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1 **Formation of necromass-derived soil organic carbon**
2 **determined by microbial death pathways**

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15 **Abstract**

16 Soil organic matter is the dominant carbon pool in terrestrial ecosystems and its management is of
17 increasing policy relevance. Soil microbes are the main drivers of soil organic carbon sequestration,
18 especially through accumulation of their necromass. However, since the direct characterization of
19 microbial necromass in soil is challenging, its composition and formation remain unresolved. Here,
20 we provide evidence that *microbial death pathways* (the distinct processes of microbial dying) in soil
21 affect necromass composition and its subsequent fate. Importantly, the composition of derived
22 microbial necromass does not equal that of microbial biomass. From biomass to necromass, distinct
23 chemical transformations lead to increases in cell wall : cytoplasm ratios, while nutrient contents and
24 easily degradable compounds are depleted. The exact changes depend on environmental conditions
25 and the relative significance of different microbial death pathways, e.g. predation, starvation or
26 anthropogenic stresses. This has far-reaching consequences for mechanisms underpinning
27 biogeochemical processes: (i) the quantity and persistence of microbial necromass is governed by
28 microbial death pathways, not only the initial biomass composition; (ii) efficient recycling of nutrients
29 within microbial biomass presents a possible pathway of organic carbon sequestration that
30 minimizes nitrogen losses; (iii) human-induced disturbances affect the causes of microbial death and
31 consequently necromass composition. Thus, new research focusing on microbial death pathways
32 holds great potential to improve management strategies for soil organic carbon storage. Not only
33 microbial growth, but also death drives the soil *microbial carbon pump*.

34

35 **Introduction**

36 Soil organic matter (SOM) represents the largest terrestrial organic carbon (C) stock, and thus
37 managing this pool to balance rising atmospheric CO₂ levels is of increasing policy relevance,
38 especially in agroecosystems¹. To achieve a lasting increase of C stored in soil, it is essential to
39 understand the nature of SOM and the processes that contribute to its formation. During the last

40 century soil science made tremendous progress in understanding basic principles: The traditional
41 view of SOM as *humic substances* derived from *recalcitrant* plant litter was replaced by an emerging
42 understanding that large portions of C compounds in soil are channeled through microorganisms.
43 Major parts of SOM in fact consist of microbial residues, especially necromass². This phenomenon is
44 referred to as the *soil microbial carbon pump*³. Indeed, recent global assessments of biomarkers in
45 soil indicate that, while living microbial biomass makes up less than 5% of soil organic carbon (SOC),
46 microbial necromass accounts for more than half^{4,5}. This several-fold increase indicates that residues
47 of dead microorganisms accumulate in soil, persisting over time. Mineralization of these residues,
48 but also interactions with mineral soil surfaces and the formation of bioorganic complexes are
49 regarded as main factors driving necromass stabilization in soil, mechanisms which are dependent on
50 soil type but also on the chemical composition of necromass^{6,7}. Thus, further insights into the
51 formation and chemical nature of necromass are urgently needed to conceptually integrate it into
52 the existing framework of biogeochemical cycles and C sequestration dynamics. Developing this
53 fundamental line of research may also reveal how soil management strategies can be adapted to
54 exploit microbial pathways for optimizing soil C storage⁸.

55 The direct characterization of necromass is analytically impeded by the complex nature of soil⁹.
56 However, microbiological research offers insights into necromass characteristics and relevant
57 knowledge about the processes of microbial dying. By taking a microbial perspective it becomes
58 apparent that microbial biomass is not exposed to “sudden death”, but experiences a series of
59 controlled events during its transformation to necromass, here referred to as *microbial death*
60 *pathways (MDP)*. MDP comprise distinct chemical transformations dependent on the cause of death
61 and the organisms involved, but inevitably result in microbial necromass that differs from microbial
62 biomass (Table 1); hence we posit that microbial necromass does not equal microbial biomass in soil.
63 In this Perspective we explore how soil microorganisms die and, based on microbial physiology,
64 elaborate the chemical transformations during MDP that influence the molecular and nutrient
65 composition of necromass. We thereby suggest that MDP themselves represent important

66 determinants of soil organic C sequestration, and their implementation in concepts of soil C and
67 nutrient cycling has far-reaching consequences for understanding the mechanisms underpinning
68 biogeochemical processes (summarized in Box 1).

69

70 **Microbial death pathways in soil microorganisms**

71 It can easily become a philosophical question whether a microbial cell is alive, dead or even
72 dormant¹⁰. We here focus on the unavoidable transition of microbial biomass to necromass, with
73 awareness that the duration and also complexity of this transition is highly variable. Current
74 biogeochemical models use microbial biomass and different compartments of SOM as individual
75 pools¹¹. Accordingly, we treat living biomass as one pool, describe possible MDP that vary in extent
76 and speed of chemical transformation, and subsequently define necromass as an end-product of the
77 completed MDP. Microorganisms in soil (biomass pool) are exposed to a range of mortality risks,
78 including not only natural developmental aging (senescence), but also starvation, desiccation,
79 predation, viral attack, competition or anthropogenic disturbances. The relative contribution of each
80 is so far unknown, but likely depends on environmental conditions, soil types and organism groups
81 involved (Table 1, Fig. 1). To understand the underlying mechanisms, we will first focus on
82 senescence and other forms of programmed cell death (PCD), and then elaborate the link to other
83 relevant pathways affecting necromass characteristics.

84

85 Senescence and programmed cell death in microorganisms

86 The old paradigm of microorganisms being immortal under optimal conditions was dismantled some
87 time ago, first by the observation of asymmetric cell division in bacterial cells and yeasts, leading to
88 subsequent aging of mother cells^{12,13}. Likewise, filamentous fungi show a “progressive loss of growth
89 potential” over time¹⁴. Such natural aging of individuals over longer time periods probably has
90 limited relevance in unstable soil environments, especially in unicellular organisms. However, in

91 filamentous fungi, senescence occurs as a by-product of growth and likely represents a prominent
92 mechanism of necromass formation due to the modular fungal growth form. Fungi *move* through soil
93 by the formation of new hyphae, consequently leaving behind large amounts of hyphal fragments¹⁵.
94 Most importantly, new hyphal growth as well as fungal sporulation and fruiting are subsidized by
95 internal recycling from older hyphal parts, resulting in efficient reuse of cytoplasmic components,
96 lipids and even cell wall fragments like chitin^{16,17}. This mechanism is of particular significance during
97 nutrient limitations and starvation (Table 1)^{18,19}. We describe this whole process as compartmental
98 senescence (Fig. 1f), an analogue to leaf senescence in which valuable resources are withdrawn as a
99 natural developmental process up to leaf abscission²⁰. Similar to leaf litter, senescent hyphal parts
100 diverge in their chemical composition from actively growing hyphae: Older hyphae (distant from
101 growing tips) are characterized by vacuolization and cytoplasmic reductions following the activity of
102 autocatalytic enzymes^{21,22}, and strong reductions in DNA content²³ and nutrient concentrations²⁴.
103 Senescence-derived fungal necromass will therefore be depleted in cytoplasmic components, storage
104 compounds and growth-limiting elements relative to biomass²⁵ (Fig. 1f). The relative proportion of
105 the cell wall fraction will increase, with consequences for C-to-nutrient ratios and chemical
106 complexity: Fungal cell walls are rich in complex interlinked polysaccharides, with varying
107 concentrations of chitin and melanin depending on species identity²⁶.

108 In bacteria, surprisingly similar recycling processes are induced under nutrient-limited or stressful
109 conditions (common in heterogeneous soil environments) despite their unicellular growth form²⁷,
110 especially within colonies and biofilms. This is represented in the literature by the generic concept of
111 programmed cell death (PCD)^{28,29}, and will be categorized here as starvation- or stress-induced PCD
112 (Table 1). Bacterial PCD is governed by a highly controlled genetic programme, involving cellular lytic
113 degradation^{30,31}. As a most simple mechanism, endospore formation induced under stressful
114 conditions is supported by autocatalysis of the mother cell and even surrounding daughter cells^{28,32}.
115 Similarly, under starvation, PCD is a strategy in *Myxococcus* to provide nutrients for fruiting body
116 formation, while individual cell death in filamentous *Streptomyces* colonies supports neighbouring

117 cells²⁸. Such unicellular *suicide* may seem paradoxical, but several authors describe this widespread
118 phenomenon as a form of altruistic behavior with the main goal of nutrient replenishment for
119 genetically related survivors (kin selection)^{28,29,33}. Especially in the context of recent suggestions that
120 the majority of soil bacteria and archaea occur in colonies embedded in EPS and biofilms, these
121 mechanisms may be highly relevant^{33,34}. Within bacterial colonies, close proximity allows cellular
122 components released by cell lysis to be recycled efficiently by survivors, especially under resource-
123 limited conditions²⁷. Again, the resulting necromass will be depleted in easily degradable cytoplasmic
124 compounds and growth-limiting elements. In addition, starvation induces further modifications to
125 bacterial cells, such as degradation of storage compounds and a reduction in cell size. Based on
126 geometric considerations, smaller cell sizes further increase cell wall : cytosol ratios.

127 Together, these lines of evidence suggest that death in microorganisms leads to significant
128 modifications in the molecular composition of necromass compared to biomass, mainly driven by
129 decreases in cytoplasmic components with related rising C-to-nutrient ratios, in parallel to a
130 reduction of limiting and easily degradable compounds (Fig. 1).

131

132 Further types of MDP relevant in soil

133 Though the relative contribution of different causes and mechanisms for MDP in soil are currently
134 unresolved (Table 1), it is clear that in natural soil environments additional (external) causes of
135 microbial death are common. Still, parts of the mechanisms described for senescence and PCD,
136 especially resource recycling, are also relevant for other MDP. Soil microorganisms form the base of
137 the soil food web, and are consumed by a diverse and abundant soil fauna community³⁵. Bacteria can
138 also be killed by other predatory bacteria³⁶ and viruses that are highly abundant in soils^{37,38} (Table 1,
139 Fig. 1). Evidently, predated microbial biomass is transformed to varying degrees to necromass
140 residues³⁹. Here, the physiology and resource demands of the attacking agent are important in
141 determining the resulting chemical transformations. Predation by fauna and protozoa is known to

142 release excess N in mineral forms, a concept referred to as the *microbial loop*⁴⁰ (Fig. 1c). Fauna needs
143 to maintain homeostatic C:N:P ratios and invest C into both catabolism and anabolism, which
144 necessitates the release of excess mineralized N, especially following ingestion of bacteria with low
145 C:N ratios. In parallel, non-digested microbial necromass residues will be emitted in fecal pellets or
146 excreted (in the case of protozoa), with the chemical composition of these residues depending on the
147 digestive capacities of the predator species^{41,42} and their specificity of prey intake³⁵. The exact
148 chemical composition depends on many factors, but relative proportions of less easily degradable
149 compounds will generally increase (Fig. 1c). Predatory bacteria, by contrast, ingest mainly the
150 cytoplasm of bacterial prey, leaving behind cell wall fragments as necromass residues³⁶ (Fig. 1e). Even
151 viral attack produces modified bacterial residues that are depleted in N and especially P, and thus C
152 enriched³⁷ (Fig. 1d). Another relevant mechanism to consider during viral or pathogenic infection are
153 self-defence mechanisms present in bacterial colonies: Via quorum sensing infected bacterial cells
154 partly initiate cell lysis (PCD), which some authors also describe as a mechanism to make resources
155 available to neighboring daughter cells^{28,43}, again allowing resource recycling within colonies (Fig. 1d).

156 Other forms of MDP exist in soil, with the list discussed here likely being incomplete (Fig. 1b).

157 Antagonistic interactions during microbial competition can have lethal outcomes. Microbial species
158 strongly compete for resources in soil environments. On the one hand, more efficient resource
159 exploitation by one species may lead to starvation and subsequent (compartmental) death of
160 another, inducing PCD mechanisms as described above⁴⁴. On the other hand, interference
161 competition involves the excretion of antimicrobial toxins with potentially lethal effects^{45,46}.

162 Regarding chemical transformations during MDP induced by antagonism, certain degrees of internal
163 resource recycling in response to this stressor are likely, depending on the lethality and
164 concentrations of toxins, especially during stress-induced spore formations in bacteria or within
165 fungal mycelia⁴⁷.

166 Another relevant mortality agent in light of global change is MDP induced by anthropogenic
167 disturbances. Examples are pesticide applications and other forms of soil pollution (Fig. 1g), soil

168 compaction, more intense drought or heat events as a consequence of climate change, or osmotic
169 stress induced by salinity (as a consequence of inappropriate management). Water stress also occurs
170 regularly under natural conditions and microorganisms have adapted to such soil conditions over
171 evolutionary time⁴⁸ - abiotic stresses are likely relevant MDP in soil (including desiccation, starvation,
172 freezing, anoxia, oxidative stress). However, sudden and severe stress events, including xenobiotic
173 chemicals, may lead to more rapid death and subsequent release of complete cell components,
174 characterized by lower resource retention and less efficient reuse than observed in natural MDP⁴⁹
175 (Table 1, Fig. 1g).

176

177 **Relevance of MDP in environmental contexts**

178 Different types of MDP differ not only in the relative amount of necromass produced, but also in the
179 chemical transformations induced, with further contrasts created among different microbial groups.
180 For example, while compartmental senescence in fungal mycelia produces necromass residues
181 dominated by complex, C-rich cell wall fragments, lysis of bacterial cells likely releases more
182 cytoplasmic compounds and cell wall fragments containing more N, since bacterial cell walls contain
183 higher proportions of peptides^{26,50}. Predation, by contrast, will retain more C within the soil food web
184 but also release complex necromass residues together with mineral nutrients available to plants.
185 Thus, it can be expected that fungal : bacterial ratios, predator load, viral abundances and
186 competitive dynamics in soil communities will affect the relative importance of different MDP types,
187 with consequences for necromass quantity and quality (Fig. 2a). Since the community composition of
188 soil microbes, fauna and viruses varies among soils and further responds to environmental change,
189 MDP and the strength of chemical transformations will vary accordingly (Fig. 2)^{38,51,52}. In parallel, the
190 efficiency of C versus nutrient recycling within microbial biomass will respond to soil nutrient
191 limitations⁵³, affecting the C:N and N:P ratios of microbial necromass (Fig. 2a). Anthropogenic (lethal)
192 stressors, especially extreme events⁵⁴, may have even more substantial impacts on necromass

193 formation and composition. Rapid, uncontrolled death of microorganisms in soil not only increases
194 the quantity of necromass produced, but also reduces its chemical transformation as opposed to
195 natural MDP (Fig. 1g, Table 1).

196 Not only microbial growth rates are affected by environmental parameters, but also MDP, which
197 subsequently determine the amount of C (i) remaining within microbial biomass or the soil food web,
198 (ii) being retained as SOC by mineral and organic interactions or (iii) available for mineralization by
199 necromass-degrading microbes. Predictions of the long-term persistence of necromass-derived SOC
200 are important research priorities, though challenging to conduct due to the different mechanisms
201 and high context-dependency involved (Fig. 2)⁶. Based on metabolic theory, necromass that is richer
202 in easily available C and nutrients (alongside C-rich molecules) will be more exposed to microbial
203 mineralization than more transformed complex polymeric necromass⁵⁵. Indeed, meshbag
204 experiments indicate that necromass mineralization rates are positively correlated with N content,
205 and negatively with the abundance of highly complex components like melanin⁵⁶. On the other hand,
206 mineral sorption is discussed as a more prevalent factor determining necromass persistence, which
207 acts most strongly on proteinaceous and phosphorylated molecules⁵⁷. Thus, MDP and resulting
208 necromass chemistry are relevant to all stages of the *necromass continuum*⁵⁸, namely *production*,
209 *recycling* and *stabilization*, though the relative significance of each stage will likely depend on
210 microbial necromass composition and diversity, together with soil properties (Fig. 2a).

211 Another relevant factor for C persistence represents the heterogeneity introduced by spatial and
212 temporal diversity in soil⁵⁹, with this complexity further enhanced by diverse and spatially
213 differentiated MDP. The latter affect molecular composition and diversity of microbial necromass as
214 well as nutrient release from biomass and its spatial distribution. The way cells disintegrate, e.g.,
215 leakage of cytosolic compounds, altered particle size distributions and the spatial arrangement of
216 cellular remains within soil particles further increases spatial heterogeneity (Fig. 1). Additionally,
217 temporal effects on MDP will be present at various scales, from short term to seasonal fluctuations⁶⁰.
218 In conclusion, diverse MDP, chemical transformations and their responses to spatial and temporal

219 fluctuations will increase *molecular diversity, spatial heterogeneity* and *temporal variability* – all
220 relevant factors determining SOC sequestration⁵⁹.

221

222 **Conclusions and future research directions**

223 We have detailed how microbial dying represents a distinct process with consequences for the
224 quantity and molecular composition of microbial necromass. Despite a lack of direct measurements
225 in soil, knowledge derived from (i) microbial physiology, (ii) trophic interactions and (iii) soil
226 community ecology provides strong evidence for the mechanisms of MDP described. At the current
227 stage the relation between microbial parameters and soil organic C storage is not fully resolved,
228 often related to missing information on microbial traits, interactions of necromass with soil minerals
229 and responses to environmental change^{61,62}. Here, we argue that an understanding of the processes
230 and rates of microbial death and resulting necromass characteristics will improve the
231 implementation of microbial contributions to SOC sequestration in biogeochemical models. Microbial
232 death, interactively with microbial growth, drives the soil *microbial carbon pump*, where the
233 correlations among biomass and necromass abundance and composition are highly context-
234 dependent (Fig. 2). Current soil organic matter research takes microbial growth and carbon-use
235 efficiency as a proxy for microbial C inputs⁶³. However, as presented here, mortality rates and
236 chemical transformations will also determine the quantity and composition of microbial necromass
237 in soil (Box 1).

238 The insights provided on biomass-to-necromass transformations add important novel perspectives
239 on soil biogeochemical processes (Box 1). Still, it is clear that MDP represent only one component of
240 a complex multifactorial soil system, which affects SOC sequestration interactively with microbial
241 biomass characteristics and soil chemical properties (Fig. 2). An important opportunity provided by
242 these new insights is to rethink the energy-efficient channeling of C within microbial communities as
243 well as high nutrient-use efficiencies due to resource recycling mechanisms. It was proposed that C

244 sequestration in microbial residues may be limited by N demands⁶⁴. However, if N is reused or
245 released in mineral forms prior to necromass formation, N (or other nutrients) may under certain
246 conditions not limit C sequestration. In line with this, increases in C sequestration also do not
247 necessarily decrease nutrients available to plants, an aspect especially relevant for the management
248 of agricultural soils with untapped C storage potential^{4,5}.

249 Future research must test these concepts experimentally in soil and microbial systems, but also
250 establish whether the incorporation of MDP improves predictive strength of biogeochemical models
251 (Box 1). We hope this Perspective will stimulate deeper exploration of the topic exploiting novel
252 techniques and interdisciplinary approaches, and motivate a new research focus in the field of soil
253 organic carbon cycling and microbial ecology. As the direct analysis of microbial necromass in soil is
254 challenging, this also applies to the examination of MDP. However, analytical tools in soil science and
255 microbiology are evolving rapidly: Detailed applications of stable isotope probing allow analyses of
256 microbial growth and death within highly resolved food web dynamics^{60,65}, while higher resolution in
257 imaging and spectroscopic techniques may provide insights on microbial interactions and processes
258 at the level of individual organisms and populations^{66,67}. Furthermore, by integrating MDP, we
259 hypothesize that experiments with *real* necromass - not autoclaved biomass - will provide more
260 detailed insights into its fate and stabilization (Box 1). Most likely, the often observed biphasic
261 mineralization (*two-pool model*) is an artefact derived from this experimental bias driven by easily
262 mineralizable cytosolic compounds^{68,69}. Future experiments should also address responses of MDP to
263 global change scenarios. Such knowledge and conceptual insight holds great potential to improve
264 mechanistic understanding of organic C storage via microbial necromass, increase the precision of
265 biogeochemical models and develop agricultural management strategies to exploit the C storage
266 potential of soils.

267

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269

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275

276 **Author contributions**

277 T.C. and J.L. generated the initial conceptual ideas. T.C. led the writing and literature search. K.M.-J.,
278 I.M., M.C.R., J.L. and T.C. developed the final concepts. All authors contributed to writing and editing.

279

280 **Competing interests**

281 The authors declare no competing interests.

282

283 **Reference list**

- 284 1. Bradford, M. A. *et al.* Soil carbon science for policy and practice. *Nature Sustainability* **2**,
285 1070-1072 (2019).
- 286 2. Lehmann, J. & Kleber, M. The contentious nature of soil organic matter. *Nature* **528**, 60-68
287 (2015).
- 288 3. Liang, C., Schimel, J. P. & Jastrow, J. D. The importance of anabolism in microbial control over
289 soil carbon storage. *Nature Microbiology* **2**, 17105 (2017).

- 290 4. Liang, C., Amelung, W., Lehmann, J. & Kästner, M. Quantitative assessment of microbial
291 necromass contribution to soil organic matter. *Glob. Change Biol.* **25**, 3578-3590 (2019).
- 292 5. Wang, B. R., An, S. S., Liang, C., Liu, Y. & Kuzyakov, Y. Microbial necromass as the source of
293 soil organic carbon in global ecosystems. *Soil Biol. Biochem.* **162**, 108422 (2021).
- 294 6. Kästner, M. & Miltner, A. Chapter 5 - SOM and Microbes—What Is Left From Microbial Life.
295 In *The Future of Soil Carbon* (eds Garcia, C., Nannipieri, P., & Hernandez, T.) (Academic Press,
296 2018).
- 297 7. Buckeridge, K. M. *et al.* Sticky dead microbes: Rapid abiotic retention of microbial necromass
298 in soil. *Soil Biol. Biochem.* **149**, 107929 (2020).
- 299 8. Kallenbach, C. M., Grandy, A. S., Frey, S. D. & Diefendorf, A. F. Microbial physiology and
300 necromass regulate agricultural soil carbon accumulation. *Soil Biology and Biochemistry* **91**,
301 279-290 (2015).
- 302 9. Kallenbach, C. M., Frey, S. D. & Grandy, A. S. Direct evidence for microbial-derived soil
303 organic matter formation and its ecophysiological controls. *Nature Communications* **7**, 13630
304 (2016).
- 305 10. Emerson, J. B. *et al.* Schrödinger's microbes: Tools for distinguishing the living from the dead
306 in microbial ecosystems. *Microbiome* **5**, 86 (2017).
- 307 11. Zhang, Y. *et al.* Simulating measurable ecosystem carbon and nitrogen dynamics with the
308 mechanistically defined MEMS 2.0 model. *Biogeosciences* **18**, 3147-3171 (2021).
- 309 12. Ackermann, M., Stearns Stephen, C. & Jenal, U. Senescence in a Bacterium with Asymmetric
310 Division. *Science* **300**, 1920-1920 (2003).
- 311 13. Aguilaniu, H., Gustafsson, L., Rigoulet, M. & Nyström, T. Asymmetric inheritance of
312 oxidatively damaged proteins during cytokinesis. *Science* **299**, 1751-1753 (2003).
- 313 14. Maheshwari, R. & Navaraj, A. Senescence in fungi: the view from *Neurospora*. *FEMS*
314 *Microbiol Lett* **280**, 135-143 (2008).

- 315 15. See, C. R. *et al.* Hyphae move matter and microbes to mineral microsites: Integrating the
316 hyphosphere into conceptual models of soil organic matter stabilization. *Glob. Change Biol.*
317 **28**, 2527-2540 (2022).
- 318 16. Pusztahelyi, T. *et al.* Comparative studies of differential expression of chitinolytic enzymes
319 encoded by chiA, chiB, chiC and nagA genes in *Aspergillus nidulans*. *Folia Microbiologica* **51**,
320 547-554 (2006).
- 321 17. Bartoszewska, M. & Kiel, J. A. The role of macroautophagy in development of filamentous
322 fungi. *Antioxidants & redox signaling* **14**, 2271-2287 (2011).
- 323 18. Josefsen, L. *et al.* Autophagy provides nutrients for nonassimilating fungal structures and is
324 necessary for plant colonization but not for infection in the necrotrophic plant pathogen
325 *Fusarium graminearum*. *Autophagy* **8**, 326-337 (2012).
- 326 19. Heaton, L. L., Jones, N. S. & Fricker, M. D. Energetic Constraints on Fungal Growth. *Am Nat*
327 **187**, E27-40 (2016).
- 328 20. Taiz L, Zeiger E. *Plant Physiology*, 4th Edition edn. Spektrum Akademischer Verlag (2008).
- 329 21. Bowman EJ, Bowman BJ. Vacuoles in Filamentous Fungi. In: *Cellular and Molecular Biology of*
330 *Filamentous Fungi* (eds Borkovich K, Ebbole D). ASM Press (2010).
- 331 22. Voigt, O. & Pöggeler, S. Self-eating to grow and kill: autophagy in filamentous ascomycetes.
332 *Applied Microbiology and Biotechnology* **97**, 9277-9290 (2013).
- 333 23. Grimmett, I. J., Shipp, K. N., Macneil, A. & Barlocher, F. Does the growth rate hypothesis
334 apply to aquatic hyphomycetes? *Fungal Ecol.* **6**, 493-500 (2013).
- 335 24. Camenzind, T., Philipp Grenz, K., Lehmann, J. & Rillig, M. C. Soil fungal mycelia have
336 unexpectedly flexible stoichiometric C:N and C:P ratios. *Ecology Letters* **24**, 208-218 (2021).
- 337 25. Mason-Jones, K., Robinson, S. L., Veen, G. F., Manzoni, S. & van der Putten, W. H. Microbial
338 storage and its implications for soil ecology. *The ISME Journal* **16**, 617-629 (2022).
- 339 26. Gow, N. A. R., Latge, J. P. & Munro, C. A. The Fungal Cell Wall: Structure, Biosynthesis, and
340 Function. *Microbiol Spectr* **5**, FUNK-0035-2016 (2017).

- 341 27. Steiner, U. K. Senescence in Bacteria and Its Underlying Mechanisms. *Front Cell Dev Biol* **9**,
342 668915-668915 (2021).
- 343 28. Allocati, N., Masulli, M., Di Ilio, C. & De Laurenzi, V. Die for the community: an overview of
344 programmed cell death in bacteria. *Cell Death & Disease* **6**, e1609 (2015).
- 345 29. Peeters, S. H. & de Jonge, M. I. For the greater good: Programmed cell death in bacterial
346 communities. *Microbiological Research* **207**, 161-169 (2018).
- 347 30. Wang, J. & Bayles, K. W. Programmed cell death in plants: lessons from bacteria? *Trends in*
348 *plant science* **18**, 133-139 (2013).
- 349 31. Nagamalleswari, E., Rao, S., Vasu, K. & Nagaraja, V. Restriction endonuclease triggered
350 bacterial apoptosis as a mechanism for long time survival. *Nucleic Acids Research* **45**, 8423-
351 8434 (2017).
- 352 32. Kysela, D. T., Brown, P. J. B., Huang, K. C. & Brun, Y. V. Biological consequences and
353 advantages of asymmetric bacterial growth. *Annu Rev Microbiol* **67**, 417-435 (2013).
- 354 33. Bayles, K. W. Bacterial programmed cell death: making sense of a paradox. *Nature reviews.*
355 *Microbiology* **12**, 63-69 (2014).
- 356 34. Flemming, H.-C. & Wuertz, S. Bacteria and archaea on Earth and their abundance in biofilms.
357 *Nature Reviews Microbiology* **17**, 247-260 (2019).
- 358 35. Coleman DC, Wall DH. Chapter 5 - Soil Fauna: Occurrence, Biodiversity, and Roles in
359 Ecosystem Function. In: Soil Microbiology, Ecology and Biochemistry (Fourth Edition) (ed Paul
360 EA). Academic Press (2015).
- 361 36. Hungate, B. A. *et al.* The Functional Significance of Bacterial Predators. *mBio* **12**, e00466-
362 00421 (2021).
- 363 37. Kuzyakov, Y. & Mason-Jones, K. Viruses in soil: Nano-scale undead drivers of microbial life,
364 biogeochemical turnover and ecosystem functions. *Soil Biology and Biochemistry* **127**, 305-
365 317 (2018).
- 366 38. Williamson, K. E., Fuhrmann, J. J., Wommack, K. E. & Radosevich, M. Viruses in Soil
367 Ecosystems: An Unknown Quantity Within an Unexplored Territory. **4**, 201-219 (2017).

- 368 39. Sokol, N. W. *et al.* Life and death in the soil microbiome: how ecological processes influence
369 biogeochemistry. *Nature Reviews Microbiology* **20**, 415-430 (2022).
- 370 40. Bonkowski, M. & Clarholm, M. J. A. P. Stimulation of Plant Growth through Interactions of
371 Bacteria and Protozoa: Testing the Auxiliary Microbial Loop Hypothesis. *Acta Protozoologica*
372 **51**, 237-247 (2012).
- 373 41. Potapov, A. M., Pollierer, M. M., Salmon, S., Šustr, V. & Chen, T.-W. Multidimensional trophic
374 niche revealed by complementary approaches: Gut content, digestive enzymes, fatty acids
375 and stable isotopes in Collembola. *Journal of Animal Ecology* **90**, 1919-1933 (2021).
- 376 42. Esteban GF, Fenchel TM. Feeding. In: *Ecology of Protozoa: The Biology of Free-living*
377 *Phagotrophic Protists* (eds Esteban GF, Fenchel TM). Springer International Publishing (2020).
- 378 43. Koksharova, O. A. Bacteria and phenoptosis. *Biochemistry. Biokhimiia* **78**, 963-970 (2013).
- 379 44. Tilman, D. Resource competition and community structure. *Monographs in population*
380 *biology* **17**, 1-296 (1982).
- 381 45. Boddy, L. Interspecific combative interactions between wood-decaying basidiomycetes.
382 *FEMS Microbiology Ecology* **31**, 185-194 (2000).
- 383 46. Hibbing, M. E., Fuqua, C., Parsek, M. R. & Peterson, S. B. Bacterial competition: surviving and
384 thriving in the microbial jungle. *Nature Reviews Microbiology* **8**, 15-25 (2010).
- 385 47. Müller, S. *et al.* Predation by *Myxococcus xanthus* Induces *Bacillus subtilis* To Form Spore-
386 Filled Megastructures. *Applied and Environmental Microbiology* **81**, 203-210 (2015).
- 387 48. Laskowska, E. & Kuczyńska-Wiśnik, D. New insight into the mechanisms protecting bacteria
388 during desiccation. *Current Genetics* **66**, 313-318 (2020).
- 389 49. Rillig, M. C., Ryo, M. & Lehmann, A. Classifying human influences on terrestrial ecosystems.
390 *Glob. Change Biol.* **27**, 2273-2278 (2021).
- 391 50. Dörr, T., Moynihan, P. J. & Mayer, C. Editorial: Bacterial Cell Wall Structure and Dynamics.
392 *Frontiers in Microbiology* **10**, 02051 (2019).
- 393 51. Corredor, B., Lang, B. & Russell, D. Effects of nitrogen fertilization on soil fauna in a global
394 meta-analysis. Preprint at <https://doi.org/10.21203/rs.3.rs-1438491/v1> (2022).

- 395 52. Blankinship, J. C., Niklaus, P. A. & Hungate, B. A. A meta-analysis of responses of soil biota to
396 global change. *Oecologia* **165**, 553-565 (2011).
- 397 53. Manzoni, S., Chakrawal, A., Spohn, M. & Lindahl, B. D. Modeling Microbial Adaptations to
398 Nutrient Limitation During Litter Decomposition. *Frontiers in Forests and Global Change* **4**,
399 686945 (2021).
- 400 54. Frank, D. *et al.* Effects of climate extremes on the terrestrial carbon cycle: concepts,
401 processes and potential future impacts. *Glob. Change Biol.* **21**, 2861-2880 (2015).
- 402 55. Gunina, A. & Kuzyakov, Y. From energy to (soil organic) matter. *Glob. Change Biol.* **28**, 2169-
403 2182 (2022).
- 404 56. Fernandez, C. W. & Koide, R. T. Initial melanin and nitrogen concentrations control the
405 decomposition of ectomycorrhizal fungal litter. *Soil Biology and Biochemistry* **77**, 150-157
406 (2014).
- 407 57. Kästner, M., Miltner, A., Thiele-Bruhn, S. & Liang, C. Microbial Necromass in Soils—Linking
408 Microbes to Soil Processes and Carbon Turnover. *Frontiers in Environmental Science* **9**,
409 756378 (2021).
- 410 58. Buckeridge, K. M., Creamer, C. & Whitaker, J. Deconstructing the microbial necromass
411 continuum to inform soil carbon sequestration. *Funct. Ecol.* **36**, 1396-1410 (2022).
- 412 59. Lehmann, J. *et al.* Persistence of soil organic carbon caused by functional complexity. *Nature*
413 *Geoscience* **13**, 529-534 (2020).
- 414 60. Blazewicz, S. J. *et al.* Taxon-specific microbial growth and mortality patterns reveal distinct
415 temporal population responses to rewetting in a California grassland soil. *The ISME Journal*
416 **14**, 1520-1532 (2020).
- 417 61. Kallenbach, C. M., Wallenstein, M. D., Schipanski, M. E. & Grandy, A. S. Managing
418 Agroecosystems for Soil Microbial Carbon Use Efficiency: Ecological Unknowns, Potential
419 Outcomes, and a Path Forward. *Frontiers in Microbiology* **10**, 1146 (2019).
- 420 62. Liang, C. Soil microbial carbon pump: Mechanism and appraisal. *Soil Ecology Letters* **2**, 241-
421 254 (2020).

- 422 63. Sinsabaugh, R. L., Manzoni, S., Moorhead, D. L. & Richter, A. Carbon use efficiency of
423 microbial communities: stoichiometry, methodology and modelling. *Ecology Letters* **16**, 930-
424 939 (2013).
- 425 64. van Groenigen, J. W. *et al.* Sequestering Soil Organic Carbon: A Nitrogen Dilemma.
426 *Environmental Science & Technology* **51**, 4738-4739 (2017).
- 427 65. Greenlon A, et al. Quantitative stable-isotope probing (qSIP) with metagenomics links
428 microbial physiology and activity to soil moisture in Mediterranean-climate grassland
429 ecosystems. Preprint at <https://doi.org/10.1101/2022.05.02.490339> (2022).
- 430 66. Mafla-Endara, P. M. *et al.* Microfluidic chips provide visual access to in situ soil ecology.
431 *Communications Biology* **4**, 889 (2021).
- 432 67. Schaible, G. A., Kohtz, A. J., Cliff, J. & Hatzenpichler, R. Correlative SIP-FISH-Raman-SEM-
433 NanoSIMS links identity, morphology, biochemistry, and physiology of environmental
434 microbes. *ISME Communications* **2**, 52 (2022).
- 435 68. See, C. R. *et al.* Distinct carbon fractions drive a generalisable two-pool model of fungal
436 necromass decomposition. *Funct. Ecol.* **35**, 796-806 (2021).
- 437 69. Wang, C. *et al.* Stabilization of microbial residues in soil organic matter after two years of
438 decomposition. *Soil Biology and Biochemistry* **141**, 107687 (2020).
- 439 70. Veresoglou, S. D., Halley, J. M. & Rillig, M. C. Extinction risk of soil biota. *Nature*
440 *Communications* **6**, 8862 (2015).
- 441 71. Potapov, A. M. *et al.* Feeding habits and multifunctional classification of soil-associated
442 consumers from protists to vertebrates. *Biological Reviews* **97**, 1057-1117 (2022).
- 443 72. Trap, J., Bonkowski, M., Plassard, C., Villenave, C. & Blanchart, E. Ecological importance of soil
444 bacterivores for ecosystem functions. *Plant and Soil* **398**, 1-24 (2016).
- 445 73. Dooley, S. R. & Treseder, K. K. The effect of fire on microbial biomass: a meta-analysis of field
446 studies. *Biogeochemistry* **109**, 49-61 (2012).

- 447 74. Muñoz-Leoz, B., Ruiz-Romera, E., Antigüedad, I. & Garbisu, C. Tebuconazole application
448 decreases soil microbial biomass and activity. *Soil Biology and Biochemistry* **43**, 2176-2183
449 (2011).
- 450 75. Meyer, M., Diehl, D., Schaumann, G. E. & Muñoz, K. Agricultural mulching and fungicides—
451 impacts on fungal biomass, mycotoxin occurrence, and soil organic matter decomposition.
452 *Environmental Science and Pollution Research* **28**, 36535-36550 (2021).
- 453 76. Thiery, S. & Kaimer, C. The Predation Strategy of *Myxococcus xanthus*. *Frontiers in*
454 *Microbiology* **11**, 2 (2020).
- 455 77. Laloux, G. Shedding Light on the Cell Biology of the Predatory Bacterium *Bdellovibrio*
456 *bacteriovorus*. *Frontiers in Microbiology* **10**, 3136 (2020).

457 **Table 1:** Summary of described microbial death pathways (MDP) and their characteristics.

Microbial death pathway (MDP)	Affected organismal groups	Attacking/antagonistic agent	Internal resource recycling	Necromass characteristics ¹			Estimates of death rates and relevance
				C-to-nutrient ratio ²	cell wall : cytoplasm ratio	easily degradable compounds	
(Compartmental) senescence	mostly fungi	-	high	↑	↑	↓	average hyphal length estimates for soil: 102 m cm ⁻³ ; turnover rate estimates 0.3 – 6.3 month ⁻¹ ¹⁵
Starvation/stress-induced PCD	bacteria; in fungi similar to senescence	-	high	↑	↑	↓	no data
Predation (soil fauna)	bacteria and fungi	fauna, protozoa	reuse by attacking agent	↓	?	↓	soil fauna abundance 60 - 11 × 10 ⁷ individuals m ⁻² soil ⁷⁰ (for individual groups see ⁷¹); 16% reduction in mic. biomass by protozoa and nematodes ⁷²
Predation (bacterial)	bacteria	predatory bacteria	reuse by attacking agent	?	↑	↓	7.4% of bacteria belong to (facultative and obligate) predator groups ³⁶ ; death rates unknown
Viral attack	bacteria	bacteriophages	medium	↑	↑-	↓-	10 ³ - 10 ¹⁰ virus particles (g ⁻¹ soil) ³⁸ ; 30-80% of bacteria in soil carry prophages ³⁷ ; death rates unknown
Interspecific competition	bacteria and fungi	bacteria and fungi	medium	↑	↑	↓	no data
Anthropogenic stress	bacteria and fungi	-	low	-	↑-	↓-	mostly unknown; drought events 25% death within 3 hours ⁶⁰ ; fire reduces mic. biomass by 33% ⁷³ ; pesticide effects on microbial biomass depend on chemicals and systems involved ^{74,75}

458

459 ¹necromass characteristics are described in direct comparison to microbial biomass. Arrows indicate expected transformations by MDP

460 ²outcomes may change depending on the limiting element in the system – selective internal recycling of limiting elements

461 PCD: programmed cell death

462 **Figure legends**

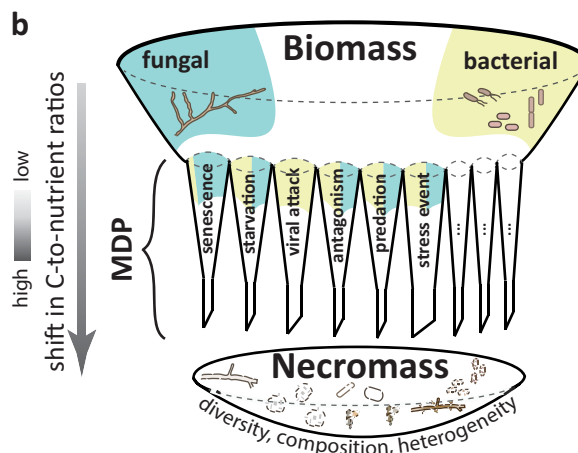
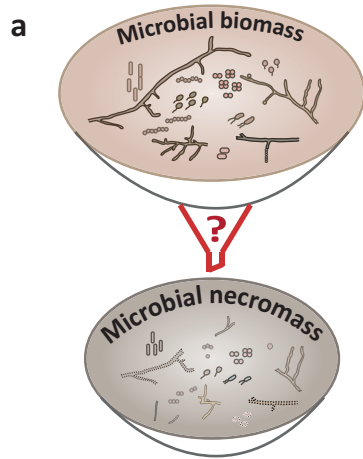
463 **Fig. 1:** Visual illustration of microbial death pathways (MDP) including molecular transformations
464 from microbial biomass to necromass. **a** The general question addressed. **b** Overview of different
465 forms of MDP with simultaneous chemical modifications. Funnels depict the different types of MDP
466 described, narrower lower funnel parts reflect higher internal recycling activity (Table 1). Blue and
467 yellow colour schemes visualize the likely relevance of MDP for fungi and bacteria, respectively. **c-g**
468 Specific examples are provided for individual types of MDP that are discussed in the literature.
469 Known cellular and molecular transformations are illustrated, as well as directions of resource flow
470 (black arrows).

471 **Fig. 2:** Visualizing the dependencies of microbial death pathways (MDP) on biotic and abiotic soil
472 properties and environmental factors. **a** Processes relevant for microbial necromass composition and
473 its fate are illustrated (solid arrows), as well as the impact of soil properties on these processes
474 (dashed arrows). Variables of microbial biomass, necromass and the chemical and physical soil
475 environment relevant for the respective processes are listed. **b** Simplified visualization of the
476 strength of chemical transformations during MDP and factors relevant in this context. Following
477 MDP, necromass may be fairly similar to the initial biomass (left); whereas certain MDP may lead to
478 significant transformation of the initial biomass (right).

479

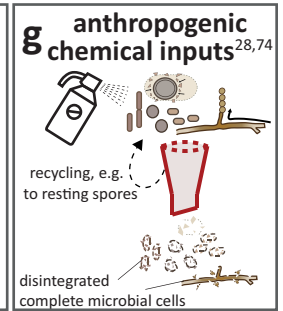
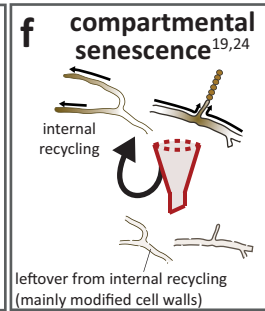
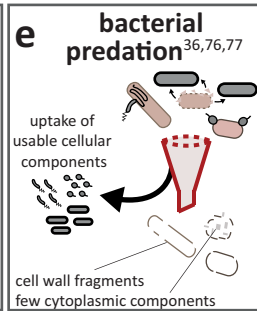
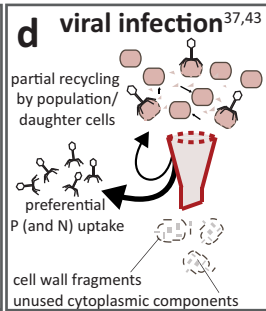
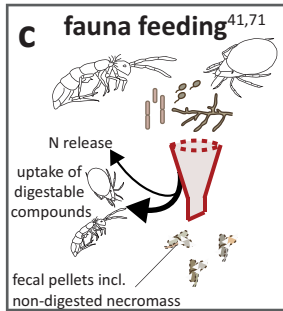
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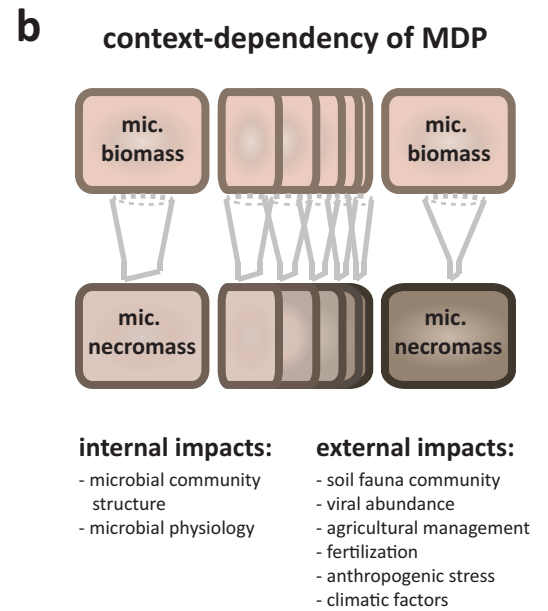
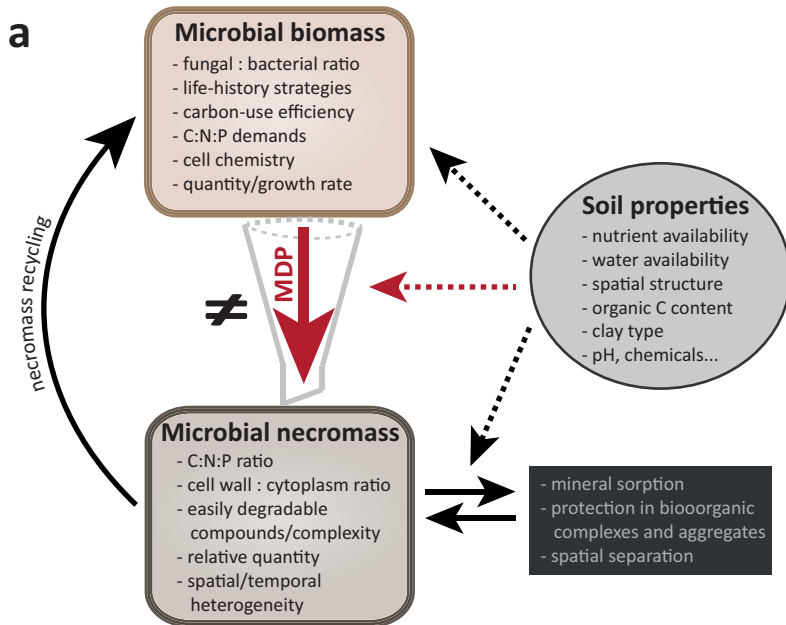
481



molecular transformations

- (i) increase in cell wall : cytosol ratios,
- (ii) relative reduction in easily degradable compounds and
- (iii) limiting resources





Box 1 | Implementing microbial death pathways in the conceptual understanding of biogeochemical processes

Microbial death pathways (MDP): The distinct processes of microbial dying, including chemical transformations dependent on the cause of death and the organisms involved

Why to implement? A short summary

- Not only microbial growth, but also the process of dying represents a relevant driver of the soil *microbial carbon pump*
- The chemical composition of biomass is altered during MDP, leading to distinct characteristics of resultant necromass (see examples in Fig. 1c-g) → Microbial necromass ≠ microbial biomass
- The chemical composition of microbial necromass affects its persistence (mean residence time), having impacts on both its mineralization and stabilization rates
- Individual types of MDP affect necromass composition differently: SOC sequestration and microbial community dynamics depend on the types of MDP relevant in soil
- (Re)use of components from biomass during natural MDP - by the species itself or attacking agents - leads to efficient channeling of C, nitrogen (N) and energy in soil
- Under certain conditions C sequestration via microbial pathways is not limited by N availability, and also does not necessarily reduce plant nutrient availability → high relevance for agricultural management
- Global change factors have direct impacts on the process and rate of microbial death
- differences in MDP among functional microbial groups explain community-driven effects, especially the increased C storage in fungal dominated systems: Fungal mycelia produce large amounts of C-enriched hyphal leftovers (necromass)

In more practical terms:

- C:N estimates and conversion factors for biomarkers of microbial necromass (derived from measurements in biomass) must be corrected
- Ecological experiments with microbial necromass should use *real* necromass derived from the completed MDP (metaphorically, leaf litter decomposition experiments also do not use fresh leaves)

How to implement? Some first ideas

In experiments:

- Understand individual MDP in more detail based on controlled experiments: Microbial strains/communities may be exposed to different stressors under laboratory conditions (agar media, artificial soil) and the chemical composition of derived necromass analyzed. Examples: inoculation with viruses or predators, exposure to sudden drought events, pesticide additions, reduction of nutrients. Necromass may be distinguished by life/death stains or isotope tracers, but also the chemical analysis of microbial biomass under stressed conditions will improve estimates of necromass chemistry (i.e., compared to biomarker conversion factors based on microbes grown on rich agar media)
- Preparing *real* necromass for experiments: (i) Microbial biomass exposed to different forms of MDP (see point above; including ¹³C labels) can be used for subsequent experiments in soil; (ii) bacterial and fungal isolates cultivated for necromass production may not be only autoclaved, but grown over longer time spans under suboptimal conditions; (iii) spatial and temporal sampling of the dying part of the microorganisms may allow to capture microbial cells most closely resembling the *real* necromass.
- Analyze mortality rates and turnover in microbial biomass and individual groups under varying conditions⁶⁷ and determine the relevance of different MDP under varying conditions/soil types using novel techniques (i.e., stable isotope probing, microfluidic devices)^{58, 66}.

In biogeochemical models:

- Simple parameters to include: (i) Biomass turnover times/mortality rates → necromass quantity (relative to microbial growth); (ii) adjusted relevance of pathways in the necromass continuum⁶⁴ depending on MDP and necromass composition (e.g., stabilization vs. destabilization); (iii) *death traits* of relevant microbial groups
- theoretical models can be used to test the relevance of MDP for C sequestration and persistence