ENVIRONMENTAL RESEARCH
LETTERS

PURPOSE-LED PUBLISHING™

LETTER • OPEN ACCESS

Continental-scale patterns of extracellular enzyme activity in the subsoil: an overlooked reservoir of microbial activity

To cite this article: Nicholas C Dove *et al* 2020 *Environ. Res. Lett.* **15** 1040a1

View the article online for updates and enhancements.

You may also like

- Bursting core-localized ellipticity-induced Alfvén eigenmodes driven by energetic electrons during EAST ohmic discharges
P. Su, H. Lan, C. Zhou et al.
- *IRIS* AND *SDO* OBSERVATIONS OF RECURRENT EXPLOSIVE EVENTS
G. R. Gupta and Durgesh Tripathi
- SOFT X-RAY EXTENDED EMISSIONS OF SHORT GAMMA-RAY BURSTS AS ELECTROMAGNETIC COUNTERPARTS OF COMPACT BINARY MERGERS: POSSIBLE ORIGIN AND DETECTABILITY
Takashi Nakamura, Kazumi Kashiyama, Daisuke Nakauchi et al.

This content was downloaded from IP address 137.75.80.24 on 18/03/2025 at 17:49

Environmental Research Letters

CrossMark

OPEN ACCESS

RECEIVED
23 April 2020

REVISED
6 August 2020

ACCEPTED FOR PUBLICATION
19 August 2020

PUBLISHED
9 October 2020

Original content from this work may be used under the terms of the Creative Commons Attribution 4.0 licence. Any further distribution of this work must maintain attribution to the author(s) and the title of the work, journal citation and DOI.

LETTER

Continental-scale patterns of extracellular enzyme activity in the subsoil: an overlooked reservoir of microbial activity

Nicholas C Dove[1,17,2], Keshav Arogyaswamy[3], Sharon A Billings[4], Jon K Botthoff[5], Chelsea J Carey[6], Caitlin Cisco[7], Jared L DeForest[8], Dawson Fairbanks[9], Noah Fierer[10], Rachel E Gallery[11], Jason P Kaye[12], Kathleen A Lohse[13], Mia R Maltz[3], Emilio Mayorga[14], Jennifer Pett-Ridge[15], Wendy H Yang[7,16], Stephen C Hart[17] and Emma L Aronson[3]

[1] Environmental Systems Graduate Group, University of California, Merced, CA, United States of America
[2] Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN, United States of America
[3] Department of Microbiology and Plant Pathology, University of California, Riverside, CA, United States of America
[4] Department of Ecology and Evolutionary Biology, Kansas Biological Survey, University of Kansas, Lawrence, KS, United States of America
[5] Center for Conservation Biology, University of California, Riverside, CA, United States of America
[6] Point Blue Conservation Science, Cypress Drive, Suite 11, Petaluma 3820, CA, United States of America
[7] Department of Plant Biology, University of Illinois, Urbana, IL, United States of America
[8] Department of Environmental and Plant Biology, Ohio University, Athens, OH, United States of America
[9] Department of Soil, Water and Environmental Science, University of Arizona, Tucson, AZ, United States of America
[10] Cooperative Institute for Research in Environmental Sciences, Department of Ecology and Evolutionary Biology, University of Colorado, Boulder, CO, United States of America
[11] School of Natural Resources and the Environment, Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, Arizona, United States of America
[12] Department of Ecosystem Science and Management, Pennsylvania State University, University Park, PA, United States of America
[13] Department of Biological Sciences, Idaho State University, Pocatello, ID, United States of America
[14] Applied Physics Laboratory, University of Washington, Seattle, WA, United States of America
[15] Physical and Life Sciences Directorate, Lawrence Livermore National Laboratory, Livermore, CA, United States of America
[16] Department of Geology, University of Illinois, Urbana, IL, United States of America
[17] Department of Life & Environmental Sciences and Sierra Nevada Research Institute, University of California, Merced, CA, United States of America

E-mail: ndove7@gmail.com

Keywords: acid phosphatase, β-glucosidase, N-acetylglucosaminidase, critical zone, ecological stoichiometry, extracellular enzymes, microbial ecology, phospholipid fatty acids, subsoil

Supplementary material for this article is available online

Abstract

Chemical stabilization of microbial-derived products such as extracellular enzymes (EE) onto mineral surfaces has gained attention as a possibly important mechanism leading to the persistence of soil organic carbon (SOC). While the controls on EE activities and their stabilization in the surface soil are reasonably well-understood, how these activities change with soil depth and possibly diverge from those at the soil surface due to distinct physical, chemical, and biotic conditions remains unclear. We assessed EE activity to a depth of 1 m (10 cm increments) in 19 soil profiles across the Critical Zone Observatory Network, which represents a wide range of climates, soil orders, and vegetation types. For all EEs, activities per mass of soil correlated positively with microbial biomass (MB) and SOC, and all three of these variables decreased logarithmically with depth ($p < 0.05$). Across all sites, over half of the potential EE activities per mass soil consistently occurred below 20 cm for all measured EEs. Activities per unit MB or SOC were substantially higher at depth (soils below 20 cm accounted for 80% of whole-profile EE activity), suggesting an accumulation of stabilized (i.e. mineral sorbed) EEs in subsoil horizons. The pronounced enzyme stabilization in subsurface horizons was corroborated by mixed-effects models that showed a

The United States Government retains and the publisher, by accepting the article for publication acknowledges that the Unted States Government retains a non-exclusive, paid-up,irrevocable, world-wide license to publish orreproduce the published form of this manuscript, or allow others to do so, for United States Government purposes. The DOE will provide public access to these results of federally sponsored research in accordance with the DOE Public Access Plan (http://energy.gov/downloads/doe-public-access-plan).

© 2020 The Author(s). Published by IOP Publishing Ltd

significant, positive relationship between clay concentration and MB-normalized EE activities in the subsoil. Furthermore, the negative relationships between soil C, N, and P and C-, N-, and P-acquiring EEs found in the surface soil decoupled below 20 cm, which could have also been caused by EE stabilization. This finding suggests that EEs may not reflect soil nutrient availabilities deeper in the soil profile. Taken together, our results suggest that deeper soil horizons hold a significant reservoir of EEs, and that the controls of subsoil EEs differ from their surface soil counterparts.

1. Introduction

Globally, soils store approximately 1500 Pg of soil organic carbon (SOC) in the upper meter of the soil profile, with 50%–67% of SOC occurring below 20 cm (Jobbágy and Jackson 2000). The persistence of this C pool is, in part, controlled by extracellular enzymes (EEs) primarily released by soil microorganisms that decompose soil organic matter (Burns *et al* 2013). However, even though the majority of SOC occurs in the subsoil, most studies of soil microorganisms and the EEs they secrete focus on the upper soil layers (Yost and Hartemink 2020). While the age (and thus persistence) of SOC increases with depth (Trumbore *et al* 1996, Paul *et al* 1997, Rumpel *et al* 2002), recent studies have shown that subsoil (>20 cm depth) C is still vulnerable to decomposition. Indeed, subsoil microbial communities have resource demands that rival those of surface soils when normalized to a microbial biomass (MB) basis (Jones *et al* 2018). Understanding subsurface processes is critical in an age of global change because vulnerability of SOC to EE attack could be enhanced by increased temperatures or wetting/drying cycles (Schimel *et al* 2011, Hicks Pries *et al* 2017). Hence, if subsoils are disturbed (either physically or through altered environmental conditions), portions of the soil organic matter pool at depth could become accessible to EEs, resulting in the mineralization of significant quantities of C and nutrients. Therefore, increased understanding of EE patterns at depth could help elucidate the mechanisms of subsoil organic matter decomposition and aid in predicting how pools of SOC and nutrients will be affected by ongoing global change factors.

Because EEs both respond to and influence soil properties, the study of EEs has led to greater insights into soil C persistence (Billings and Ballantyne 2013, Birge *et al* 2015, Dove *et al* 2019), nitrogen (N) and phosphorus (P) mineralization (Weintraub and Schimel 2003, Waring *et al* 2014, Chen *et al* 2018), ecosystem development (Olander and Vitousek 2000, Selmants and Hart 2010, Turner *et al* 2014), and microbial metabolism (Sinsabaugh and Shah 2011, 2012, Sinsabaugh *et al* 2013). Given that the methods for measuring EE activity in soils are relatively high-throughput, inexpensive, and reproducible across laboratories (Dick *et al* 2018), it is one of the most common soil biogeochemical measurements ('soil extracellular enzyme activity' resulted in 2013 records using Clarivate Analytics Web of Science as of Jan. 28, 2020). However, despite the widespread measurement of soil EEs, most studies have focused on EE activities in surface horizons, with few studies exploring EE activity patterns in soil horizons below 20 cm (but see Taylor *et al* 2002, Kramer *et al* 2013, Stone *et al* 2014, Taş *et al* 2014, Schnecker *et al* 2015, Loeppmann *et al* 2016, Jing *et al* 2017).

Numerous soil physical and biogeochemical properties change with depth. As organic matter (both SOC and organically bound nutrients) moves into the subsoil, it becomes increasingly more microbially processed and sorbed onto charged mineral surfaces (Rumpel and Kögel-Knabner 2010), which concomitantly increase with depth. Soil pH may also increase with depth in instances where the parent material is enriched in so-called 'base' cations (i.e. calcium, magnesium, potassium, and sodium; Brubaker *et al* 1993). These gradients in soil properties result in subsoil microbial communities that are vastly different than their surface soil counterparts (Eilers *et al* 2012, Brewer *et al* 2019). Soil pH (Sinsabaugh *et al* 2008, Kivlin and Treseder 2014), substrate availability and demand (Olander and Vitousek 2000, Dove *et al* 2019), and microbial community composition (Schnecker *et al* 2015) influence EE activities in surface soils. Because these factors change along soil profiles, EE activities should also change with soil depth. Two main generalizations have emerged from the few studies that have investigated EE activities in subsoils: (1) EE activities decline with depth in association with decreases in soil organic matter concentrations and decreases in MB (Taylor *et al* 2002, Stone *et al* 2014, Loeppmann *et al* 2016); and (2) EE activities at depth are less responsive to surface conditions, manipulations, and management practices (Kramer *et al* 2013, Jing *et al* 2017, Yao *et al* 2019). However, our ability to quantify the total EE pool and elucidate the controls on EEs in subsoils has been hindered by unstandardized ancillary measurements, assay parameters, and depths of sampling across studies (Nannipieri *et al* 2018).

Systematic, continental- and global-scale assessments and meta-analyses of EEs in surface soils have begun to clarify controls and correlates of EE activity (Sinsabaugh *et al* 2008, 2009, Xiao *et al* 2018). For instance, EE stoichiometry (the ratio of C-, N-, and P-acquiring enzymes), which can represent

the relative C, N, and P demand (Sinsabaugh and Shah 2012), scales at 1:1:1 (C:N:P) globally across soil, freshwater, and saltwater ecosystems, suggesting that the plasticity of microbial resource demand is somewhat constrained (Sinsabaugh *et al* 2008, 2009). These large-scale assessments also confirm that pH, substrate availability, and microbial demand influence EE activity in surface soils (Sinsabaugh *et al* 2008, 2009, Xiao *et al* 2018). However, it is currently unknown if these controls in surface soils extend into the subsoil. We posit that EE activities at depth may follow different patterns than in the surface horizons given that EEs at depth are less responsive to environmental perturbations (Jing *et al* 2017), subsoils have greater spatial heterogeneity of organic substrates than at the surface (Salomé *et al* 2010), and the microbial communities at depth are dominated by oligotrophic microorganisms (Brewer *et al* 2019).

To quantify EE activities and elucidate their controls throughout the soil profile, we sampled the upper meter of mineral soil at 10 cm increments in 19 soil pits across the 10 United States National Science Foundation-supported Critical Zone Observatories (CZOs; http://criticalzone.org/national/). We hypothesized that EE activities per mass of soil would decline with depth due to decreased SOC and MB concentrations; however, a significant proportion of EE activity in the top meter of soil would occur below 20 cm depth. We also hypothesized that the fundamental controls on EE activities would differ between surface and subsoil horizons due to shifting biological, chemical, and physical conditions throughout the soil profile. Specifically, as organically bound microbial resources decrease with depth, mineral sorption of both substrates and EEs will become a more dominant control of potential EE activity. Our overall goal was to quantify potential EE activity in the subsoil over a diverse set of soils, ecosystems, and climates to elucidate how EE activity mediates subsoil C and limiting nutrient availabilities.

2. Methods

2.1. Site selection and sampling

Samples were collected from the network of ten CZOs (http://criticalzone.org) across the USA, which represents a wide range of hydrogeological provinces, soil orders, and vegetation types as described in Brewer *et al* (2019). Soils were collected at peak greenness (as estimated from NASA's MODerate-resolution Imaging Spectroradiometer, or MODIS) between April 2016 and November 2016, with the exception of the Eel River CZO samples, which were collected in May 2017 (also at peak-greenness). At each CZO, we excavated two separate soil profiles ('sites') selected to represent distinct soil types and landscape positions (table 1). Any organic horizon was first removed, and then mineral soils were sampled in 10 cm increments with a sterile hand trowel dug into the face of each soil pit to a depth of at least 100 cm or to refusal (e.g. bedrock, hardpan, coarse regolith).

All soil samples were shipped overnight at 4 °C to the University of California, Riverside for processing. A portion of each field sample was sieved (<2 mm), homogenized, divided into subsamples for further analyses, and frozen (−20 °C). For some soils (particularly some wet, finely textured depth intervals), sieving was impractical. These samples were homogenized and larger root and rock fragments were removed by hand. In addition, as samples from SHAL (70–100 cm depth; see table 1 for site abbreviations) consisted almost entirely of medium-sized weathered bedrock (Cr material), soil was collected by manually crushing weathered bedrock with a ceramic mortar and pestle with this material then passed through a 2 mm sieve.

2.2. Soil physiochemical measurements

Soil pH, gravimetric water content, and clay concentration were measured using modified long-term ecological research protocols (Robertson *et al* 1999). Briefly, soil pH was determined in a 1:2 (weight to volume) solution using 5 g of oven-dried soil and 10 ml of Milli-Q water (Millipore Sigma, Burlington, MA, USA). The solution was measured on an Orion DUAL STAR pH meter and an epoxy combination electrode (Orion 9165BNWP Combination Sure-Flow pH Electrode; Thermo Fisher Scientific, Waltham, MA, USA). For determining gravimetric water content, approximately 7 g field-moist soil was dried at 105 °C for a minimum of 24 h. Soil texture was measured on oven-dried and sieved soil using the hydrometer method following Gee and Bauder (2018).

Prior to soil total organic C and N analysis, soils were freeze-dried using a Savant Novalyphe-NL500 freezer dryer (Savant, Farmingdale, NY, USA) and ground to a fine powder using a roller mill. If effervescence occurred when a drop of 1 M HCl was added to a subsample of each soil sample, then inorganic C was removed from 2 g of the soil sample by twice-washing with 30 ml 0.1 N HCl (allowing the soil slurry to stand for 1 h during each wash), twice-washing with 30 ml DI, and then freeze-dried. The soil samples were analyzed for total organic C and total N by continuous-flow, direct combustion using a Vario Micro Cube elemental analyzer (Elementar, Hanau, Germany).

Microbially available orthophosphate, referred hereafter as Olsen P, was estimated by extracting 1 g of soil with 200 ml of 0.5 M $NaHCO_3$ at pH 8.5 (Olsen *et al* 1954). This measurement includes both directly available phosphate and phosphate bound to calcium minerals that could become potentially available to microbes. Briefly, slurries were shaken for

Table 1. Characteristics of the 19 study sites across ten Critical Zone Observatories (CZOs).

Site	CZO	Latitude	Longitude	$pH_{1:2(water)}$ [a]	Elevation (m)	MAP (mm)	MAT (°C)	Parent Material	Soil Order	Vegetation
AGRI	Christina	39.8622	−75.7834	4.55–5.07	105	1145	12	fluvium	Inceptisol	Forest
BSLT	Reynolds Creek	43.1171	−116.7258	6.09–6.64	1917	479	6.3	basalt	Mollisol	Shrubland
CTNA	Catalina-Jemez	32.4293	−110.7610	4.72–5.31	2100	840	12	granite	Entisol	Forest
FLUD	Christina	39.8625	−75.7830	4.71–5.11	113	1145	12	quartzite	Ultisol	Forest
GARN	Shale Hills	40.6949	−77.9199	3.24–4.29	554	1050	9.5	sandstone	Inceptisol	Forest
GOOS	IML	40.4374	−88.5552	7.08–7.51	250	1000	11	fluvium	Mollisol	Cropland
GRNT	Reynolds Creek	43.1927	−116.8105	5.65–7.55	1565	616	7	granite	Mollisol	Shrubland
HARD	Calhoun	34.6064	−81.7234	4.91–5.34	183	1250	16	gneiss	Ultisol	Forest
ICAC	Luquillo	18.2814	−65.7909	4.05–4.34	690	5000	19	quartzite	Inceptisol	Forest
LVRD	Luquillo	18.3237	−65.8185	4.27–4.77	343	3456	23	volcaniclastic	Oxisol	Forest
MDRN	Eel River	39.7294	−123.6419	–	487	1500	12	sandstone	Alfisol	Forest
MEAD	Boulder Creek	40.0210	−105.4796	5.54–5.68	2642	519	5.1	gneiss	Mollisol	Grassland
NSLP	Boulder Creek	40.0125	−105.4690	4.29–5.06	2521	519	5.1	gneiss	Inceptisol	Forest
PINE	Calhoun	34.6074	−81.7228	4.88–5.72	184	1250	16	gneiss	Ultisol	Forest
PRAR	IML	40.4275	−88.6032	5.88–7.88	250	1000	11	loess	Mollisol	Cropland
PROV	Southern Sierra	37.0675	−119.1950	4.77–5.28	2016	1200	8	granite	Inceptisol	Shrubland
SCST	Catalina-Jemez	32.4263	−110.7612	5.49–6.11	2100	840	12	schist	Entisol	Forest
SHAL	Shale Hills	40.6640	−77.9064	4.19–4.78	282	1050	9.5	shale	Ultisol	Forest
SJER	Southern Sierra	37.1088	−119.7314	–	405	513	16.4	granite	Alfisol	Grassland

[a]pH was not measured on MDRN and SJER soils because of limited soil collected.

30 min and filtered through Whatman No. 42 filters. Orthophosphate was measured colormetrically using a Lachat AE Flow Injection Auto Analyzer (Method 12-115-01-1-Q, Lachat Instruments, Inc. Milwaukee, WI, USA).

2.3. Phospholipid fatty acid analysis

We used phospholipid fatty acids (PLFAs) to determine differences in the MB and the ratios of fungal to bacterial biomass. Briefly, total lipids were extracted using 10 ml of methanol, 5 ml chloroform, and 4 ml of a 50 mM phosphate buffer (pH = 7.4) from 5 g of lyophilized soil (White *et al* 1979, Deforest *et al* 2004). To determine analytical recovery, phospholipid 19:0 (1,2-dinonadecanoyl-*sn*-glycero-3-phosphocholine) and 21:0 (1,2-diheneicosanoyl-*sn*-glycero-3-phosphocholine) standards (Avanti Polar Lipids, Inc. Alabaster, AL, USA) were added during the extraction phase (Deforest *et al* 2012). Polar lipids were separated from other lipids using silicic acid solid-phase chromatography columns (500 mg 6 ml^{-1}; Thermo Scientific, Waltham, MA, USA), and the separated polar lipids were converted to fatty acid methyl esters (FAME) through methanolysis (Guckert *et al* 1985). The resulting FAMEs were separated using a HP GC-FID (HP6890 series, Agilent Technologies, Inc. Santa Clara, CA, USA) gas chromatograph, and peaks/biomarkers were identified using the Sherlock System (v. 6.1, MIDI, Inc. Newark, DE, USA). External FAME standards (K104 FAME mix, Grace, Deerfield, IL, USA) were used to determine concentrations. The sum of all detected 14–19 C-length PLFAs was used to calculate MB because longer PLFAs can be indicators of mosses and higher plants (Zelles 1999). Ratios of fungal to bacterial biomass (fungi:bacteria) were calculated by dividing the amount (mol) of the fungal biomarker 18:2ω6c by the sum of all other microbial biomarkers (i.e. mol 18:2ω6c/(mol MB—mol 18:2ω6 c)).

2.4. EE activity

We measured potential EE activity (i.e. activity not limited by substrate concentrations) of α-glucosidase (AG), β-glucosidase (BG), cellobiohydrolase (CB), β-xylosidase (BX), N-acetylglucosaminidase (NAG), leucine aminopeptidase (LAP), and acid phosphatase (AP) fluorometrically following Bell *et al* (2013). Briefly, an 800 µl soil slurry consisting of 2.75 g of field-moist soil in 91 ml of 50 mM sodium acetate buffer (pH = 5.5) was incubated with 200 µl of each of the 100 µM 4-methylumbelliferone (MUB)-linked or 7-amido-4-methylcoumarin (AMC)-linked substrates (only LAP was AMC-linked) in 96-deep well plates. After a 3 h incubation at 20 °C, plates were centrifuged, and the supernatant was transferred to black, flat-bottom 96-well plates. Fluorescence was measured on a Tecan M200 Pro (Tecan Group Ltd., Männedorf, Switzerland) using an excitation wavelength of 365 nm and an emission wavelength of 450 nm.

The choice of buffer pH in EE activity assays depends on the research question (Burns *et al* 2013) and, as such, we decided to use a consistent pH of 5.5 for all soils assayed similar to other cross-site soil EE studies (Deforest 2009, Dick *et al* 2018). The intensity of florescence of MUB is pH dependent (Mead *et al* 1955), therefore comparisons across sites must be done at a consistent pH to avoid attributing biological phenomena to the chemistry of the florescent substrate. A buffer pH of 5.5 was chosen because this is within the range of soil pH for most of our sites (table 1) and the range of pH optima for our enzymes (4.0–6.5, as determined in a variety of biomes; Parham and Deng 2000, Niemi and Vepsäläinen 2005, Turner 2010, Min *et al* 2014). Nevertheless, we recognize that our buffer pH may not be indicative of the native soil pH (or pH within the microsites in which EEs operate), which may reduce our ability to quantify *in situ* EE activity.

The enzymes, AG, BG, BX, and CB are involved in the degradation of organic C, and total C-acquiring enzyme activity (C_{sum}) was operationally defined as the sum of these four enzyme activities. The enzyme, NAG is involved in releasing N-acetylglucosamine from aminopolysaccharides such as chitin and peptidoglycan, and LAP catalyzes the hydrolysis of leucine residues at the N-terminus of peptides and proteins. Both NAG and LAP are considered N-acquiring enzymes and were similarly summed to define the variable N_{sum}, which we use as a proxy for N acquisition by decomposition. Acid phosphatase is involved in releasing phosphate from monoester bonds, representing a P-mineralizing enzyme (Burns *et al* 2013). This suite of EEs, while not inclusive of all relevant enzymatic substrates, represents many of the most frequent hydrolytic reactions during decomposition of organic matter (Sinsabaugh and Shah 2012). Furthermore, these EEs have been extensively studied across numerous surface soils (Sinsabaugh *et al* 2008, 2009) to which we can compare with our deep-soil measurements.

Extracellular enzyme activities were expressed per soil mass (mmol EE activity kg^{-1} soil h^{-1}), SOC (mmol EE activity kg^{-1} SOC h^{-1}), and MB (mmol EE activity kg^{-1} MB h^{-1}). These latter two variables are called SOC-normalized and MB-normalized, respectively, in this paper. We also measured the ratio of C-, N-, and P-acquiring enzymes. Because EEs mediate nutrient acquisition for soil microorganisms, they can be used to determine relative nutrient demand (Olander and Vitousek 2000, Sinsabaugh and Shah 2012). Hence, we used C_{sum}:N_{sum}, C_{sum}:AP, and N_{sum}:AP as proxies for C:N, C:P, and N:P relative demand ratios, respectively.

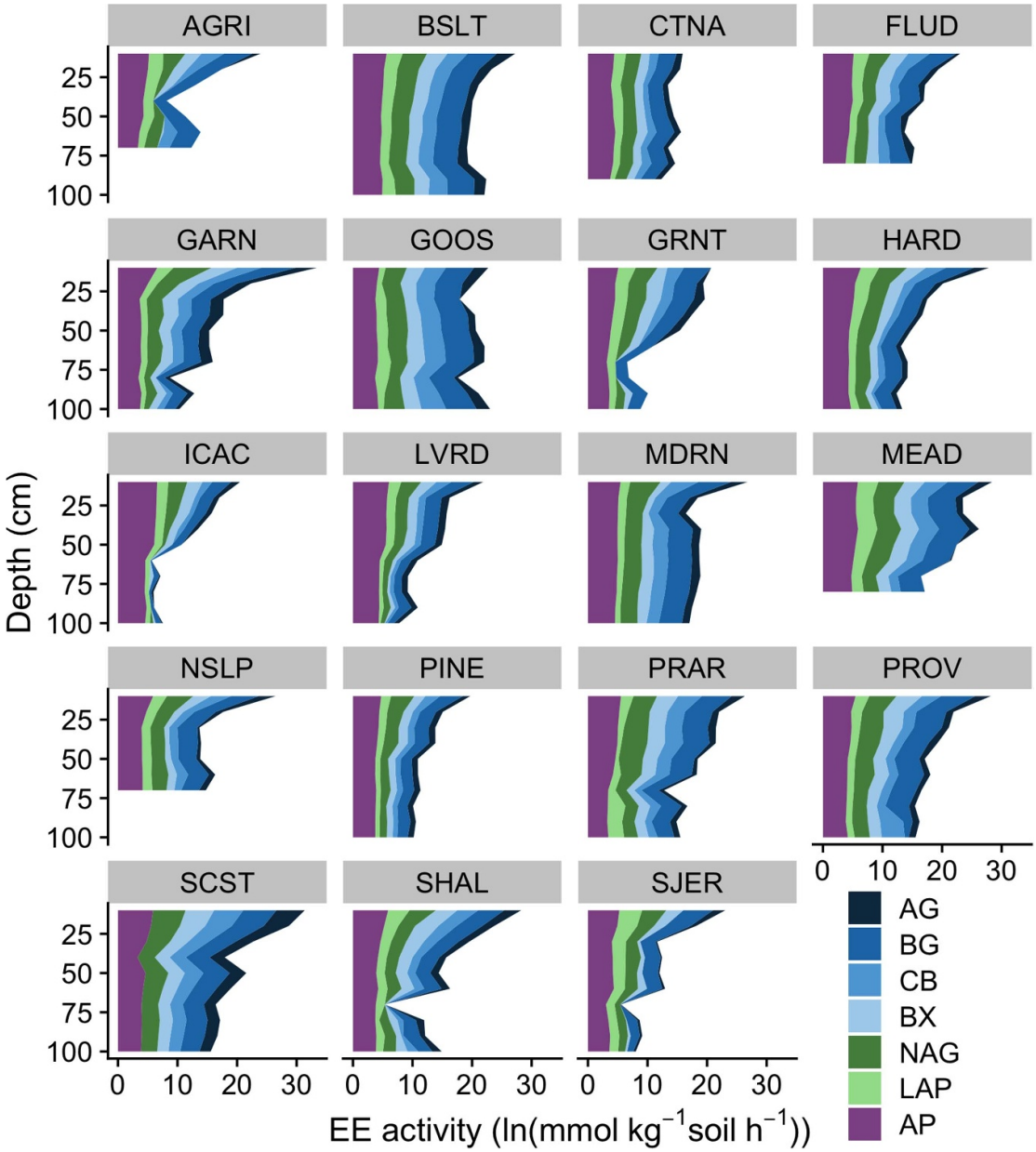

Figure 1. Distribution of activity of α-glucosidase (AG), β-glucosidase (BG), β-xylosidase (BX), cellobiohydrolase (CB), N-acetylglucosaminidase (NAG), leucine aminopeptidase (LAP), and acid phosphatase (AP) per soil mass as a function of depth throughout the top meter of soil across sites. See table 1 for site abbreviations.

2.5. Statistical analysis

All statistical tests and visualizations were conducted in R (R Development Core Team 2008) using the lme4 (Bates *et al* 2015) and MuMin (Barton 2020) packages. We used mixed-effects models with site as a random effect to examine the relationship between depth, SOC, MB, clay, and fungi:bacteria and EE activity (expressed on soil mass, SOC, and MB bases). We similarly used mixed-effects models with site as a random effect to examine the effect of soil stoichiometry (using ratios of SOC, total N, and available P) on enzyme stoichiometry. These models were conducted on the complete dataset, the surface soil dataset (depth $\leq$ 20 cm), and the subsoil dataset (depth > 20 cm) to determine differences in the controls of EE activities between the surface and subsoils. Because we did not characterize the horizonation of the sampling pits, we *a priori* chose 20 cm to represent the subsoil because most EE studies do not sample below this depth. However, we also conducted our analysis using a 30 cm threshold, and the overall interpretation remained unchanged (see appendix A). Therefore, for clarity, we report results using only the 20 cm threshold for the subsoil. To denote the variance explained by the models, we report the marginal R^2 value, which expresses the increase in explained variance by including the fixed effect(s) (Nakagawa and Schielzeth 2013). We also

used ANOVA and Pearson's correlation to determine if the fraction of EE activity below 20 cm differed by soil order and if the aggregate surface and subsoil EE activities were correlated, respectively. We assessed significance at the $\alpha = 0.05$ level and marginal significance at $\alpha = 0.10$. If significant differences were detected, we used Tukey's Test of Honest Significant Differences to determine which soil orders were significantly different.

We used QQ-plots and scale-location plots to inspect normality and homoscedasticity, respectively. Because many of the mixed-effects models failed to meet parametric assumptions, all dependent and independent continuous variables were natural log-transformed and re-analyzed. The resulting models, along with the ANOVAs, met the assumptions of parametric tests. For visualization purposes, data are left untransformed unless otherwise stated.

3. Results

3.1. Whole profile soil properties among sites

Soil organic C, total N, available P, and fungi:bacteria decreased while clay percentage increased with depth across the CZO network (all: $p < 0.001$, figures S1(A)–(E) (available online at stacks.iop.org/ERL/15/1040a1/mmedia)). Across all sites, soil pH increased slightly with depth (on average 0.1 pH units over 1 m, $p = 0.028$, figure S1(F)).

3.2. Distribution of EE activity is related to MB and organic carbon throughout the top meter of soil

For all assayed EEs, EE activity per mass of soil declined logarithmically with depth ($p < 0.001$, figures 1 and S2), with the strongest decline for NAG ($\beta = -0.223$) and the weakest for AG ($\beta = -0.109$). However, about 50% of the total-profile EE activity kg^{-1} soil in the top meter occurred below 20 cm (figure 2(A)). The proportion of the EE activity below 20 cm differed by the soil order for many of the assayed EEs (tables S1 and S2). Mollisols had about a 1.5 times greater percentage of the sum of C- and N-acquiring EE activity kg^{-1} soil below 20 cm than Inceptisols or Ultisols ($p < 0.05$ for all comparisons, figure 2(B)). For AP, the 39% higher proportion in the subsoil for Mollisols compared to Inceptisols was only marginally significant ($p = 0.063$). Neither mean annual temperature (MAT) nor precipitation (MAP) significantly correlated with the proportion of EE activity below 20 cm ($p > 0.05$, figures S3 and S4).

There were also differences in the percentage of MB and SOC in the subsoil among soil orders (MB: $p < 0.001$, SOC: $p = 0.013$), with Mollisols having an almost two times greater proportion of MB and SOC below 20 cm than Inceptisols (MB: $p = 0.006$, SOC: $p = 0.013$; figure 2(B)). While the proportion of MB below 20 cm was significantly higher in Mollisols compared to Ultisols (about 1.5 times greater, $p = 0.001$), the difference in the proportion of SOC below 20 cm between Mollisols and Ultisols was only marginally significant ($p = 0.057$).

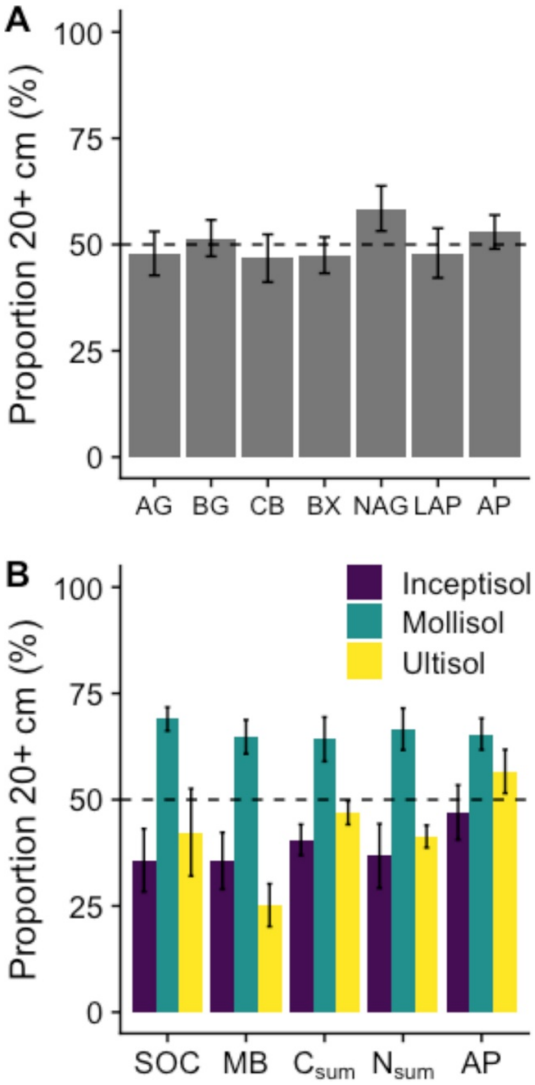

Figure 2. Percentage of α-glucosidase (AG), β-glucosidase (BG), cellobiohydrolase (CB), β-xylosidase (BX), N-acetylglucosamine (NAG), leucine aminopeptidase (LAP), and acid phosphatase (AP) activity below 20 cm in the top meter (A); and proportion of soil organic carbon (SOC), microbial biomass (MB), sum of C-degrading enzymes (C_{sum} = AG + BG + CB + BX), sum of nitrogen-mineralizing enzymes (N_{sum} = NAG + LAP), and acid phosphatase (AP) below 20 cm in the top meter of soil among soil orders (B). Error bars show ± one standard error of the mean (Figure panel A: $n = 19$; Figure panel B: Inceptisol: $n = 5$, Mollisol: $n = 5$, Ultisol: $n = 4$).

Microbial biomass-normalized EE activity increased with depth for all enzymes (figure S5; all: $p < 0.05$). The strongest increases were for LAP and AP, which increased six- and seven-fold, respectively, from the 0–10 cm to the 90–100 cm depth, while NAG and BG increased by 85% and 103%, respectively. Throughout the top meter, over 80% of MB-normalized EE activity occurred below 20 cm (figure S6(A)). However, because the proportion of MB below 20 cm also varied among soil orders, the proportion of MB-normalized EE activity below 20 cm was consistent among soil orders for most assayed

EEs (AG: $p = 0.333$, BG: $p = 0.175$, CB: $p = 0.278$, BX: $p = 0.211$, NAG: $p = 0.027$, LAP: $p = 0.537$, AP: $p = 0.048$; figure S6(A)). Nevertheless, the proportion of MB-normalized NAG activity below 20 cm was 15% greater in Ultisols compared to Inceptisols ($p = 0.025$), and the proportion of MB-normalized AP activity below 20 cm was 17% greater in Ultisols compared to Mollisols ($p = 0.042$).

There were inconsistent patterns of EE activity normalized by SOC with depth. N-acetylglucosaminidase normalized by SOC decreased with depth ($p = 0.004$); AG, LAP, and AP increased with depth (AG: $p = 0.016$, LAP: $p = 0.002$, AP: $p < 0.001$); and BG, CB, and BX did not change with depth (BG: $p = 0.322$, CB: $p = 0.344$, BX: $p = 0.198$; figure S7). Similar to the proportion of MB-normalized EE activity below 20 cm, the proportion of EE activity normalized by SOC below 20 cm averaged about 80% and did not differ among soil orders (all: $p > 0.1$; figure S8).

With a few exceptions, aggregate EE activity (per mass of soil, MB, and SOC) below 20 cm correlated with the aggregated activity in the upper 20 cm (table S3). On average, these correlations were strongest for SOC-normalized EE activities and weakest for MB-normalized EE activities. As such, aggregate surface soil AG, CB, and BX activity normalized by MB was not correlated with respective aggregate activities in the subsoil ($p > 0.05$).

3.3. Controls on EE activity throughout the top meter of soil

Consistently, MB, SOC, and fungi:bacteria were better predictors of EE activities per mass of soil than pH or clay concentrations (table S4). This was generally consistent among surface soil- and subsoil-only datasets except for fungi:bacteria, which was only a strong predictor in the surface soil (table S5).

Normalized by MB, soil pH was generally not a significant predictor of the assayed EE activities (table S6). This pattern was mostly consistent among surface soil- and subsoil-only datasets, with the exception of surface soil CB ($p = 0.023$) and subsoil LAP ($p = 0.042$, table 2). In contrast, normalized by SOC, soil pH had a variable effect on EE activities. In the surface soil, pH was positively correlated with BG ($p = 0.001$), CB ($p = 0.002$), BX ($p = 0.042$), and LAP ($p = 0.004$, table 2). However, in the subsoil, pH was negatively correlated with CB ($p = 0.025$) and AP ($p < 0.001$), and positively correlated with LAP ($p < 0.001$, table 2).

When EE activities were normalized per unit MB, clay concentrations and fungi:bacteria were generally correlated positively with EE activities (table S6). When surface and subsoil EE data were analyzed separately, the effect of clay concentrations and fungi:bacteria on MB-normalized EE activities was more often significant in the subsoil (table 2).

3.4. Relating soil and EE stoichiometries throughout the top meter of soil

When considering soils from all depth increments, only $soil_{C:N}$ and $EE_{C:N}$ were correlated (C:N: $p = 0.013$, C:P: $p = 0.292$, N:P: $p = 0.276$), but this negative correlation between $soil_{C:N}$ and $EE_{C:N}$ was relatively weak (marginal $R^2 = 0.038$; figure S9). However, using the surface soil-only dataset, all soil and EE stoichiometries were negatively correlated (C:N: $p = 0.003$, marginal $R^2 = 0.268$; C:P: $p = 0.002$, marginal $R^2 = 0.193$; N:P: $p = 0.004$, marginal $R^2 = 0.260$; figure 3). In the subsoil, these correlations decoupled such that none of the stoichiometries were significantly correlated (C:N: $p = 0.288$, C:P: $p = 0.358$, N:P: $p = 0.282$; figure 3). Split amongst 10 cm increment sample depths, negative correlations between soil and enzyme stoichiometry were generally significant ($p < 0.05$) only in the upper soil layers (figure S10).

4. Discussion

Our continental-scale sampling efforts show that microbial activity at depth is non-negligible, and the relative proportion of EE activity (kg^{-1} soil) at depth depends predominately on soil development (i.e. soil order; figure 2(B)). Although replication of each soil order was relatively small ($n = 4$–5), this finding was strikingly consistent despite large gradients in MAT and MAP for each soil order (e.g. MAP spanned an order of magnitude for Inceptisols; table 1). Our analysis shows that climate is an unlikely driver of the relative vertical distribution of EE activity. Instead, this phenomenon is likely due to changes in the vertical distribution of substrate (organic C) and MB among these soil orders (Batjes 1996; figure 2(B)), which strongly correlate with EE activity (Sinsabaugh *et al* 2008; table S4). Hence, we show that SOC and MB are the strongest controls of EE activities throughout the soil profile.

We hypothesize that increases in the MB-normalized EE activities at depth suggest an accumulation of EEs chemically stabilized on mineral and organic surfaces. While MB-normalized EE activity is often related to the relative activity of the microbial community or differences in metabolic strategies among microbial taxa (Boerner *et al* 2005), we alternatively hypothesize that the increase in MB-normalized EE activity is due to EE stabilization, namely the sorption of the EEs onto clay or organic matter particles that impedes EE degradation (Sarkar *et al* 1989, Burns *et al* 2013). Because EE activities are often measured in a salt-buffered soil slurry that disrupts the stabilization of EEs (as is the case in our study), EE activity assays generally measure both active and stabilized EEs (Burns *et al* 2013). We hypothesize that higher subsoil MB-normalized EE activities is primarily a product of EE stabilization instead of differences in the metabolic capabilities

Table 2. Marginal R^2 values for mixed-effects models with soil clay concentration, pH, or fungi:bacteria ratio as the sole fixed effect, and soil pit as a random effect on extracellular enzyme (EE) activity normalized by microbial biomass (MB) or soil organic carbon (SOC) concentration in surface- (≤20 cm) and sub-soils (>20 cm) across all sites. Key: α-glucosidase (AG), β-glucosidase (BG), cellobiohydrolase (CB), β-xylosidase (BX), N-acetylglucosamine (NAG), leucine aminopeptidase (LAP), and acid phosphatase (AP) activity. Bolded values represent a significant ($\alpha = 0.05$) effect and ± signifies the direction of the effect (surface soil: $n = 29$, subsoil: $n = 114$).

	MB-normalized[a]			SOC-normalized[b]		
EE	Clay	pH	fungi:bacteria	Clay	pH	fungi:bacteria
Surface soil						
AG	<0.001	0.015	0.016	0.002	0.023	0.016
BG	<0.001	0.135	0.013	0.001	**+0.366**	0.008
CB	0.003	**+0.119**	0.052	0.002	**+0.301**	0.002
BX	0.004	0.076	0.011	<0.001	**+0.161**	**−0.095**
NAG	0.067	<0.001	**+0.298**	0.011	0.122	**+0.146**
LAP	0.004	0.024	0.007	**+0.020**	**+0.142**	0.039
AP	0.004	0.024	< 0.001	**+0.102**	0.009	**−0.226**
Subsoil						
AG	**+0.097**	0.013	0.019	0.019	0.073	0.005
BG	0.063	0.017	**+0.171**	0.001	0.001	0.014
CB	0.043	0.007	**+0.037**	<0.001	**−0.106**	0.001
BX	**+0.094**	0.002	**+0.146**	0.002	0.035	0.001
NAG	0.020	0.005	**+0.080**	0.032	0.075	0.006
LAP	0.001	**+0.088**	0.001	0.009	**+0.086**	<0.001
AP	**+0.142**	0.081	0.002	0.210	**−0.455**	0.002

[a]Enzyme activity per unit microbial biomass

[b]Enzyme activity per unit soil organic carbon

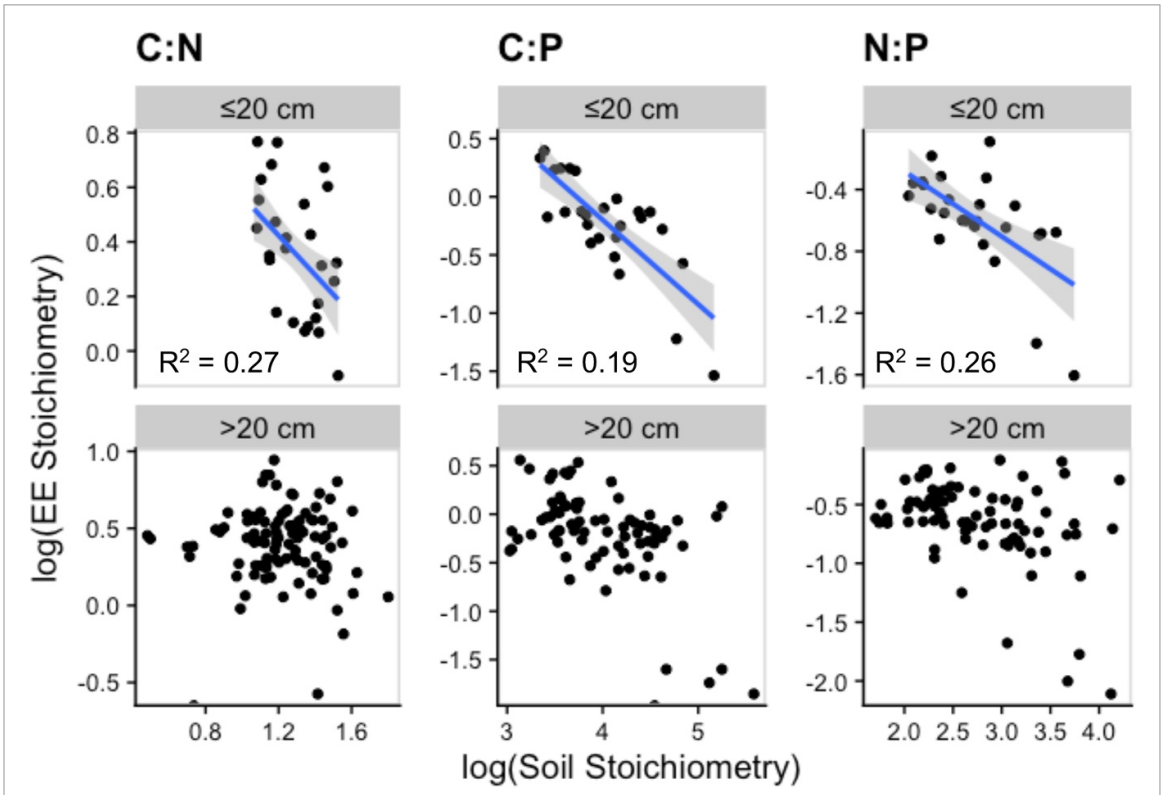

Figure 3. Correlations between soil and extracellular enzyme (EE) stoichiometry (i.e. the ratio of elements by mass and extracellular enzyme activities that target these same elements) of carbon (C), nitrogen (N), and phosphorus (P) in surface (≤20 cm depth) and subsoils (>20 cm depth across all sites). Blue lines show significant ($\alpha = 0.05$) mixed-effects models of the relationship between soil and EE stoichiometry (site was used as a random effect; lines were not drawn where correlations were not significant). Gray ribbons show the standard error of the model. Data points represent individual soil samples (depths within each pit). Note the scales of the axes differ among plots.

of the microbial community for three reasons. First, MB-normalized respiration (i.e. microbial metabolic quotient), which is another measure of the relative activity of the microbial community, generally does not increase with depth (Dominy and Haynes 2002, Fang and Moncrieff 2005; but see Lavahun *et al* 1996).

Secondly, the relative abundance of fungi, which produce more EEs per unit MB than bacteria (Romaní *et al* 2006), decreased with depth. Finally, the decoupling of soil stoichiometry and EE stoichiometry at depth suggests that EE activities are not responsive to altered nutrient availabilities. Taken together, these results suggest that the physiochemical process of EE stabilization, a largely abiotic process, is the major control of EE activity in the subsoil.

Extracellular enzyme stabilization as a major mechanism in the subsoil is corroborated by our finding that the influence of clay concentration on MB-normalized EE activity is higher in the subsoil than the surface soil (table 2). Furthermore, we may have underestimated EE activity in high clay soils because clay can increase the pH optima of EEs 1–2 pH units (Mclaren and Estermann 1957, Ramírez-Martínez and Mclaren 1966). Whereas many EEs have native pH optima between 4.0 and 6.5 (Parham and Deng 2000, Niemi and Vepsäläinen 2005, Turner 2010, Min *et al* 2014), an increase of two pH units would be significantly higher than the pH of our assay buffer (pH = 5.5). Therefore, we conclude that EE stabilization is a major process when microbial activity is relatively low and clay concentrations are relatively high, which is often the case in subsurface soil layers.

Extracellular enzyme stabilization may be partially responsible for the muted treatment effects on subsoil EE activity commonly found throughout the literature (e.g. Kramer *et al* 2013, Jing *et al* 2017, Yao *et al* 2019). When the stabilized EE pool is significantly greater than the active EE pool, the ability to detect changes in the active pool is decreased. For example, if we assume that there is negligible EE stabilization in the surface soil and that the actualized MB-normalized EE activity *in situ* is constant throughout the soil profile, our results show that at least 29%–71% of the assayed MB-normalized EE activity at depth can be attributed to stabilized EEs across our study sites, depending on the EE (equation (1)).

$$Z = ((Y - X)/Y) * 100 \quad (1)$$

X = Average MB-normalized EE activity in surface soil

Y = Average MB-normalized EE activity in subsoil

Z = Percent MB-normalized EE activity in subsoil attributed to stabilized EEs

This equation calculates the difference between MB-normalized EE activity in surface and subsoil as a percentage of the MB-normalized EE activity in the subsoil and, adhering to the aforementioned assumptions, represents the percentage of MB-normalized EE activity in the subsoil attributed to EE stabilization. This calculation likely represents the lower bound of the estimated stabilized MB-normalized EE activity because any stabilization in the surface soil (X), would increase Z, and the relative proportion of fungal biomass, which release comparatively more EEs than bacteria per unit MB (Romaní *et al* 2006), decreased with depth. Nevertheless, this implies that if the stabilized EE pool is resistant to treatment effects in experiments (e.g. Kramer *et al* 2013, Jing *et al* 2017, Yao *et al* 2019), the ability to detect significant changes in microbial activity at depth using EE assays is also reduced by at least 29%–71%. In instances where the magnitude of the treatment effect is modest, it is unlikely that a significant change in subsoil EE activity will be detected. However, this

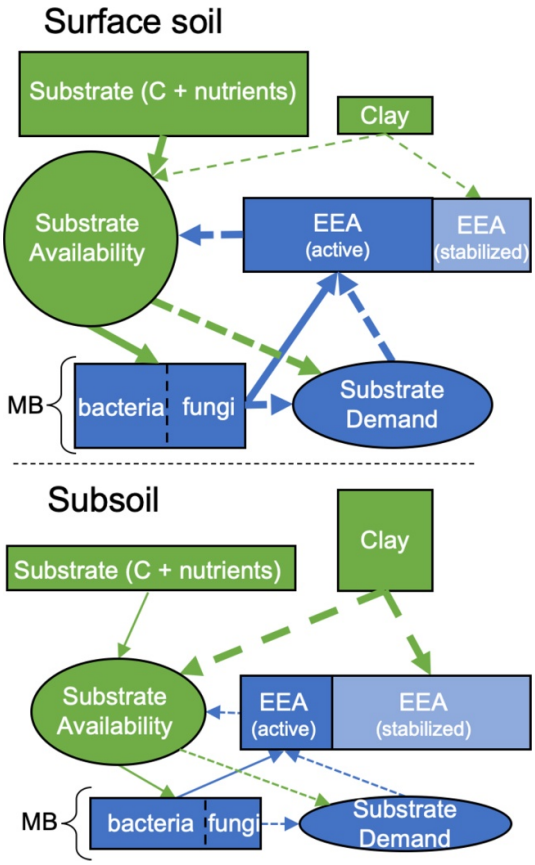

Figure 4. Conceptual model of changing controls on extracellular enzyme activity (EEA) between surface soil and subsoil. Solid lines represent fluxes and dashed lines represent moderating controls. Boxes represent pools or concentrations, and other shapes represent moderating variables. Blue parameters represent microbial parameters, and green boxes represent edaphic variables such as substrate (including carbon [C] and nutrients) and clay concentrations. The differences in the size of boxes between the surface and subsoil represent the relative size of the pool, and differences in the thickness of arrows between the surface and subsoil represent the hypothesized relative magnitude of the flux or control. A portion of the substrate pool is available to microbial biomass (MB) and is moderated by clay concentration and active EEA. Substrate availability moderates substrate demand. Bacterial biomass, fungal biomass, and substrate demand influence active EEA. Additionally, our conceptual model incorporates stabilized EEA (i.e. EEs sorbed onto clay particles), which is primarily influenced by clay concentrations. At depth, the impact of clay on substrate availability and stabilized EEA increases, while the absolute impact of substrates and microbial properties (i.e. microbial biomass and substrate demand) decreases.

should not necessarily be interpreted as a lack of microbial response, and caution should be exercised in interpreting the effect of a surface manipulation or treatment on subsoil EE activity.

The discrepancy between soil and EE stoichiometry at depth may also be caused by the increased discontinuity of substrates in the subsoil and the reduced ability of the microbial community to respond to changes in resource availability (Allison *et al* 2007). This would prevent subsoil microorganisms altering their EE stoichiometry to different nutrient conditions. Resource availability is typically higher in surface soils than in subsoils (Salomé *et al* 2010). Recent work in soil enzymography show that C-degrading EE activities are enriched only 0.5–2.0 mm from C-rich rhizodeposits (Ma *et al* 2018). The EE assays that we and most other researchers use disrupt the spatial arrangement of EEs and substrates such that our results express bulk EE activities and bulk resource concentrations, which may not be representative of more localized heterogeneity in resources.

Our finding that aggregated surface soil EE activity (normalized by mass of soil, MB, or SOC) generally correlates with aggregated activity in the subsoil suggests that it may be possible to extrapolate EE measurements at the surface into deeper layers. Interestingly, MB and SOC, which we demonstrate correlate with EE activity (per mass of soil), did not follow these same patterns. It is possible that high concentrations of EEs in the surface soils percolated into the subsoil. However, correlation of surface and deeper EE activities, instead, could be due to similarities in microbial community composition throughout the soil profile. Indeed, microbial community composition assessed by 16S rRNA gene sequencing of these same soils showed a stronger effect of soil location than soil depth (Brewer *et al* 2019). This finding provides further evidence of the linkages between microbial community composition and metabolic strategies in soils (e.g. Schnecker *et al* 2015) and demonstrates association between surface soils and subsoils.

Discrepancies in the effect of soil pH between MB-normalized and SOC-normalized EE activities likely reflects the impact of soil pH on SOC stabilization and how well our bulk MB and SOC measurements correlate with microbial-available SOC. In numerous ecosystems, low soil pH is associated with greater SOC stabilization due to an increased charge of clay minerals and Al- and Fe-oxyhydroxides resulting in an increase of their sorption capacity (Rasmussen *et al* 2018). Therefore, increasing pH (and decreasing SOC stabilization) likely reflects greater available SOC as a fraction of total SOC, which would result in higher SOC-normalized EE activities. Soil pH was not a significant mediator of MB-normalized activities possibly because our MB measurements better reflect the available SOC pool, given that microbial growth is generally substrate-limited (Jones *et al* 2018). These results highlight the interactions between SOC, MB, and soil stabilization of microbial substrates and products and provide further evidence for the strong effect of soil stabilization in regulating EE activities throughout the soil profile.

Taken together, our results suggest that the relative importance of the different controls on EE activities change with depth. We summarize this in a conceptual model, where the active EE pool is controlled by microbial EE production (proximately influenced by MB and resource demand), and the stabilized EE pool is primarily influenced by EE stabilization onto clay particles (figure 4). Because MB and resource demand decrease with depth as C becomes more limiting and clay concentrations increase, the subsoil total EE pool is maintained because of the relatively large proportion of stabilized (sorbed on soil colloids) EEs that decay slower than unstabilized (present in the bulk soil solution) EEs. Understanding how soil texture affects EE stabilization and decay dynamics is a critical knowledge gap in enzyme-explicit microbial models (e.g. Schimel and Weintraub 2003, Manzoni *et al* 2016, Abramoff *et al* 2017, Sulman *et al* 2018). For instance, Schimel *et al* (2017) estimated EE decay dynamics in multiple soils by measuring EE activities for weeks after sterilization. While these soils varied in texture, there did not appear to be a consistent pattern between soil texture and EE decay, possibly because of changes in other edaphic factors (i.e. moisture, substrate, etc.). Future work should systematically study EE decay and its relation to multiple edaphic factors including clay concentration to test our proposed conceptual model.

Overall, the suite of EEs studied here exhibit similar patterns with depth across a wide range of sites and represent a diverse set of biochemical reactions. Hence, we posit that these patterns are robust and may be applicable to other EEs released by soil microorganisms. Our findings imply that the vast majority of EE studies are missing a large portion of the total EE activity in soils, and that the unmeasured subsoil EE activity varies in its response to environmental conditions. Nevertheless, if undisturbed, extrapolating surface soil EE values into the subsoil may be appropriate. As numerous other experiments have shown (Blume *et al* 2002, Taş *et al* 2014), ignoring subsoils, and exclusively focusing on surface soils, can limit our ability to understand whole-profile EE-dynamics and soil C storage.

Acknowledgments

We thank N. Blair, A. Bissett, T. Brewer, A.N. Campbell, G. King, M. Firestone, C. Lehmeier, M. Leon,

G. Logan, N. Lu, F. Meyer, S.M. Owens, A. Packman, A.F. Plante, D.D. Richter, W.L. Silver and E. Starr for their contributions to this research effort and B. Boudinot for assistance with PLFA analysis. This research was supported by the NSF EarthCube program (ICER-1541047), the Critical Zone Observatory Network (EAR-1331939), and a University of California Merced Graduate Fellowship Award derived from a match provided by the Southern Sierra Critical Zone Observatory (to NCD). Work conducted by researchers at Lawrence Livermore National Laboratory was performed under the auspices of the U.S. Department of Energy (DOE) by under contract DE-AC52-07NA27344, and supported by a US Department of Energy Early Career Research Program Award to J. Pett-Ridge (SCW1478). Postdoctoral development funds from Oak Ridge National Laboratory also supported N. Dove (OakRidge National Laboratory is managed by UT-Battelle, LLC, for the U.S. DOE under contract DEAC05-00OR22725). Support for this research was also provided by National Science Foundation for RC CZO Cooperative agreement, EAR-1331872.

Data availability statement

The data that support the findings of this study are openly available at the following URL/DOI: https://doi.org/10.6071/M3D104.

Author contributions

All authors contributed to this project by designing the cross-site study, collecting/processing samples, characterizing soils, analyzing data, or some combination thereof. E.L.A. was primarily responsible for leading this cross-site effort and for coordinating the research activities across all project personnel. Laboratory analyses were conducted by K.A., C.C., J.L.D., S.C.H., W.H.Y, and N.C.D. Data analysis was led by N.C.D. The manuscript was written by N.C.D. and S.C.H., with critical input from all coauthors.

Appendix A

In the main text of this study, we use the threshold of 20 cm to delineate the surface and subsoil. We provide the following analysis to show that the same analysis with the same extracellular enzymes (EEs) (e.g. α-glucosidase [AG], β-glucosidase [BG], cellobiohydrolase [CB], β-xylosidase [BX], N-acetylglucosaminidase [NAG], leucine aminopeptidase [LAP], and acid phosphatase [AP]) conducted with a 30 cm threshold to show that the general interpretation remains the same.

Table A1. Mean proportion (and standard error, $n = 19$) of extracellular enzyme activity (kg^{-1} soil) below 30 cm across the three main soil orders represented in the study. Different superscript letters represent significant differences among soil orders for each enzyme ($\alpha = 0.05$). Key: AG = α-glucosidase, BG = β-glucosidase, CB = cellobiohydrolase, BX = β-xylosidase, LAP = leucine aminopeptidase, NAG = N-acetylglucosamine, AP = acid phosphatase.

Enzyme	Inceptisols	Mollisols	Ultisols
AG	26.2% (7.7)	46.3% (6.4)	52.0% (7.0)
BG	31.0% (4.3)^{a}	54.0% (7.0)^{b}	36.8% (2.3)^{ab}
CB	34.5% (10.3)	47.8% (9.8)	28.7% (4.5)
BX	20.8% (5.1)^{a}	51.7% (5.0)^{b}	38.6% (6.7)^{ab}
NAG	23.6% (7.0)^{a}	52.2% (6.2)^{b}	31.7% (2.5)^{ab}
LAP	41.6% (2.7)^{ab}	61.4% (8.0)^{b}	37.3% (4.3)^{a}
AP	35.7% (4.1)	52.9% (5.1)	44.5% (4.3)

Table A2. Means (and standard errors) of the aggregate EE activity (mmol kg^{-1} soil h^{-1}) in the upper 30 cm and below 30 cm across soil orders. Key: AG = α-glucosidase, BG = β-glucosidase, CB = cellobiohydrolase, BX = β-xylosidase, LAP = leucine aminopeptidase, NAG = N-acetylglucosamine, AP = acid phosphatase; Inceptisol: $n = 5$, Mollisol: $n = 5$, Ultisol: $n = 4$.

		Inceptisols	Mollisols	Ultisols
AG	≤30 cm	19.3 (8.3)	16.1 (4.0)	13.7 (5.2)
	>30 cm	10.4 (5.4)	16.0 (5.4)	12.2 (1.6)
BG	≤30 cm	269.1 (94.0)	294.2 (35.6)	143.2 (25.6)
	>30 cm	129.2 (53.1)	422.7 (118.4)	82.2 (14.2)
CB	≤30 cm	42.4 (12.1)	64.7 (11.1)	39.5 (9.7)
	>30 cm	34.4 (20.2)	88.2 (36.5)	14.2 (2.2)
BX	≤30 cm	60.8 (22.2)	50.4 (7.0)	48.6 (18.8)
	>30 cm	20.4 (9.8)	57.6 (10.9)	24.3 (4.4)
NAG	≤30 cm	201.6 (110.5)	114.0 (15.0)	98.3 (21.3)
	>30 cm	50.2 (21.9)	138.3 (27.3)	46.1 (12.2)
LAP	≤30 cm	19.3 (2.2)	29.4 (10.0)	30.8 (8.9)
	>30 cm	13.5 (0.8)	40.7 (5.9)	16.0 (2.7)
AP	≤30 cm	870.4 (292.3)	524.3 (118.3)	582.5 (149.8)
	>30 cm	529.0 (234.3)	588.0 (143.6)	430.2 (64.5)

Table A3. Pearson correlations between the aggregated surface (≤30 cm) and subsoil (>30 cm) extracellular enzyme (EE) activities per mass soil, microbial biomass (MB), and soil organic carbon (SOC) across all sites. Bolded values represent a significant ($\alpha = 0.05$) positive correlation. Note: these are correlations of natural-log transformed data.

EE	mass^{-1} soil	mass^{-1} MB	mass^{-1} SOC
AG	**0.766**	0.276	**0.743**
BG	**0.767**	0.465	**0.836**
CB	**0.717**	0.377	**0.713**
BX	**0.469**	**0.478**	**0.536**
NAG	**0.584**	**0.561**	**0.876**
LAP	**0.784**	**0.763**	**0.947**
AP	**0.584**	**0.671**	**0.735**

Distribution of EE activity is related to microbial biomass and organic carbon throughout the top meter of soil

About 40% of the total-profile EE activity kg^{-1} soil in the top meter occurred below 30 cm (figure A1(A)).

Table A4. Marginal r^2 values for mixed-effects models with soil microbial biomass (MB), soil organic carbon (SOC) concentration, clay concentration, pH, or fungi:bacteria as the sole fixed effect, and soil pit as a random effect on extracellular enzyme (EE) activities (kg^{-1} soil) in surface ($\leq$30 cm) and subsoils (>30 cm) across all sites. Key: α-glucosidase (AG), β-glucosidase (BG), cellobiohydrolase (CB), β-xylosidase (BX), N-acetylglucosamine (NAG), leucine aminopeptidase (LAP), acid phosphatase (AP), sum of C-degrading enzymes (C_{sum} = AG + BG + CB + BX), and sum of nitrogen-mineralizing enzymes (N_{sum} = NAG + LAP). Bolded values represent a significant ($\alpha = 0.05$) effect and ± signifies the direction of the effect (surface soil MB, SOC, fungi:bacteria: $n = 38$, subsoil MB, SOC, fungi:bacteria: $n = 140$, surface soil clay & pH: $n = 29$, subsoil clay and pH: $n = 114$).

EE	MB (mol PLFA)	SOC (%)	Clay (%)	pH (1:2 w v^{-1} H_2O)	fungi:bacteria
Surface soil					
C_{sum}	**+0.232**	**+0.337**	**−0.235**	0.012	**+0.270**
AG	**+0.188**	**+0.325**	**−0.060**	0.008	**+0.260**
BG	**+0.257**	**+0.326**	**−0.186**	0.020	**+0.272**
CB	**+0.264**	**+0.328**	**−0.153**	0.044	**+0.261**
BX	**+0.242**	**+0.296**	**−0.109**	0.001	**+0.166**
N_{sum}	**+0.397**	**+0.562**	**−0.188**	< 0.001	**+0.507**
NAG	**+0.389**	**+0.542**	**−0.159**	0.001	**+0.496**
LAP	**+0.162**	**+0.173**	**−0.225**	0.072	**+0.159**
AP	**+0.500**	**+0.611**	**−0.140**	**−0.262**	**+0.323**
Subsoil					
C_{sum}	**0.195**	**0.149**	**−0.690**	0.026	<0.001
AG	**0.030**	**0.043**	< 0.001	0.005	0.002
BG	**0.300**	**0.176**	0.054	<0.001	0.003
CB	**0.071**	**0.073**	< 0.001	0.018	<0.001
BX	**0.257**	**0.211**	0.031	0.016	<0.001
N_{sum}	**0.321**	**0.240**	0.057	<0.001	0.002
NAG	**0.259**	**0.131**	0.030	0.050	0.003
LAP	**0.050**	**0.243**	0.035	**+0.276**	0.002
AP	**0.307**	**0.165**	0.064	**−0.208**	0.006

Table A5. Marginal R^2 values for mixed-effects models with soil clay concentration, pH, or fungi:bacteria as the sole fixed effect, and soil pit as a random effect on extracellular enzyme (EE) activity normalized by microbial biomass (MB) or soil organic carbon (SOC) concentration in top- ($\leq$30 cm) and sub-soils (>30 cm) across all sites. Key: α-glucosidase (AG), β-glucosidase (BG), cellobiohydrolase (CB), β-xylosidase (BX), N-acetylglucosamine (NAG), leucine aminopeptidase (LAP), and acid phosphatase (AP) activity. Bolded values represent a significant ($\alpha = 0.05$) effect and ± signifies the direction of the effect (surface soil: $n = 29$, subsoil: $n = 114$)..

	MB-normalized[a]			SOC-normalized[b]		
EE	Clay	pH	fungi:bacteria	Clay	pH	fungi:bacteria
Surface soil						
AG	0.016	0.041	0.003	−0.003	<0.001	0.029
BG	0.003	**+0.131**	0.008	0.021	**+0.247**	0.004
CB	0.027	**+0.191**	0.044	0.021	**+0.247**	0.008
BX	0.011	0.032	0.002	0.041	0.107	0.037
NAG	−0.022	0.008	**+0.196**	0.003	0.050	**+0.093**
LAP	< 0.001	0.022	**−0.014**	**+0.021**	**+0.118**	**−0.023**
AP	< 0.001	0.033	**−0.004**	**+0.091**	0.046	**−0.092**
Subsoil						
AG	**+0.079**	0.009	0.009	0.028	0.042	0.001
BG	0.041	0.028	**0.163**	0.001	0.001	0.020
CB	0.038	0.008	0.034	0.001	0.072	0.003
BX	**+0.077**	< 0.001	**0.160**	0.001	0.046	0.013
NAG	0.002	< 0.001	**0.052**	0.027	0.059	0.018
LAP	< 0.001	0.086	0.004	0.006	**+0.072**	< 0.001
AP	**+0.099**	0.080	< 0.001	0.011	**−0.493**	0.002

[a]Enzyme activity per unit microbial biomass

[b]Enzyme activity per unit soil organic carbon

The proportion of the EE activity below 30 cm differed by the soil order for many of the assayed EEs (tables A1 and A2). Mollisols had about a 1.5 times greater percentage of the sum of carbon (C)- and nitrogen (N)-acquiring EE activity kg^{-1} soil below 30 cm than Inceptisols ($p < 0.050$ for all comparisons, figure A1(B)). For AP, differences among soil orders was only marginally significant ($p = 0.057$). Neither mean annual temperature nor precipitation significantly correlated with the proportion of EE activity below 30 cm ($p > 0.05$, figures A2 and A3).

There were also differences in the percentage of microbial biomass (MB) and soil organic C (SOC) in the subsoil among soil orders (MB: $p < 0.001$, SOC: $p = 0.009$), with Mollisols having an almost two times greater proportion of MB and SOC below 30 cm

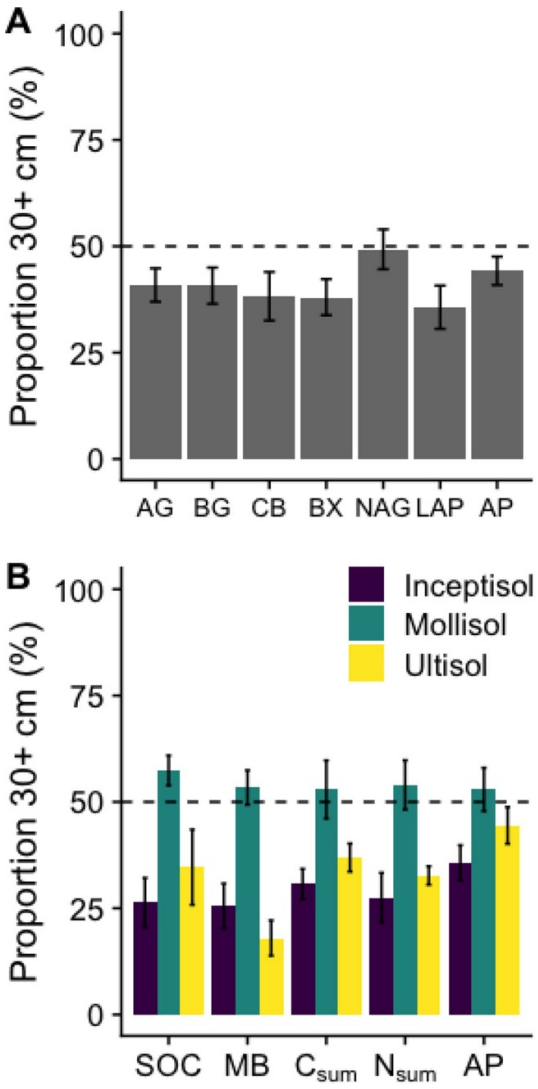

Figure A1. Percentage of α-glucosidase (AG), β-glucosidase (BG), cellobiohydrolase (CB), β-xylosidase (BX), N-acetylglucosamine (NAG), leucine aminopeptidase (LAP), and acid phosphatase (AP) activity below 30 cm in the top meter (A); and proportion of soil organic carbon (SOC), microbial biomass (MB), sum of C-degrading enzymes (C_{sum} = AG + BG + CB + BX), sum of nitrogen-mineralizing enzymes (N_{sum} = NAG + LAP), and acid phosphatase (AP) below 30 cm in the top meter of soil among soil orders (B). Error bars show ± one standard error of the mean (Figure panel A: $n = 19$; Figure panel B: Inceptisol: $n = 5$, Mollisol: $n = 5$, Ultisol: $n = 4$).

than Inceptisols (MB: $p = 0.003$, SOC: $p = 0.008$; figure A1(B)). While the proportion of MB below 30 cm was significantly higher in Mollisols compared to Ultisols (about 1.5 times greater, $p < 0.001$), the difference in the proportion of SOC below 30 cm between Mollisols and Ultisols was only marginally significant ($p = 0.059$).

Throughout the top meter, about 75% of MB-normalized EE activity occurred below 30 cm (figure A4(A)). However, because the proportion of MB below 30 cm also varied among soil orders, the proportion of MB-normalized EE activity below 30 cm was consistent among soil orders for all assayed EEs (AG: $p = 0.251$, BG: $p = 0.334$, CB: $p = 0.332$, BX: $p = 0.367$, NAG: $p = 0.081$, LAP: $p = 0.670$, AP: $p = 0.154$; figure A4(A)). Similar to the proportion of MB-normalized EE activity below 30 cm, the proportion of EE normalized by SOC below 30 cm averaged about 70% and did not differ among soil orders (all: $p > 0.1$; figure A5).

With a few exceptions, aggregate EE activity (per mass of soil, MB, and SOC) below 30 cm correlated with the aggregated activity in the upper 30 cm (table A3). On average, these correlations were strongest for SOC-normalized EE activities and weakest for MB-normalized EE actives. As such, aggregate surface soil AG, BG, and CB, activity normalized by MB was not correlated with respective aggregate activities in the subsoil ($p > 0.05$).

Controls on EE activity throughout the top meter of soil

While EE activities (kg^{-1} soil) were always correlated with MB and SOC for both the surface and subsoil datasets, clay concentration and the ratio of fungi-to-bacteria (fungi:bacteria) were only correlated with EE activities in the surface soil (table A4). With the exception of surface- and subsoil AP, which positively correlated with pH, and subsoil LAP, which negatively correlated with soil pH, pH was not a significant predictor of EE activities (table A4). Normalized by SOC or MB, soil pH had a variable effect on EE activities (table A5). In the surface soil, pH correlated positively with BG and CB regardless of the normalization, while pH positively correlated with LAP only when normalized by SOC. In the subsoil soil pH positively correlated with LAP and negatively correlated with AP only when normalized by SOC.

Relating soil and EE stoichiometries throughout the top meter of soil

Using the surface soil-only dataset, all soil and EE stoichiometries were negatively correlated (C:N: $p = 0.004$, marginal $R^2 = 0.201$; C:P: $p = 0.002$, marginal $R^2 = 0.193$; N:P: $p = 0.028$, marginal $R^2 = 0.146$; figure A6). In the subsoil, these correlations decoupled such that none of the stoichiometries were significantly correlated (C:N: $p = 0.257$, C:P: $p = 0.409$, N:P: $p = 0.385$; figure A6).

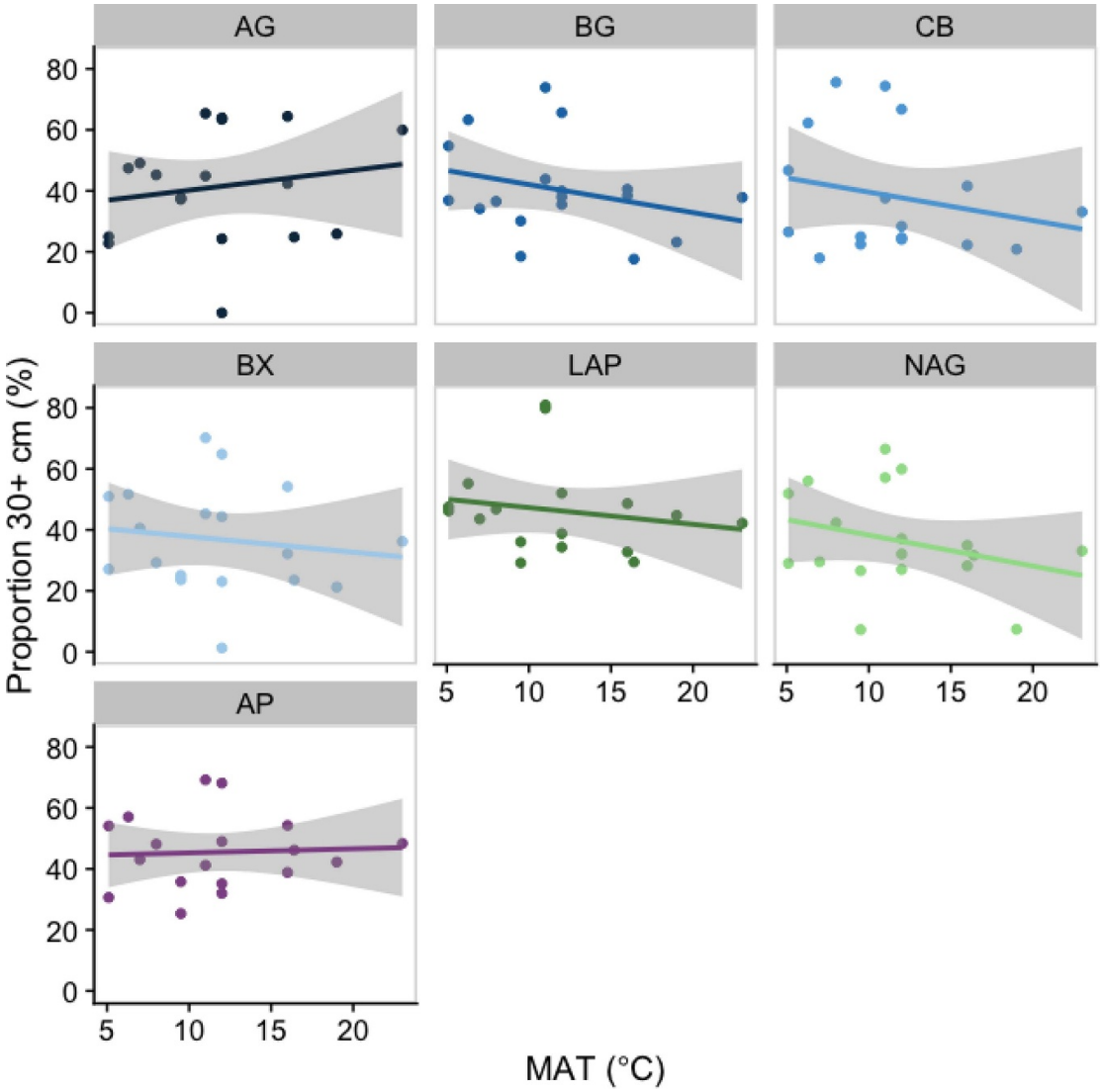

Figure A2. Relationship between mean annual temperature (MAT) and the proportion of α-glucosidase (AG), β-glucosidase (BG), β-xylosidase (BX), cellobiohydrolase (CB), N-acetylglucosaminidase (NAG), leucine aminopeptidase (LAP), and acid phosphatase (AP) below 30 cm across all sites. Line represents the best-fit linear regression, and gray ribbon represents the standard error of the regression.

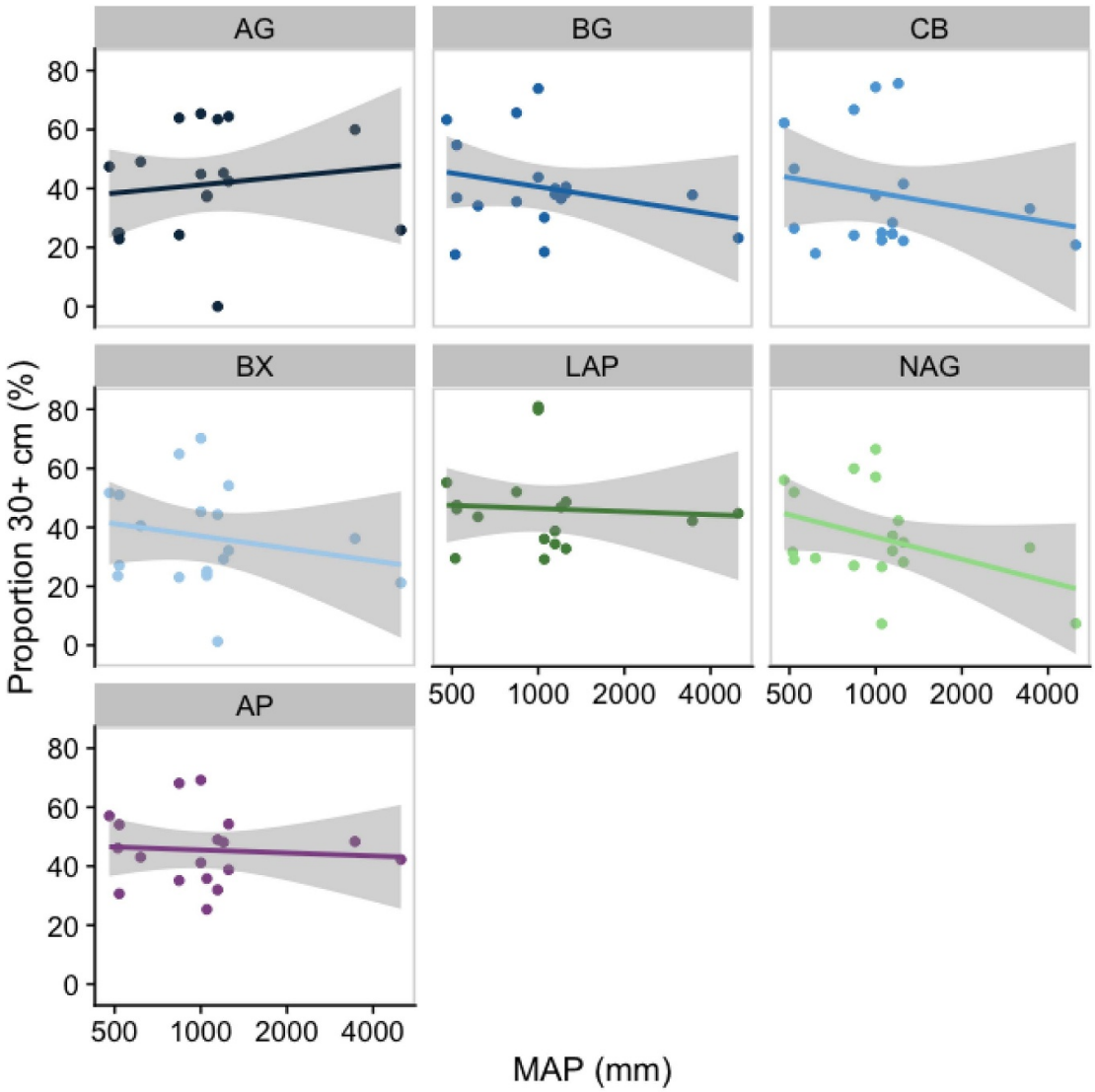

Figure A3. Relationship between mean annual precipitation (MAP) and the proportion of α-glucosidase (AG), β-glucosidase (BG), β-xylosidase (BX), cellobiohydrolase (CB), N-acetylglucosaminidase (NAG), leucine aminopeptidase (LAP), and acid phosphatase (AP) below 30 cm across all sites. Line represents the best-fit linear regression, and gray ribbon represents the standard error of the regression. Note: *x*-axis (i.e. MAP) is on log10 scale.

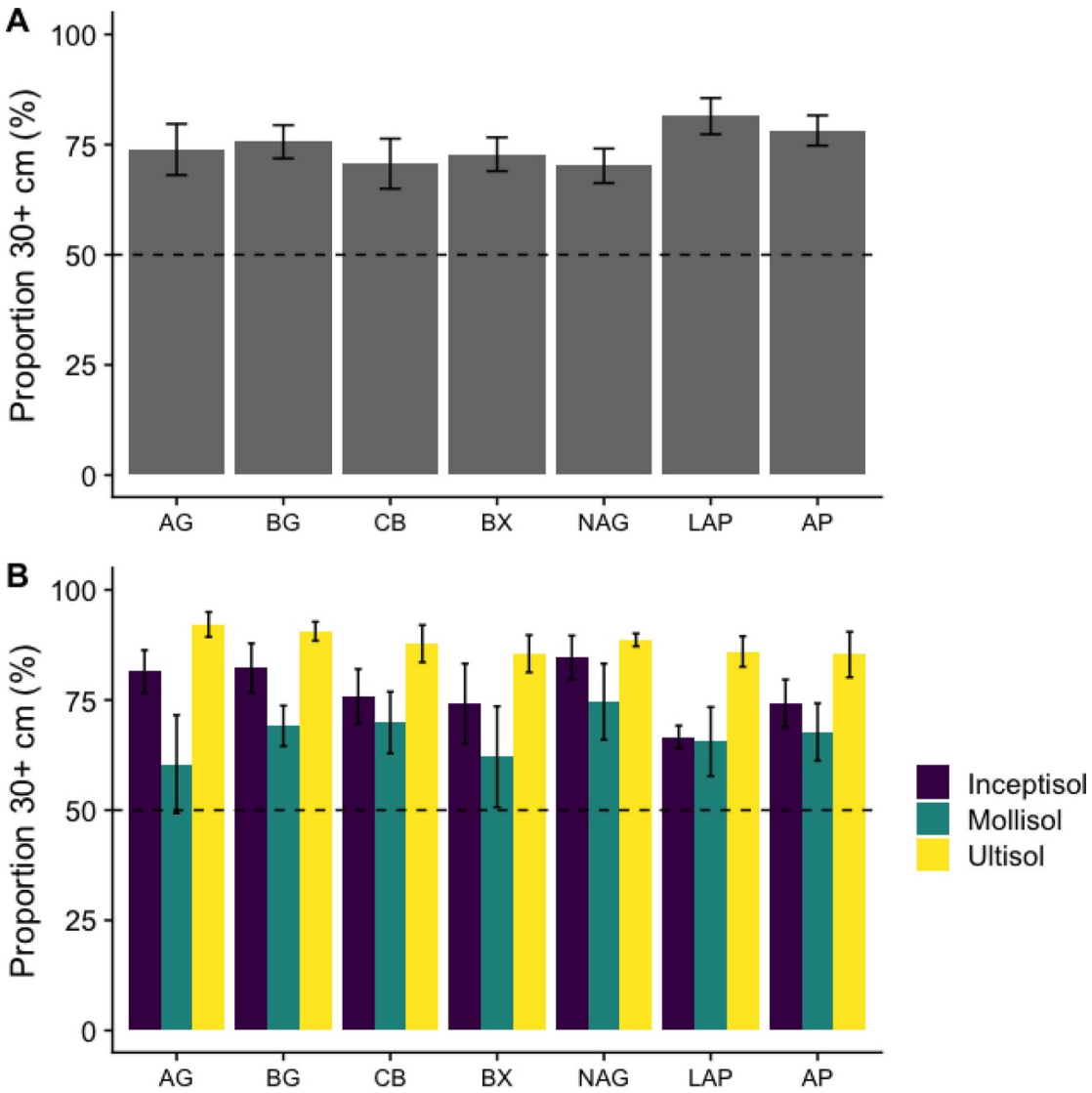

Figure A4. Proportion of soil microbial biomass-normalized extracellular enzyme activity below 30 cm in the top meter for α-glucosidase (AG), β-glucosidase (BG), cellobiohydrolase (CB), β-xylosidase (BX), N-acetylglucosamine (NAG), leucine aminopeptidase (LAP), and acid phosphatase (AP) across (A) and among (B) soil orders. Error bars show standard error of the mean (Figure panel A: $n = 19$; Figure panel B: Inceptisol: $n = 5$, Mollisol: $n = 5$, Ultisol: $n = 4$).

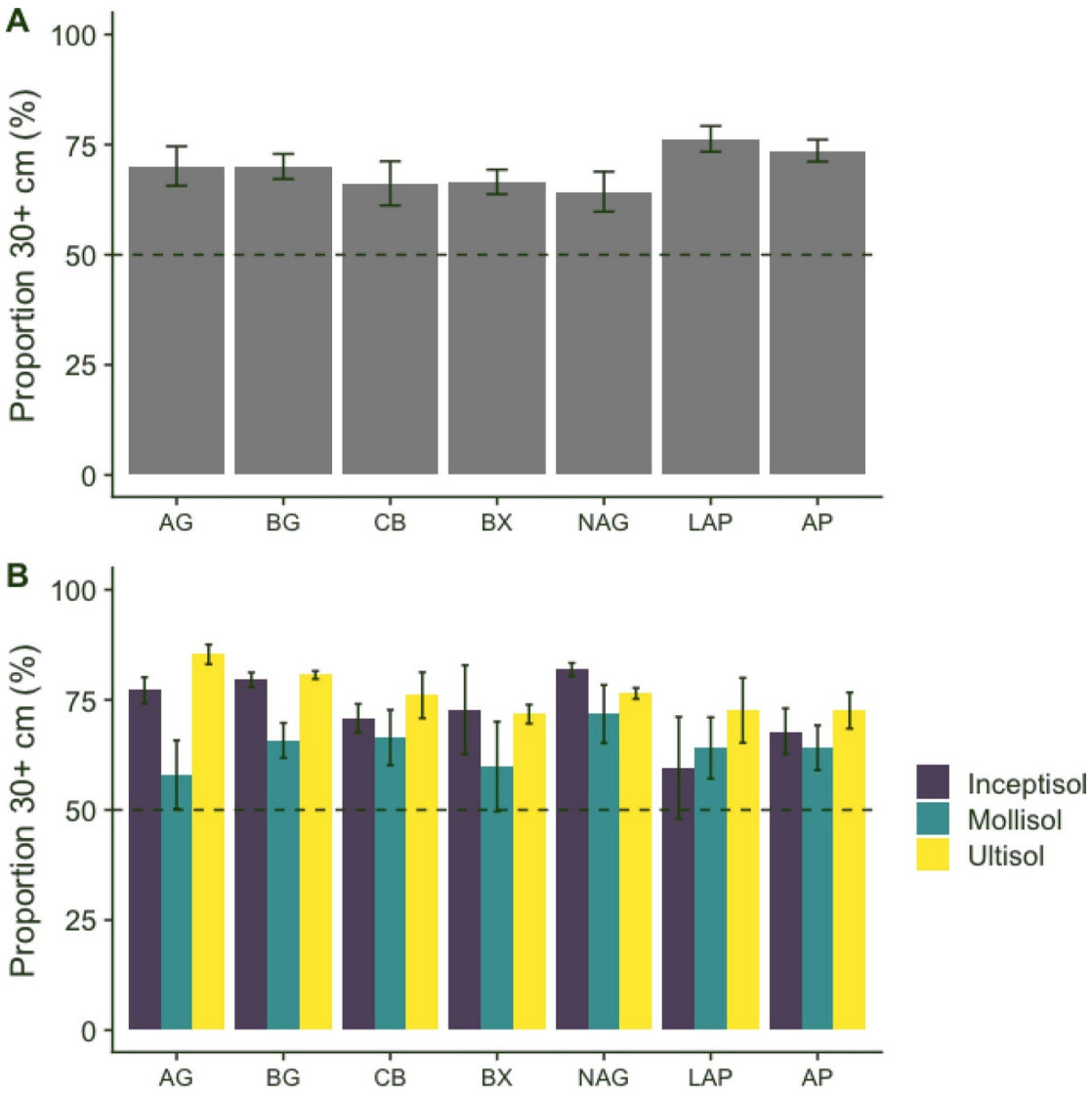

Figure A5. Proportion of extracellular enzyme activity (kg^{-1} soil organic carbon [C]) below 30 cm in the top meter for α-glucosidase (AG), β-glucosidase (BG), cellobiohydrolase (CB), β-xylosidase (BX), N-acetylglucosamine (NAG), leucine aminopeptidase (LAP), and acid phosphatase (AP) across (A) and among (B) soil orders. Error bars show standard error of the mean (Figure panel A: $n = 19$; Figure panel B: Inceptisol: $n = 5$, Mollisol: $n = 5$, Ultisol: $n = 4$).

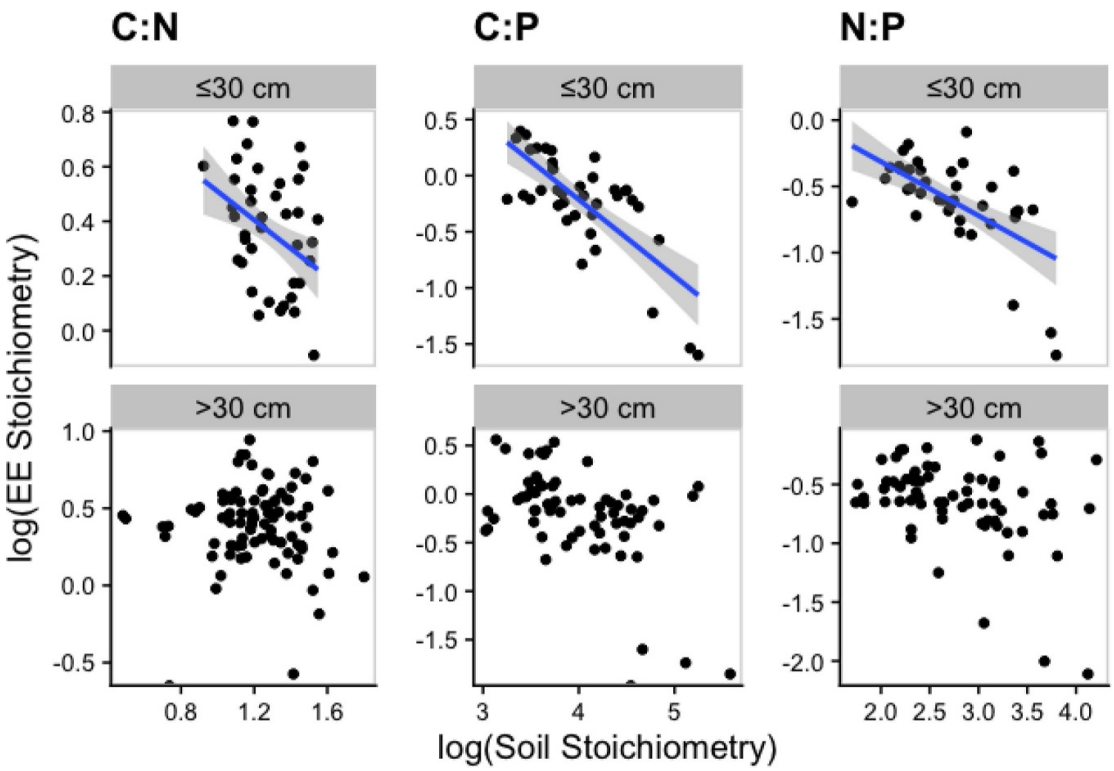

Figure A6. Correlations between soil and extracellular enzyme (EE) stoichiometry (i.e. the ratio of elements by mass and extracellular enzyme activities that target these same elements) of carbon (C), nitrogen (N), and phosphorus (P) in surface ($\leq$30 cm depth) and subsoils (>30 cm depth across all sites). Blue lines show significant ($\alpha = 0.05$) mixed-effects models of the relationship between soil and EE stoichiometry (site was used as a random effect; lines were not drawn where correlations were not significant). Gray ribbons show the standard error of the model. Data points represent individual soil samples (depths within each pit). Note the scales of both axes differ among plots.

ORCID iDs

Nicholas C Dove https://orcid.org/0000-0003-1152-956X
Jared L DeForest https://orcid.org/0000-0002-8390-9126
Rachel E Gallery https://orcid.org/0000-0002-9159-8778
Kathleen A Lohse https://orcid.org/0000-0003-1779-6773

References

Abramoff R Z, Davidson E A and Finzi A C 2017 A parsimonious modular approach to building a mechanistic belowground carbon and nitrogen model *J. Geophys. Res. Biogeosci.* **122** 2017JG003796

Allison S D, Gartner T B, Holland K, Weintraub M and Sinsabaugh R L 2007 Soil enzymes: linking proteomics and ecological processes *Manual of Environmental Microbiology* Third Edition pp 704–11 (Washington, D.C.: ASM Press)

Barton K 2020 MuMIn: Multi-Model Inference https://CRAN.R-project.org/package\protect$\relax=$MuMIn

Bates D, Maechler M, Bolker B and Walker S 2015 Fitting linear mixed-effects models using lme4 *J. Stat. Softw.* **67** 1–48

Batjes N H 1996 Total carbon and nitrogen in the soils of the world *Eur. J. Soil Sci.* **47** 151–63

Bell C W, Fricks B E, Rocca J D, Steinweg J M, Mcmahon S K and Wallenstein M D 2013 High-throughput fluorometric measurement of potential soil extracellular enzyme activities *J. Vis. Exp.* **81** e50961

Billings S A and Ballantyne F 2013 How interactions between microbial resource demands, soil organic matter stoichiometry, and substrate reactivity determine the direction and magnitude of soil respiratory responses to warming *Glob. Chang. Biol.* **19** 90–102

Birge H E, Conant R T, Follett R F, Haddix M L, Morris S J, Snapp S S, Wallenstein M D and Paul E A 2015 Soil respiration is not limited by reductions in microbial biomass during long-term soil incubations *Soil Biol. Biochem.* **81** 304–10

Blume E, Bischoff M, Reichert J M, Moorman T, Konopka A and Turco R F 2002 Surface and subsurface microbial biomass, community structure and metabolic activity as a function of soil depth and season *Appl. Soil Ecol.* **20** 171–81

Boerner R E J, Brinkman J A and Smith A 2005 Seasonal variations in enzyme activity and organic carbon in soil of a burned and unburned hardwood forest *Soil Biol. Biochem.* **37** 1419–26

Brewer T E *et al* 2019 Ecological and genomic attributes of novel bacterial taxa that thrive in subsurface soil horizons *mBio* **10** e01318-19

Brubaker S C, Jones A J, Lewis D T and Frank K 1993 Soil properties associated with landscape position *Soil Sci. Soc. Am. J.* **57** 235–9

Burns R G, Deforest J L, Marxsen J, Sinsabaugh R L, Stromberger M E, Wallenstein M D, Weintraub M N and Zoppini A 2013 Soil enzymes in a changing environment: current knowledge and future directions *Soil Biol. Biochem.* **58** 216–34

Chen H, Li D, Zhao J, Xiao K and Wang K 2018 Effects of nitrogen addition on activities of soil nitrogen acquisition enzymes A meta-analysis *Agric. Ecosyst. Environ.* **252** 126–31

Deforest J L 2009 The influence of time, storage temperature, and substrate age on potential soil enzyme activity in acidic forest soils using MUB-linked substrates and l-DOPA *Soil Biol. Biochem.* **41** 1180–6

Deforest J L, Smemo K A, Burke D J, Elliott H L and Becker J C 2012 Soil microbial responses to elevated phosphorus and pH in acidic temperate deciduous forests *Biogeochemistry* **109** 189–202

Deforest J L, Zak D R, Pregitzer K S and Burton A J 2004 Atmospheric nitrate deposition and the microbial degradation of cellobiose and vanillin in a northern hardwood forest *Soil Biol. Biochem.* **36** 965–71

Dick R P *et al* 2018 Cross-laboratory comparison of fluorimetric microplate and colorimetric bench-scale soil enzyme assays *Soil Biol. Biochem.* **121** 240–8

Dominy C and Haynes R 2002 Influence of agricultural land management on organic matter content, microbial activity and aggregate stability in the profiles of two Oxisols *Biol. Fertil. Soils* **36** 298–305

Dove N C, Stark J M, Newman G S and Hart S C 2019 Carbon control on terrestrial ecosystem function across contrasting site productivities: the carbon connection revisited *Ecology* **100** e02695

Eilers K G, Debenport S, Anderson S and Fierer N 2012 Digging deeper to find unique microbial communities: the strong effect of depth on the structure of bacterial and archaeal communities in soil *Soil Biol. Biochem.* **50** 58–65

Fang C and Moncrieff J B 2005 The variation of soil microbial respiration with depth in relation to soil carbon composition *Plant Soil* **268** 243–53

Gee G W and Bauder J W 2018 Particle-size analysis *Methods of Soil Analysis* (New York: Wiley) pp 383–411

Guckert J B, Antworth C P, Nichols P D and White D C 1985 Phospholipid, ester-linked fatty acid profiles as reproducible assays for changes in prokaryotic community structure of estuarine sediments *FEMS Microbiol. Ecol.* **1** 147–58

Hicks Pries C E, Castanha C, Porras R C and Torn M S 2017 The whole-soil carbon flux in response to warming *Science* **355** 1420–3

Jing X *et al* 2017 Nitrogen deposition has minor effect on soil extracellular enzyme activities in six Chinese forests *Sci. Total Environ.* **607–608** 806–15

Jobbágy E G and Jackson R B 2000 The vertical distribution of soil organic carbon and its relation to climate and vegetation *Ecol. Appl.* **10** 423–36

Jones D L, Magthab E A, Gleeson D B, Hill P W, Sánchez-Rodríguez A R, Roberts P, Ge T and Murphy D V 2018 Microbial competition for nitrogen and carbon is as intense in the subsoil as in the topsoil *Soil Biol. Biochem.* **117** 72–82

Kivlin S N and Treseder K K 2014 Soil extracellular enzyme activities correspond with abiotic factors more than fungal community composition *Biogeochemistry* **117** 23–37

Kramer S, Marhan S, Haslwimmer H, Ruess L and Kandeler E 2013 Temporal variation in surface and subsoil abundance and function of the soil microbial community in an arable soil *Soil Biol. Biochem.* **61** 76–85

Lavahun M F E, Joergensen R G and Meyer B 1996 Activity and biomass of soil microorganisms at different depths *Biol. Fertil. Soils* **23** 38–42

Loeppmann S, Blagodatskaya E, Pausch J and Kuzyakov Y 2016 Enzyme properties down the soil profile - A matter of substrate quality in rhizosphere and detritusphere *Soil Biol. Biochem.* **103** 274–83

Ma X, Zarebanadkouki M, Kuzyakov Y, Blagodatskaya E, Pausch J and Razavi B S 2018 Spatial patterns of enzyme activities in the rhizosphere: effects of root hairs and root radius *Soil Biol. Biochem.* **118** 69–78

Manzoni S, Moyano F, Kätterer T and Schimel J 2016 Modeling coupled enzymatic and solute transport controls on decomposition in drying soils *Soil Biol. Biochem.* **95** 275–87

Mclaren A D and Estermann E F 1957 Influence of pH on the activity of chymotrypsin at a solid-liquid interface *Arch. Biochem. Biophys.* **68** 157–60

Mead J A R, Smith J N and Williams R T 1955 Studies in detoxication. 67. The biosynthesis of the glucuronides of umbelliferone and 4-methylumbelliferone and their use in fluorimetric determination of β-glucuronidase *Biochem. J.* **61** 569–74

Min K, Lehmeier C A, Ballantyne F, Tatarko A and Billings S A 2014 Differential effects of pH on temperature sensitivity of

organic carbon and nitrogen decay *Soil Biol. Biochem.* **76** 193–200
Nakagawa S and Schielzeth H 2013 A general and simple method for obtaining R2 from generalized linear mixed-effects models *Methods Ecol. Evol.* **4** 133–42
Nannipieri P, Trasar-Cepeda C and Dick R P 2018 Soil enzyme activity: a brief history and biochemistry as a basis for appropriate interpretations and meta-analysis *Biol. Fertil. Soils* **54** 11–19
Niemi R M and Vepsäläinen M 2005 Stability of the fluorogenic enzyme substrates and pH optima of enzyme activities in different Finnish soils *J. Microbiol. Methods* **60** 195–205
Olander L P and Vitousek P M 2000 Regulation of soil phosphatase and chitinase activity by N and P availability *Biogeochemistry* **49** 175–90
Olsen S R, Cole C V, Watanabe F S and Dean L A 1954 *Estimation of Available Phosphorus in Soils by Extraction with Sodium Bicarbonate (USDA Circular No. 939)* (Washington, D.C.: U.S. Government Printing Office)
Parham J A and Deng S P 2000 Detection, quantification and characterization of β-glucosaminidase activity in soil *Soil Biol. Biochem.* **32** 1183–90
Paul E A, Follett R F, Leavitt S W, Halvorson A, Peterson G A and Lyon D J 1997 Radiocarbon dating for determination of soil organic matter pool sizes and dynamics *Soil Sci. Soc. Am. J.* **61** 1058–67
R Development Core Team 2008 *R: A Language and Environment for Statistical Computing* (Vienna, Austria: R Foundation for Statistical Computing)
Ramírez-Martínez J R and Mclaren A D 1966 Some factors influencing the determination of phosphatase activity in native soils and in soils sterilized by irradiation *Enzymologia* **31** 23–38
Rasmussen C *et al* 2018 Beyond clay: towards an improved set of variables for predicting soil organic matter content *Biogeochemistry* **137** 297–306
Robertson G P *et al* 1999 *Standard Soil Methods for Long-term Ecological Research* (Oxford: Oxford University Press)
Romaní A M, Fischer H, Mille-Lindblom C and Tranvik L J 2006 Interactions of bacteria and fungi on decomposing litter: differential extracellular enzyme activities *Ecology* **87** 2559–69
Rumpel C and Kögel-Knabner I 2010 Deep soil organic matter—a key but poorly understood component of terrestrial C cycle *Plant Soil* **338** 143–58
Rumpel C, Kögel-Knabner I and Bruhn F 2002 Vertical distribution, age, and chemical composition of organic carbon in two forest soils of different pedogenesis *Org. Geochem.* **33** 1131–42
Salomé C, Nunan N, Pouteau V, Lerch T Z and Chenu C 2010 Carbon dynamics in topsoil and in subsoil may be controlled by different regulatory mechanisms *Glob. Chang. Biol.* **16** 416–26
Sarkar J M, Leonowicz A and Bollag J-M 1989 Immobilization of enzymes on clays and soils *Soil Biol. Biochem.* **21** 223–30
Schimel J P and Weintraub M N 2003 The implications of exoenzyme activity on microbial carbon and nitrogen limitation in soil: a theoretical model *Soil Biol. Biochem.* **35** 549–63
Schimel J P, Wetterstedt J Å M, Holden P A and Trumbore S E 2011 Drying/rewetting cycles mobilize old C from deep soils from a California annual grassland *Soil Biol. Biochem.* **43** 1101–3
Schimel J, Becerra C A and Blankinship J 2017 Estimating decay dynamics for enzyme activities in soils from different ecosystems *Soil Biol. Biochem.* **114** 5–11
Schnecker J *et al* 2015 Microbial community composition shapes enzyme patterns in topsoil and subsoil horizons along a latitudinal transect in Western Siberia *Soil Biol. Biochem.* **83** 106–15
Selmants P C and Hart S C 2010 Phosphorus and soil development: Does the Walker and Syers model apply to semiarid ecosystems? *Ecology* **91** 474–484
Sinsabaugh R L *et al* 2008 Stoichiometry of soil enzyme activity at global scale *Ecol. Lett.* **11** 1252–64
Sinsabaugh R L, Hill B H and Follstad Shah J J 2009 Ecoenzymatic stoichiometry of microbial organic nutrient acquisition in soil and sediment *Nature* **462** 795–8
Sinsabaugh R L, Manzoni S, Moorhead D L and Richter A 2013 Carbon use efficiency of microbial communities: stoichiometry, methodology and modelling *Ecol. Lett.* **16** 930–9
Sinsabaugh R L and Shah J J F 2011 Ecoenzymatic stoichiometry of recalcitrant organic matter decomposition: the growth rate hypothesis in reverse *Biogeochemistry* **102** 31–43
Sinsabaugh R L and Shah J J F 2012 Ecoenzymatic stoichiometry and ecological theory *Annu. Rev. Ecol. Evol. Syst.* **43** 313–43
Stone M M, Deforest J L and Plante A F 2014 Changes in extracellular enzyme activity and microbial community structure with soil depth at the Luquillo Critical Zone Observatory *Soil Biol. Biochem.* **75** 237–47
Sulman B N *et al* 2018 Multiple models and experiments underscore large uncertainty in soil carbon dynamics *Biogeochemistry* **141** 109–23
Taş N, Prestat E, Mcfarland J W, Wickland K P, Knight R, Berhe A A, Jorgenson T, Waldrop M P and Jansson J K 2014 Impact of fire on active layer and permafrost microbial communities and metagenomes in an upland Alaskan boreal forest *Isme J.* **8** 1904–19
Taylor J P, Wilson B, Mills M S and Burns R G 2002 Comparison of microbial numbers and enzymatic activities in surface soils and subsoils using various techniques *Soil Biol. Biochem.* **34** 387–401
Trumbore S E, Chadwick O A and Amundson R 1996 Rapid exchange between soil carbon and atmospheric carbon dioxide driven by temperature change *Science* **272** 393–6
Turner B L 2010 Variation in pH optima of hydrolytic enzyme activities in tropical rain forest soils *Appl. Environ. Microbiol.* **76** 6485–93
Turner S *et al* 2014 Mineralogical impact on long-term patterns of soil nitrogen and phosphorus enzyme activities *Soil Biol. Biochem.* **68** 31–43
Waring B G, Weintraub S R and Sinsabaugh R L 2014 Ecoenzymatic stoichiometry of microbial nutrient acquisition in tropical soils *Biogeochemistry* **117** 101–13
Weintraub M N and Schimel J P 2003 Interactions between carbon and nitrogen mineralization and soil organic matter chemistry in arctic tundra soils *Ecosystems* **6** 0129–43
White D C, Davis W M, Nickels J S, King J D and Bobbie R J 1979 Determination of the sedimentary microbial biomass by extractible lipid phosphate *Oecologia* **40** 51–62
Xiao W, Chen X, Jing X and Zhu B 2018 A meta-analysis of soil extracellular enzyme activities in response to global change *Soil Biol. Biochem.* **123** 21–32
Yao Y, Shao M, Fu X, Wang X and Wei X 2019 Effects of shrubs on soil nutrients and enzymatic activities over a 0–100 cm soil profile in the desert-loess transition zone *CATENA* **174** 362–70
Yost J L and Hartemink A E 2020 How deep is the soil studied – an analysis of four soil science journals *Plant Soil* **452** 5-18
Zelles L 1999 Fatty acid patterns of phospholipids and lipopolysaccharides in the characterisation of microbial communities in soil: a review *Biol. Fertil. Soils* **29** 111–29