



Data in Brief

Cultivation-independent comprehensive investigations on bacterial communities in serofluid dish, a traditional Chinese fermented food



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ABSTRACT

Serofluid dish (or *Jiangshui*, in Chinese), a traditional food in the Chinese culture, is made from vegetables by fermentation. In this study, bacterial community of the fermented serofluid dish was assessed by Illumina amplicon sequencing. The metagenome comprised of 49,589 average raw reads with an average 11,497,917 bp and G+C content is 52.46%. This is the first report on V4 hyper-variable region of the 16S rRNA metagenome sequence employing Illumina platform to profile the microbial community of this little known fermented food from Gansu Province, China. The metagenome sequence can be accessed at NCBI, SRA database accession no. SRP065370.

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Specifications

Organism/cell line/tissue	Metagenome of serofluid dish
Sex	Not applicable
Sequencer or array type	Illumina HiSeq2500
Data format	Raw data: FASTQ file
Experimental factors	Environmental sample
Experimental features	V4 hypervariable region of 16S rRNA was sequenced using paired end Illumina Hi-Seq technology, sequence analyzed by QIIME data analysis package.
Consent	Not applicable
Sample source location	A total of 12 serofluid dish samples were collected from 10 handmade areas from Gansu Province, China.

1. Direct link to deposited data

<http://www.ncbi.nlm.nih.gov/sra/?term=SRP065370>.

2. Experimental design, materials and methods

Serofluid dish is a naturally fermented dish from vegetables such as Chinese cabbage and celery that are also called *Jiangshui*, in Chinese due

to its white serofluid [1]. It has been found that serofluid dish making techniques have a history of over two thousand years. In recent years, serofluid dish has been confirmed to be clinically effective for promoting digestion, lowers cholesterol levels, and fall blood pressure *in vitro* and *in vivo* [2]. In addition, microbes involved in serofluid dish fermentation have been studied previously [3,4]. Taxonomically diverse groups of lactic acid bacteria (LAB) have been identified during the fermentation of serofluid dish [5]. However, most of the diversity studies in the last two decades have shown that less than 1% of the microbes of a community are possibly cultured *in vitro* with known cultivation approach, but 99% still remain unexplored [6]. Culture-based approaches have known limitations in terms of reproducibility and challenges in the culturability of some microbes [7]. Therefore, the set of cultured isolates may not reflect the true microbial composition of fermented serofluid dish. With the advancement of culture independent technique using next generation sequencing or clone library construction, it is time to analyze the entire population in the community as well as their functional potentiality in fermented food [8,9]. Therefore, the present research was designed to investigate the bacterial community composition by using Illumina based metagenomic approach in serofluid dish, which may represent novel species within this genus which was reported for the first time in association with serofluid dish.

A total of 26 serofluid dish samples were collected from 10 handmade areas across Gansu Province, China (35.22°–36.33°N, 103.59°–105.10°E). The V4 hypervariable region of the 16S rRNA gene was amplified using 515 F and 806R primer combination (5′-GTGCCAGC

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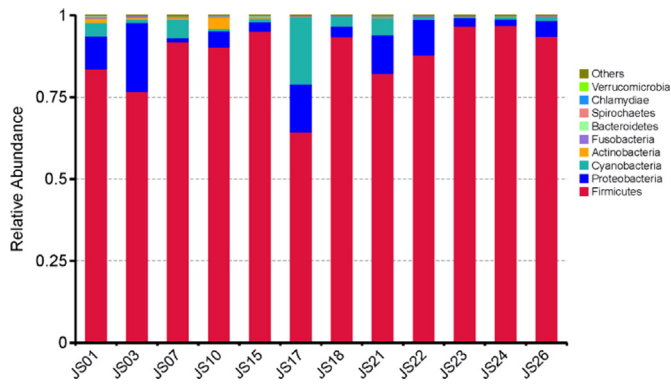


Fig. 1. Taxonomy classification of reads at phylum level. Only top 10 enriched class categories are shown in the figure.

MGCCGCGTAA-3' and 5'-GGACTACHVGGGTWTCTAAT-3', respectively [10]. A 6-bp error-correcting tag was added to the forward primer [11]. A total of 12 serofluid dish samples were sent to Novogene Bioinformatics Technology (Beijing, China) to perform amplicon sequencing according to HiSeq protocols. Amplicon pyrosequencing was performed on the Illumina HiSeq PE250 platforms at Novogene Bioinformatics Technology (Beijing, China). Bioinformatic analysis was performed by QIIME data analysis package [12]. Complete data sets are submitted to the NCBI Short Read Archive under accession numbers SRR2919186, SRR2919188, SRR2919190-SRR2919199.

The output file comprised 113 MB data with a total of 595,067 high qualities read having 52.46% GC content. In the serofluid dish sample studied, the classified OTUs represent distinct phyla dominated by Firmicutes (87.79%), Proteobacteria (7.50%) and Cyanobacteria (3.69%) (Fig. 1). At the family level, Lactobacillaceae (81.01%) was predominant followed by Acetobacteraceae (2.43%), Pseudomonadaceae (1.19%), Enterobacteriaceae (1.53%) and Bacillaceae (0.83%) (Fig. 2). The leading genera were *Lactobacillus* (74.65%), *Pediococcus* (5.92%), *Acetobacter* (2.43%), *Bacillus* (0.34%) and *Cetobacterium* (0.33%) (Fig. 3). Our data provide the first scientific report on the composition of the bacterial community, using Illumina sequencing method, from the undeveloped serofluid dish located in northwest China region. The most dominated phylum in this study was *Lactobacillus* which is known to produce beneficial metabolites useful for gut microbiota and human health. 16S rRNA metagenome analysis of serofluid dish revealed the presence of microorganism key functional characteristics. It may contribute to further studies on critical process for human gut microbiota and probiotics, such as nutrient absorption, cholesterol decomposition and blood-pressure control. Consequently, these results indicate that both serofluid dish formation complex and distinct bacterial structure which were not reported before.

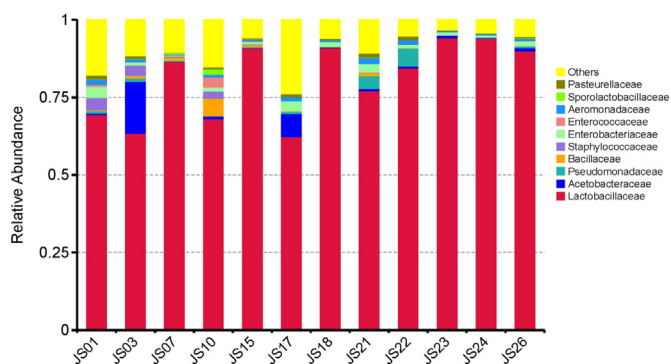


Fig. 2. Taxonomy classification of reads at family level. Only top 10 enriched class categories are shown in the figure.

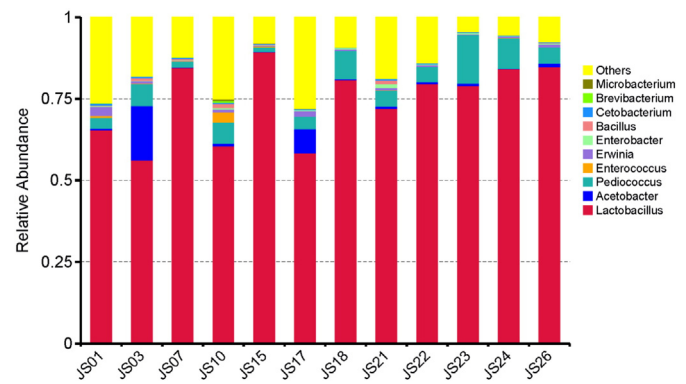


Fig. 3. Taxonomy classification of reads at genera level. Only top 10 enriched class categories are shown in the figure.

3. Nucleotide sequence accession number

Metagenome sequence data are available on NCBI, SRA database accession no. SRP065370.

Competing Interests

The authors declare that there are no competing interests.

Acknowledgments

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