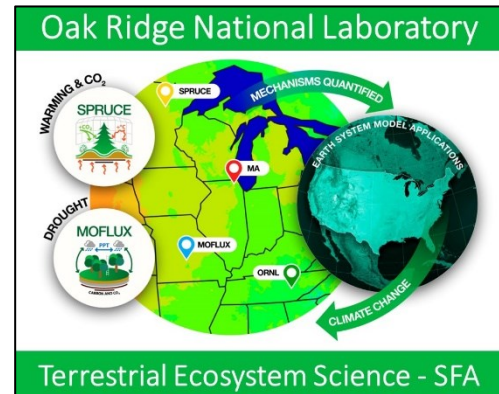


Responses of Drying-rewetting (Transient Soil Moisture) and Steady State Soil Moisture Incubation on Soil Organic Carbon Dynamics in Three US Soils, 2017

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1. Data Set Overview:

This data set contains measurements of soil characteristics (aggregate size distribution and mean size, total aggregate associated carbon, extractable organic C, and microbial biomass C), microbial respiration, and soil metabolite concentrations from a transient and steady soil moisture incubation experiment using soils of different textures (sandy, loamy, and clayey). The study investigated mechanisms driving the Birch effect (increased carbon mineralization pulses with wetting following a drying period) in differing soil textures.

Three different soils of distinctly different textures were collected from 0-15cm depth in Georgia (sandy, 2017-05-01), Missouri (loamy, 2017-06-14), and Texas (clayey, December 2017). Soils were incubated for 140 days with destructive harvests done on days 1, 29, 33, 56, 112, 116, and 140 in transient soil moisture incubation and on days 1, 33, 116, and 140 in steady state soil moisture incubation. This dataset contains six data files in comma separate (.csv) format.

Relevant Publication:

The measurements and results of this study have been described in the following publications:

Singh, S, MA Mayes, SN Kivlin, & S Jagadamma. 2023. How the Birch effect differs in mechanisms and magnitudes due to soil texture. *Soil Biology and Biochemistry*, 179, 108973. <https://doi.org/10.1016/j.soilbio.2023.108973>

Singh, Shikha. "Soil Moisture Sensitivity of Microbial Processing of Soil Organic Carbon. " PhD diss., University of Tennessee, 2020. https://trace.tennessee.edu/utk_graddiss/6187

Data Citation:

Cite this data set as follows:

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2. Data Characteristics:

This data set contains 10 comma separate (*.csv) files.

Spatial Coverage

This was a lab incubation study using soils from mixed forests from the following locations in Georgia, Missouri, and Texas:

- Taylor County in Georgia (32.54°N, 84.22°W)
- Missouri Ozark AmeriFlux (MOFLUX) site in central Missouri (38.74°N, 92.20°W)
- Bowie County, Texas (33.44°N, 94.48°W)

Temporal Coverage

The soil sampling for loamy soil (Georgia) was done on June 14, 2017, sandy soil (Missouri) on May 1, 2017, and clayey (Texas) in December 2017. The incubation study lasted 140 days. Gas samples were collected frequently in both incubations. Destructive soil sampling was done days 1, 29, 33, 56, 112, 116, and 140 for transient soil moisture incubation and days 1, 33, 116, and 140 for steady state moisture incubation to determine the extractable organic C, microbial biomass C, , aggregate size distribution and associated C, and metabolites.

Data File Description

These data are considered at **Quality Level 1**. Level 1 indicates an internally consistent data product that has been subjected to quality checks and data management procedures.

This data set contains 10 files in comma separate (.csv) format:

- *Incubation_data.csv*: Contains the proportion of aggregates in the following size categories: > 2 mm, 2000-250 µm, 250-53 µm, and <53 µm, mean weight diameter , total aggregate associated carbon, extractable organic C, and microbial biomass C. Measurements were made at the destructive harvest time points for both steady and transient soil moisture incubations.
- *Metabolites_clayey.csv*: Contains metabolites data in clayey soil for transient and steady soil moisture incubations.

- *Metabolites_loamy.csv*: Contains metabolites data in loamy soil for transient and steady soil moisture incubations.
- *Metabolites_sandy.csv*: Contains data on metabolites data in sandy soil for transient and steady soil moisture incubations.
- *Microbial_respiration_steady.csv*: Contains microbial respiration rate across the 140 days of incubation (steady state soil moisture conditions) for the three soil types.
- *Microbial_respiration_transient.csv*: Contains microbial respiration rate across the 140 days of incubation (transient state soil moisture conditions) for the three soil types.

Missing data are indicated by -9999.

Data Dictionary for *Incubation_data.csv*

Column Name	Units	Description
ID		Unique ID. Created by aggregating Days, Soil_type, Soil_moisture, and Rep.
Days		Shows the days the readings were taken.
Soil_type		Soil types include clayey, loamy, and sandy
Soil_moisture		Shows if the incubation is transient or steady state soil moisture. Transient incubations were subjected to five cycles of soil drying (~10% WHC) and wetting (100% WHC) while while steady state incubations maintained 55% WHC.
Rep		Treatment replicate number
Prop_less_than_53_um		Proportion aggregates less than 53 um
Prop_250_53_um		Proportion aggregates from 250-53um
Prop_2000_250_um		Proportion aggregates from 2000-250um
Prop_greater_than_2mm		Proportion of aggregates greater than 2 mm
Mean_weight_diameter	mm	Average aggregate size in mm
Extractable_organic_C	mg kg ⁻¹ soil	Extractable organic soil carbon
Microbial_biomass_C	µg g ⁻¹ soil	Microbial biomass carbon
Total_aggregate_associated_C	g kg ⁻¹ soil	Total aggregate associated carbon

Data Dictionary for *Metabolites_clayey.csv*

Column Name	Units	Description
Soil_type	N/A	Soil types include clayey, loamy, and sandy
Soil_moisture	N/A	Shows if the incubation is transient or steady state soil moisture. Transient incubations were subjected to five cycles of soil drying (~10% WHC) and wetting (100% WHC) while while steady state incubations maintained 55% WHC.
Day	N/A	Shows the days the readings were taken.
Aconitate	N/A	Aconitate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.

Adenosine	N/A	Adenosine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Creatine	N/A	Creatine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Disaccharide	N/A	Disaccharide relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Fumarate	N/A	Fumarate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Glucose_phosphate	N/A	Glucose phosphate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Glutaric_acid	N/A	Glutaric acid relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Inosine	N/A	Inosine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Leucine_Isoleucine	N/A	Leucine Isoleucine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Myo-Inositol	N/A	Myo-Inositol relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Pyroglutamic_acid	N/A	Pyroglutamic acid relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Taurine	N/A	Taurine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.

Data Dictionary for *Metabolites_loamy.csv*

Column Name	Units	Description
Soil_type	N/A	Soil types include clayey, loamy, and sandy
Soil_moisture	N/A	Shows if the incubation is transient or steady state soil moisture. Transient incubations were subjected to five cycles of soil drying (~10% WHC) and wetting (100% WHC) while steady state incubations maintained 55% WHC.
Day	N/A	Shows the days the readings were taken.
3-Phosphoglycerate	N/A	3-Phosphoglycerate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.

Aconitate	N/A	Aconitate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Adenosine	N/A	Adenosine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Aminocaproic_acid	N/A	Aminocaproic_acid relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Aspartate	N/A	Aspartate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
D-Gluconate	N/A	D-Gluconate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Disaccharide	N/A	Disaccharide relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Fumarate	N/A	Fumarate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Glutamate	N/A	Glutamate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Glutaric_acid	N/A	Glutaric_acid relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Guanosine	N/A	Guanosine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Leucine_Isoleucine	N/A	Leucine_Isoleucine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Malate	N/A	Malate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Myo-Inositol	N/A	Myo-Inositol relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
N-Acetylglutamate	N/A	N-Acetylglutamate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Nicotinate	N/A	Nicotinate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.

Pyroglutamic_acid	N/A	Pyroglutamic acid relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Thymidine	N/A	Thymidine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Tryptophan	N/A	Tryptophan relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.

Data Dictionary for *Metabolites_sandy.csv*

Column Name	Units	Description
Soil_type	N/A	Soil_type
Soil_moisture	N/A	Soil_moisture
Day	N/A	Day
1-Methyladenosine	N/A	1-Methyladenosine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
3-Hydroxyisovalerate	N/A	3-Hydroxyisovalerate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
3-Phosphoglycerate	N/A	3-Phosphoglycerate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Acetyllysine	N/A	Acetyllysine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Adenosine	N/A	Adenosine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Aminocaproic_acid	N/A	Aminocaproic acid relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Aspartate	N/A	Aspartate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Creatine	N/A	Creatine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
D-Gluconate	N/A	D-Gluconate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Disaccharide	N/A	Disaccharide relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.

Glucose_phosphate	N/A	Glucose phosphate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Glutamate	N/A	Glutamate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Glutaric_acid	N/A	Glutaric acid relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Homovanillic_acid_HVA	N/A	Homovanillic acid (HVA) relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
IMP	N/A	IMP relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Leucine_Isoleucine	N/A	Leucine Isoleucine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Myo-Inositol	N/A	Myo-Inositol relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Nicotinate	N/A	Nicotinate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Pyroglutamic_acid	N/A	Pyroglutamic acid relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Succinate_Methylmalonate	N/A	Succinate Methylmalonate relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Taurine	N/A	Taurine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Tyrosine	N/A	Tyrosine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
Valine_betaine	N/A	Valine betaine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.
1-Methyladenosine	N/A	1-Methyladenosine relative concentration. The numbers are reported as relative abundances to the highest abundant metabolite for the sample.

Data Dictionary for *Microbial_respiration_Steady.csv* and *Microbial_respiration_Transient.csv*

Column Name	Units	Description
Soil_type		Soil types include clayey, loamy, and sandy
Days		Shows the days the readings were taken.
Respiration_rate	$\mu\text{g CO}_2\text{-C g}^{-1}\text{ dry soil day}^{-1}$	Microbial respiration rate
Std_error	$\mu\text{g CO}_2\text{-C g}^{-1}\text{ dry soil day}^{-1}$	Standard error of microbial respiration rate

3 Applications and Derivation

This data was collected to elucidate the relative contribution of various mechanisms to the Birch effect (spike in soil carbon loss when dry soils are rewetted). In this study, we observed different mechanisms controlling the Birch effect in different soil types. Therefore, our results show that soil texture is a major controller of microbial activity under extreme moisture changes, which ultimately controlled the mechanisms driving the Birch effect and the magnitude of CO₂ production.

4. Quality Assessment:

These data are considered at **Quality Level 1**. Level 1 indicates an internally consistent data product that has been subjected to quality checks and data management procedures. Established calibration procedures were followed.

5. Data Acquisition Materials and Methods:

Study Site

Soil samples were collected from 0-15 cm depth from Georgia (sandy soil), Missouri (loamy soil), and Texas (clayey soil) in summer 2019. The sandy soil was collected from Taylor County (32.54°N, 84.22°W) in Georgia and belonged to the Cowart series (fine-loamy, kaolinitic, thermic Typic Kanhapludults). The loamy soil was collected from the Missouri Ozark AmeriFlux (MOFLUX) site in central Missouri (38.74°N, 92.20°W) and belongs to Weller series (fine, smectitic, mesic Aquertic Chromic Hapludalfs). The clayey soil belonged to Buxin series (very fine, smectitic, thermic Aquic Hapluderts) and was collected from Bowie County, Texas (33.44°N, 94.48°W). The soil samples were transported in coolers with ice packs overnight to the research laboratory at the University of Tennessee, Knoxville.

Methods

Triplicate soil samples of the three distinct textures (sandy, loamy, and clayey) were incubated for a period of 140 days under alternate drying and wetting conditions with a total of 5 cycles (transient) and under a steady state moisture condition at 55% water holding capacity of the three soils. The incubations were done at 25 °C under either transient- or steady-state moisture status. Soil respiration was measured 52 times in 140 days.

Microbial biomass C, extractable organic C, microbial osmolytes, and aggregate changes were determined on days 1, 29, 33, 56, 112, 116 and 140 to capture particular dry or wet phases of the experiment. Microbial biomass C was measured using chloroform fumigation method (Vance et al., 1987) as the difference in C concentration in non-fumigated (extractable organic C) and fumigated soil samples (extracted using 0.5 M K₂SO₄) and dividing that with kEC (extraction efficiency) value of 0.45 (Beck et al., 1997).

Microbial respiration rate was calculated using linear response curve of change in CO₂ concentrations over time (Curiel Yuste et al., 2007). The CO₂ concentration in the gas samples was measured using a flame ionization detector on a gas chromatograph (Shimadzu GC-2014, Japan). Blank correction was done by collecting gas samples from empty jars.

Metabolite extraction was done using protocol laid out by Lu et al., (2008) and analyzed at the University of Tennessee Chemistry Core (Knoxville, TN, USA). Soil samples, stored at -20 °C, were ground using liquid nitrogen for rapid quenching and immediately extracted at 4 °C in a cold room with pre-chilled solvent (1300 µL of 40:40:20 HPLC grade acetonitrile: methanol: water with 0.1 M formic acid. After extraction, the supernatants were dried under nitrogen stream and then resuspended in 300 µL of MilliQ water.

Bacterial and fungal community structure were determined using NextGen amplicon sequencing. The raw sequences are submitted to the National Center for Biotechnology Information with accession number PRJNA922077.

Aggregate size distribution was also determined. Briefly, 25 g of soil sample (<8 mm) was sieved through a series of three sieves to obtain four aggregate size fractions: >2000 µm (large macroaggregates), 2000–250 µm (small macroaggregates), 250–53 µm (microaggregates) and <53 µm (silt and clay sized fractions) (Singh et al., 2020). Mean weight diameter (MWD) was calculated following equation (Youker and McGuinness, 1957).

$$MWD = \sum_{i=1}^n X_i W_i$$

where, x_i is the mean diameter of aggregates size on each sieve size (mm), w_i is the total weight of aggregates retained on top of each sieve size and n is the number of aggregate size fractions. Aggregate associated organic C concentration in each aggregate size was determined using the Elementar CN analyzer (Elementar Vario Max Cube, Hanau, Germany). Statistical analyses were conducted using SAS software v 9.4 (SAS Institute Inc., 2002).

6. Related References:

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7. Data Access:

Get Data

For public access to data from the US Department of Energy Terrestrial Ecosystem Science Scientific Focus Area (TES-SFA) please visit: <https://tes-sfa.ornl.gov/node/80>

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