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Short Research Communication

Draft Genome Sequence of Multidrug Resistant *Salmonella enterica* serovar Weltevreden Isolated from Seafood

Vijaya Kumar Deekshit[1], Krishna Kumar Ballamoole[1], Praveen Rai[1], Madhushankara[2], Iddya Karunasagar[3], Indrani Karunasagar[1] ✉

1. Faculty of Biomedical Sciences, Nitte University Center for Science Education and Research, UNESCO MIRCEN for Medical & Marine Biotechnology, University Enclave, Medical Sciences Complex, Deralakatte, Mangalore-575018, India
2. School of Information Science (SOIS), Manipal University, Manipal, India
3. FAO Consultant, Subba-Meena, Jayanagar, Mangalore, India

✉ Corresponding author: Prof. (Dr.) Indrani Karunasagar, Director (R & D), UNESCO MIRCEN for Medical & Marine Biotechnology, Faculty of Biomedical Sciences, Nitte University Center for Science Education and Research, University Enclave, Medical Sciences Complex, Deralakatte, Mangalore-575018, India. E.mail: karuna8sagar@yahoo.com

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Abstract

Salmonella enterica subsp. *enterica* serovar Weltevereden is the most frequent serovar isolated from Asia. Here, we report a draft genome sequence of multidrug resistant *Salmonella* Weltevreden 9 isolated from seafood. Whole-genome of this isolate and annotation will help enhance the understanding of this pathogenic multidrug-resistant serovar.

Key words: *Salmonella* Weltevreden, multidrug resistance, seafood, genome sequence

Introduction

Salmonellosis is a common foodborne disease caused by *Salmonella* spp. and is of global significance. It is a significant pathogen of food producing animals and remains a primary source of salmonellosis (1). *Salmonella* spp. has been frequently reported in environmental samples since they find their way to the environment through the excreta of humans and animals. In 2004, the European Union (EU) alone recorded 192,703 human cases of salmonellosis (2). The majority of seafood associated illness is due to the consumption of shellfish harvested from sewage polluted waters. It is well known that fish/shellfish normally do not harbour microorganism like *Salmonella* but acquire it from contaminated water from which they have been harvested (3). The work of Koonse *et al*. (2005) (4) showed *S*. Weltevreden to be the most frequent serovar at 21 % prevalence of the total serovars reported from aquaculture shrimp farms in three different countries. Similar observation were also made by Ponce *et al*. (2008) (5) who confirmed *S*. Weltevreden as the most important serovar among the 64 different serovars isolated from seafood. It has been the predominant serovar in seafood in the Asian region reported in several studies (6-8).

In this report the availability of draft genome sequence of *S*. Weltevreden (SW9) isolated from seafood in India has been announced. *S*. Weltevreden (SW9) was isolated from seafood (fish) obtained from the fish landing centre in Mangalore, located in the Southwest coast of India. Sample was immediately iced and transported to the laboratory for further analysis. Culture based technique for the isolation and phenotypic identification of the isolate using a battery of biochemical tests was performed as per FDA Bac-

teriological Analytical Manual. Genotypic identification was done by polymerase chain reaction using genus specific primers.

The isolate was resistant to 6 antimicrobials including tetracycline, chloramphenicol, nalidixic acid, ampicillin, co-trimoxazole and erythromycin. Genomic DNA was extracted from *S*. Weltevreden (SW9) using a QIAamp DNA minikit (Qiagen, Germany). A concentration of 50ng/µl was used for the genome sequencing. The raw sequence data was generated after library preparation on the Ion Torrent PGM platform and assembled using CLC Genomics Workbench version 6. Structural gene prediction and functional annotation was performed using the Rapid Annotations Subsystems Technology (RAST) server (http://rast.nmpdr.org/) as it was shown to work exceedingly well in our previous studies (9).

A total of 2, 64,365 reads with a mean read length of 150.2 bp for 200 bp fragmentation chemistry obtained from the Ion PGM was assembled into 716 contigs. The median contig length N_{50} = 6276. The draft genome had a length of 3,825,753 bp, with 6239 coding sequences and a GC content of 51.8%. The 716 contigs from SW9 were also assembled to NC_003198.1 using Geneious 8.0.3. The analysis obtained from the RAST server revealed 456 subsystems. The annotated genome had 109 genes responsible for resistance to antibiotics and toxic compounds, including 17 genes for multidrug resistance efflux pumps and 18 genes for mdtABCD multidrug resistance cluster and 8 fluoroquinolone resistant genes. There were 235 genes coding for membrane transport proteins. The multidrug resistant isolate (SW9) harbored the resistance genes to antibiotics like tetracycline, chloramphenicol, co-trimoxazole, florfenicol and presented point mutation in the quinolone resistance determining region (QRDR) responsible for resistance to nalidixic acid. The isolate was found to carry resistant genes such as *tetB*, *catA1* for tetracycline and chloramphenicol respectively (10).

Nucleotide sequence accession number

This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number JPIO00000000.1. The version described in this paper is the first version.

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Competing Interests

The authors have declared that no competing interest exists.

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