Utah State University
DigitalCommons@USU

8-28-2019

MSA: Dust as an ecosystem driver: determining the ecosystem consequences of cross-system subsidies of nutrients and microorganisms in dusts

Janice Brahney
Utah State University, janice.brahney@usu.edu

Follow this and additional works at: https://digitalcommons.usu.edu/funded_research_data

Part of the Life Sciences Commons

DATA MANAGEMENT PLAN

The project includes the collection of physical samples and the generation of analytical data. Goals of the data management plan for this project include a) protect physical samples from post-collection alteration, b) provide and maintain metadata to accompany physical samples, c) share data and results with the larger scientific community.

1. Samples and Data Types

<u>Physical samples</u> will include dry dust samples collected from Dry Sampling Inserts as well as filters generated by wet deposition analyses at the National Atmospheric Deposition Program. All physical samples will be archived in the Environmental Biogeochemistry and Paleolimnology Lab (EBPL) at Utah State University in temperature-controlled chambers. Each sample will be associated with raw data including unique sample ID and metadata including, location, sampling period, sample processing information, and mass collected.

<u>Analytical data</u> derived from this project including sample inorganic and organic composition, genomics, and the results of bioassay and source attribution studies. Additional recorded data will include climate, biogeography, and HYSLPIT back-trajectory models.

<u>Fungal sequence data</u> will be gathered and analyzed as part of the proposed work. Sequence data will be stored in fasta file format, and associated metadata will be stored as comma separated values (csv) files.

<u>Educational material</u> developed in this project, including the instructional guide and video, and lesson plans will be made available to high school teachers around the country through the national Agriculture in Classroom program and Utah Nature Explorers.

Data will be compiled and stored in Microsoft Excel spreadsheets, comma separated values files, and fasta files, and at least once per week backed-up to external hard drives and USU's Box cloud storage, which allows for centralized and secure file management. A summary table will be generated that includes the unique Sample ID, the sampling location, and information on the types of analytical results available for these samples, the dates of analyses, and the laboratory, method, and instrumentation used to generate the data. Table 1 presents examples of the analytical data types, format, and metadata standards to be used through the project and for subsequent archiving.

Table 1.

DATA	FORMAT	ARCHIVE LOCATION	METADATA STANDARD
Dust samples	physical	EBPL	local
Raw Data	.csv	DigitalCommons@USU	Qualified Dublin Core
Fungal Sequence DNA	.csv, fasta	NCBI SRA	SRA
GeoChemical Data	.csv, xlsx	EarthChem	DataCite
Data Analysis/ experimental	.csv	DigitalCommons@USU	Qualified Dublin Core
Data Analysis/ Maps	.shp	DigitalCommons@USU	Qualified Dublin Core
Curricular Materials	.pdf	DigitalCommons@USU	Qualified Dublin Core

2. Dissemination methods

The data and results of analyses generated in this project will be disseminated through publishing in peer-reviewed and widely available scientific journals and through presentations at national and local conferences by the project PI, Co-PI, and graduate and undergraduate students. Data tables generated through the project will be published as supplementary information along with journal publications. Post-publication data and articles will be archived through the Utah State University open access Digital Commons website (http://digitalcommons.usu.edu/) managed through the Merill-Cazier Library. All published articles will be deposited into NSF's Public Access repository.

3. Policies for data sharing

Prior to archiving, data and any remaining archived samples will be considered for sharing with other researchers as requested. All interested sample and or data users will be required to sign a sample and data use contract that will require them to acknowledge the investigators and NSF in any resulting publication or presentation

4. Plans for Archiving and Preserving

All remaining physical samples will be permanently archived at EBPL and stored in temperature controlled low humidity environment. All metagenomic sequence data will be deposited at NCBI's Sequence Read Archive (SRA). Sequence data will be uploaded to the SRA at the time of manuscript submission or one year following completion of the associated experiment, whichever comes first. Similarly, at the time of publication or two years following the completion of the project, geochemical data will be archived in the Integrated Earth Data Applications EarthChem database (http://www.earthchem.org/), and ecological data will be archived in Dryad (http://datadryad.org/), and DataOne (http://www.dataone.org/), as appropriate. All additional data will be archived through USU's Digital Commons, where all files are backed up at multiple sites, including cloud storage and preservation copies are stored in Amazon Web Services, with redundant storage across multiple facilities and are regularly verified for the integrity of data using checksums.

5. Roles and responsibilities

Dr Brahney will be responsible for maintaining all physical samples and ensuring her and her students appropriately store and archive dust and associated data including, physical properties, biogeochemical data, and experimental results. Generated data will be backed up to external hard-drives and through automatic daily updates to cloud storage through USU's Box subscription.

Dr. Waring will be responsible for the generation and analyses of fungal sequence libraries. Sequence files (and the QIIME scripts used to analyze them) will be backed up to the cloud daily through USU's Box subscription. Additionally, all data will be copied to an external hard drive on a weekly basis.