



Supplement of

Modeling microbial regulatory feedback in organic matter decomposition identifies copiotrophic traits as key drivers of positive priming

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SUPPLEMENTARY TEXT

S1. Trophic Strategies of Copiotrophs and Oligotrophs

In Fig. S1, we showed the behavior of oligotrophs and copiotrophs at varying labile organic matter (OM) concentrations and respective population levels based on our fixed parameter values. While oligotrophs and copiotrophs can thrive in environments with less and more than 0.1 M of labile OM (Fig. S1A), the microbial activities are also influenced by their respective population levels. The copiotrophs are more sensitive to changes in population levels, where they need to exceed the oligotroph population by more than three times under labile OM-limited conditions, and by 1.5 times under labile OM-rich conditions to equally compete for available labile OM (Fig. S1B). Therefore, we set equal initial population levels for all microbial groups in all test cases in this study to give them equal footing in accessing labile OM (see Methods). However, the complex dynamics of complex OM degradation, simultaneous labile OM uptake, and microbial population accumulation can all influence the regulation strategy of microbes. Additionally, the degraders can transform the availability of labile OM for non-degraders depending on their efficiency in degrading complex OM. Therefore, it is imperative that we not only use the end conditions to characterize the overall priming effects but also consider the transient changes in priming effects over time. The overall and transient priming outcomes for various test cases are explored in the Results and Discussion section.

S2. Priming Effects and Microbial Population Levels in Alternative Binary Consortia Configurations

We further explored additional binary consortia configurations, including ODG-OND, CDG-CND, and CDG-ODG, that were not covered in the main text. When both CDG and ODG are paired together, the extent of positive priming is not as high, and occurrences of negative priming have significantly increased compared to the single functional group model of CDG or the binary consortium of CDG and OND (cf. top panels of Fig. S2A with Fig. 2A and Fig. 3A, respectively). In CDG-ODG systems, the community consists of degraders that can thrive across a wide range of labile OM conditions (with low levels favoring ODG and high levels favoring CDG), forming a strongly degradative community even in the absence of exogenous labile OM. In this case, the addition of labile OM provides only minor enhancement of positive priming and may increase the likelihood of negative priming. Moreover, interactions between the two degraders can also potentially lead to rapid accumulation of labile OM in the system, thereby reducing the subsequent degradation of complex OM. As expected from their characteristic trophic traits, ODG fare better in labile OM-poor conditions, while CDG thrive in labile OM-rich conditions (bottom panel of Fig. S2A). Conversely, when degraders and non-degraders share similar trophic strategies, they compete equally for labile OM, resulting in less efficient triggering of positive priming effects, and increased chances of negative priming when compared with the single functional group models of the respective degraders (cf. top panels of Figs. S2B and S2C with Fig. 2). Similarly, the combination of CDG and CND tends to have

a higher frequency of negative priming compared to when CDG are paired with OND (cf. top panels of Fig. S2B with Fig. 3A). This is because CND in the former are more adept at utilizing the labile OM produced by CDG, thereby reducing the potential of positive priming. Also, CDG and CND have comparable population levels as they both equally thrive and compete in labile OM-rich conditions (bottom panel of Fig. S2B). However, the combination of ODG and OND shows fewer instances of negative priming compared to when ODG are paired with CND (cf. top panels of Fig. S2C with Fig. 3B). This is potentially because OND in the former are less effective at exploiting the degradation products produced by ODG.

SUPPLEMENTARY FIGURES

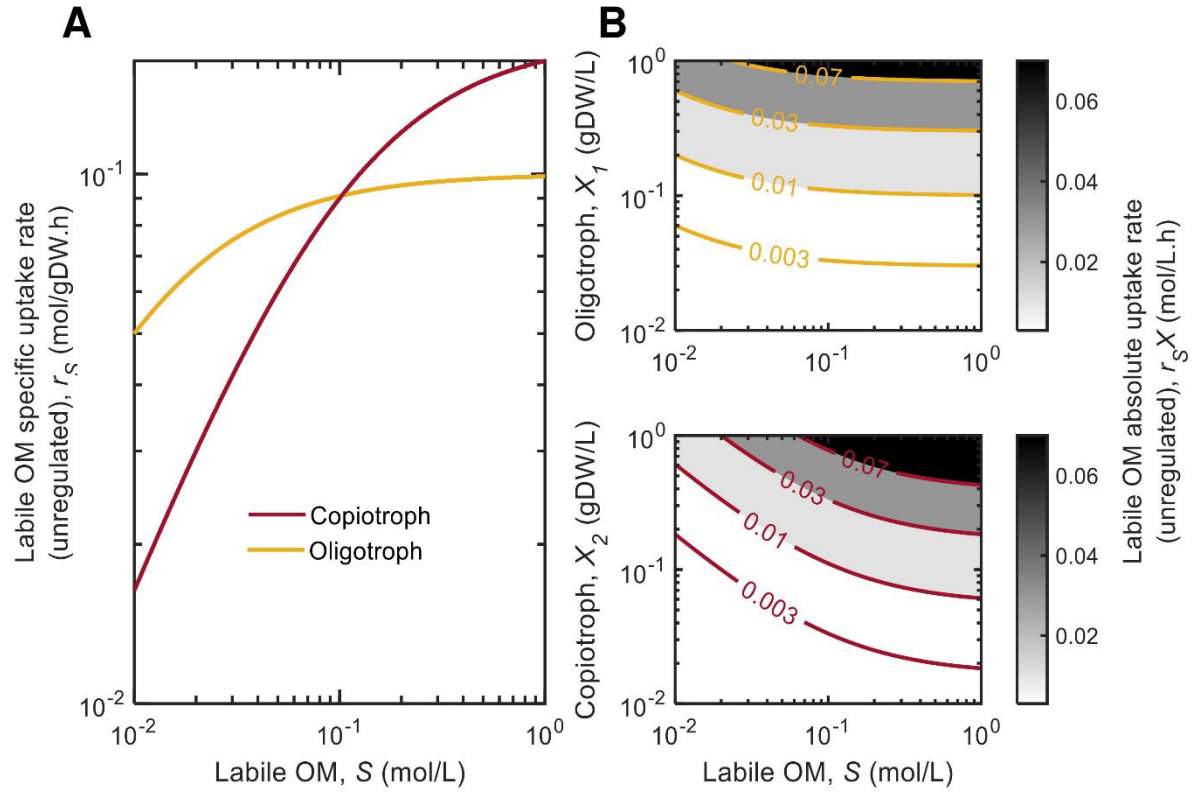


Figure S1. Differences in labile OM uptake kinetics between oligotrophs and copiotrophs visualized as **(A)** unregulated specific uptake rates with respect to only labile OM levels, and **(B)** unregulated absolute uptake rates with respect to both biomass and labile OM levels.

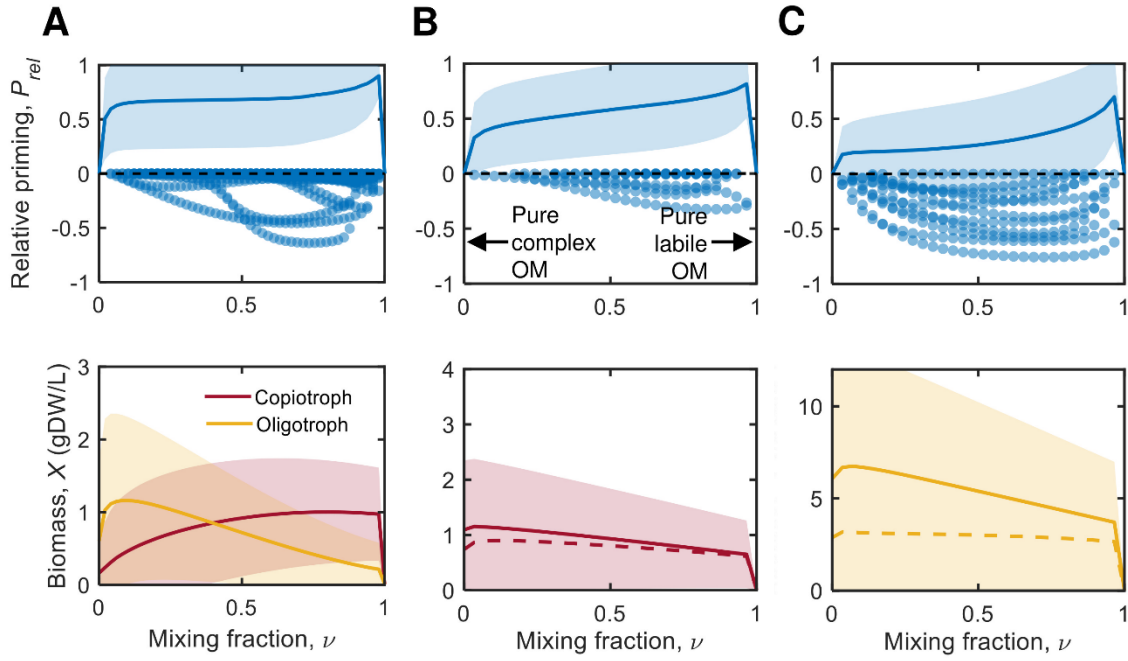


Figure S2. Overall relative priming effects and microbial population levels at various mixing compositions of complex and exogenous labile OM, evaluated for binary consortia of **(A)** copiotrophic and oligotrophic degraders, **(B)** copiotrophic degraders and non-degraders, and **(C)** oligotrophic degraders and non-degraders. The lines and shaded regions are averaged results and standard deviations of Monte Carlo simulations, respectively, while the markers are all individual runs with negative overall relative priming effects. In the population-level plots, the solid lines are degraders, and the dashed lines represent non-degraders.

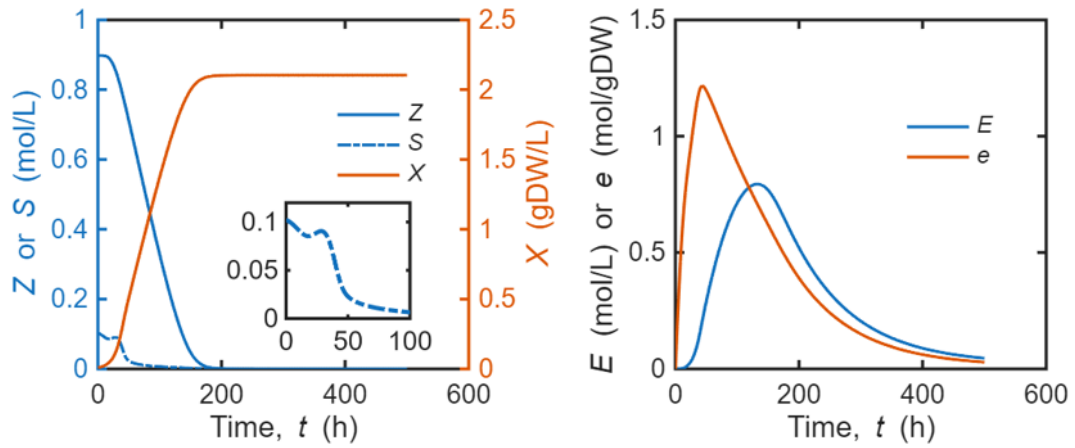


Figure S3. Dynamic model results showing the transient profiles of complex OM (Z), labile OM (S), biomass (X), exoenzymes (E), and endoenzymes (e) for a single run with randomly sampled parameters from the Monte Carlo simulations for the copiotrophic degrader case at a 10% labile OM fraction of the total OM in the complex and labile OM mixture. This figure illustrates the microbial regulatory response underlying complex OM degradation dynamics, where endoenzyme synthesis is initially upregulated to facilitate uptake of the available labile OM. The acquired energy subsequently supports exoenzyme synthesis, which enhances complex OM degradation and generates additional labile OM that is simultaneously assimilated to sustain biomass growth.

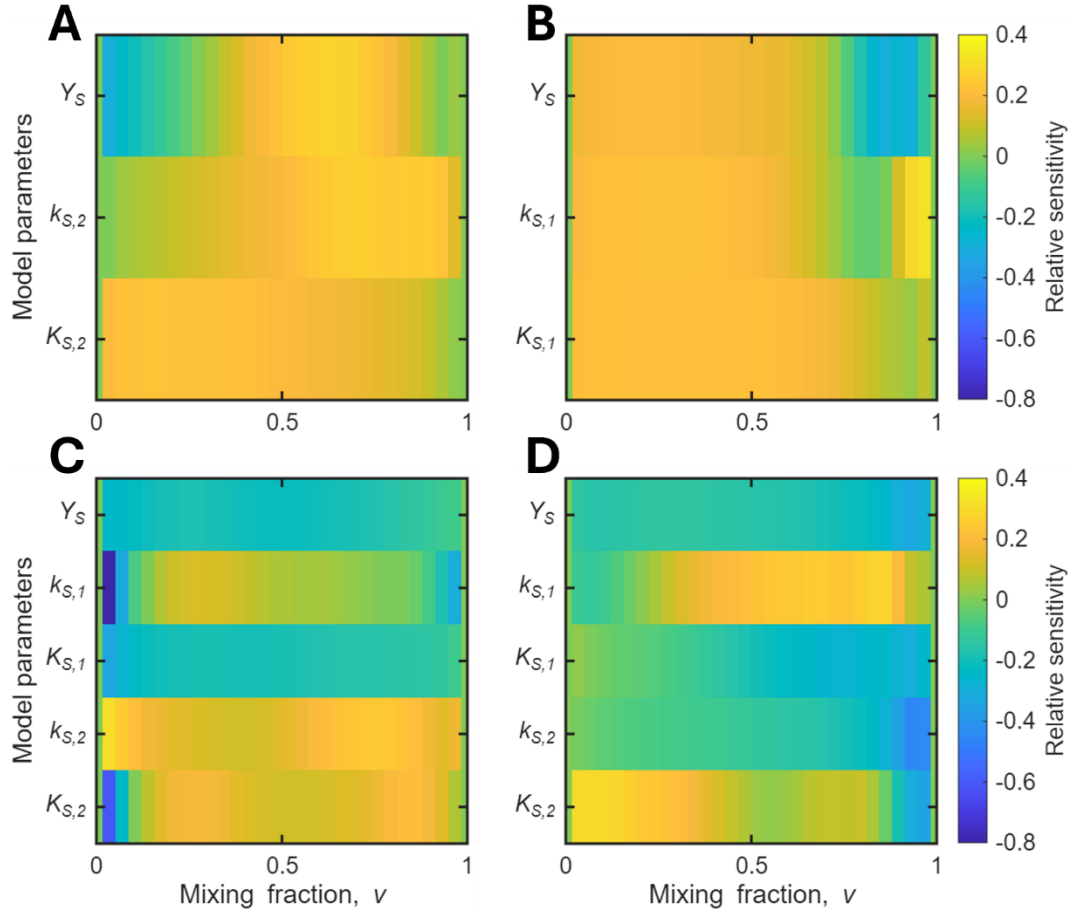


Figure S4. Relative sensitivities of model parameters on overall relative priming effects, evaluated for single functional group models of **(A)** copiotrophic degraders, **(B)** oligotrophic degraders, binary consortia of **(C)** copiotrophic degrader and oligotrophic non-degrader, and **(D)** oligotrophic degrader and copiotrophic non-degrader. Here, model parameters with subscript $i = 1$ are associated with oligotrophs, while $i = 2$ are associated with copiotrophs. A +20% perturbation was enforced for all model parameters in the sensitivity analysis. The parameters were perturbed one at a time while all other parameters were fixed at their baseline values. Relative sensitivities were quantified as the Jacobian of the model output with respect to the parameter perturbation, then scaled and normalized by the corresponding baseline parameter values. Parameters not included in the sensitivity analysis were either fixed or randomly sampled in the Monte Carlo simulations. Baseline values, fixed parameters, and randomization bounds are provided in Table S1.

SUPPLEMENTARY TABLES

Table S1. Model parameter values that were either fixed or randomized within specified bounds using uniform distributions in this study.

Model parameter	Unit	Fixed [F] or Randomized [R]	Copiotrophs	Oligotrophs	Remarks
$Y_{X,i}$	gDW/mol	R	[0, 2]	[0, 2]	-
$k_{S,i}$	mol/gDW.h	F	0.18	0.1	Copiotrophs > oligotrophs
$K_{S,i}$	mol/L	F	0.1	0.01	Copiotrophs > oligotrophs
$\alpha_{E,i}$	mol/gDW.h	R	[0, 1E-4]	[0, 1E-4]	-
$\alpha_{e,i}$	mol/gDW.h	R	$= \alpha_{E,i}$	$= \alpha_{E,i}$	Assuming basal synthesis rates of exoenzymes and endoenzymes are identical for simplicity.
$Y_{E,i}$	mol/mol	R	[0, 2]	[0, 2]	-
$Y_{e,i}$	mol/mol	R	[0, 2]	[0, 2]	-
$\beta_{E,i}$	1/h	F	0.01	0.01	-
$\beta_{e,i}$	1/h	F	0.01	0.01	-
$K_{E,i}$	mol/L	R	[0, 0.1]	[0, 0.1]	-
$K_{e,i}$	mol/gDW	R	[0, 0.1]	[0, 0.1]	-
$X_i(0)$	gDW/L	F	0.01	0.01	Made equal for all microbial groups for a fair comparison.
$Z(0)$	mol/L	F	Depending on the mixing fraction, ν		$\begin{cases} \nu = 0: Z(0) = 1; S(0) = 0 \\ \nu = 1: Z(0) = 0; S(0) = 1 \end{cases}$
$S(0)$	mol/L	F			
$E_i(0)$	mol/L	F	0	-	-
$e_i(0)$	mol/gDW	F	0	-	-
k_Z	mol/L.h	F	0.01		Fixed to exclude the effects of variability in complex OM properties on priming.
K_Z	mol/L	F	0.1		
Y_S	mol/mol	F	2		

Table S2. Summary of results for various priming models with different assortments of microbial groups exhibiting distinct trophic traits. The levels of priming (low: $P_{rel} < 0.1$, moderate: $P_{rel} = 0.1 - 0.9$, high: $P_{rel} > 0.9$) and the percentage occurrences (runs) of different priming types (positive, negative, zero) in the Monte Carlo simulations are presented. Note: CDG – copiotrophic degrader; ODG – oligotrophic degrader; CND – copiotrophic non-degrader; OND – oligotrophic non-degrader; PP – positive priming; NP – negative priming; ZP – zero priming.

	CDG	ODG
CDG	PP: High levels, 96.0% NP: 0.0% ZP: 4.0%	PP: Moderate to high levels, 94.6% NP: Low to moderate levels, 1.4% ZP: 4.0%
ODG	PP: Moderate to high levels, 94.6% NP: Low to moderate levels, 1.4% ZP: 4.0%	PP: Moderate to high levels, 95.7% NP: Low to high levels, 0.3% ZP: 4.0%
CND	PP: Low to moderate levels, 88.0% NP: Low to moderate levels, 5.3% ZP: 6.7%	PP: Moderate levels, 90.4% NP: Low to high levels, 5.6% ZP: 4.0%
OND	PP: High levels, 100.0% PP NP: 0.0% ZP: 0.0%	PP: Low to moderate levels, 82.9% NP: Low to moderate levels, 10.4% ZP: 6.7%