genomeA.00247-14.
8. **Li XQ, Zhu YH, Zhang HF, Yue Y, Cai ZX, Lu QP, Zhang L, Weng XG, Zhang FJ, Zhou D, Yang JC, Wang JF.** 2012. Risks associated with high-dose *Lactobacillus rhamnosus* in an *Escherichia coli* model of piglet diarrhoea: intestinal microbiota and immune imbalances. PLoS One **7**:e40666. http://dx.doi.org/10.1371/journal.pone.0040666.
9. **Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O.** 2008. The RAST server: Rapid Annotations using Subsystems Technology. BMC Genomics **9**:75. http://dx.doi.org/10.1186/1471-2164-9-75.