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Data in Brief

Metagenomic analysis of fungal taxa inhabiting Mecca region, Saudi Arabia

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ABSTRACT

The data presented contains the sequences of fungal Internal Transcribed Spacer (ITS) and 18S rRNA gene from a metagenome of the Mecca region, Saudi Arabia. Sequences were amplified using fungal specific primers, which amplified the amplicon aligned between the 18S and 28S rRNA genes. A total of 460 fungal species belonging to 133 genera, 58 families, 33 orders, 13 classes and 4 phyla were identified in four contrasting locations. The raw sequencing data used to perform this analysis along with FASTQ file are located in the NCBI Sequence Read Archive (SRA) under accession numbers: SRR3150823, SRR3144873, SRR3150825 and SRR3150846.

Specifications	Microbiology, mycology, biodiversity
How data was acquired	Fungal tag-encoded FLX massively parallel pyrosequencing using Roche 454 GS FLX Titanium sequence followed by bioinformatics analysis using our in-house developed java script for filtration, annotation and taxonomy assignment.
Data format	Raw data FASTQ file
Experimental factors	ITS region along with partial gene sequence of 18S rRNA were amplified using fungal specific primers (ITS1-F and ITS4-F) from isolated metagenome followed by pyrosequencing using 454 GS FLX Titanium.
Experimental features	Soil cores, 2 cm in diameter and 20 cm deep, were taken at each site. The soil samples were collected from four locations in Mecca region, Saudi Arabia.
Data source location	Mecca region, Saudi Arabia.
Data accessibility	Data are available at NCBI Biosample under accession numbers: SRR3150823 (MMKhulais_P.SS), SRR3144873 (MMMeccaORD_P.SS), SRR3150825 (MMThuwal_P.SS), SRR3150846 (MMAsfan_P.SS). Direct link to deposited data http://www.ncbi.nlm.nih.gov/sra?term=SRP069742

1. Direct link to the data

http://www.ncbi.nlm.nih.gov/sra?term=SRP069742.

2. Data, experimental design, materials and methods

2.1. Sampling

Soil samples were collected from four different locations in the Mecca region, Saudi Arabia. The field sampling only included soil and did not affect or involve endangered or protected species. 24 Tow to four soil samples for each sampling locations were collected to represent the soil profiles of the site. Soil cores, 2 cm in diameter and 20 cm deep, were taken at each site. Soils were deposited in 50 ml Falcon tubes and stored at −20 °C until analysis.

2.2. DNA extraction

Genomic DNA was extracted from an 8 g subsample of each soil sample after combining various samples at each location using the Mo Bio Power soil kit following the manufacturer's instructions. Finally, the extracted DNA was checked using 0.7% w/v agarose gel electrophoresis to verify the success of the extraction.

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2.3. Sequencing

High-throughput tag-encoded GS-FLX amplicon sequencing was used to assess fungal diversity in the selected location. Amplicon libraries were performed using a combination of tagged primers designed for the variable ITS region, as recommended for the tag-encoded pyrosequencing method [1,2]. Genomic DNA samples were amplified using the fungal-specific primer pair ITS1F (5′-XCTTGGTCATTTAGAGGAAGTAA) and ITS4 (5′-YxxxxxTCCTCCGCTTATTGATATGC), where X and Y represent the two pyrosequencing primers (CCTATCCCCTGTGTGCCTTGGCAGTCTCAGT and CCATCTCATCCCTGCGTGTCTCCGACTCAGA) and xxxxx represents the barcodes designed for sample identification. Barcodes were unique and differed from each other by at least two nucleotides. Four PCR reactions were performed per sample. Pyrosequencing was performed using the GS 454 FLX instrument with Titanium reagents (Roche, Indianapolis, IN, USA) at Macrogen Inc. (Seoul, Korea).

2.4. Data analysis

Output file containing ITS sequences with partial 18S rRNA gene sequence were analysed. Furthermore, the output fna file was converted to Fastq using the standalone phred33 conversion tool and submitted to the NCBI Biosample with accession numbers. Direct link to the data: SRP069742.

A total of 460 fungal species belonging to 133 genera, 58 families, 33 orders, 13 classes and 4 phyla were identified at the four locations.

Conflict of interest

The authors declare no conflict of interests.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.gdata.2016.07.008.

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