Soil carbon accrual and biopore formation across a plant diversity gradient

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Abstract. Plant diversity promotes soil organic carbon (SOC) gains through intricate changes in root-soil interactions and their subsequent influence on soil physical and biological processes. We assessed SOC and pore characteristics of soils under a range of switchgrass-based plant systems 12 years after their establishment. The systems represented a gradient of plant diversity with species richness ranging from 1 to 30 species. We focused on soil biopores as indicators of the legacy of root activity and explored biopore relationships with SOC accumulation. Biopores were measured using X-ray computed micro-tomography.

Plant functional richness explained 29% of bioporosity and 36% of SOC variation, while bioporosity itself explained 36% of the variation in SOC. The most diverse plant system (30 species) had the highest SOC, while long-term bare soil fallow and monoculture switchgrass had the lowest. Of particular note was a two-species mixture of switchgrass (*Panicum virgatum* L.) and ryegrass (*Elymus canadensis*), which exhibited the highest bioporosity and achieved SOC levels comparable to those of the systems with 6 and 10 plant species, and were inferior only to the system with 30 species. We conclude that plant diversity may enhance SOC through biopore-mediated mechanisms and suggest a potential for identifying specific plant combinations that may be particularly efficient for fostering biopore formation and, subsequently, SOC sequestration.

1 Introduction

Plant diversity has been found to positively influence soil organic carbon (SOC) accumulation in various ecosystems, including grasslands (Lange et al., 2015; Sprunger and Robertson, 2018) and row crop agriculture (Liebman et al., 2013; McDaniel et al., 2014). Among the mechanisms through which higher plant diversity promotes SOC storage are i) high biomass and C inputs from roots (Yang and Tilman, 2020), ii) slower root decomposition in high diversity systems due to increased root C:N ratios (Chen et al., 2017), and iii) higher microbial activity enhanced by belowground inputs, where greater quantities of plant-added C are transformed into microbial biomass (Prommer et al., 2020; Lee et al., 2023) and then necromass (Qian et al., 2023; Mou et al., 2024). This microbially-processed C is then protected through physico-chemical associations with soil minerals (Cotrufo et al., 2022).

The quantity and chemical composition of C inputs from plant roots and soil biota play an important role in ensuring SOC gains (Berhongaray et al., 2019; Lehmann et al., 2020). For instance, extensive root growth and earthworm activity can facilitate the root exudates and earthworm secretions, which in turn stimulate microbial growth, C assimilation (Kuzyakov and Blagodatskaya, 2015), and the accumulation of microbial necromass (Banfield et al., 2018). Yet, the specific locations within the soil matrix where such inputs are added and their spatial distribution patterns can be an important driver in formation of SOC and its subsequent protection. In diverse plant communities, belowground competition among plants with contrasting root architectures can lead to greater root proliferation through the soil matrix, thereby increasing the density and spatial distribution of root channels that are in direct contact with the soil matrix (Gersani et al., 2001; Bargaz et al., 2017; Wang et al., 2017). Similarly, diverse plant communities exhibit increased activity of soil mesofauna such as earthworms, whereby earthworms create new biogenic channels that expand the contact surface between soil and organic inputs (Milcu et al., 2008; Kuzyakov and Kooch, 2024). The redistribution of these soil–organic matter interfaces varies considerably with plant diversity and species composition (Marshall et al., 2016; Zahorec et al., 2022). For instance, shifts in root morphology and spatial distribution in response to neighboring plant species (Bolte and Villanueva, 2006; Wang et al., 2014) indicate that the formation of root-derived channels and the localization of C storage depend on community composition. Likewise, findings that earthworm activity differs according to the presence of legumes (Eisenhauer et al., 2009) suggest that both the quantity and spatial pattern of SOC storage depend on plant species identity and diversity.

Analysis of root-soil and mesofauna-soil interactions in diverse perennial plant communities in situ is extremely challenging due to the opaque nature of soil and the difficulty of carrying out long-term (e.g., multiyear) continuous rhizobox or greenhouse studies. Thus, much knowledge is based on speculations from the data on root volumes and architecture generated upon disturbing the system to procure the roots and upon conducting the root measurements after cleaning away the soil (Lange et al., 2015). Likewise, earthworm–soil interactions have often been examined by simple comparisons between earthworm activity and soil carbon, while only a few studies have employed the technically demanding approach of artificially creating earthworm biopores with spatial information (Hoang et al., 2016). In contrast, sampling intact soil from long-term field studies and visualizing root residues, particulate organic matter (POM), and pores via X-ray computed micro-tomography (μCT) can generate helpful information on root-soil and earthworm-soil interactions (Helliwell et al., 2013). This is where identification and quantification of biopores can be particularly advantageous, because it allows capturing the legacy of root and mesofauna proliferation through the soil matrix and estimating the volume of the soil matrix that has received their C inputs in the past.

Biopores are the soil pores originated from biological activity such as plant root growth and the movement of earthworms and other soil fauna (Dexter, 1986; Blackwell et al., 1990). Biopores act as preferential pathways for root growth, organic matter inputs, water, and nutrient flow, thereby creating microenvironments that favor microbial colonization and necromass accumulation (Guhra et al., 2022; Kautz et al., 2015; Wendel et al., 2022). Root-originated biopores, formed either by growth of living roots or by decomposition of old roots, are particularly significant as they are 40 times more abundant, especially in subsoils, compared to earthworm biopores (Banfield et al., 2018). Root biopores are tubular, round-shaped channels with sizes ranging from a few micron to several centimeters (Kautz, 2015). Since root inputs are primarily introduced into the soil through the biopores, they have >2.5 times higher soil C contents compared to bulk soil (Banfield et al., 2017). Rapid microbial

decomposition of plant residues and accumulation of microbial residues observed in root biopores (Banfield et al., 2018) suggest that root biopore characteristics may reflect the physical preferences and biochemical processes involved in the transformation and accumulation of plant-derived C.

Reuse of existing biopores by newly grown roots is a commonly observed process in annual crops such as wheat, fodder radish, and spring barley (White and Kirkegaard, 2010; Wahlström et al., 2021). Switchgrass, a North American prairie grass, currently actively explored as a potential bioenergy feedstock (Larnaudie et al., 2022; Zegada-Lizarazu et al., 2022), is known for its particularly active use of old root channels (i.e., biopore reuse), especially when grown in monoculture (Lucas et al., 2023). Because of their continuous reuse, accompanied by repeated influxes of new C and stimulated microbiota, biopores in perennial plant systems can be viewed as hotspots of C processing and are both a product of historic root-soil interactions and a current arena of such interactions. Taken together, these considerations suggest that the morphology and spatial pattern of root biopores may serve as an informative indicator of root-derived SOC within the soil matrix.

We posit that biopore information derived from X-ray μCT is particularly informative for assessing root impacts and root–soil interactions in perennial plant systems. In species-rich perennial communities, interspecific interactions generate complex root architectures and heterogeneous rooting pathways, which in turn produce spatially variable inputs of root-derived SOC (Zahorec et al., 2021). In this context, increased root-originated biopores (e.g., the volume fraction and connectivity) can indicate diversified root growth paths and intensified root–soil contact in perennial systems. Accordingly, we hypothesize that higher plant diversity promotes the abundance and formation of root biopores and that this enhanced biopore development is associated with greater gains in SOC. Specifically, our objectives are to examine (i) how a plant-diversity gradient shapes soil-pore characteristics, with emphasis on biopores, and (ii) whether the (bio)pore abundance is associated with SOC levels accrued over the preceding 12 years.

2 Materials and Methods

2.1 Experimental site and soil sampling

Soil samples were collected from the Cellulosic Biofuel Diversity Experiment site established in 2008 at Kellogg Biological Station (KBS, 42°23′47″ N, 85°22′26″ W), a part of the KBS Long-Term Ecological Research (LTER) program (Robertson and Hamilton, 2015). The soil is fine-loamy, mixed, mesic, Typic Hapludalf (Kalamazoo loam). The experiment consists of twelve plant systems representing a 12-point gradient of plant diversity (CE1-CE12), six of which were used in this study. Specifically, we sampled a bare soil system, which was kept free of vegetation since 2016 after 8 years of continuous corn (CE1), a monoculture switchgrass (*Panicum virgatum*, L.; var. Southlow) system (CE7), a mixture of two grass species, namely, switchgrass and Canadian rye (*Elymus canadensis*, L.) (CE8), a mixture of six native grasses (CE9), a mixture of six native grasses and four forbs (CE10), and a mixture of six native grasses and 24 forbs (CE12). Plant species of each system are listed in Supplementary Table S1. The experiment is in a randomized complete block design with four replicated 9.1 m x 27.4 m plots for each plant system (https://lter.kbs.msu.edu/research/long-term-experiments/cellulosic-biofuels-experiment/).

114   For soil pore analysis, intact soil cores (5 cm diameter (Ø) and 5 cm height) were taken from the 7-12

115   cm depth interval in July 2019. This depth encompasses the zone of greatest fine-root abundance and turnover,

116   where root-derived C inputs and microbial activity are most pronounced (Halli et al., 2022; Roosendaal et al.,

117   2016). Loose soil adjacent to each core was also procured for measurements of other soil characteristics. Two soil

118   cores were collected from each plot, for a total of 48 soil cores (6 systems x 4 replicate plots x 2 cores per plot).

119   Aboveground biomass was measured each autumn (Oct–Nov) from 2010 to 2019 in all plots except CE1 (bare

120   soil) (Fig. S1a). For the present analysis, we used the 2018 and 2019 biomass datasets (Fig. S1b). Soil sampling

121   for this study occurred in July 2019; thus, the 2019 fall biomass provides the most temporally proximate estimate

122   of aboveground production for the soils analyzed, while the 2018 biomass offers the preceding-year context and

123   helps mitigate interannual variability. The entire aboveground biomass from each plot was harvested with a mini

124   combine, leaving 10-15 cm of stubble, and weighed and subsampled for moisture content determination. Due to

125   destructive and intensive sampling required for belowground biomass quantification, such measurements could

126   not be undertaken. Therefore, all plant biomass estimates in this study are explicitly based on aboveground

127   components only.

128

2.2 Soil characteristics measured using destructively sampled soil

130   Soil moisture at the time of core sampling was determined gravimetrically using a 20 g subsample of

131   loose soil immediately upon collection. The remaining loose soil samples were air-dried for 2 days and sieved to

132   < 2 mm for further analysis.

133   SOC and total soil N were measured by combustion analysis using an elemental CN analyzer (Costech

134   Analytical Technologies Inc., CA, USA). SOC mineralization was measured via 10 d incubation: 10 g of air-dried

135   soil were brought to 20% gravimetric moisture, placed in a beaker that was then placed in a 450 mL Mason jar

136   with ~5 mL of purified water on the bottom for maintaining high humidity within the jar. Mason jars were kept

137   in the dark at 20 °C for 10 days, and CO_2 concentration in the headspace was measured for each jar using Infrared

138   Photoacoustic Spectroscopy (INNOVA Air Tech Instruments, Denmark).

2.3 Soil core scanning and pore structure analysis

140   Soil cores were subjected to X-ray computed micro-tomography (North Star Imaging, X3000, Rogers,

141   USA) to visualize and quantify soil pore structure. X-ray µCT is particularly suitable for biopore investigation

142   (Wendel et al., 2022), enabling the examination of accumulated evidence of past root-soil interactions (Helliwell

143   et al., 2013). The scanning was conducted with a projection energy level of 75 KV and 450 µA, with 2880

144   projections per scan. 3D reconstruction of the images was computed using efX-CT software (North Star Imaging,

145   Rogers, USA) obtaining a final scanning resolution of 18.2 µm. Reconstructed images were processed using Fiji

146   software (Schindelin et al., 2012) and simpleITK package in Python (Beare et al., 2018). A series of image pre-

147   processing steps was conducted using Fiji and its Xlib plugin (Münch and Holzer, 2008). Specifically, images

148   were cropped into 1500 x 1500 pixels with a height of 2240 pixels to remove artifacts near core edges. Then, a

149   2D non-local filter (sigma=0.1) was applied to reduce noise.

150   For pore segmentation, threshold values were obtained from eight segmentation methods, i.e., Otsu,
151 Kitler, Huang, Triangle, ISO, Li, Renyi, and Moments. Outliers that exceeded >1 standard deviation of the mean
152 were removed. This approach enabled us to minimize the side effects of using one specific thresholding method
153 and ensured robustness of the segmentation (Schlüter et al., 2014). Hereafter, we refer to the >18.2 μm Ø pores
154 as visible pores, and their total volume as visible porosity. Pore size distributions of visible pores were determined
155 by the Local Thickness method embedded in Fiji, which is based on maximal inscribed spheres approach (Silin
156 and Patzek, 2006). For biopore identification, the images were subjected to Tubeness filtering in Fiji to detect
157 tubular type pores of different radius. Detailed procedures for biopore segmentation are publicly available
158 (https://github.com/Maik-Lu/Roots_and_Biopores) (Lucas et al., 2022). Total volumes of visible pores and
159 biopores were presented as visible porosity and bioporosity. Surface area of biopores was calculated by applying
160 assumption that the biopore shape is cylindrical in a given radius, and the mean distance of soil matrix to biopores
161 was calculated using the Euclidean Distance Transform (3D) function in Fiji (Lucas et al., 2025).

162

2.4 Plant diversity indicators

164   Two plant diversity indicators were used in this study: i) plant species richness, and ii) plant functional
165 richness (Díaz and Cabido, 2001). Plant species richness was represented by the number of plant species in each
166 treatment, i.e., 0, 1, 2, 6, 10, and 30 for CE1, CE7, CE8, CE9, CE10, and CE12, respectively. For plant functional
167 richness we adopted the ecological concept of plant functional types, used to simplify plant diversity and behavior
168 in ecological models (McMahon et al., 2011). Specifically, we followed the approach used in grassland studies
169 (Mangan et al., 2011; Spiesman et al., 2018; Tilman et al., 2006) by separating species based on different
170 photosynthetic pathways (C3 vs. C4), and leaf shape (broad-leaf vs. grasses) to form three functional groups,
171 namely, C3 grasses, C4 grasses, and forbs. Based on species characteristics (Table S1), plant functional richness
172 of each treatment was equal to 0, 1, 2, 2, 3, and 3 for CE1, CE7, CE8, CE9, CE10, and CE12, respectively.

173

2.5 Statistical analysis

175   The statistical model for SOC, total soil N, C:N ratio, 10-day mineralization, visible porosity, and
176 bioporosity data consisted of plant system as a fixed effect, and experimental blocks and blocks by systems
177 interaction as random effects (Milliken and Johnson, 2009). The latter term, in essence, represents experimental
178 plots and was used as an error term to test the plant system effect. The statistical model for the aboveground
179 biomass measured during two consecutive years further included year and its interaction with the plant system as
180 fixed factors. The statistical model for pore and biopore size distribution data included the pore size class and its
181 interaction with plant system as fixed effects, and soil core nested within the plant system and experimental plot
182 as the random effect. When the ANOVA was significant, all pairwise mean comparisons among plant systems
183 were conducted within each pore size class. Normality was checked by visual inspection of normal probability
184 plots, and when found violated, the data were subjected to either square root or lognormal transformation prior to
185 the analyses. The equal variance assumption was tested by Levene's test, and when found to be violated, the
186 unequal variance model was fitted using the approach suggested by Milliken and Johnson (2009).

187   To explore associations of soil characteristics with pore and biopore data, the porosity and bioporosity

188 from two intact cores of each plot were averaged, followed by linear regression analysis. All statistical analyses

189 were conducted using SAS 9.4 software, using PROC MIXED and PROC REG procedure. Results are reported

190 as statistically significant at p<0.05 and as trends at p<0.1. P-values < 0.1, < 0.05, and < 0.01 are marked with *,

191 **, and ***, respectively.

192

3 Results

193 **3 Results**

194 **3.1 Plant biomass and SOC characteristics of the studied plant systems**

195   Total aboveground biomass (2018-2019) tended to be higher in the most diverse systems (CE10 and

196 CE12) than in grass-only systems (CE8 and CE9), while the monoculture switchgrass (CE7) was intermediate (p

197 < 0.10, Fig. S1b). Total aboveground biomass was weakly correlated with plant species richness (Fig. S2a) and

198 not correlated with plant functional richness (Fig. S2b). Total aboveground biomass was not correlated with SOC

199 contents (Fig. S2c). The plant systems with the highest diversity (CE12) had markedly higher SOC as compared

200 to the rest of the systems (Fig. 1a). However, an increase in plant diversity from a two-species (CE8) to six-species

201 (CE9) and then to a ten-species (CE10) system did not affect SOC (Fig. 1a). Soil C:N ratio was smallest in

202 monoculture switchgrass (CE7), and greatest in high diversity systems (CE10 and CE12) (p< 0.01, Fig. S3). C

203 mineralization was highest in CE12, followed by bare soil (CE1), and CE8 (Fig. 1c). C mineralization was lowest

204 in CE7 and CE10.

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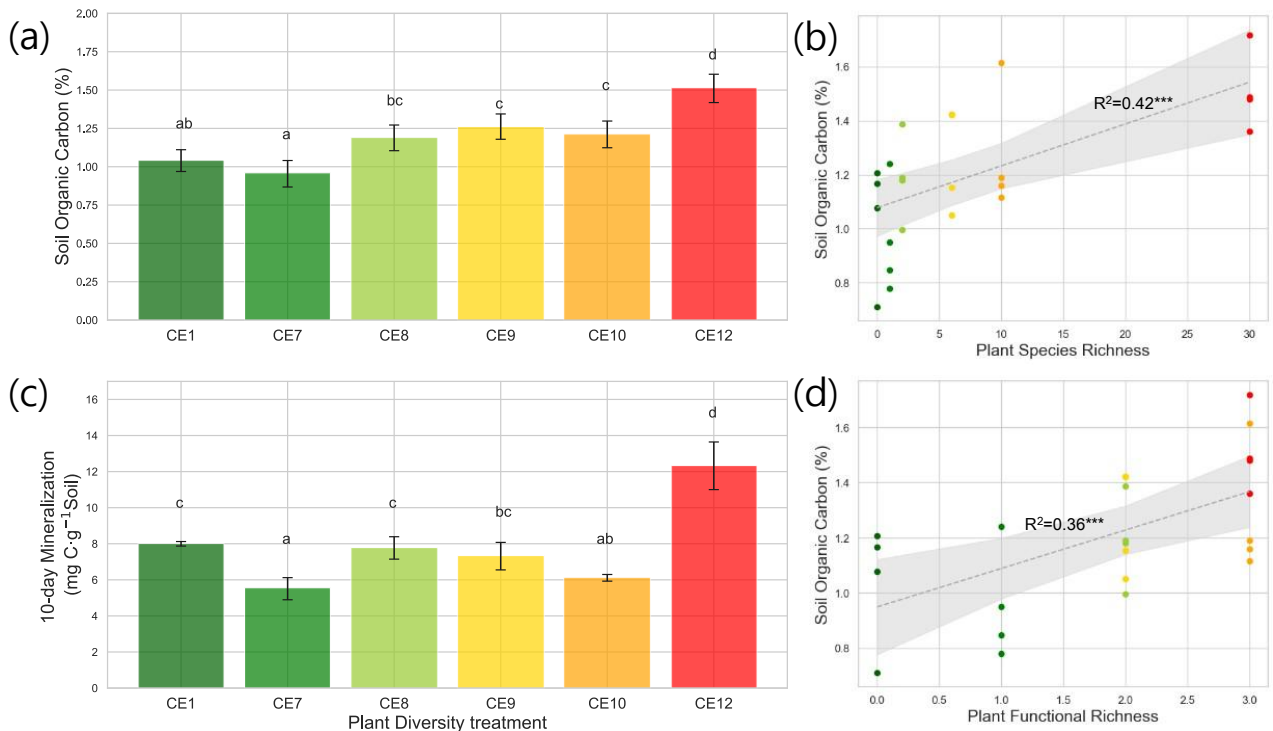
209 **Figure 1: Soil Organic Carbon (SOC) content (a) and 10-day mineralization (c) in the studied plant diversity systems**
210 **(CE1: Bare soil, CE7: Switchgrass, CE8: Switchgrass + Rye, CE9: 6 grasses, CE10: 6 grasses + 4 forbs. CE12: 6 grasses**
211 **+ 10 forbs). Correlations between SOC and Plant Species Richness (b), as well as Plant Functional Richness (d), are**
212 **shown. Error bars in (a) and (C) show standard error of the mean. Letters indicate significant differences among plant**
213 **diversity treatments (p< 0.05). Dotted gray lines in (b) and (d) represent fitted regression models, with light gray shaded**
214 **area denoting 95% confidence interval. R^2 values are provided for each model. Asterisks (***) indicate statistically**
215 **significant regression models at p< 0.01.**

216

217 **3.2 Biopore characteristics**

218   Plant systems affected pore size distributions (Fig. 2a), where CE8, CE10, and CE12 had the lowest
219 volumes of < 200 μm diameter pores and the highest volumes of >400 μm diameter pores, while an opposite trend
220 was observed for CE1, CE7, and CE9 systems. Biopores, which was segmented based on its tubular morphology,
221 tended to be larger than regular pores of arbitrary shapes (Fig. 2). For example, while the mode (i.e., the most
222 frequent value) pore diameter of the entire pore size distribution was ~100 μm (Fig. 2a), for biopores the modal
223 pore diamater was ~300 μm (Fig. 2b). Visible porosity (pores of > 18.2 μm diam.) was highest in CE9 followed
224 by CE8 (Fig. 3a). In contrast to visible porosity, bioporosity was the highest in CE8, which is comprised of
225 switchgrass and Canadian ryegrass (Fig. 3b). In addition to CE8, throughout the entire range of biopore sizes,
226 CE10 and CE12 also had consistently higher biopore volumes (Fig. 2b) as well as higher total bioporosity than
227 the rest of the systems (Fig. 3b). Total surface areas of biopores (all pores of < 1500 μm diam.) were highest in
228 CE7 and CE8, and lowest in CE1 (p< 0.05, Fig. 4a). Mean distance of soil matrix to biopores showed an opposite
229 trend from surface area, i.e., farthest in CE1 and CE9 and shortest in CE8 (p< 0.05, Fig. 4d).

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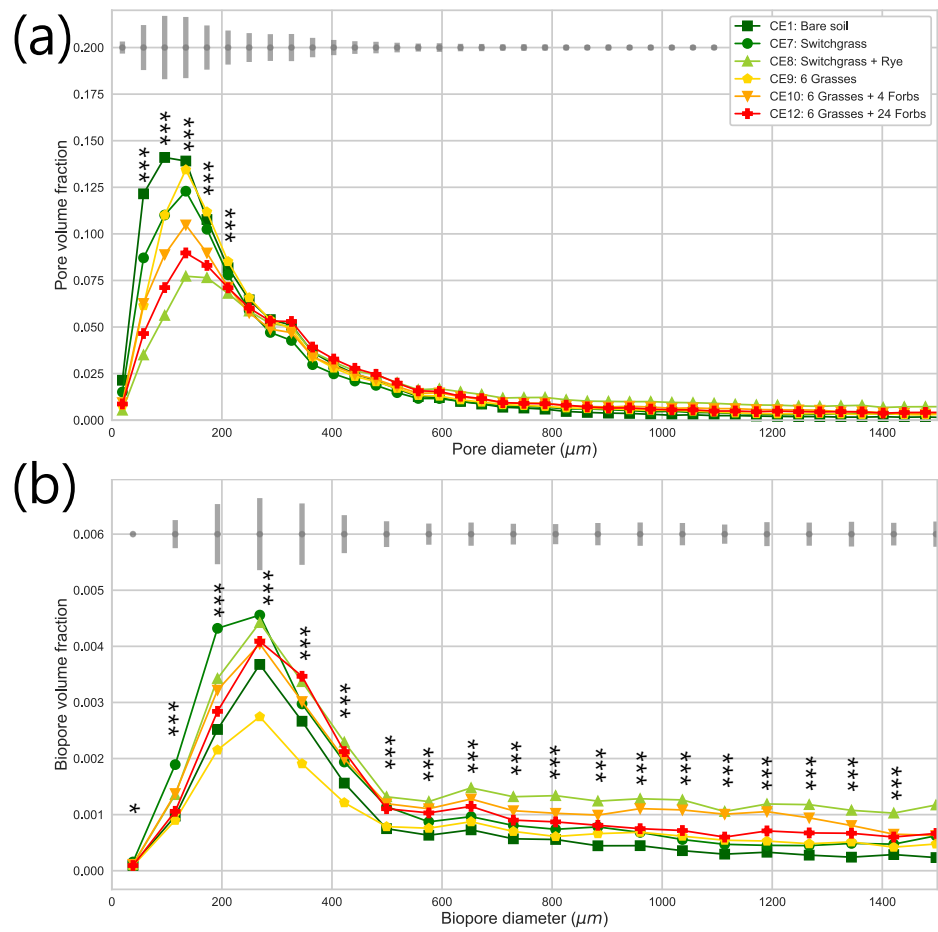
Figure 2: Pore size distribution (a) and biopore size distribution (b) in the studied plant diversity systems (CE1: Bare soil, CE7: Switchgrass, CE8: Switchgrass + Rye, CE9: 6 grasses, CE10: 6 grasses + 4 forbs. CE12: 6 grasses + 10 forbs). Gray bars indicate the least significant difference (LSD) in each (Bio)pore diameter group. Asterisks *** and * mark significant differences among the plant diversity treatments at each (Bio)pore diameter at p < 0.01 and p< 0.10 significance.

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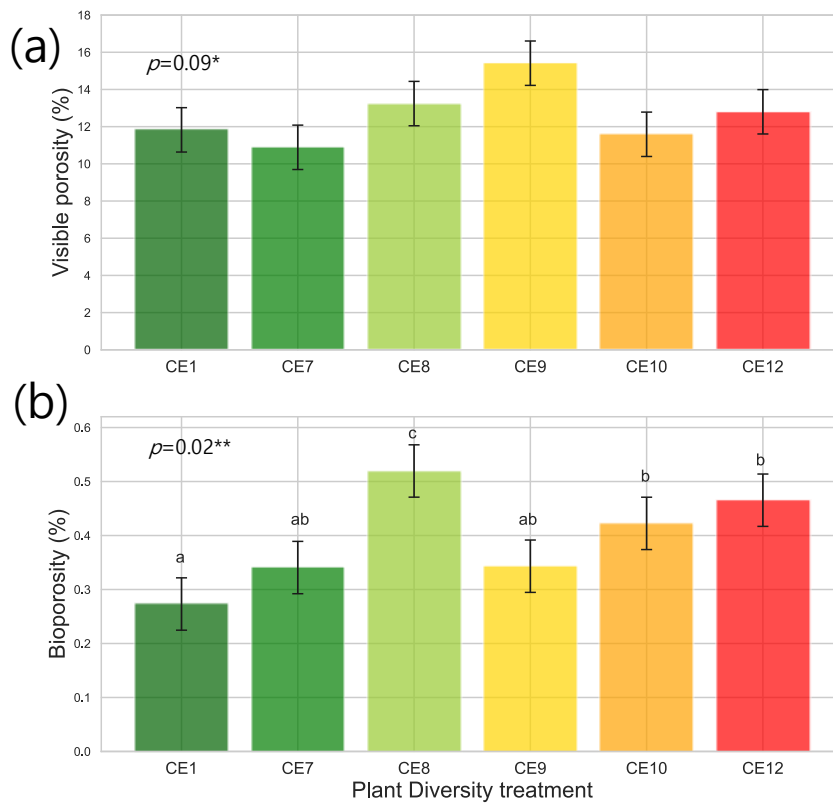
Figure 3: Visible porosity (a) and bioporosity (b) in the studied plant diversity systems (CE1: Bare soil, CE7: Switchgrass, CE8: Switchgrass + Rye, CE9: 6 grasses, CE10: 6 grasses + 4 forbs. CE12: 6 grasses + 10 forbs). Error bars show standard error of the mean. Asterisks * and ** indicate statistically significant differences among plant diversity treatments at p< 0.10 and 0.05, respectively. Letters indicate significant differences among plant diversity treatments (p< 0.05).

3.3 Correlation between plant diversity, pore characteristics, and SOC

Plant species richness and plant functional richness were both positively associated with SOC, with species richness explaining 42% of the variance in SOC ($p < 0.01$; Fig. 1b) and functional richness explaining 36% ($p < 0.01$; Fig. 1d). Within the pore metrics, biopore surface area was positively related to bioporosity ($R^2 = 0.50$, $p < 0.01$; Fig. 4b), whereas the mean distance from the soil matrix to the nearest biopore was negatively related to bioporosity ($R^2 = 0.46$, $p < 0.01$; Fig. 4d). Bioporosity increased with plant diversity. Species richness explained 10% of the variance in bioporosity ($p < 0.01$; Fig. S4a), and functional richness explained 29% ($p < 0.05$; Fig. 5a). Consistent with these patterns, bioporosity was positively correlated with SOC ($R^2 = 0.36$, $p < 0.01$; Fig. 5b).

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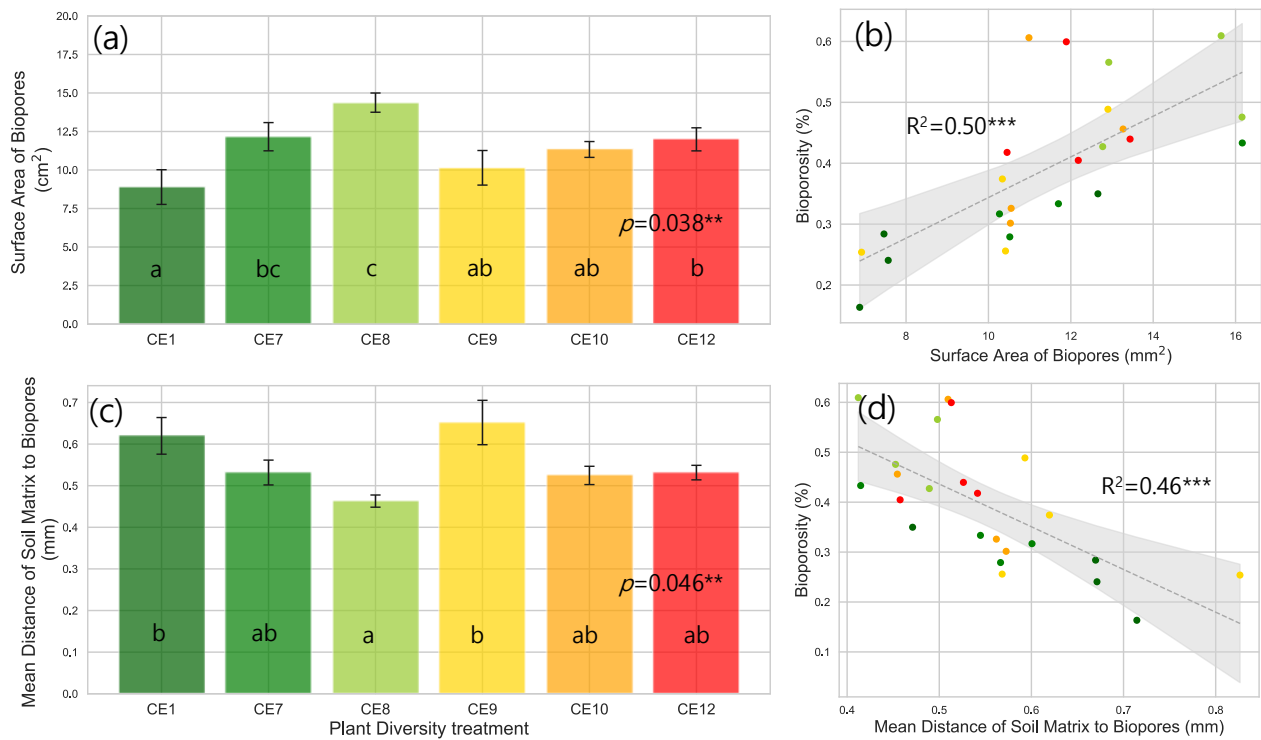
253 **Figure 4: Surface area of biopores (a) and mean distance of soil matrix to biopores (c) in the studied plant diversity**

254 **systems (CE1: Bare soil, CE7: Switchgrass, CE8: Switchgrass + Rye, CE9: 6 grasses, CE10: 6 grasses + 4 forbs. CE12:**

255 **6 grasses + 10 forbs). Error bars in (a) and (c) show standard error of the mean. Correlations between bioporosity and**

256 **surface area of biopores (b), as well as mean distance of soil matrix to biopores (d), are shown. Letters indicate**

257 **significant differences among plant diversity treatments (p< 0.05). Dotted gray lines in (b) and (d) represent fitted**

258 **regression models, with light gray shaded area denoting 95% confidence interval. R^2 values are provided for each**

259 **model. Asterisks (***) indicate statistically significant regression models at p< 0.01.**

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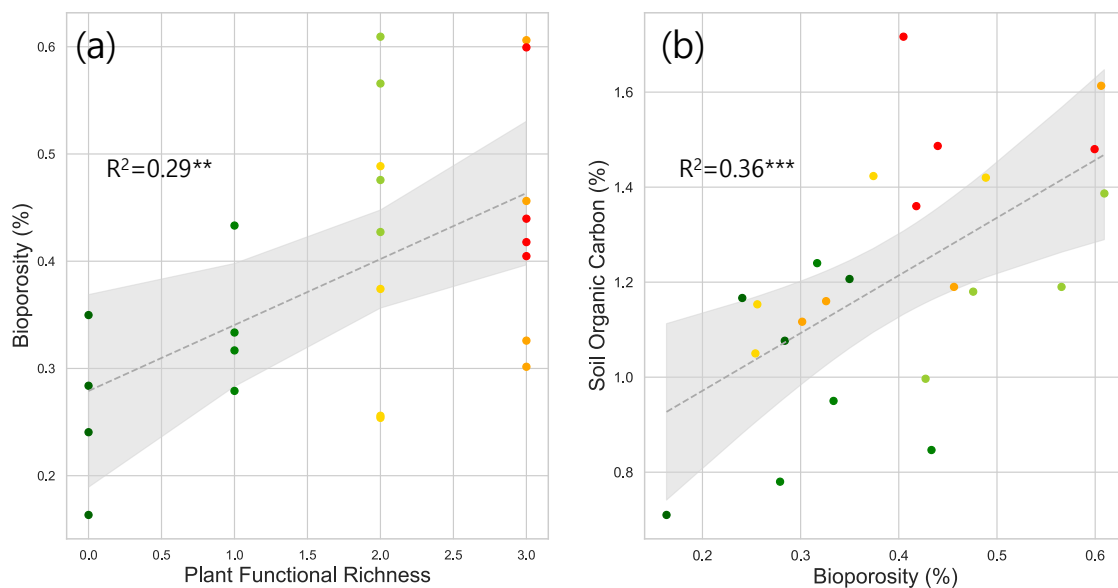
262 **Figure 5: Correlation between plant functional richness and bioporosity (a), and between bioporosity and SOC (b). R^2**

263 **values are provided for each model. Dotted gray lines represent fitted regression models, with light gray shaded area**

266 **4 Discussion**

267 **4.1 Biopores link plant diversity and SOC accumulation**

268   Consistent with our expectations and previous literature (Lange et al., 2015; Prommer et al., 2020; Yang

269 and Tilman, 2020), 12 years of contrasting vegetation was sufficient to develop differences in SOC among the

270 studied plant systems, with the highest SOC observed in the soil under the most diverse plant community (Fig. 1a,

271 b, and d). However, the lack of correlation between the plant aboveground biomass and SOC observed here (Fig.

272 S2c) suggests that greater plant biomass did not itself significantly contribute to SOC increases. This lack of

273 impact is even more obvious when comparing CE7 (monoculture) and CE8 (two-species system), where CE8 had

274 the lowest aboveground biomass but its SOC was comparable to that from the systems with 3~5 times higher plant

275 species richness and higher aboveground biomass (CE9 and 10, Fig. 1a and S1b).

276   The positive association between SOC and bioporosity was another result consistent with our

277 expectations (Fig. 5b). The correlation between plant richness and SOC was largely driven by the highest species

278 richness of 30, which was a high leverage point in our regression analysis (Fig. 1b and d). Thus, even though the

279 R^2 for bioporosity-SOC regression was lower than that from species richness-SOC (0.36 vs. 0.42), bioporosity

280 could be viewed as a better predictor of SOC. Moreover, the CE8 system with its unexpectedly high SOC turned

281 out to have higher bioporosity and higher volumes of biopores of all sizes than the other studied systems (Figs.

282 2b and 3b). This observation is consistent with previous reports identifying biopores as sites of high inputs of labile

283 substrates (Pierret et al., 1999; Xiong et al., 2022), increased microbial abundance and activity (Wendel et al.,

284 2022), and enhanced necromass accumulation (Banfield et al., 2018), all of which highlight the role of biopores

285 in contributing to SOC accrual. It should be noted that belowground biomass was not directly measured in this

286 study, which may have influenced estimates of biopore-related parameters. Direct belowground measurements

287 would allow disentangling root-biomass–driven biopore formation from species-interaction effects, and would

288 further clarify the contribution of belowground biomass to SOC accrual and the independent role of biopores.

289   The biopores in CE8 had the greatest surface area, followed by the most diverse system (Fig. 4a). The

290 mean distance of soil matrix to biopores was the shortest in CE8, followed by diverse systems (CE10 and CE12)

291 (Fig. 4c). The surface area of biopores is critical as it represents the specific portion of the soil matrix that directly

292 intercepts root-derived C inputs, i.e., rhizodeposits (Keller et al., 2021) and decomposed root residues processed

293 by soil microbes (Kim et al., 2022). A shorter mean distance from soil matrix to biopores indicates that root-

294 derived C was accessible to a large community of soil microorganisms, probably facilitating efficient transfer and

295 sequestration of microbially processed C into the soil matrix (Kravchenko et al., 2019). These findings emphasize

296 the currently underestimated importance of formation, abundance, and surface properties of biopores in affecting

297 soil biochemical status, specifically, influencing plant-derived inputs and their potential protection within the soil

298 matrix. Our study suggests that this role might be particularly pronounced in ecosystems with high plant species

299 diversity.

300   Our C mineralization results (Fig. 1c) did not much correspond with previous reports indicating that

301 higher plant diversity enhances microbial C use efficiency (Eisenhauer et al., 2009), likely driven by greater

302 chemical heterogeneity and enhanced substrate accessibility to soil microbes (Mellado-Vázquez et al., 2016;
303 Domeignoz-Horta et al., 2024). We suggest that future studies incorporate more detailed assessments of microbial
304 biomass, community composition, and diversity to better elucidate carbon processes occurring in biopores. These
305 inconsistencies highlight the need for further investigation of microbial activities and net C balance to identify the
306 specific microbial pathways operating in biopores. In particular, the integration of X-ray μCT with pore-scale
307 microbial analyses, as recently demonstrated by Li et al. (2024), represents a promising approach to advance our
308 understanding of SOC accumulation mediated by soil microorganisms in biopores structures.

4.2 Future research directions: winning plant species combinations?

310 Interestingly, while bioporosity was not affected by the number of plant species within the system, it
311 was positively correlated with the systems' functional diversity (Fig. 5a). This implies that greater diversity of
312 functional groups – rather than a greater diversity of plant species per se – may lead to a more thorough exploration
313 of the soil matrix in part through biopore formation, subsequently enhancing SOC accumulation. Moreover, our
314 results suggest that certain combinations of plant species, e.g., CE8 (Switchgrass + Canadian rye) in this study,
315 can be more "effective" in building biopores, and potentially furthering SOC accumulation through rapid
316 processing of added substrates (Banfield et al., 2017; Banfield et al., 2018). We hypothesize that Canadian rye
317 could be viewed as a species with a keystone effect on bioporosity and SOC accumulation.

318 A "keystone effect" refers to beneficial effect of a certain plant species on ecosystem function (Mills et
319 al., 1993). For instance, legume species added to grasslands have been found to disproportionately affect biomass
320 productivity and root C accrual (Minns et al., 2001; Fornara and Tilman, 2008; Lange et al., 2015; Yang et al.,
321 2019) due to N assimilation by legumes and consequent utilization of that N by grasses (Minns et al., 2001;
322 Mangan et al., 2011; Mou et al., 2024). Introduction of a C3 plant, i.e., Canadian rye, into a monoculture C4
323 switchgrass community may have altered switchgrass root growth and exudation patterns. This conjecture is
324 supported by a report on sensitivity of chemical composition of switchgrass root exudates to neighbouring plant
325 species (e.g., C3 *Koeleria macrantha* Ledeb.), with subsequent increases in microbial biomass C and changes in
326 bacterial diversity in the switchgrass rhizosphere (Ulbrich et al., 2022). We see the need for further investigation
327 into the role that individual members of grassland communities may play in stimulating soil pore structure
328 development and SOC accumulation. Identifying keystone species enabling more efficient C accumulation can
329 guide plant restoration and SOC accrual efforts.

5. Conclusion

331 The 12-year grassland experiment demonstrates that SOC accumulation is governed by plant diversity, with the
332 benefits of high plant diversity being, in part, exhibited via development of biopores. Yet, certain species
333 combinations may lead to biopore formation and SOC accumulation benefits disproportional to the actual level
334 of the plant system diversity. Specifically, the two-species mixture of C4 switchgrass and C3 Canadian rye created
335 the greatest bioporosity, shortest mean soil-to-pore distance, and the largest biopore surface area, thereby
336 accelerating microbial processing and stabilization of root-derived C in the surrounding matrix. These findings
337 highlight bioporosity as a more reliable proxy for SOC gains than plant species number alone, and point to
338 potential existence of specific "keystone" species combinations that may disproportionately enhance soil structure

339 and C sequestration. Identifying and deploying such functionally complementary plant species can offer a targeted
340 pathway for optimizing grassland restoration and long-term SOC storage.

341 **Acknowledgements**

342 This work was supported by a 2019 Kellogg Biological Station LTER Fellowship. Support for this research was
343 provided by the U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research
344 (Award DE-SC0018409), by the National Science Foundation Long-term Ecological Research Program (DEB
345 2224712) at the Kellogg Biological Station, and by Michigan State University AgBioResearch. This work was
346 also supported by the New Faculty Startup Fund from Seoul National University.
347

348 **Code/Data availability**

349 All data underlying the main article are provided in the Supplementary Information (Tables S2 and S3).

350 **Author contribution**

351 K. K Formal analysis, investigation, Writing-original draft, visualization
352 M.G: Software, Validation, Writing-Review & Editing
353 G. P. R: Resources, Project administration, Writing-Review & Editing
354 A. K: Conceptualization, Resources, Writing-Review & Editing, Supervision, Funding acquisition

355 **Competing interests**

356 The authors declare that they have no known competing financial interests or personal relationships that could
357 have appeared to influence the work reported in this paper.

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