Metadata Rivas et al. Environmental Sequencing

Table 1. Metadata associated with environmental sequencing of dust samples including methods used for extraction, location of sequencing facility, data pipeline, and primer combinations used to characterize prokaryotes and eukaryotes found in dust.

Title of dataset	Dust environmental sequencing
URL of dataset	datarepo.bioinformatics.utep.edu/ getdata?acc=ACIEJDV41U1ZN5I
Abstract	To study movement of aquatic biota by wind at regional scales we performed total DNA analysis on collected dust (n=19) from dust events from various locations. Using conserved DNA primers we identified 31,761 eukaryotic OTUs.
Keywords	NGS, 18S, Environmental Sequencing, Dust
Dataset lead author	Jonathon Mohl
Position of data author	Systems Analyst, Staff
Address of data author	The University of Texas at El Paso, 500 W University, El Paso, TX 79968
Email address of data author	jemohl@utep.edu
Primary contact person for dataset	Elizabeth J. Walsh
Position of primary contact person	Biological Sciences Professor, Principal Investigator
Address of primary contact person	The University of Texas at El Paso, Department of Biological Sciences, 500 W University, El Paso, TX 79968
Email address of primary contact person	ewalsh@utep.edu
Organization associated with the data	The University of Texas at El Paso
Usage Rights	publicly available and free to use
Geographic region	Samples analyzed included Texas, New Mexico, and China
Geographic coverage	HTSPHS= Hueco Tanks State Park and Historic Site; 31.926927 N, -106.041183 W; 1384 m University of Texas El Paso; 31.76873 N, -106.504067 W; elevation 1170 m White Sands Missile Range; 32.437503 N, -106.168744 W; 1249 m: 32.542026 N, -106.194941 W; 1222 m Yellow Lake playa 33.823477 N, -102.459967 W; 1040 m Jornada, LTER 32.608625, -106.730238; 1327 m
Temporal coverage - Begin date	3/28/02
Temporal coverage - End date	3/24/16
General study design	The purpose of this study was to quantify the transport of aquatic micro-invertebrate resting stages in dust storms. Falling sediment was passively collected from 2011–2016 using standard marble dust collectors (MDCOs), Modified Wilson and Cooke (MWAC) or Big Spring Number Eight (BSNE) samplers.
Methods description	0.25 g of dust from each sample was used for analysis. Total DNA was extracted from dust samples (n=19) using a PowerSoil kit (MoBio, Carlsbad, CA)

	following the manufacturer's protocol.
Laboratory, field, or other analytical methods	DNA was submitted to MRDNA labs (Shallowater, TX) for 18S tag-encoded FLX-Titanium amplicon pyrosequencing using the SSU_F04//SSU_R22 primer set. Sequencing reads were analyzed using QIIME. Reads were clustered at 99% sequence identity to delineate operational taxonomic units (OTUs). OTUs were then taxonomically assigned using BLAST (Altschul et al. 1990) against the Silva reference (eukaryotic OTUs) (v.128; (Yilmaz et al. 2014).
Quality control	Some samples were done in replicate to monitor reproducibility.
Additional information	Metadata includes; 1) Excel sheet with collection dates, GPS locations; folder containing SSU sequences with i) mapping files that contain barcodes and sample ids; ii) Fasta file that contains the raw sequences; iii) quality file that contains sequence quality data for sample

Table 2. Date and locality of dust collection and sequences obtained using the 18S primer set.

Column name	**Definition**	**Units**
Date	Date samples were collected	Calendar date
Collection Location	Location were the samples were located	GPS
18S Sequences	Next-generation sequences using SSU_F04//SSU_R22 primer sets	each