

1 **Soil Extracellular Enzyme Activities, Soil Carbon and Nitrogen Storage under Nitrogen**  
2 **Fertilization: A Meta-analysis**

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19 *Abstract.* Nitrogen (N) fertilization affects the rate of soil organic carbon (SOC)  
20 decomposition by regulating extracellular enzyme activities (EEA). Extracellular enzymes,  
21 excreted by soil microbes, have not been represented in global biogeochemical models, it is  
22 thus imperative to elucidate the possible relationships between EEA and SOC, soil N (TN) or  
23 soil microbial biomass carbon (MBC) under N fertilization. Based on 59 published studies,  
24 we synthesized  $\alpha$ -1,4-Gulcosidase (AG),  $\beta$ -1,4-Glucosidase (BG),  $\beta$ -D-Cellobiosidase (CBH),  
25  $\beta$ -1,4-Xylosidase (BX),  $\beta$ -1,4-N-Acetyl-glucosaminidase (NAG), Leucineamino peptidase  
26 (LAP), Urease (UREA), acid phosphatase (AP), Phenol Oxidase (PHO) and Peroxidase  
27 (PEO). The *C-acq*, *N-acq* and *OX* were calculated as the sum of AG, BG, CBH and BX,  
28 NAG and LAP, and PHO and PEO, respectively. The relationships were explored between  
29 response ratios (RR) of EEA and SOC, TN or MBC when they were reported simultaneously.  
30 Results showed N fertilization significantly increased CBH, *C-acq*, BG, BX, AP and UREA  
31 activities by 5.9, 9.0, 11.0, 12.0, 12.0 and 19.0%, but decreased PEO, *OX* and PHO by 6.4,  
32 9.2 and 12.0%, respectively. N fertilization enhanced SOC and TN by 7.7% and 16.0%,  
33 respectively, but inhibited MBC by 9.0%. Significant positive correlations were found only  
34 between the RR of *C-acq* and MBC suggesting changes in combined hydrolases activities  
35 might act as a proxy for MBC under N fertilization. In contrast with other variables, the RR  
36 of AP, MBC and TN showed monotonic trends under different edaphic, environmental and  
37 physiological conditions. Our results provide the first set of evidence on how hydrolase and  
38 oxidase activities respond to N fertilization over various ecosystems. To improve long-term  
39 model projections, this study highlights the need for further investigations specifically on  
40 how slow cycling soil C pools and oxidases respond to global change scenarios.

41 **Key words:** Nitrogen fertilization; Extracellular enzyme activities (EEA); Soil organic  
42 carbon (SOC); Microbial biomass carbon (MBC); Meta-analysis

## 43 **1. Introduction**

44 Nitrogen (N) fertilization is the major contributor to the global reactive nitrogen  
45 inputs, which is estimated to increase from 86 Tg N in 1995 to 135 Tg N in 2050 (Gallo et al.  
46 2004). This enhanced N availability can alter decomposition and formation of soil organic  
47 matter (SOM) due to essential coupling of carbon (C) and N cycling in terrestrial ecosystems  
48 (Vitousek et al. 1997, Thornton et al. 2007, Galloway et al. 2008, Schlesinger 2009). Because  
49 soils contain the largest reservoir of terrestrial organic C in the biosphere, i.e. 2344 Pg C in  
50 the top 3 meter soil (Jobbágy and Jackson 2000), elevated N bioavailability could alter soil C  
51 turnover and exert strong feedbacks on global climate change (Federle et al. 1986, Davidson  
52 and Janssens 2006, Friedlingstein et al. 2006, Billings and Ziegler 2008, Schimel 2013, Li et  
53 al. 2014). As extracellular enzymes are important agents of soil C decomposition (Sinsabaugh  
54 1994, Sinsabaugh et al. 2008), it highlights the significance of studying N fertilization effects  
55 on extracellular enzyme activities (EEA). In spite of increasing number of field and  
56 laboratory studies on this topic, no syntheses have yet explored the N fertilization effect on  
57 EEA in fertilization to their relationships with soil C, N and nutrient changes.

58 A wide range of EEA have been measured associated with C and N turnover (Burns  
59 1982, Dick 1994, Wallenstein and Burns 2011). In general, soil extracellular enzymes include  
60 hydrolases and oxidases which decompose different substrates with varying complexity  
61 (Sinsabaugh 2010, Sinsabaugh and Shah 2012). Briefly, cellulase is a group of hydrolytic  
62 enzymes that soil microbes produce to decompose polysaccharides and they include  
63  $\alpha$ -1,4-Galactosidase (AG),  $\beta$ -1,4-Glucosidase (BG),  $\beta$ -D-Cellobiosidase (CBH) and  
64  $\beta$ -1,4-Xylosidase (BX) (Deng and Tabatabai 1994). The enzymes associated with microbial N  
65 acquisitions include  $\beta$ -1,4-N-Acetyl-glucosaminidase (NAG), Leucine amino peptidase (LAP)  
66 and urease (UREA), which target chitin, protein and urea, respectively (Tabatabai and

67 Bremner 1972). The enzymes associated with P acquisition cleave  $\text{PO}_4^{3-}$  from P-containing  
68 organic compounds and they include acidic phosphatase (AP) and alkaline phosphatase  
69 (Tabatabai and Bremner 1972, Eivazi and Tabatabai 1977, Hui et al. 2013). Oxidative  
70 enzymes productions incur high energy costs and they are produced by microbes to  
71 specifically decompose slow cycling substrates (i.e. lignin). Phenol oxidase (PHO) and  
72 peroxidase (PEO) are two most frequently assayed oxidases (Sinsabaugh 2010, Wang et al.  
73 2012).

74 The responses of EEA under N fertilization have been studied for decades and  
75 generally showed high variations in both direction and magnitude across studies (Fog 1988,  
76 Sinsabaugh et al. 1993, Sinsabaugh and Findlay 1995, Ajwa et al. 1999, Carreiro et al. 2000,  
77 Lucas et al. 2011, Ramirez et al. 2012). The effects of N fertilization on BG activities were  
78 found to be positive in temperate forest and grassland soils (Saiya-Cork et al. 2002, Waldrop  
79 et al. 2004a, Sinsabaugh et al. 2005), while the positive effect could be diminished with the  
80 increasing soil age in grassland ecosystems, or remain constant in the oldest grassland soil  
81 (Zeglin et al. 2007). However, BG activities decreased by 24% with N fertilization averaged  
82 from 28 soils across North America (Ramirez et al. 2012). NAG activities can be stimulated  
83 or suppressed with N fertilization among different sites. For example, activities of NAG with  
84 N fertilization was 76% of unfertilized soils collected from Duke FACE experiment after an  
85 18 hour incubation (Billings and Ziegler 2008), whereas NAG activity increased by 14% in a  
86 sugar-maple dominated forest in Michigan (Saiya-Cork et al. 2002). Stimulation of AP  
87 activities under N fertilization has been widely observed across studies (Ajwa et al. 1999,  
88 Olander and Vitousek 2000, Henry et al. 2005, Stursova et al. 2006). Carreiro et al. (2000)  
89 first reported ligninolytic enzyme activities were suppressed under N fertilization and  
90 resulted in a declined decay rate of high-lignin oak litter. Responses of oxidative enzymes

91 activities were also found to vary with litter C:N ratios under N fertilization (Carreiro et al.  
92 2000). Waldrop et al. (2004b) reported that under N fertilization, PHO increased in forest  
93 where litter contains lower C:N ratio by 16% to 36%, whereas decreased by 20% in forest  
94 had higher C:N ratio. Li et al. (2013) reported that PHO increased by 70~170% with adding  
95 litter of high N concentration under warming. Allison et al. (2008) however found no  
96 significant N fertilization effect on PHO at a boreal forest soil in Alaska.

97 N fertilization also affected microbial growth and activities which directly altered  
98 SOC turnover and subsequently lead to changes in C and N pool sizes. N fertilization caused  
99 reductions by 8%~11% in microbial respiration (Treseder 2008, Liu and Greaver 2010) and  
100 by 15%~35% in microbial biomass C (MBC) (Treseder 2008, Liu and Greaver 2010,  
101 Ramirez et al. 2010). This suppressing effect is a net effect of either positive or negative  
102 changes in relative abundance of different fungal and bacterial communities (Ramirez et al.  
103 2012). For example, N fertilization increased the relative abundance of *Actinobacteria* and  
104 *Firmicutes* by 11.8% and 2.0%, respectively, and decreased the relative abundance of  
105 *Acidobacteria* and *Verrucomicrobia* by 13.5% and 5%, respectively (Ramirez et al. 2012). A  
106 number of studies revealed that N fertilization can enhance soil C storage. Hyvonen et al.  
107 (2008) showed that N fertilization increased SOC sequestration in the fertilized plots but not  
108 in control plots. Pregitzer et al. (2008) found long-term N fertilization significantly increased  
109 surface soil (0-10 cm) C content by 26% due to retarding the decomposition rate, and did not  
110 enhance the C input in a boreal forest. However, it was also reported that N fertilization had  
111 no effect or a negative effect on soil C concentration in tundra ecosystems (Neff et al. 2002,  
112 Mack et al. 2004). A recent meta-analysis showed that N fertilization had no effect on C  
113 storage in forests and grasslands, but significantly increased C storage in agricultural  
114 ecosystems by 3.5% (Lu et al. 2011b).

115 N fertilization generally increased N stock in soil and plants (Liu and Greaver 2010,  
116 Lu et al. 2011b, Lu et al. 2013, García-Palacios et al. 2015). Various experimental studies  
117 showed varying magnitudes of soil N pool response to N fertilization. For example, Koyama  
118 et al. (2013) found increase in total N content in the organic horizons in Arctic tundra soils,  
119 while Lagomarsino et al. (2009) found no effect of N fertilizer on total N in the bulk soil of a  
120 *Triticum durum* and *Zeamais* farmland in central Italy. Lu et al. (2011a) reported that N  
121 fertilization increased N content by about 6.0% in both organic and mineral soil horizons.

122 Given the increasing availability of soil EEA measurements in the last decade, it  
123 becomes feasible to use meta-analysis to synthesize various EEA responses to N fertilization  
124 (Gurevitch and Hedges 1999, Hedges et al. 1999, Luo et al. 2006, Lu et al. 2013). In this  
125 study, we collected and synthesized 59 independent studies to elucidate the impact of N  
126 fertilization on EEA associated with soil C, N and P acquisition, SOC, soil N (TN), and  
127 microbial biomass C (MBC) pool sizes. This study also explored the relationships between  
128 EEA and C and N pool sizes. We hypothesize that 1) N fertilization would significantly  
129 increase EEA associated with C and P acquisitions but depress EEA associated with N and  
130 lignin or oxidative C acquisitions. The possible explanation is the linkages between nutrient  
131 availability to soil decay on the basis of microbial allocation of resources to extracellular  
132 enzyme production (Sinsabaugh et al. 1993, Sinsabaugh and Findlay 1995); 2) N fertilization  
133 will increase SOC and TN but decrease MBC; and 3) positive correlations exist between SOC  
134 and *OX* or MBC and *C-acq*. We further explored these patterns across different edaphic,  
135 environmental and physiological conditions. This study is expected to summarize the  
136 important microbial extracellular enzyme changes and the subsequent impact on soil C and N  
137 dynamics given the increasing N inputs in terrestrial ecosystems.

138

## 139 **2. Materials and methods**

### 140 **2.1 Data collection**

141 The search engine of Web of Science was used to locate published journal articles.  
142 We used different combinations of terms to including “soil”, “extracellular enzyme” and  
143 either “nitrogen fertilization”, “nitrogen deposition” or “chronic nitrogen fertilization”. A  
144 total of 400 papers were found and 59 of them were identified to contain at least one of our  
145 targeted variables (i.e. EEA in Table 1). Data were extracted according to the following  
146 criteria: (1) if data were only reported in graphs and figures, the means and standard  
147 deviations (SD) were extracted using GetData Graph Digitizer 2.26  
148 (<http://www.getdata-graph-digitizer.com/index.php>). If replicate numbers (n) and standard  
149 errors (SE) were reported, they were converted to standard deviations (SD) using  $SD = SE$   
150  $\times \sqrt{n}$ ; (2) If one article reports multiple independent manipulative experiments, e.g. two  
151 experiments at two separate locations, each of them was considered as an independent study  
152 and incorporated into our dataset (García-Palacios et al. 2015); (3) For studies with multiple  
153 global change or ecological factors being manipulated (i.e. altered temperature, carbon  
154 dioxide concentration or precipitation regime), we only extracted data from control plots and  
155 N fertilization plots (García-Palacios et al. 2015); (4) If one article contains results from  
156 multiple sampling date and soil depth, we used the measurement of latest sampling time and  
157 the upmost soil layer. The complete dataset and 59 publications were attached in  
158 Supplementary Material.

159 In total, data of ten different extracellular enzymes were collected (Table 1). We  
160 further integrated individual EEA into combined EEA targeting specific nutrient acquisition.  
161 The combined EEA was calculated as the average of multiple individual enzyme activities  
162 measured in each study by assuming that the absolute values from potential assays

163 correspond to meaningful differences in functional rates (Li et al. 2012, Li et al. 2013). The C  
164 acquired enzymes (*C-acq*) denoted the average enzyme activity of AG, BG, BX and CBH; N  
165 acquired enzyme (*N-acq*) denoted the average enzyme activity of NAG and LAP; and  
166 oxidative enzyme (*OX*) denoted the average enzyme activity of PHO and PEO. A ratio of  
167 enzymatic C over N acquisition (*C:N-acq*) was obtained by the *C-acq* divided by *N-acq*. Soil  
168 organic carbon content (SOC), soil nitrogen (TN) and microbial biomass carbon (MBC) were  
169 also collected based on studies reporting EEA simultaneously, which will allow us to explore  
170 relationship between EEA and these C or N pool sizes.

171 For each site, we also collected its edaphic, climatic and experimental information.  
172 The edaphic properties included soil type, soil texture, soil depth and ecosystem type;  
173 climatic properties included mean annual temperature (MAT) and mean annual precipitation  
174 (MAP); experimental properties included experimental type, duration of experiment, quantity  
175 and form of N fertilization. Soil type and soil texture records were extracted from the original  
176 publications, or they were determined based upon soil characteristics and literature searching  
177 based upon USDA soil taxonomy (Soil Survey Staff, 1999). Given the fact that N fertilization  
178 could be carried out in the field or during lab incubation, the experiment type was categorized  
179 into “field” and “lab”, respectively. We further divided continuous variables (i.e. MAT, MAP,  
180 experimental duration and N fertilization quantity) into categorical variables to conduct group  
181 meta-analysis. Different schemes of categorical groups and multiple tests were conducted  
182 given the number of observations in each category and the outputs of each test. The following  
183 categorical groups were established in this study. MAT was divided into “ $\leq 5$  °C”, “5-10 °C”,  
184 “10-20 °C” and “ $>20$  °C” while MAP was divided into “ $\leq 250$  mm”, “250-1000 mm” and  
185 “ $>1000$  mm”. Experiment duration was categorized into “ $\leq 1$  year”, “1-10 years” and “ $>10$   
186 years”. N fertilization quantity as fertilizers was grouped into “ $\leq 50$  kgN/ha/yr”, “50-150



187 kgN/ha/yr” and “> 150 kgN/ha/yr”, while N fertilizer form was grouped into “NO<sub>3</sub><sup>-</sup>”, “NH<sub>4</sub><sup>+</sup>”,  
 188 “NH<sub>4</sub><sup>+</sup>&NO<sub>3</sub><sup>-</sup>”, “urea”, “organic N” and “organic N & inorganic N (ON & IN)”.

## 189 2.2 Meta-data analysis

190 The response ratio (RR) was calculated by the natural log of the ratio between a given  
 191 variable in the treatment group ( $\bar{x}_t$ ) to that in the control group ( $\bar{x}_c$ ):

$$192 \quad RR = \ln\left(\frac{\bar{x}_t}{\bar{x}_c}\right) = \ln(\bar{x}_t) - \ln(\bar{x}_c) \quad (1)$$

193 The variance of effect size ( $v$ ) was calculated as below:

$$194 \quad v = \frac{s_t^2}{n_t \bar{x}_t^2} + \frac{s_c^2}{n_c \bar{x}_c^2} \quad (2)$$

195 where  $s_t$ ,  $s_c$ ,  $n_t$  and  $n_c$  represented standard deviation of treatment group and control groups,  
 196 replicate numbers of treatment and control groups, respectively. In order to derive the overall  
 197 response effect, we used the weighted (or average) response ratio  $RR_{++}$ , defined as (Hedges et  
 198 al. 1999, Luo et al. 2006, Lu et al. 2013):

$$199 \quad RR_{++} = \frac{\sum_{i=1}^m \sum_{j=1}^k w_{ij} RR_{ij}}{\sum_{i=1}^m \sum_{j=1}^k w_{ij}} \quad (3)$$

200 The standard error of  $RR_{++}$  was calculated by:

$$201 \quad s(RR_{++}) = \sqrt{\frac{1}{\sum_{i=1}^m \sum_{j=1}^k w_{ij}}} \quad (4)$$

202 The  $w$  in equation (3) and (4) was defined as weighting factor, the inverse of the  
 203 pooled variance ( $w_{ij} = 1/v$ ),  $m$  was the number of compared groups, and  $k$  was the number of  
 204 comparisons in the corresponding groups.

205 95% confidence interval (95% CI) for the  $RR_{++}$  was derived by the following  
 206 equation:

$$207 \quad 95\% \text{ CI} = RR_{++} \pm 1.96 \times s(RR_{++}) \quad (5)$$

208           When a 95% CI value of the response valuable did not overlap 0, we considered the  
209 effect of nitrogen fertilization on the variable was significantly different between control and  
210 treatment group. A transformation from average response ratio to percentage change was  
211 conducted in order to evaluate the effect directly using the equation below:

$$212 \qquad \text{Percentage change} = [\exp(RR_{++}) - 1] \times 100\% \quad .(6)$$

### 213 **2.3 Data analysis**

214           The meta-analysis method was used to calculate the mean effect size and 95% CI of  
215 overall effect of N fertilization on EEA and C and N dynamic. We also applied meta-analysis  
216 to explore the effect of N fertilization on each variable under different groups. In categorical  
217 group analysis, the heterogeneities within groups ( $Q_W$ ) and between groups ( $Q_B$ ) were  
218 reported and chi-square test was applied to determine whether there was significant  
219 difference in heterogeneity between groups, i.e.  $Q_B$  (Treseder 2008, Bai et al. 2013). To  
220 elucidate publication bias, we plotted the number of study against RR of EEA by removing  
221 one publication from dataset each time and calculating the average RR and 95% CI (Deng et  
222 al. 2015). If the 95% CI without a specific publication is significantly different from the  
223 entire dataset's 95% CI, the observations in that publication were removed and the rest  
224 dataset were reanalyzed.

225           In fertilization, we conducted regression analyses and plotted RR versus number of  
226 observations by randomly selecting a certain number of observations (starting from 20 and  
227 adding 5 each time until all observations) and calculating the RR (Philibert et al. 2012,  
228 Loladze 2014, Deng et al. 2015). Meta-analysis was conducted by MetaWin 2.1  
229 (SinauerAsSOMiates Inc., Sunderland, MA, USA) using random-effect models.  
230 Pearson-moment correlation coefficients were obtained between different RR of enzyme  
231 activities, SOC, MBC and TN by R (R Core Team 2015).

232

### 233 **3. Results**

#### 234 **3.1 N fertilization effects on EEA and soil C and N pools**

235 N fertilization significantly increased CBH, BG, BX, AP and UREA activities by  
236 5.9%, 11.2%, 11.7%, 12.0% and 18.6% ( $P < 0.05$ ), but significantly decreased the activities of  
237 PEO and PHO by 6.4% and 11.8%, respectively (Figure. 1). As for the combined enzymes, N  
238 fertilization significantly increased *C-acq* by 9.0% but decreased *OX* by 9.2%. AG, NAG,  
239 LAP, and *N-acq* were not significantly altered by N fertilization. The ratio of C:N acquisition  
240 enzyme activity increased by 1.2% in response to N fertilization, though statistically  
241 insignificant. Based on studies reporting SOC, TN, MBC with EEA simultaneously, N  
242 fertilization significantly increased SOC and TN contents by 7.7% and 16%, respectively,  
243 while significantly decreased MBC content by 9.0% (Figure. 1). The publication bias and  
244 independence tests of our dataset satisfied the requirements for our meta-analysis  
245 (Supplementary Figs. S1-S2).

#### 246 **3.2 Correlations between response ratios of EEA, soil C and N pools**

247 Significant positive correlations were found between any two of AG, BG, BX and  
248 CBH, and between each individual C acquired enzymes with NAG or AP (Table 2).  
249 Significant positive correlations were also observed between PHO and NAG, or between  
250 PEO and BG (Table 2). Significant correlations were also present between any two of the  
251 combined enzyme groups (*C-acq*, *N-acq* and *OX*). Significant positive correlations were  
252 found for the *C:N-acq* with *C-acq*, BG or CBH, but significant negative correlations were  
253 present for the *C:N-acq* with *N-acq*, NAG or LAP.

254 Among EEA, SOC, TN and MBC, significant correlations were found between  
255 MBC and *C-acq* or MBC and BG (Table 2). Further regression analysis revealed a linear

256 relationship between the response ratio (RR) of soil carbon-acquiring enzymes (*C-acq*) and  
257 RR of MBC ( $y=0.29*x-0.12$   $R^2=0.20$ ,  $P<0.05$ ). We further explore this relationship under  
258 different conditions (Figure 2). Significant difference of the relationships (i.e. slopes in  
259 Figure. 2) was found only between forest and farmland ( $P<0.05$ ).

### 260 **3.3 N fertilization effects on *C-acq*, *N-acq*, *OX* and *C:N\_acq* under different conditions**

261 The most pronounced results are presented regarding N fertilization on EEA and C  
262 and N pool sizes given specific conditions.

263 Percentage changes of *C-acq* were significantly negative for Histosols and Aridsols,  
264 which contrasted with the significantly positive percentage changes for other soil types  
265 (Figure 3). There are either insignificant or significantly positive percentage changes in all  
266 other edaphic, climatic and physiological conditions (Figure 3).

267 Percentage changes of *N-acq* were significantly negative for Histosols, Gelisols and  
268 Andisols, but significantly positive for Alfisol and Aridsols (Figure 4). Percentage changes  
269 were significantly negative when N load is higher than 150 kg/ha/yr or when inorganic and  
270 organic N fertilizers were simultaneously applied, or when MAT is between 10° C and 20° C  
271 (Figure 4). Percentage change is significantly positive for loamy soils. Percentage changes of  
272 *OX* were either significantly negative or insignificant for any specific conditions (Figure 5).

273 Percentage changes of *C:N\_acq* were significantly negative for Aridsoils, for  
274 grassland or farmland, for  $\text{NH}_4^+$  or urea treated fertilization experiment, but significantly  
275 positive for Gelisols, for organic N fertilizer input, for experiments longer than 10 years, for  
276 forest ecosystems, for sites with MAP less than 250mm or for N fertilizer input less than 50  
277 or more than 150 kg/ha/yr (Figure 6).

### 278 **3.4 N fertilization effects on soil C and N pools under different conditions**

279 Percentage changes of SOC were significantly negative only for Oxisols. There are  
280 either insignificant or significantly positive percentage changes in all other edaphic, climatic  
281 and physiological conditions (Figure 7). Percentage changes of MBC were either  
282 significantly negative or insignificant for specific conditions (Figure 8). Percentage changes  
283 of TN were either significantly positive or insignificant for specific conditions (Figure 9).

284

## 285 **4. Discussion**

### 286 **4.1 N fertilization stimulated hydrolytic EEA but depressed oxidative EEA**

287 The growing understanding of the role of extracellular enzymes in soil C dynamics  
288 and its feedback to climate change has drawn the attention of scientists especially for  
289 improving mechanistic models and prediction (Tang and Riley 2015). Our study represented  
290 a comprehensive synthesis and strived to reveal the effect of N fertilization on soil EEA, and  
291 possible linkages between EEA and soil C and N dynamics.

292 In our first hypothesis, we speculate N fertilization decreased EEA associated with  
293 microbial N and oxidative C acquisitions, and increased EEA associated with hydrolytic C  
294 and P acquisitions. Results concluded from this meta-analysis partially supported the first  
295 hypothesis. Three out of four EEA associated with hydrolytic C acquisition increased  
296 significantly, including BG, BX and CBH (Figure 1). Meanwhile, AP increased significantly  
297 by 12%, although lower than 46% revealed in a former study (Marklein and Houlton 2012),  
298 possibly due to a larger number of observations in this study including all former ones (i.e.  
299 155 vs. 80). As a result of N fertilization, sufficient N supply sustains soil microbes to  
300 produce fewer extracellular enzymes associated with hydrolytic C-acquisition to satisfy their  
301 metabolism demand and stoichiometry, resulting in overall lower energy acquisition costs.  
302 These stimulated EEA responses suggest that soil microbial communities are likely

303 constrained by C or P under N fertilization.

304 We did not observe significant changes in LAP, NAG or their sum, thus our first  
305 hypothesis was not supported in this regard. Zeglin et al. (2007) found responses of LAP and  
306 NAG to N fertilization were related with LAP to NAG ratio in grassland ecosystems. That is,  
307 when the LAP to NAG ratio was high, N fertilization reduced LAP activity and increased  
308 NAG; where the ratio was low, N fertilization increased LAP and depressed NAG. This could  
309 lead to no significant change in the sum of LAP and NAG, which is supportive to our  
310 synthesis result on *N-acq*. Sinsabaugh and Follstad Shah (2012) showed that at ecosystem  
311 scale, microbial N-acquiring EEAs didn't have a simple relationship with N availability. As  
312 LAP and NAG attack different classes of substrates, this was not unexpected.

313 It is worthy to note, *N-acq* showed significantly negative percentage changes when N  
314 load was high ( $>150 \text{ kg ha}^{-1} \text{ yr}^{-1}$ ) or both inorganic and organic N fertilizers were  
315 simultaneously applied. This demonstrates a large quantity of soil available N could have  
316 substantially relieved N limitations for microbes thus causing more conservative production  
317 of N-associated enzymes (Sinsabaugh et al. 2008). Another interesting finding is that NAG  
318 activity was significantly depressed in Histosols, Gelisols and Andisols, but significantly  
319 enhanced in Alfisols and Aridsols. This demonstrates a modulating effect of edaphic  
320 properties in regulating N retention and supply. In particular, Alfisols and Aridsoils represent  
321 low fertility soil where the tight N demand may stimulate N acquisition in their respective  
322 ecosystems (Sinsabaugh et al. 2008).

323 It should be noted that the ratio of C acquisition to N acquisition enzyme activities  
324 (C:N<sub>acq</sub>) was not significantly affected by N fertilization, which is consistent with the well  
325 constrained stoichiometry of EEA across large scale studies (Sinsabaugh et al. 2008). It  
326 reflected the intrinsic microbial acquisitions for C and nutrients even if the environment is

327 below the N saturation conditions.

328         However, PHO, PEO and combined *OX* all significantly decreased under N  
329 fertilization (Figure 1). Other studies have also observed inhibited PHO and PEO activities,  
330 especially in ecosystems with high lignin litter content (Waldrop et al. 2004b, Sinsabaugh et  
331 al. 2009, Hobbie et al. 2012). The possible explanation is that added N drives microbial  
332 community toward hydrolytic substrate decomposition resulted from increased aboveground  
333 and belowground litter input. There are other possibilities as well, such as added N  
334 suppressing fungi that produce these enzymes (Matocha et al. 2004, Allison et al. 2008) or  
335 less lignin decomposition due to plentiful N content in lignin (Taylor et al. 1989, Hobbie et al.  
336 2012, Talbot and Treseder 2012).

#### 337 **4.2 N fertilization enhanced SOC but depressed MBC pool sizes**

338         Consistent with our second hypothesis, SOC content significantly increased by 7.7%  
339 due to N fertilization, which is a little larger than 3.2% in Lu et al. (2011b). In fact, increasing  
340 evidence supported that N fertilization enhanced SOC sequestration in terrestrial ecosystems  
341 (DeForest et al. 2004, Hyvonen et al. 2008, Pregitzer et al. 2008). One mechanism for  
342 explaining the phenomena is that the lignin-rich substrates, as the major portion of total  
343 inputs, are preserved from decomposition due to depressed oxidative activities with N  
344 fertilizations (Waldrop and Firestone 2004). Our result indeed showed 11.8% and 6.4%  
345 decreases in phenol oxidase and peroxidase activities due to N fertilization, respectively.  
346 Waldrop and Firestone (2004) also explored relationships between response ratios of SOC  
347 pool and phenol oxidase or peroxidase, however, no significant correlations were detected.  
348 This creates a need to synthesize the slow cycling SOC pool specifically in order to explore  
349 its relationship with oxidative enzyme activities. Although this preserving mechanism is  
350 currently derived from a single site, it is likely via data syntheses to establish a sound

351 relationship between the oxidative C pool sizes and oxidase activities across multiple sites.

352 In support of our hypothesis, N fertilization significantly decreased MBC by 9.0%.  
353 In Treseder (2008), MBC declined by 15% based on 29 studies. The widely observed  
354 decrease in MBC under N fertilization has been attributed to microbial composition changes.  
355 Ramirez et al. (2012) found the relative abundance of *Acidobacteria* and *Verrucomicrobia*  
356 were decreased by 13.5% and 5%, respectively under N fertilization. Because *Acidobacteria*  
357 is abundant in the soil (Janssen 2006, Jones et al. 2009), changes of its size and relative  
358 abundance may contribute substantially to the overall microbial biomass change under N  
359 fertilization. However, it remains unclear why microbial biomass and soil respiration  
360 decreased under N fertilization (Treseder 2008, Ramirez et al. 2010), while soil  
361 microbially-mediated activities were still enhanced. In particular, the roles of the key  
362 bacterial and fungal groups still remain elusive in terrestrial ecosystems, thus it is imperative  
363 to further study microbial group responses to N fertilization and elucidate their contributions  
364 to the biomass change.

365

#### 366 **4.3 Correlation between response ratios of *C-acq* and MBC**

367 If a time-integrated variable can somewhat be linked with SOC pool size, it will  
368 make soil modeling and long-term prediction much easier. Some current soil microbial  
369 models all included EEA as an independent C pool and catalyst for SOC decompositions  
370 (Allison et al. 2010, Wang et al. 2013, Li et al. 2014). A type of linear correlation between  
371 EEA and SOC may be needed because it can substantially simplify the current soil models. A  
372 single or a combined EEA is such a candidate variable. MBC and EEA were simultaneously  
373 collected at each site, we thus have a unique opportunity to explore their relationship.  
374 Furthermore, our analysis can reveal the differences in this relationship under different



375 conditions, such as by ecosystem or soil type. Our synthetic results showed a significantly  
376 positive linear relationship between response ratios of *C-acq* and MBC, but not between  
377 *C-acq* and SOC. This supported the modeling efforts that hydrolytic enzyme C is linearly  
378 proportional to the microbial biomass C pool (Schimel and Weintraub 2003, Allison et al.  
379 2010, Wang et al. 2013, Li et al. 2014).

380         The positive relationships between response ratios of *C-acq* and MBC varied under  
381 different ecosystems, experimental duration, MAT and N forms (Figure 2). In particular, the  
382 pronounced difference between forests and farmland provided likely useful information to  
383 improve the parameterization of the enzyme C pool when models were applied to different  
384 ecosystems. This difference could be attributed to varied microbial community compositions  
385 and structures. For example, fungi were relatively more abundant in the forest soil and  
386 Gram-positive bacteria were more abundant in cropland soil, thus the fungal:bacterial PLFA  
387 ratio was higher in the forest soil than most of the agricultural soils (Jangid et al. 2008). The  
388 difference in community structure between cropland and pasture soils was not as dramatic as  
389 the difference between agricultural and forest soils (Jangid et al. 2008). Bacterial  
390 communities in forest soils were less diverse than in agricultural soils (Upchurch et al. 2008).  
391 On the other hand, this difference is attributed to the sensitivities of distinct microbial groups  
392 in response to N fertilization in these ecosystems. N fertilizer amendments had a larger effect  
393 on bacterial communities specifically including *Acidobacteria*, *Baacteroidetes* and  
394 *Proteobacteria* than in forests and pastures (Jangid et al. 2008). Because bacteria  
395 communities are a primary group of decomposer on cellulose via production of hydrolases  
396 (Bayer et al. 2006), this substantial inhibitive effect of N fertilization on bacterial groups can  
397 directly lead to depressed production of *C-acq* in agricultural soils.

398

399 **5. Conclusion**

400 Extracellular enzyme activities (EEA) have not been explicitly represented in global  
401 biogeochemical models due to unclear relationship between EEA and soil C and N dynamics.  
402 This study summarized hydrolases and oxidases activities, SOC, TN and MBC pool sizes  
403 under N fertilizations based on 59 published studies. In general, N fertilization stimulated  
404 hydrolases associated with C and P but depressed oxidases, while has no significant effect on  
405 hydrolases associated with N. In particular, a significantly positive relationship was found  
406 between response ratios (RRs) of the combined hydrolases with C acquisition (i.e. *C-acq*) and  
407 MBC suggesting changes in combined hydrolases activities might act as a proxy for MBC  
408 under N fertilization. This study provides the first set of evidence on how hydrolase and  
409 oxidase activities respond to N fertilization and how they correlate to soil C and N pools over  
410 various ecosystems. Due to importance of slow cycling soil C pools for quantifying soil  
411 feedback to climate while the scarcity of such measurements, future studies should  
412 investigate the relationship between slow cycling soil C and oxidases.

413

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420

421

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