

Complete genome analysis of *Bacillus subtilis* Miz-8 isolated from “Bekang” traditional fermented soybean food of Mizoram, India

Elavarashi E*, Harini Keerthana S, Trishala G, Tapasya K and Kumar P

Department of Biotechnology, Sri Ramachandra Faculty of Biomedical Sciences & Technology, Sri Ramachandra Institute of Higher Education and Research, (SRIHER), Deemed to be University, Chennai, India

Purpose: Fermented soybean Foods (FSF) is popularly consumed in the South-East Asian countries. *Bacillus* species, a predominant microorganism present in these foods have demonstrated beneficial and deleterious impacts on human health. These microorganisms produce bioactive compounds during fermentation that have beneficial impacts in improving human health.

Objective: To perform complete genome analysis of *Bacillus subtilis* Miz-8 isolated from “bekang” traditional fermented soybean food, an Eastern state of India.

Methods: *Bacillus subtilis* Miz-8 was subjected to whole genome sequencing by Illumina Hiseq sequencing technology and analysis were performed using various bioinformatic tools. For a reliable identification of the strain Miz-8, phylogenetic and Multilocus Sequence Typing (MLST) analysis were performed.

Mining of secondary metabolites, antibiotic resistance genes, virulence genes, and prophage clusters were determined.

Findings: Complete genome of *Bacillus subtilis* Miz-8 consists of a chromosome and a plasmid which were uploaded in NCBI (GenBank ID: CP076731.1, CP076732.1) respectively. The strain Miz-8 belongs to *Bacillus subtilis* subsp. *subtilis* by MLST analysis. Strain Miz-8 revealed few secondary metabolites such as surfactin, fengycin, bacillibactin and antibiotic resistance related genes such as *tmrB*, *vmlR*, *aadK*. Virulence genes encoding immune evasion, iron acquisition and toxin genes were detected. Thirteen prophage regions were identified, among them one intact and two questionable and the rest were incomplete regions.

Recent Publications

1. Trishala G, Harini Keerthana S, Kumar P, Elavarashi E. Impact of *Bacillus* in fermented soybean foods on human health. *Annals of Microbiology* 2021; 71, <https://doi.org/10.1186/s13213-021-01641-9>.
2. Ramaraj V, Vijayaraman RS, Elavarashi E, Rangarajan S, Kindo AJ. Molecular strain typing of clinical isolates, *Trichophyton rubrum* using non-transcribed spacer (NTS) region as a molecular marker. *Journal of Clinical and Diagnostic Research* 2017; 11, 10.7860/JCDR/2017/21994.9843.
3. Elavarashi E, Kindo AJ, Sudha R. Enzymatic and non-enzymatic virulence activities of dermatophytes on solid media. *Journal of Clinical and Diagnostic Research* 2017; 11, 10.7860/JCDR/2017/23147.9410.

Microbial Interactions 2021

Pharmaceutical Microbiology 2021

October 06-07, 2021

WEBINAR

4. Elavarashi E, Kindo AJ, Kalyani J, Sudha R. Application of PCR fingerprinting using (GACA)₄ primer in the rapid discrimination of dermatophytes. Indian Journal of Medical Microbiology 2014; 32, 10.4103/0255-0857.136548.
5. Elavarashi E, Kindo AJ, Kalyani J. Optimization of PCR-RFLP directly from the skin and nails in cases of dermatophytosis, targeting the ITS and the 18S ribosomal DNA regions. Journal of Clinical and Diagnostic Research 2013; 7, 10.7860/JCDR/2013/5363.2873.

Biography

Elavarashi E, is a recipient of SRU Chancellor Fellowship Grant for full-time PhD programme in April 2009 at Sri Ramachandra Institute of Higher Education and Research (SRIHER), Chennai, India. She has done PhD in Microbiology on 'Phenotypic and genotypic characterization of dermatophytes from clinical specimens using novel markers'. Now her current research interest is to isolate potent probiotic *Bacillus* strains from various sources like fermented soybean foods and soil. She has worked on *Bacillus* since 2019, isolated *Bacillus* isolates from various sources and evaluated extracellular enzyme activity, biofilm formation and antimicrobial activity of *Bacillus* spp. against pathogens. Recently, she has analysed the complete genome of *Bacillus* and is yet to be published.