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Whole-Genome Sequence of *Listeria monocytogenes* Strains from Clinical and Environmental Samples from Varanasi, India

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We present here the whole-genome sequences of *Listeria monocytogenes* from Ganges River water, agricultural soil, and human clinical samples from Varanasi, India, which will be used for a comparative analysis.

Received 11 December 2014 **Accepted** 29 December 2014 **Published** 5 February 2015

Citation Soni DK, Singh KM, Ghosh A, Chikara SK, Joshi CG, Dubey SK. 2015. Whole-genome sequence of *Listeria monocytogenes* strains from clinical and environmental samples from Varanasi, India. Genome Announc 3(1):e01496-14. doi:10.1128/genomeA.01496-14.

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Listeria monocytogenes is the Gram-positive pathogenic bacterium that causes listeriosis and results in high mortality (20 to 30%) and hospitalization rates (1, 2). *L. monocytogenes* encompasses a variety of strains that vary in their pathogenic potential in hosts (3, 4). *L. monocytogenes* strains group into 13 serotypes, of which 1/2a, 1/2b, and 4b represent the majority of the pathogenic strains (5, 6). To obtain a better understating of the molecular mechanisms of *L. monocytogenes* pathogenicity with special reference to their different ecological niche, the genome sequences of the isolates recovered from Ganges River water, agricultural soil, and human clinical samples (placenta bit) were analyzed.

Genomic DNA was extracted using the QIAamp DNA minikit (Qiagen, Milan, Italy), according to the manufacturer's protocol. Whole-genome shotgun sequencing was performed using the 318 Chip and 300-bp chemistry Ion Torrent PGM platform, per the manufacturer's instructions. The reads were quality filtered using Prinseq-lite-0.20.3. *De novo* assembly was carried out using Newbler version 2.6. The gene annotation and screening for RNAs were performed by submitting the sequences to the Rapid Annotations using Subsystems Technology (RAST) server (7). The resulting assemblies generated 13, 19, and 15 contigs representing the genomes of *L. monocytogenes* BHU1 (Ganges River water), *L. monocytogenes* BHU2 (agriculture soil), and *L. monocytogenes* BHU3 (human placenta bit), respectively, with an average sequencing coverage of ~89× for all three samples. The estimated genome size is 2.9 Mb, and G+C contents of 39%, 38%, and 38% were evident for the *L. monocytogenes* strains BHU1, BHU2, and BHU3, respectively. The annotation pattern suggested the genomes to contain 3,030, 3,011, and 3,005 protein-coding genes (CDSs) for *L. monocytogenes* BHU1, BHU2, and BHU3, respectively, which includes the hypothetical and RNA genes.

The genome analysis showed all the isolates to possess a relatively high number of CDSs involved in carbohydrate and amino acid metabolism, as well as virulence-defense mechanisms. More significantly, the availability of these *L. monocytogenes* genome sequences offers the opportunity to conduct further comparative genomics studies between pathogenic and nonpathogenic isolates and their listeriosis potential in India. This will also facilitate the development of newer comprehensive genotype assays for *L. monocytogenes*.

Nucleotide sequence accession numbers. The whole-genome sequences described here have been deposited in DDBJ/EMBL/GenBank under the accession numbers JUKE00000000, JUKF00000000, and JUKG00000000 for *L. monocytogenes* BHU1, *L. monocytogenes* BHU2, and *L. monocytogenes* BHU3, respectively.

ACKNOWLEDGMENTS

This study was supported by the Indian Council of Medical Research (ICMR), Government of India, New Delhi, through research project 5/3/3/10/2007-ECD-I. D.K.S. is grateful to the Centre of Advanced Study, Botany, BHU, for financial support in the form of JRF.

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