



Metagenomic data of fungal internal transcribed spacer from serofluid dish, a traditional Chinese fermented food



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ARTICLE INFO

Article history:

Received 21 December 2015

Accepted 30 December 2015

Available online 31 December 2015

Keywords:

Serofluid dish

Jiangshui

Fungal ITS

Cultivation-independent

Microbial diversity

ABSTRACT

Serofluid dish (or *Jiangshui*, in Chinese), a traditional food in the Chinese culture for thousands of years, is made from vegetables by fermentation. In this work, microorganism community of the fermented serofluid dish was investigated by the culture-independent method. The metagenomic data in this article contains the sequences of fungal internal transcribed spacer (ITS) regions of rRNA genes from 12 different serofluid dish samples. The metagenome comprised of 50,865 average raw reads with an average of 8,958,220 bp and G + C content is 45.62%. This is the first report on metagenomic data of fungal ITS from serofluid dish employing Illumina platform to profile the fungal communities of this little known fermented food from Gansu Province, China. The Metagenomic data of fungal internal transcribed spacer can be accessed at NCBI, SRA database accession no. SRP067411.

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Specifications

Organism/cell line/tissue	Fungal internal transcribed spacer from serofluid dish (<i>Jiangshui</i>)
Sex	Not applicable
Sequencer or array type	Illumina HiSeq 2500
Data format	Raw data: FASTQ file
Experimental factors	Environmental sample
Experimental features	ITS region of serofluid dish (<i>Jiangshui</i>) was amplified using fungal ITS specific primers from isolated metagenome followed by pyrosequencing using Illumina Hi-Seq technology.
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=SRP067411>.

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2. Experimental design, materials and methods

Chinese traditional fermented vegetable foods, such as serofluid dish (also called *Jiangshui*, in Chinese), have served as low-calorie food that have been one of the major carbohydrate and vitamin sources in Chinese diet for more than two thousand years [1]. In recent years, fermented vegetable foods have attracted considerable interest due to their remarkable nutritional value. They are also well known as functional foods due to their antihypertensive effect, improvement in the intestinal function, and preventing diabetes and anticancer properties [2]. Therefore, they are predicted to become significant for human health [3].

Although diverse eukaryotic microbes were found in serofluid dish by cultivation and microscopy, the abundance and diversity of naturally occurring fungi have not been well characterized [4]. Culture-independent methods based on the rRNA genes of microbes were usually used to study the microbial communities in natural habitats [5]. The internal transcribed spacer (ITS) regions of fungal rRNA genes have been identified as particular targets for molecular biology analysis of fungal communities and their high sequence variability relative to the flanking sequences that makes them valuable for genus- and species-level identification [6]. Therefore, the present research was designed to investigate the fungal communities' 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.

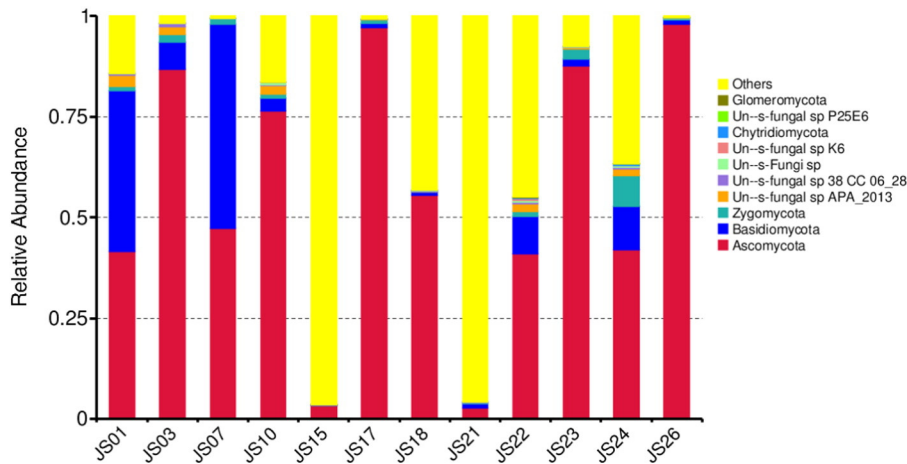


Fig. 1. Taxonomy classification of reads at phylum level. Only top 10 enriched class categories are shown in the figure.

A total of 26 serofluid dish samples were collected from 10 hand-made areas across Gansu Province, China (35.22°–36.33°N, 103.59°–105.10°E). The fungal internal transcribed spacer was amplified using ITS1 and ITS4 primer combination (5'-GGAAGTAAAAGTCGTAACAAGG-3' and 5'-GCTGCGTTCATCGATGC-3', respectively). A 6-bp error-correcting tag was added to the forward primer [7]. 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 [8]. Complete data sets are submitted to the NCBI Short Read Archive under accession numbers SRR3003942, SRR3003943, SRR3003944, SRR3003945, SRR3003947, SRR3003948, SRR3004055, SRR3004201, SRR3004236, SRR3004274, SRR3004275 and SRR3009902, respectively.

The output file comprised 151 MB data with a total of 610,379 high quality reads having 45.62% GC content. In the serofluid dish sample studied, the classified OTUs represent distinct phyla dominated by Ascomycota (56.62%), Basidiomycota (10.55%), Zygomycota (1.54%) and others (31.29%) (Fig. 1). At the family level, *Candida xylopsoci* (23.96%) was predominant followed by *Sporopachydermia* sp. (10.36%), *Cystofilobasidiaceae* (7.73%), *Debaryomycetaceae* (4.46%), *Trichocomaceae* (3.69%), *Cyberlindnera* (3.40%), *Dipodascaceae* (1.17%), *Ascomycota* sp. (1.06%), *Rhodotorula mucilaginosa* (0.94%), *Mortierellales* sp. (0.55%) and others (42.68%) (Fig. 2). The leading genera were

Candida (23.96%), *Sporopachydermia* (10.36%), *Guehomyces* (7.72%), *Scheffersomyces* (4.0%), *Cyberlindnera* (3.40%), *Penicillium* (3.16%), *Ascomycota* sp. (1.06%) and others (44.44%) (Fig. 3). The remaining sequences were not associated to any known fungi or fungal sequences in the public database.

Our data provide the first scientific report on the composition of the fungal communities, using Illumina sequencing method, from the underdeveloped serofluid dish located in northwest China region. The most dominated phylum in this study was Ascomycota and Basidiomycota which are known to produce beneficial metabolites useful for human health, such as organic acid, antibiotic, polysaccharide, and vitamin. The metagenome analysis of fungal ITS regions from serofluid dish revealed the presence of fungal key functional characteristics. Therefore, these results indicate that both serofluid dish formation complex and distinct fungal communities structure which were not reported before.

Nucleotide sequence accession number

Metagenome sequence data are available on NCBI, SRA database accession no. SRP067411.

Competing interests

The authors declare there are no competing interests.

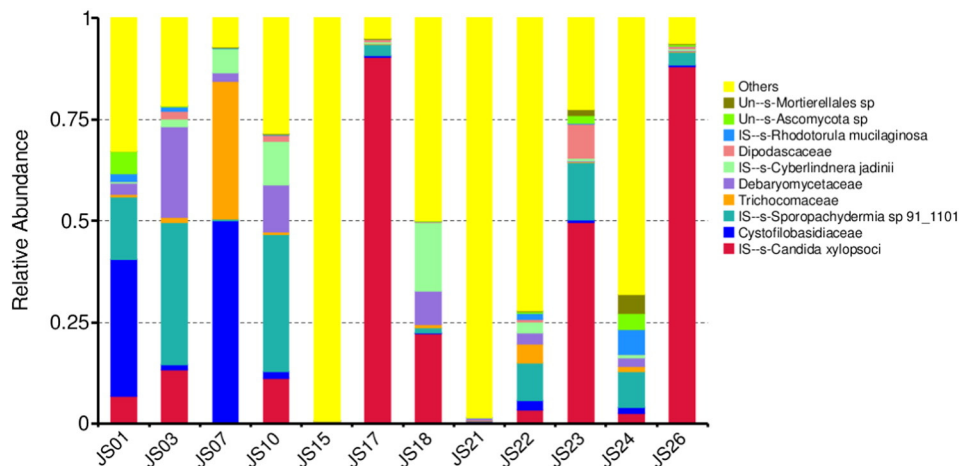


Fig. 2. Taxonomy classification of reads at family level. Only top 10 enriched class categories are shown in the figure.

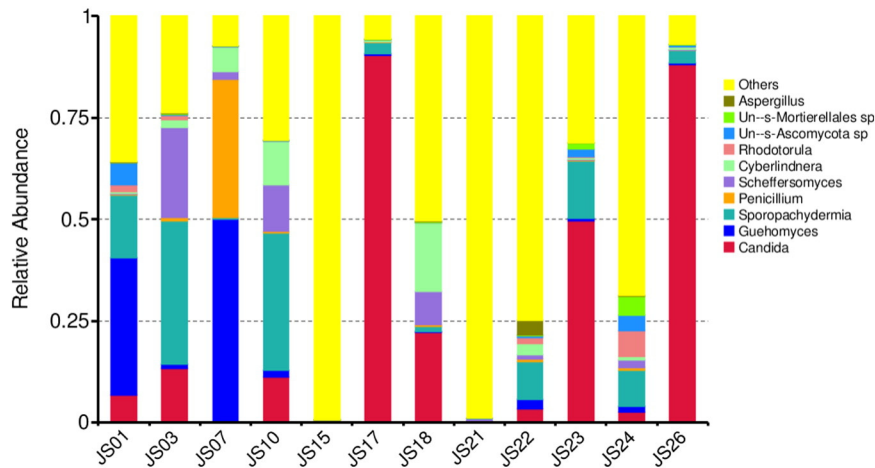


Fig. 3. Taxonomy classification of reads at genera level. Only top 10 enriched class categories are shown in the figure.

Acknowledgments

This work was supported by Gansu Province Science Foundation for Distinguished Young Scholars (Grant No. 1308RJDA014), Longyuan Support Project for Young Creative Talents (Grant No. GANZUTONGZI [2014] no.4), Technology Program of Lanzhou City (Grant No. 2015-3-142, Grant No. 2015-3-97), and The Fundamental Research Funds for the Central Universities of China (Grant No. lzujbky-2015-57).

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