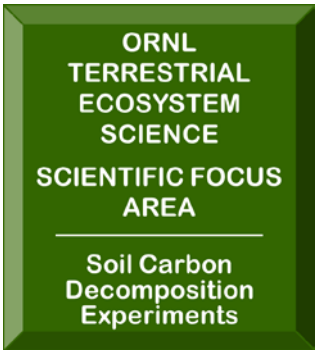

Organic Carbon Sorption and Decomposition in Selected Global Soils

Summary:

This data set reports the results of lab-scale experiments conducted to investigate the dynamics of organic carbon (C) decomposition from several soils from temperate, tropical, arctic, and sub-arctic environments. Results were used to test the newly developed soil microbe decomposition C model -- Microbial-ENzyme-mediated Decomposition (MEND) (Wang et al., 2013).

We conducted a series of laboratory-scale experiments to better understand the microbial processing of organic C in response to diverse substrates and soil types, and to provide data to create an improved mechanistic model of cycling of organic C in soils. The interaction of diverse substrate types was determined in batch sorption experiments and the microbial decomposition of these compounds was determined by long-term incubation experiments. We used radiocarbon labeling approach in order to study the turnover of added substrate ^{14}C through different C pools and to separately quantify the respiration of substrate ^{14}C and native soil organic carbon (SOC).

Two types of experiments were conducted:

1. Year-long incubation experiments -- where four uniformly-labeled organic ^{14}C substrates (glucose, starch, cinnamic acid and stearic acid) were added to the soils and their decomposition was measured along with the decomposition of native SOC. Incubations were conducted with bulk soils and also in particulate and mineral-associated organic C fractions (POC and MOC, respectively) separated by size-based fractionation approach. Microbial biomass C (MBC), dissolved organic C (DOC), and microbial gene copy numbers were measured at selected time points in the bulk soil incubation microcosms.

2. Eight-hour long sorption experiments -- where sorbate solutions of ^{14}C labeled and unlabeled compounds (glucose, starch, cinnamic acid and stearic acid) were added to MOC fraction isolated from A and B soil horizons. After 8 hours of incubation, the amount of C solution sorbed on soil minerals was calculated.

There are 25 *.csv data files included in this data set, a Data Dictionary, and two of the resulting published articles.

Figure 1. Left: Laboratory set up of incubation jars. Right: Close up of microcosm containing soil in specimen cup and CO_2 trap in glass vial.

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Data and Documentation Access:

Get Data

For public access to data please visit the ORNL TES-SFA Web Site: http://tes-sfa.ornl.gov/home

Description and Links to Supplemental Information

Data Dictionary: **Soil_C_Decomp_Data_Dictionary_20140616.pdf**

Published Papers included as companion files: Wang et al., 2013 and Jagadamma et al., 2014(b)

ORNL TES-SFA Data Policy: **Archiving, Sharing, and Fair-Use**

Related Data Sets: MEND Model with supplemental data, Wang et al., 2013

Data Citation:

Cite this data set as follows:

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Project Description

The top meter of soil contains 1500 Pg of C, and contemporary models often simulate C dynamics by determining pool sizes and turnover rates *post hoc*. This traditional modeling framework does not explicitly consider microbial activities, and this lack of microbial representation means that some key mechanisms controlling C turnover as a result of environmental and climate change could be ignored.

We conducted a series of laboratory-scale experiments to better understand the microbial processing of organic C in response to diverse substrates and soil types, and to provide data to create an improved mechanistic model of cycling of organic C in soils. The interaction of diverse substrate types on a global suite of soils was determined in batch sorption experiments and the microbial decomposition of these compounds was determined by long-term incubation experiments. We used radiocarbon labeling approaches to study the turnover of added substrate ^{14}C through different C pools and to separately quantify the respiration of substrate ^{14}C and SOC.

The ultimate outcome was a microbial process-rich soil C cycling model (MEND) (Wang et al., 2013) tested using the coupled sorption and degradation measurements described here.

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2 Data Characteristics
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1. Data Set Overview:

This data set reports results from the lab-scale experiments conducted to understand the effect of substrate quality on organic C decomposition from a global suite of soils. Two major experiments were conducted: (i) one year long incubation experiment, and (ii) 8 h long sorption experiment. Both experiments used four ^{14}C labeled organic carbon substrates (glucose, starch, cinnamic acid and stearic acid). Experiments were conducted with bulk soils and also with physically-separated POC and MOC fractions.

2. Data Characteristics:

Spatial Coverage

The soils for the lab experiments were selected from four contrasting climatic zones—temperate, tropical, sub-arctic, and arctic.

Site boundaries: Latitude and longitude given in decimal degrees.

Site (Region)	Soil Order	Westernmost Longitude	Easternmost Longitude	Northernmost Latitude	Southernmost Latitude
Reykjanes, Iceland	Andisol	-22.7	-22.7	63.8	63.8
Alaska, USA	Gelisol	-147.7	-147.7	64.8	64.8
Illinois, USA	Mollisol	-88.2	-88.2	41.8	41.8
La Selva, Costa Rica	Oxisol 2	-83.6	-83.6	10.2	10.2
Minas Gerais, Brazil	Trop-Ultisol	-43.8	-43.8	-17.9	-17.9
Minas Gerais, Brazil	Oxisol 1	-43.8	-43.8	-17.9	-17.9
Tennessee, USA	Temp-Ultisol	-86.6	-86.6	35.5	35.5
Tennessee, USA	Alfisol	-88.8	-88.8	35.9	35.9

User Note: All the soils in the table were used for the 8 hr sorption experiments, however, only the first five soils (Andisol, Gelisol, Mollisol, Oxisol-2 and Trop-Ultisol) were used for the 1 yr incubation experiments.

Temporal Coverage

This data set was compiled from the lab-scale experiments conducted to understand the dynamics of organic carbon decomposition from a global suite of soils.

Time period: The one-year-long incubation experiment was conducted during 2011-2012. The sorption experiments were conducted during May-June 2011. The time period for this data set is designated as May 1, 2011 through August 31, 2012.

Data File Description

The data are provided in 25 comma separated (*.csv) ASCII files that have been compressed into a single file for convenience. **Data File: Soil_C_Decomp_Data.zip**

Data Dictionary:

The Data Dictionary for the data files is included as a separate document to use a more convenient format and to keep overall document length reasonable. The individual data file descriptions are organized in the same directory/subdirectory structure as the Data File listing below. **link to Soil_C_Decomp_Data_Dictionary_20140519.pdf**

Data File Listing:

- Files are organized in the following directory/subdirectory structure with file names (*.csv) as denoted by the bullet items (e.g., Characterization_bulk_soils.csv). First are the results for bulk soils and then results from soil fractions.

Experiments using bulk soils

Bulk soils

Characterization_bulk_soils

- Characterization_bulk_soils

14C_Substrate_C_respiration

- 14C_respiration_bulk_soils_glucose
- 14C_respiration_bulk_soils_starch
- 14C_respiration_bulk_soils_cinnamic_acid
- 14C_respiration_bulk_soils_stearic_acid

Native_soil_C_respiration

- SoilC_respiration_bulk_soils_unamended
- SoilC_respiration_bulk_soils_glucose

- SoilC_respiration_bulk_soils_starch
- SoilC_respiration_bulk_soils_cinnamic_acid
- SoilC_respiration_bulk_soils_stearic_acid

Mineralization_kinetics (pool sizes and fluxes)

- Mineralization_kinetics_nativesoilC_bulk_soils
- Mineralization_kinetics_substrate14C_bulk_soils

DOC_microbial_C_biomass_bulk_soils

- DOC_microbial_C_biomass_bulk_soils

Microbial_gene_copy_numbers

- Bacterial_fungal_gene_copy_numbers_bulk_soils

Experiments using soil fractions

Soil fractions

14C_Substrate_C_respiration

- 14C_respiration_fractions_glucose
- 14C_respiration_fractions_starch
- 14C_respiration_fractions_cinnamic_acid
- 14C_respiration_fractions_stearic_acid

Native_soil_C_respiration

- SoilC_respiration_fractions_unamended
- SoilC_respiration_fractions_glucose
- SoilC_respiration_fractions_starch
- SoilC_respiration_fractions_cinnamic_acid
- SoilC_respiration_fractions_stearic_acid

Characterization_mineral_fraction

- Characterization_mineral_fraction

Sorption_mineral_fraction

- Sorption_parameters_mineral_fraction

3. Data Application and Derivation:

Our objective was to inform microbial processes of soil C decomposition in a new soil C model. Results were used to test the microbial-process rich soil carbon (C) model -- Microbial-Enzyme-mediated Decomposition (MEND) (Wang et al., 2013; Wang et al., 2014).

4. Quality Assessment:

These data are considered at **Quality Level 2**. Level 2 indicates a complete, externally consistent data product that has undergone interpretative and diagnostic analyses. The data product has been subjected to quality checks and data management procedures (Level 1). Established calibration procedures were followed.

5. Data Acquisition Materials and Methods:

The experiments were conducted in the laboratory at ambient conditions using 8 soil types collected from around the globe. Soil descriptions were provided in Jagadamma et al., 2014a. Two sets of experiments were conducted in triplicates, one year long incubation experiments and 8 hour long sorption experiments. Incubation experiments were conducted on bulk soils (<2 mm) and on soil fractions POC and MOC separated from the bulk soils by size-based fractionation approach. The detailed fractionation protocol is described in Jagadamma et al., 2013 and Jagadamma et al., 2014a.

Incubation Experiments

The microcosms were set up in 1 L glass Mason jars at 20^{o}C in the dark in a temperature and humidity controlled room. The Mason jars contain specimen cups with bulk soils or soil fractions, which were amended with four C substrates (glucose, starch, cinnamic acid and stearic acid) at the rate of 0.4 mg C g^{-1} after labeling them with 296 Bq g^{-1} of corresponding ^{14}C compounds (Fig. 2). Mason jars also contain 0.02 L glass vials with NaOH solution which traps the CO_2 evolved by the decomposition of C present in soils. The NaOH traps were removed 15 times during one year of the experiment and the trapped CO_2 -both ^{14}C-CO_2 and native soil CO_2 - were measured. Microbial biomass C and dissolved organic C were measured at 5 time points (day 4, day 30, day 150, day 270 and day 365) and microbial gene copy numbers were measured at 3 time points (day 4, day 30 and day 27) from the bulk soil microcosms.

Figure 2. Laboratory set up of incubation jars.

Sorption Experiments

Sorption experiments were conducted in the MOC fraction isolated from A and B horizons of all the 8 soil types (Jagadamma et al., 2014a). Sorbate solutions were prepared by adding 74Bq mL^{-1} ^{14}C labeled compounds (glucose, starch, cinnamic acid and stearic acid) to a series of concentrations (1 to 100 mg L^{-1}) of corresponding unlabeled compounds. Solution (0.03 L) was added to glass vials containing 0.5 g MOC fraction. After shaking gently on a reciprocal shaker for 8 h, the mixtures were centrifuged at 1500 g for 15 min and the supernatants were collected. The amount of C solutions sorbed on soil minerals was calculated by Langmuir isotherm modeling. More details can be found in Jagadamma et al., 2014a.

Table 1
Soil collection locations and taxonomy.

Soils	Location	B horizon	Soil taxonomy
Temperate			
Alfisol	Milan, Tennessee, USA	Btx	Oxyaquic Fraglossudalfs
Mollisol	Batavia, Illinois, USA	Btg1	Typic Endoaquolls
Temp-Ultisol	Walker Br, Tennessee, USA	2Bt1	Typic Paleudults
Tropics			
Trop-Ultisol	Lavras, Minas Gerais, Brazil	Bt2	Typic Hapludult
Oxisol-1	Lavras, Minas Gerais, Brazil		Humic Rhodic Acrudox
Oxisol-2	La Selva Biological Station, Costa Rica	Bt1	Haplic Haploperox
Sub-arctic			
Gelisol	Fairbanks, Alaska, USA	Cgf[a]	Typic Aquiturbels
Andisol	Krýsuvíkurheiði, Reykjanes, Iceland	Bw	Haplic Andosol[b]

[a] Permafrost layer.
[b] Based on World Reference Base system, all others are based on USDA–NRCS system.

Figure 3. Table 1 from Jagadamma et al., 2014a.

Description of measurements and analyses:

Soil characterization before experiment

Before the incubation experiment, the 5 soil types used for incubation experiments were characterized for basic physical, chemical and biological properties using standard analytical protocols. The properties analyzed include soil pH, organic C and total N concentrations, soil texture, MBC and DOC concentrations, and microbial gene copy numbers. The MOC fractions of all the 8 soil types were analyzed for pH, organic C, clay, dithionate-oxalate-pyrophosphate extractable Fe and Al. There are 2 data files containing the characterization data.

- Characterization_bulk_soils
- Characterization_mineral_fraction

^{14}C respiration

Evolution of CO_2 originated from substrate C was determined by measuring the activity of $^{14}CO_2$ trapped in NaOH solutions collected from the microcosms with a Packard Tri-Carb Liquid Scintillation Counter (LSC) after mixing with 0.05 L of the NaOH solution with 0.010 L of the scintillation cocktail Ultima Gold XR. The respiration data was expressed as the % of added substrate C. There are 8 data files in total: 4 from bulk soils and 4 from soil fractions.

Data files from bulk soils:

- 14C_respiration_bulk_soils_glucose
- 14C_respiration_bulk_soils_starch
- 14C_respiration_bulk_soils_cinnamic_acid
- 14C_respiration_bulk_soils_stearic_acid

Data files from POC and MOC fractions:

- 14C_respiration_fractions_glucose
- 14C_respiration_fractions _starch
- 14C_respiration_fractions _cinnamic_acid
- 14C_respiration_fractions_stearic_acid

Soil C respiration

Total mineralized C from each microcosm was determined by titrating an aliquot of CO_2 trapped NaOH solution collected at each sampling time with HCL by an automatic titrator. Before the titration, the CO_2 collected in NaOH solution was precipitated as barium carbonate ($BaCO_3$) by adding 0.02 L 10% barium chloride ($BaCl_2$). The volume of acid needed to neutralize the remaining NaOH (unreacted with CO_2) was determined by the titration, which was used to calculate the concentration of CO_2 trapped in the NaOH solution. In the case of substrate amended soils, the amount of native soil derived CO_2 is calculated by subtracting the substrate

derived $^{14}CO_2$ from the total CO_2 and in the case of unamended soils, the native soil derived CO_2 is equal to the total CO_2. The data are represented as cumulative native soil C respiration in mg C /g soil. There are 10 data files in total: 5 from bulk soils and 5 from soil fractions.

Data files from bulk soils:

- SoilC_respiration_bulk_soils_unamended
- SoilC_respiration_bulk_soils_glucose
- SoilC_respiration_bulk_soils_starch
- Soil4C_respiration_bulk_soils_cinnamic_acid
- SoilC_respiration_bulk_soils_stearic_acid

Data files from POC and MOC fractions:

- SoilC_respiration_fractions_unamended
- SoilC_respiration_fractions_glucose
- SoilC_respiration_fractions _starch
- SoilC_respiration_fractions _cinnamic_acid
- SoilC_respiration_fractions_stearic_acid

Dissolved organic C and microbial biomass C

DOC and MOC - both total and ^{14}C derived -measurements were conducted 5 time points (day 4, day 30, day 150, day 270, day 365) during the course of incubation experiment using bulk soils. Twenty g (oven-dry basis) samples were divided into two sub-samples of equal weight. Sub-sample one was added to 0.04 L 0.5 M K_2SO_4, shaken for one hr in a reciprocal shaker and filtered. Sub-sample two was fumigated for three days using ethanol-free chloroform followed K_2SO_4 extraction (Vance et al. 1987). Total DOC and total MBC (µg C per g soil) were analyzed using a Shimadzu Total C Analyzer. Organic carbon values for sub-sample one represented the DOC. Organic carbon values for the fumigated sub-sample two represented both DOC and MBC. Substrate-derived DOC and MBC were measured by counting the ^{14}C activity of the extract using LSC. Due to the limitation of the mass of incubated fractions, only one replicate analysis was possible. Below is the data file for the DOC and MBC.

- DOC_microbial_C_biomass_bulk_soils

Bacterial and fungal gene copy numbers

These measurements were conducted 3 time points (day 4, day 30, day 270) during the length of incubation using bulk soils. Microbial DNA extraction was conducted first with 0.25 g of moist soil using the PowerSoil DNA Isolation Kit (MOBIO Laboratories, Inc., CA, USA). The abundance of the rRNA genes was determined by quantitative real time polymerase chain reaction (qPCR) on a CFX96TM Real-Time PCR Detection System with group specific ribosomal DNA gene primers using iQ SYBR Green Supermix (Bio-Rad, CA, USA). A small

segment of the sample DNA was amplified using primer pairs that targeted the conserved region of the rRNA. Gene copy numbers for bacteria and fungi were determined in analytical triplicates using standard curves constructed from group specific microorganisms and were expressed in dry weight basis. Below is the data file for the bacterial and fungal gene copy numbers.

- Bacterial_fungal_gene_copy_numbers_bulk_soils

Mineralization kinetics

The respiration data (both the substrate C and SOC) from incubation experiments using bulk soils were tested using a double and a triple pool first order exponential decay model using Sigma plot v11 (Systat Software Inc., IL, USA). Native soil C respiration was best modeled by the double pool exponential decay model with fast pool size, C_1 and slow pool size, C_2 and their corresponding mineralization rates k_1 and k_2. Substrate C respiration was best modeled by the triple pool model with fast pool size, C_1, intermediate pool size, C_2 and slow pool size, C_3, and their corresponding mineralization rates, k_1, k_2 and k_3. The mean mineralization parameters along with their standard errors corresponding to native SOC and substrate C respiration are provided in the following data files.

- Mineralization_kinetics_nativesoilC_bulk_soils
- Mineralization_kinetics_substrate14C_bulk_soils

Sorption parameters [Jagadamma et al., 2014(a)]

Two most common sorption parameters, maximum sorption capacity (Q_{max}) and binding coefficient (k), were calculated after adding ^{14}C labeled substrates to the MOC fractions isolated from the A and B horizons of the soils. The mean Q_{max} and k, and their standard errors (n=3) are available in the following data file.

- Sorption_parameters_mineral_fraction

6. References:

Jagadamma, S., Steinweg, J.M., Mayes, M.A., Wang, G., and Post, W.M. 2013. Decomposition of added and native organic carbon from physically separated fractions of diverse soils. Biology and Fertility of Soils 50:613-621. http://dx.doi.org/10.1007/s00374-013-0879-2

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Vance, E.D., Brookes, P.C., and Jenkinson, D.S. 1987. An extraction method for measuring soil microbial biomass C. Soil Biology and Biochemistry 19:703–7077.

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7. Data Access:

This data is available through the Oak Ridge National Laboratory (ORNL) Carbon Dioxide Information Analysis Center (CDIAC).

Data Archive Center:

Contact for Data Center Access Information:

E-mail: http://cdiacservices.ornl.gov/feedback.cfm