Complete Draft Genome Sequence of *Escherichia coli* JF733

Gabriele R. M. Kleiner, a Daniel Wibberg, b Anika Winkler, b Jörn Kalinowski, b John E. Wertz, c Karl Friehs a, b

Fermentation Engineering, Bielefeld University, Bielefeld, Germany; Center for Biotechnology, Bielefeld University, Bielefeld, Germany; Department of Molecular, Cellular and Developmental Biology, E. coli Genetic Stock Center, Yale University, New Haven, Connecticut, USA

*Escherichia coli* JF733 is a strain with a long history on research on membrane proteins and processes. However, tracing back the strain development raises some questions concerning the correct genotype of JF733. Here, we present the complete draft genome of *E. coli* JF733 in order to resolve any remaining uncertainties.

The strain has a long history, and CGSC tries to collect and update all information about their available strains and their characteristics. Sequencing of *E. coli* JF733 enables the clarification of remaining uncertainties and gives new insight into the genetic background of *E. coli* JF733.

*E. coli* JF733 was created based on the parental strain *E. coli* AT3143 (CGSC #4539) (1, 2). The latter is an *E. coli* K-12 derivate that emerged from mating AT3055, also known as JF733. Further studies of outer membrane proteins and porins (3) as well as on the relationship to loci tolF (4) were described in 2008 (5, 6). The following *JF733* genotype is currently published by the CGSC (cgsc.biology.yale.edu): [F-, lacY29, proC24, tss-63, purE41, λ−, ompA252, his-53, ompC262, rpsL97(strR), xyl-14, metB65, cycA1, ilv-277, cysB2?], 2016-01-27.

Initial studies using *E. coli* JF733 were focused on functional studies of outer membrane proteins and porins (3–5) as well as on their contribution to bacteriophage and colicin sensitivity (2, 6). Furthermore, production and secretion of recombinant proteins like anti-αTF using JF733 were described in 2008 (7).

To resolve remaining uncertainties concerning the JF733 genotype for further research, the draft genome sequence of *E. coli* JF733 was established on the Illumina MiSeq system as recently described for other microorganisms (8–10). A paired-end sequencing run (2 × 300-bp) yielded 2,266,996 reads with a total size of 646.20 Mb. Assembly using the GS de novo assembler version 2.8 resulted in 107 contigs and 58 scaffolds for the JF733 draft genome. Annotation of the genome was accomplished within the GenDB platform (11). The chromosome has a size of 4,518,620 bp with a G+C content of 50.78%. In total, 4,218 coding sequences, 70 tRNA genes, and 3 species of rRNA genes were identified by the gene and RNA prediction tools.

Sequencing of the *E. coli* JF733 genome and comparison to *E. coli* W3110 (GenBank: AP009048.1) confirmed most of the indicated mutations and resulted in a specification of three affected genes, namely, hisD, ilvD, and xylR. No mutations in ompC, metB (and metC), and cyC were detected. Whereas the latter is not annotated for *E. coli* W3110, a potential deletion within tss could not be verified with certainty using the obtained data. Although no mutation within ompC was detected, a base-pair substitution located in the –10 promoter region 90 bp upstream of ompC (12) was found, which could explain the described lack of protein Ib (2).

**Nucleotide sequence accession numbers.** The *E. coli* JF733 draft genome sequence was deposited in the EMBL database under the accession numbers FBSE0100001 to FBSE01000058.

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**REFERENCES.**

1. Foulds J. 1976. tolF locus in *Escherichia coli*: chromosomal location and relationship to loci cmlB and tolD. J Bacteriol 128:604–608.

2. Foulds J, Chai TJ. 1979. Isolation and characterization of isogenic *E. coli* strains with alterations in the level of one or more major outer membrane
proteins. Can J Microbiol 25:423–427. http://dx.doi.org/10.1139/m79-065.
3. Parr TR, Jr, Poole K, Crockford GWK, Hancock REW. 1986. Lipopolysaccharide-free Escherichia coli OmpF and Pseudomonas aeruginosa protein P porins are functionally active in lipid bilayer membranes. J Bacteriol 165:523–526.
4. Woodruff WA, Parr TR, Jr, Hancock REW, Hanne LF, Nicas TI, Iglewski BH. 1986. Expression in Escherichia coli and function of Pseudomonas aeruginosa outer membrane porin protein F. J Bacteriol 167:473–479.
5. Kim JE, Arjara G, Richards JH, Gray HB, Winkler JR. 2006. Probing folded and unfolded states of outer membrane protein A with steady-state and time-resolved tryptophan fluorescence. J Phys Chem B 110:17656–17662. http://dx.doi.org/10.1021/jp061991t.
6. Chai TJ, Wu V, Foulds J. 1982. Colicin A receptor: role of two Escherichia coli outer membrane proteins (OmpF protein and btuB gene product) and lipopolysaccharide. J Bacteriol 151:983–988.
7. Wich G, Dassler T. 2008. Process for the fermentative production of antibodies. US patent 2008/0206818 A1.
8. Wibberg D, Rupp O, Jelonk L, Krober M, Verwaaijen B, Blom J, Winkler A, Goesmann A, Grosch R, Pühler A, Schlüter A. 2015. Improved genome sequence of the phytopathogenic fungus Rhizoctonia solani AG1-IB 7/3/14 as established by deep mate-pair sequencing on the MiSeq (Illumina) system. J Biotechnol 203:19–21. http://dx.doi.org/10.1016/j.jbiotec.2015.03.005.
9. Maus I, Cibis KG, Wibberg D, Winkler A, Stolze Y, König H, Pühler A, Schlüter A. 2015. Complete genome sequence of the strain Defluvivitoga tunisiensis L3, isolated from a thermophilic, production-scale biogas plant. J Biotechnol 203:17–18. http://dx.doi.org/10.1016/j.jbiotec.2015.03.006.
10. Wibberg D, Alkhateeb RS, Winkler A, Albersmeier A, Schatschneider S, Albaum S, Niehaus K, Hublik G, Pühler A, Vorhöltler FJ. 2015. Draft genome of the xanthan producer Xanthomonas campestris NRRL B-1459 (ATCC 13951). J Biotechnol 204:45–46. http://dx.doi.org/10.1016/j.jbiotec.2015.03.026.
11. Meyer F, Goesmann A, McHardy AC, Bartels D, Bekel T, Clausen J, Kalinowski J, Linke B, Rupp O, Giegerich R, Pühler A. 2003. GenDB—an open source genome annotation system for prokaryote genomes. Nucleic Acids Res 31:2187–2195. http://dx.doi.org/10.1093/nar/gkg312.
12. Mizuno T, Mizushima S. 1986. Characterization by deletion and localized mutagenesis in vitro of the promoter region of the Escherichia coli ompC gene and importance of the upstream DNA domain in positive regulation by the OmpR protein. J Bacteriol 168:86–95.