

Bacterial BEF relationships: degradation metabolic trade-offs with growth rate but not with nitrogen processing pathways

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Abstract

Biodiversity-ecosystem function (BEF) relationships have been a major topic since the 1990's, increasing in importance due to sustainability and extinction crises. However, the shapes of BEF relationships are not easily correlated with habitat, taxa, or diversity. We propose and test two predictors for BEF relationship shapes: 1) individual species growth rates (as indicative of coexistence and competitive abilities) and functional performance, and 2) BEF shapes of specific functions underlying a broader function. *Darlingtonia californica* is a carnivorous plant with modified leaves housing bacteria that contribute toward insect prey degradation and nitrogen provision. We isolated 14 distinct bacterial strains from fluid obtained from *D. californica*'s modified leaves. We grew the isolates in monoculture and mixed culture and evaluated each culture using degradation assays, and protein, ammonia, nitrate, chitinase, and protease quantification assays. We ask three specific questions related to our two proposed predictors of BEF shapes: 1) can we predict the function and assembly of a community based on individual species functions? 2) does a species function and growth rate correlate? 3) does degradation overall correlate with other functions in the metabolic processing of nitrogen? We found that increased degradative function was correlated with decreased species growth rates, highly functioning mixed cultures could result from both highly functioning isolates or moderately functioning isolates, and degradative function did not rely on nitrogen processing pathways. Our analysis suggests that BEF relationships present a metabolic trade-off between degradative function and bacterial division rates, but not with nitrogen processing. Additionally, while species with strong functional contributions can also be good competitors, they may also be poor competitors or play complex roles in community assembly.

Introduction

Biodiversity-ecosystem function (BEF) relationships have received renewed attention in the past decade due to current sustainability and extinction crises [1, 2]. While this has been a major topic in ecological research since the 1990's, identifying a cause for ecosystem function variation remains challenging [3]. Major BEF research has attempted to link these relationships to habitat, taxa, and research methods, yet we continuously find BEF shapes ranging from positive to negative [4]. Even when similar environmental conditions are present, very different communities can arise depending on timing of species introduction [5, 6]. Therefore, we should be focusing on differences in assembly mechanisms that dictate the relationship between biodiversity, community composition, and ecosystem functions [7–9]. We propose that to better predict BEF relationships, it may not be enough to simply track biodiversity; perhaps we must explicitly account for each species functional contribution and ecological role within the community in terms of growth and interspecific interactions.

Species can contribute to ecosystem function in three central ways. First, a species can both dominate as a competitor and as a contributor to function. Second, function can be distributed amongst multiple cooperative species through facilitation or niche partitioning. Third, species may contribute strongly to function but may be overshadowed due to poor competitive abilities. These patterns were described as two mechanisms by Loreau and Hector [10]: (1) selection and (2) complementarity. As an example of

positive complementarity, nitrogen-fixing legumes can increase the productivity of other plants when grown together [10, 11]. In contrast, as an example of negative complementarity, arbuscular mycorrhizal fungi, although often beneficial, when grown on some plants can lead to decreased N availability for the plant [12]. In terms of positive selection, there are plants, such as Norway spruce and Douglas fir which yield far higher biomass in monoculture than any mixed cultures in study, not only performing highly functionally but also managing to be strong competitors [13]. However, negative selection may appear in the case of invasive species who succeed in outcompeting native flora and fauna but reduce food web efficiencies [14]. Rather than experimentally examining every species interaction to establish the driving BEF mechanism, determining species driving functions can be used to predict BEF patterns and mechanisms.

BEF research over the last 20 years has revealed (1) communities with fewer species generally function less efficiently and (2) primary productivity has been the focal function of interest [15, 16]. Meta-analysis of over 100 experiments with abundance or biomass as the response variable revealed, on average, a loss in biomass resulted in a loss of function [17]. From these studies, it is evident that positive selection effects are common when examining biodiversity-biomass relationships within a trophic level [18], and this can be accounted for by a combination of complementarity and negative selection [19]. However primary production and respiration is performed broadly by all trophic groups, including consumers, predators, and primary producers [17], and critiques of current research point out that many early studies used simple systems lacking trophic complexity; in more complex systems we may not expect to observe positive BEF relationships consistently [3, 15]. Diverse assemblages of species often fail to produce more biomass than the highest performing single species, indicating that loss of function is dependent on the species lost [17]. To establish driving mechanisms behind BEF, it may be instrumental to find unifying links between biodiversity and other functions supplemental to primary production.

Decomposition and degradative metabolic processes play a complex role in biogeochemical cycling and ecosystem function, yet we know little of their relationship with other ecological traits. Breakdown of complex organic products requires specific genes and enzymes, some of which are limited specifically to microbial taxa [20]. Microorganisms drive and maintain the key degradative processes of nitrification, denitrification, and ammonification [21]. While the processes of microbial assembly that maintain these specific genes and complex decomposition functions are not well understood, previous research has revealed that bacterial nitrification and denitrification processes have a significant, albeit low, relationship with species richness [7, 20, 22]. Based on a review of 14 studies, Jiang and collaborators [18] found that decomposition of simple substrates such as cellulose positively related to biodiversity, while complex substrates such as leaf, wood, and wheat mass had relationships trending from positive to neutral to negative in relation to biodiversity [18]. If substrate complexity has distinct relationships with biodiversity in terms of decomposition, we must consider specific trade-offs between functions and community composition.

Microbial communities within the leaves of the carnivorous plant *Darlingtonia californica* are an ideal model system for measuring relationships between microbial traits and decomposition. Previous

research shows that bacterial diversity within the plant can be linked to the leaf nitrogen uptake, and research on nitrogen requirements reveals that the plant can acquire up to 76.4% of its nitrogen from insects [23, 24]. In the case of insect degradation, chitin degrading pathways require specialized enzymes and result in the freeing of carbon and nitrogen compounds, including smaller chitin chains, fat, proteins, amino acids, and other carbohydrates [25, 26]. *D. californica* research has reported no digestive enzymes, and other plants in the same family may excrete low efficiency enzymes [27, 28]. Because insect-derived nitrogen seems to be a key nutrient in this system affected by microbial diversity [23, 24], the BEF relationships between bacteria and nitrogen functions present a unique opportunity to examine functional contribution, interspecific interactions, and bacterial growth patterns.

In this study, we evaluated three questions about degradative function and its relationship with bacterial growth: (1) can the best functioning community be predicted based on isolate function, (2) can function be explained by bacterial growth rates, and (3) can function be explained by nitrogen processing. We evaluated degradative function in bacteria isolated from *Darlingtonia californica*. Fourteen isolated bacteria were subjected to a degradation experiment in monoculture and in coculture. Given that more expansive experiments on BEF relationships in degradation and decomposition have found correlations ranging from positive to negative, we instead focus on the processes that may be driving the relationships. While this small group of culturable bacteria cannot fully represent the functions of the complex communities observed in the field, the aim is to understand how individual species grow and impact nitrogen cycling, and how these trends are disrupted when these species coexist with one or more other species.

Materials and Methods

Isolation, Storage, and Identification of Bacterial Isolates

Fourteen cryopreserved bacterial isolates were revived using LB broth. Isolates were previously obtained by Dr. Cuellar-Gempeler from greenhouse and field collections of *Darlingtonia* fluid and maintained in cryovials using 2% DMSO. Stored isolates were thawed and 1mL aliquot was transferred to a microcentrifuge tube, and sample was centrifuged at 100xg for 10 minutes. DMSO supernatant was removed, and bacteria pellet was mixed into LB broth which was incubated for 48 hours at 30°C. Broth was streaked onto LB plates to confirm purity.

To perform colony PCR, a needle was used to remove bacteria from a single colony and diluted in tube with 20 µL ultrapure water. PCR cocktail consisted of 25 µL DreamTaq PCR Mastermix, 23 µL Nuclease-Free Water, 0.5 µL forward primer (27F), 0.5 µL reverse primer (1492R) per sample. 49 µL of PCR cocktail was combined with 1 µL of diluted bacterial sample. Samples were run in the thermocycler with settings: 35 cycles, 95°C 4 minutes, 94°C 1 minute, 58°C 1 minute, 72°C 7 minutes, 4°C upon completion of 35 cycles. Samples were submitted to Eurofins for Sanger sequencing.

Cultured Community

Once isolates were acclimated to lab condition, they were streaked on LB agar media to confirm purity and then plated to quantify abundance. Samples were diluted with LB broth to 10^7 cells/mL. They were then inoculated into duplicate monocultures by adding 5mL of 10^7 cell/mL culture to 40 mL LB broth for a total of 28 samples, plus two media controls, and incubated at room temperature for 48 hours. Five groups each of 2, 3, 4, and 5 mixed cultures were randomly assembled in equal amounts. For mixed cultures with 2 species, 2.5mL of each species was added, for mixed cultures with 3 species, 1.67 mL of each species was added. For mixed cultures with 4 species, 1.25mL of each species was added. For mixed cultures with 5 species, 1mL of each species was added. This equated to adding a total of 5mL of 10^7 cells/mL culture to 40mL LB broth for a total of 20 samples, plus two media controls; these were incubated at room temperature for 48 hours. Bacterial species and composition of groups are detailed in Table 1 and Table 2 respectively.

Table 1
Bacterial isolate identities.

Isolate Number	Scientific Name	Percent Identity	Acquisition Number
1	<i>Bacillus sp. WYT007</i>	98.30%	JQ807855.1
2	<i>Curtobacterium sp. b213 4</i>	90.75%	KF733315.1
3	<i>Leucobacter sp. 1</i>	98.14%	MH671536.1
4	<i>Staphylococcus equorum 1</i>	87.03%	KC513844.1
5	<i>Acinetobacter sp.</i>	99.18%	MF462948.1
6	<i>Leucobacter sp. 4</i>	93.75%	MH671536.1
7	<i>Arthrobacter gandavensis 1</i>	85.32%	MT539758.1
8	<i>Leucobacter sp. 2</i>	98.14%	MH671536.1
9	<i>Bacillus pumilus</i>	81.56%	AJ494732.1
10	<i>Curtobacterium sp. b213 3</i>	90.40%	KF733315.1
11	<i>Staphylococcus equorum 2</i>	95.05%	JX134628.1
12	<i>Curtobacterium sp. b213 2</i>	90.29%	KF733315.1
13	<i>Curtobacterium sp. b213 1</i>	92.32%	KF733315.1
14	<i>Leucobacter sp. 3</i>	99.15%	MH671536.1

Table 2
Composition of mixed culture communities.

Group Name	Bacteria Included (By isolate number)
Mix 1	7, 13
Mix 2	4, 7
Mix 3	8, 9
Mix 4	11, 14
Mix 5	3, 9
Mix 6	8, 10, 13
Mix 7	9, 12, 14
Mix 8	3, 6, 13
Mix 9	5, 7, 14
Mix 10	10, 12, 14
Mix 11	3, 4, 6, 8
Mix 12	1, 6, 11, 14
Mix 13	1, 3, 6, 11
Mix 14	1, 5, 11, 14
Mix 15	7, 10, 11, 12
Mix 16	1, 7, 8, 10, 11
Mix 17	3, 8, 10, 13, 14
Mix 18	1, 6, 9, 10, 13
Mix 19	5, 8, 12, 13, 14
Mix 20	5, 7, 11, 13, 14

Because *Bacillus sp. WYT007* did not produce single colonies upon plating (it formed filamentous mats), counts for this species have been converted from a percentage of plate coverage into colony counts by taking that percent of coverage and multiplying it by the maximum species abundance counted, that being of *Curtobacterium sp. b213 2* at an abundance of 1.2×10^{11} cells/mL, as they visually looked the most similar at max coverage.

Fruit Fly Preparation for Degradation Experiments

Drosophila fruit flies were purchased from Arcata Pet Supply in Arcata, CA. Culture was then frozen over night at -20°C to sacrifice flies. Flies were then collected and dried for 48 hours at 60°C and autoclaved to sterilize. These were then transferred into sterile 1.5mL cages, produced by drilling 24 holes into a 1.5mL centrifuge tube to allow for flow of fluid and bacteria, for a total of 12-15mg of flies per 1.5mL cage. Exact mass per cage was recorded by recording each cage without flies and with flies.

Degradation Experiment

The cultured community and serial dilution community were subjected to the following degradation experiment. Following acclimation of the communities, samples were plated to calculate cell density at the start of the degradation. Fruit fly cages were placed in each sample and samples were loosely capped to allow for airflow. Samples were then incubated at room temperature for 11 days in still conditions to simulate the still conditions in which *Darlingtonia* leaves live. Samples were inverted once daily to encourage flow of bacteria in and out of the fruit fly cages for the duration of the degradation experiment. At the end of the 11 days, 1.5 mL fluid was collected for each solubilized protein, protease, and chitinase quantification, and 10 mL was collected for nitrate and ammonia quantification. Samples were plated to quantify end of experiment densities.

Relevant Measures of Specific Nitrogen Function Assays

Following degradation, samples were collected for measurement of specific nitrogen metabolic functions and frozen at -20°C until measurement. Degradation rate, enzymatic activity of protease and chitinase, solubilized protein, nitrate, and ammonia were measured. Degradation rate was measured by drying fly cages at 60°C for 3 days and subtracting from pre-degradation mass to calculate fly mass loss. Chitinase activity was quantified using the Chitinase Microplate Assay Kit from MyBioSource (catalog #MBS8243204) and read on Spectra iMax at 585 nm. Protease activity was quantified using the Protease Assay Kit from ThermoScientific (catalog #23263) and read on the Spectra iMax at 450 nm. Solubilized protein was quantified using a Bradford assay and reading on a Nanodrop 1000 at 595 nm. Solubilized protein and enzymatic activity of chitinase and protease were measured in duplicate to verify accuracy of spectrophotometric quantification. Ammonia and nitrate was quantified using the Orion™ High Performance Ammonia Electrode and calibrated using standards from USAbluebook.

Bioinformatics and Data Analysis

Sanger sequences were read using the package `sangerseqR` (version 1.30.1) [29]. Reverse sequences were reversed using the function `reverseComplement` from the package `Biostrings` (version 2.60.2) [30]. Low quality bases were trimmed and sequences were merged using the package `sangeranalyseR` (version 0.1.0) [31]. Files were saved using the function `write.dna` from the package `ape` (version 5.5) [32]. DNA sequences were then matched to previously isolated strains in the NCBI database using BLAST.

We calculated degradation and growth rates from the monocultures to establish relationships between these parameters. To calculate bacterial growth rates at the start of degradation, we subtracted bacterial cell concentration upon inoculation from bacterial cell concentration at the start of the 11 day degradation experiment. To calculate end of degradation growth, we subtracted cell concentration at the start of the degradation experiment from cell concentration at the end of the experiment. Significance of correlation was tested using a linear model with a significance test for linear regression using the function `lm`. All analyses and plots were performed and produced using the R statistical environment (version 4.1.1, R Core Team, 2020). Relationships were plotted and visualized using the `ggplot2` package (version 3.3.6) [33]. P-values were adjusted using the Benjamini and Hochberg method; degradation rate was the dependent variable and specific nitrogen functions were the explanatory variables [34].

To establish the biodiversity-function relationship in the mixed community experiments, we used a linear regression model with diversity metrics as the explanatory variables and function metrics as the dependent variable. We used function `lm` which included a significance of correlation test.

To evaluate the relationship between the cultured communities and complementarity and selection, we used the `partitionBEFsp` package (version 1.0) [35]. Monoculture and coculture plate counts were used and functions `calculate_DRY` and `classic_partition` were used to calculate complementarity and selection values. These values were plotted using a linear regression model and function `lm` was used to measure significance of correlation.

Results

No results correlated with end of degradation experiment cell densities and diversity, therefore throughout the results we focus specifically on cell densities and diversity recorded at the start of the 11 day degradation experiment.

Degradation rates of the 14 species grown in monoculture are visualized in Fig. 1A. *Bacillus mycoides* cultures performed the highest degradation (11.2 mg), with 8 species resulting in fly mass retention compared to the control average of 5.3 mg, with the lowest recorded average degradation rate being – 2.3 mg. Cell abundances of the 14 species, in contrast, show an overall increase from *Bacillus mycoides* to *Leucobacter sp. 3* (Fig. 1B).

The 14 bacteria grown in monoculture performed degradation at varying rates, with *Bacillus mycoides* being related to highest degradative function and *Leucobacter sp. dR13-9* being related to lowest degradative function. The solid black line indicates control average, the dash line indicates zero. (B) Monoculture cell abundances measured at the start of the degradation experiment. The dash line indicates zero.

In the monocultures, degradation rate correlated negatively with growth rates (Fig. 2, $df = 26$, $R^2 = 0.17$, $F = 5.50$, $p = 0.027$), but no other specific function correlated with growth rate (Table 3). No specific

nitrogen function correlated with degradative function (S1). No trend was found between bacterial abundance and the specific nitrogen functions.

Species with higher growth rates had lower degradation rates at the end of the experiment. The dash line indicates zero, the solid line indicates the linear regression model fitted to fly mass loss and cell abundance.

Table 3
Monoculture bacterial growth rate vs. function Results of linear regression significance test of bacterial growth rate compared with each functional assay. Degrees of freedom for all tests were 26. Significance results are highlighted in bold.

Functional Assay	<i>R</i> -squared	<i>F</i> -statistic	<i>p</i> -value
Degradation Rate	0.1429	5.501	0.02691*
Bradford	0.01209	1.33	0.2592
Nitrate	-0.0233	0.385	0.5403
Ammonia	0.02776	1.771	0.1948
Chitinase	-0.0276	0.2758	0.6039
Protease	0.01138	1.311	0.2627

In mixed culture, degradation rate correlated positively with species richness (Fig. 3, $df = 18$, $R^2 = 0.31$, $F = 8.14$, $p = 0.011$). In contrast, no other correlation was found between other nitrogen metrics and species richness (Table 4) or between degradation rate compared with specific nitrogen assays (S2).

The degradation rate correlated positively with species richness. The dash line indicated zero, the solid black line represents the linear regression model fitted to fly mass loss and species richness.

Table 4
Mixed culture species richness vs. function Results of linear regression significance test of species richness compared with each functional assay. Degrees of freedom for all tests were 18. Significance results are highlighted in bold.
*Represents significance to the $p < 0.05$.

Functional Assay	<i>R</i> -squared	<i>F</i> -statistic	<i>p</i> -value
Degradation Rate	0.2731	8.14	0.01056*
Bradford	-0.05516	0.006743	0.9355
Nitrate	0.02025	1.393	0.6333
Ammonia	-0.03524	0.3533	0.9328
Chitinase	0.04893	1.978	0.6333
Protease	-0.04992	0.09655	0.9355

Importantly, diversity treatments did not always result in consistent richness for the duration of the experiment. While 5 groups were inoculated with 5 species, only Group 16 and 19 continued to maintain this richness level by the start of the experiment. Group 17, 18, and 20 reduced to 4, 4, and 3 species respectively. Group 16 and 19 also had two of the three highest fly loss measures.

Evaluating the effects of complementarity and selection on mixed culture function revealed no significant relationship (S3).

Further evaluation of the species involved in this study reveals relationships with degradative and nitrogen processing functions, including presence of chitinolytic and proteolytic activity (Table 5).

Table 5

Species involved in this study and degradative and nitrogen processing traits found in previous literature.

Family	Relevant Genus	Degradative Metabolic Traits	Nitrogen Processing Traits	Reference
<i>Bacillus</i>	<i>WYT007</i> <i>Pumilus</i>	Proteolytic, amylolytic, cellulolytic activity; lipolysis	Proteins	Chan et. al. 2016; Howard et. al. 2013
<i>Curtobacterium</i>	<i>B213</i>	All Identified Carbohydrate substrates		Chase et. al. 2016
<i>Leucobacter</i>		Amino acid metabolism	Amino acids	Percudani 2013
<i>Staphylococcus</i>	<i>Equorum</i>	Carbohydrate utilization, proteolytic activity	Peptide hydrolysis	Lee, Heo, & Jeong, 2018
<i>Acinetobacter</i>		Carbon and aromatic compounds, lipolysis		Howard et. al. 2013
<i>Arthrobacter</i>	<i>Gandavensis</i>	Nitrogen fixation	Nitrogen fixation	Özdoğan, Akçelik, & Akçelik, 2022

Discussion

As we advance our understanding of biodiversity-ecosystem function relationships, a central goal should be to understand assembly mechanisms, functional contributions, and ecological roles of species within a diverse community. In this study, we aimed at testing two predictors of BEF relationships, underscored by species traits and the relationship between broad and specific functions, yet we found that these straightforward factors still did not explain the BEF patterns observed. Overall, we found positive BEF relationships in the mixed culture experiment, driven by degradation in groups 16, 17, and 19. Instead of strong contribution from highly functional species as expected from selection effects models [10, 11] it would seem these patterns result from complementarity (although not statistically significant) between intermediate performers. In fact, we found a significant negative relationship between bacterial growth rates and degradative function, suggesting that the degradative function may have a fitness cost. This has been previously linked to negative selection effects and negative BEF relationships [18, 36]. At the same time, we found no relationships between nitrogen metabolic pathways and degradative function, suggestive that specific functions, at least within nitrogen processing, are poor predictors of insect degradation in this system.

Addition of species increases degradative function, aligning with several BEF studies that found positive relationships between species richness and community function [22, 37, 38], but the most functional groups do not necessarily contain the most functional individual species. While *Bacillus sp. WYT007* was highly functional in monoculture, mixed cultures of which it was a member performed highly (group 16) and weakly (group 12, 13, 14, 18). Groups comprised of lower functioning species perform similarly

to groups with high functioning species, likewise, all groups with 3 or fewer species perform similarly. Because of the small pool of 14 species in this study, the BEF relationship observed is difficult to compare to the breadth of diversity that would be observed in natural systems; but recognizing that loss of a highly functioning species in a community may not necessarily lead to a loss of overall function is important. Complementarity effects may bear more weight in this community, and ecological process coverage from different species may allow the overall community function to be higher than that of a single high-functioning species [7].

Viewing degradation in *D. californica* as a function of bacterial growth rate may allow us to understand one of the aspects influencing community diversity and BEF relationships. We found that bacterial growth and abundance correlates negatively with degradative function (Fig. 2), indicating a fitness cost of degradation. Metabolic strategies represented include rapid growth, prioritized during resource abundant conditions, and slow growth, prioritized during resource scarce conditions [39, 40]. Slow growth may be energetically efficient [39], allowing bacteria like *Bacillus sp. WYT007* to succeed in monoculture. However, the highly functioning communities of group 16, 17, and 19 were dominated by fast-growth species, which is successful in cases of high resource availability, and may be indicative of complementarity due to the production of enzymes or nutrients available to the whole community [39, 41]. Evidently, the presence of both metabolic strategies has positive impacts on community function, as communities consisting of slow growth-high degraders and rapid growth-low degraders have the potential to produce highly functioning communities, as observed in the mixed-culture portion of our experiment. Metabolism and degradation are ultimately complex, and depend on a wide variety of nutritional substrates, organismal factors, and community factors.

Nitrogen metabolic pathways do not correlate with overall insect degradation and are not a strong indicator of this community's function. Chitin, an aminopolysaccharide, and protein generally respectively make up 30–42% and 44–61% of insects by dry weight [42], so the role of degradation of these compounds was not expected to be nominal. Conversely, insect prey is approximately 10% nitrogen by weight [43], and many of the isolates present in this study have been shown to process lipids, carbohydrates, and other non-nitrogen substrates in other systems (Table 7). Other studies have found positive correlations in carbon substrate utilization and community degradation function [38]. Therefore, despite the large presence of nitrogen-based compounds, like chitin and protein, it may be important to consider the role of carbon substrate degradation in this system as well.

In addition to the nitrogen requirement expectations of the lab-based cultures used in this experiment, *D. californica* acquires approximately 76.5% of its nitrogen from insects [24]. Evidently, the necessity for insect-derived nitrogen is not a considerable driver behind bacterial nitrogen processing. While cultures were not grown within the host plant for the duration of the experiment, and therefore were not directly influenced by the nutrient requirements of the host, microbial growth rates correlate more with the nutrient availability they evolved with than the current nutrient availability [44]. Despite these expectations, ammonia and nitrate concentration had no correlation with degradative function, indicating that insect degradation is not driven solely by nitrogen requirements of the plant.

Conclusion

The BEF relationships behind degradative function are complex, linked negatively with bacterial growth rates but surprisingly not with nitrogen processing. Despite *D. californica* acquiring a vast majority of its nitrogen from insects, insect degradation does not appear to correlate with nitrogen processes in the bacteria that live within the pitcher. This indicates that bacterial metabolism is not influenced by the metabolic needs of the host plant, and instead that microbial assembly and metabolic networks may respond to processes intrinsic to the microbial community, more related to competition, predation, colonization, and habitat filtering or drift. Although research on BEF relationships has vastly improved our understanding of how individual species' metabolic traits affect community function, we still lack unifying drivers that can be used to predict community function across a broad number of systems. We suggest that bacterial growth strategies present a valuable tool in understanding community complementarity, competition, and function.

Declarations

Competing Interests

Authors declare there were no competing financial interests in relation to the work in this article.

Author Contribution

MT and CCG wrote the main manuscript text and MT prepared figures 1-3, tables 1-5, and supplementary information. All authors reviewed the manuscript.

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Data Availability

The datasets generated and analyzed during the current study are available in the Zenodo repository [doi: 10.5281/zenodo.10149994]. Bacterial 16S rRNA sequences have been submitted to NCBI SRA (SUB14137204).

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Figures

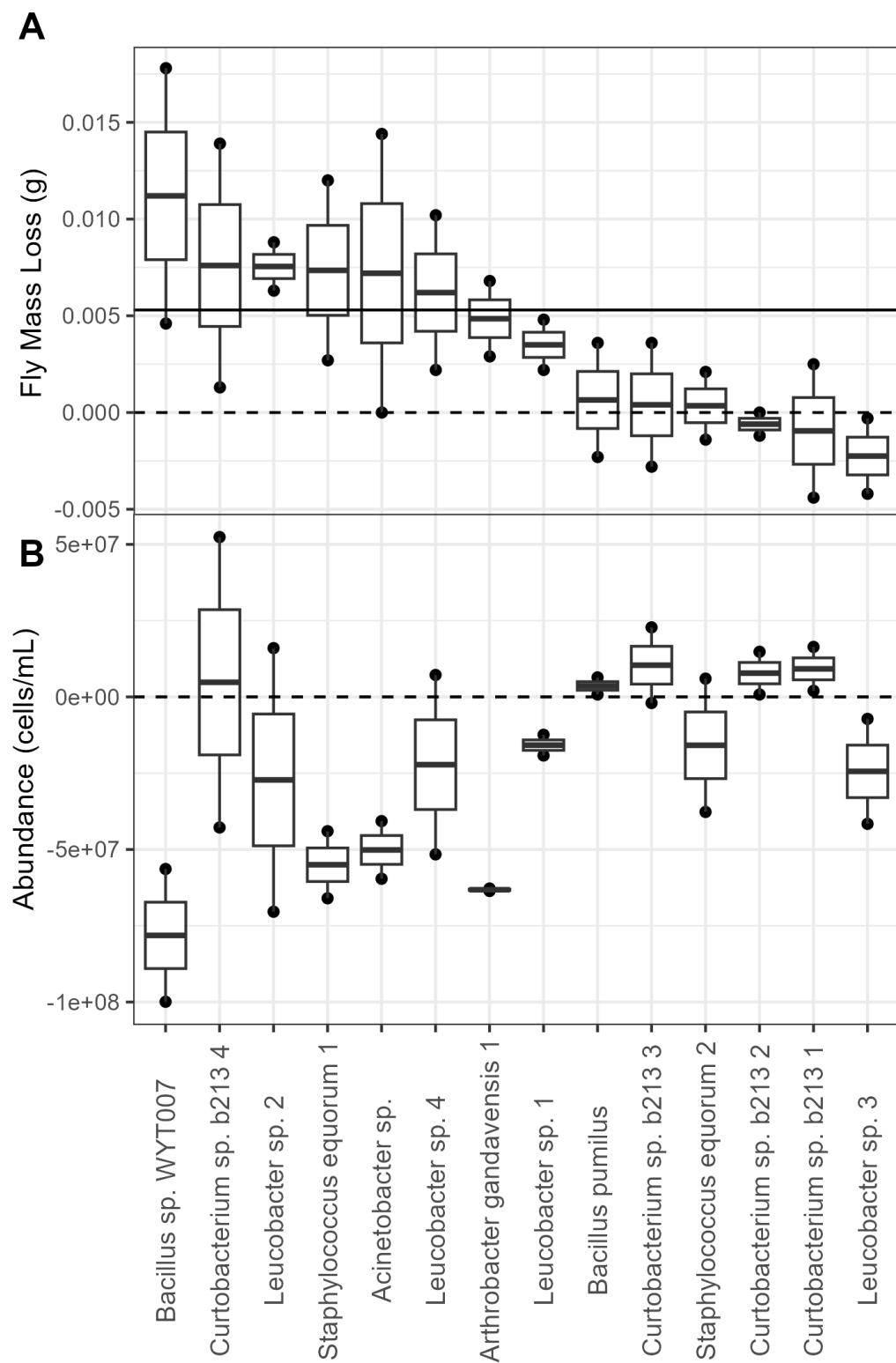


Figure 1

(A) Monoculture Degradation Rates.

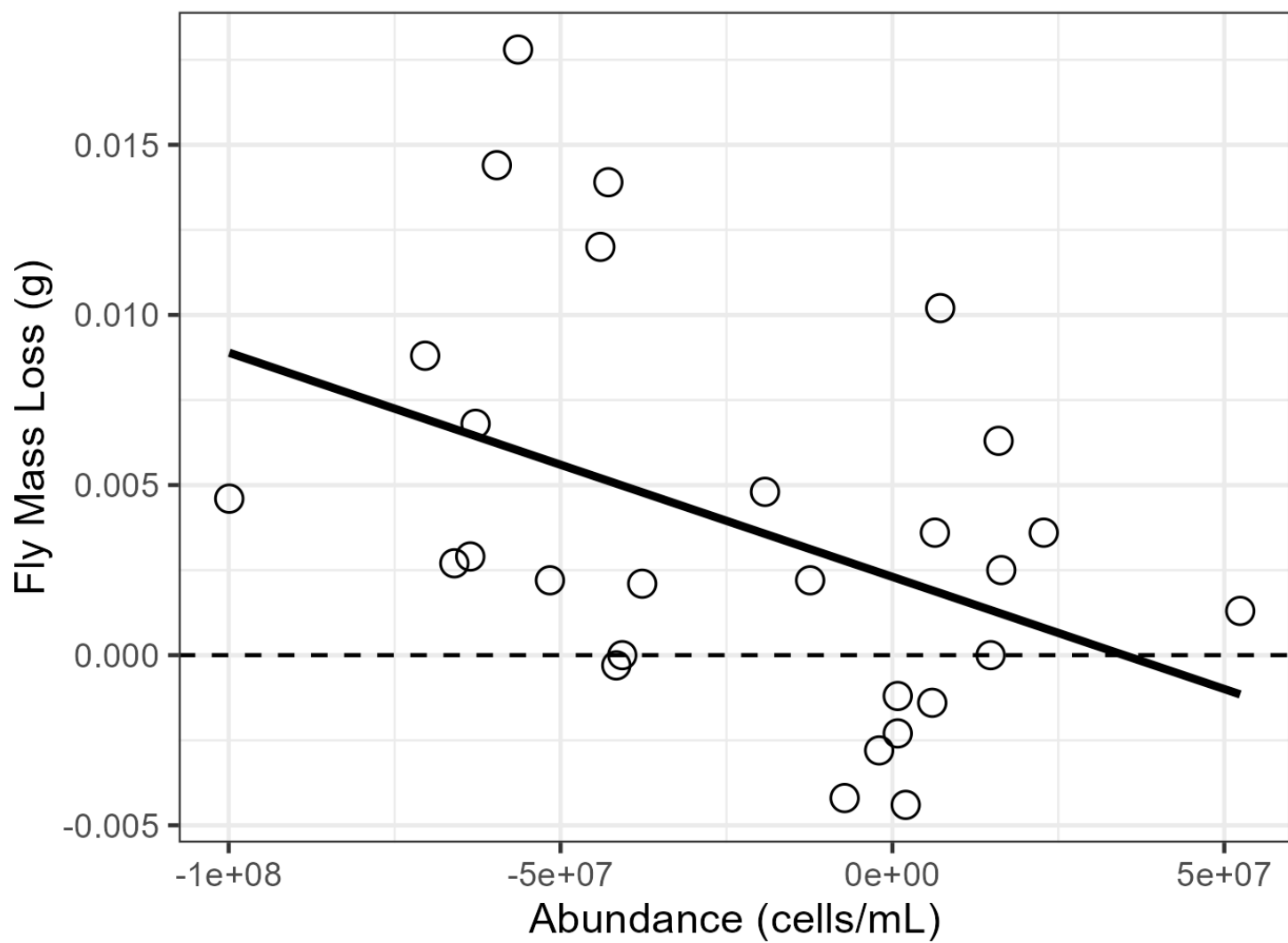


Figure 2

Monoculture bacterial growth vs. degradation rate.

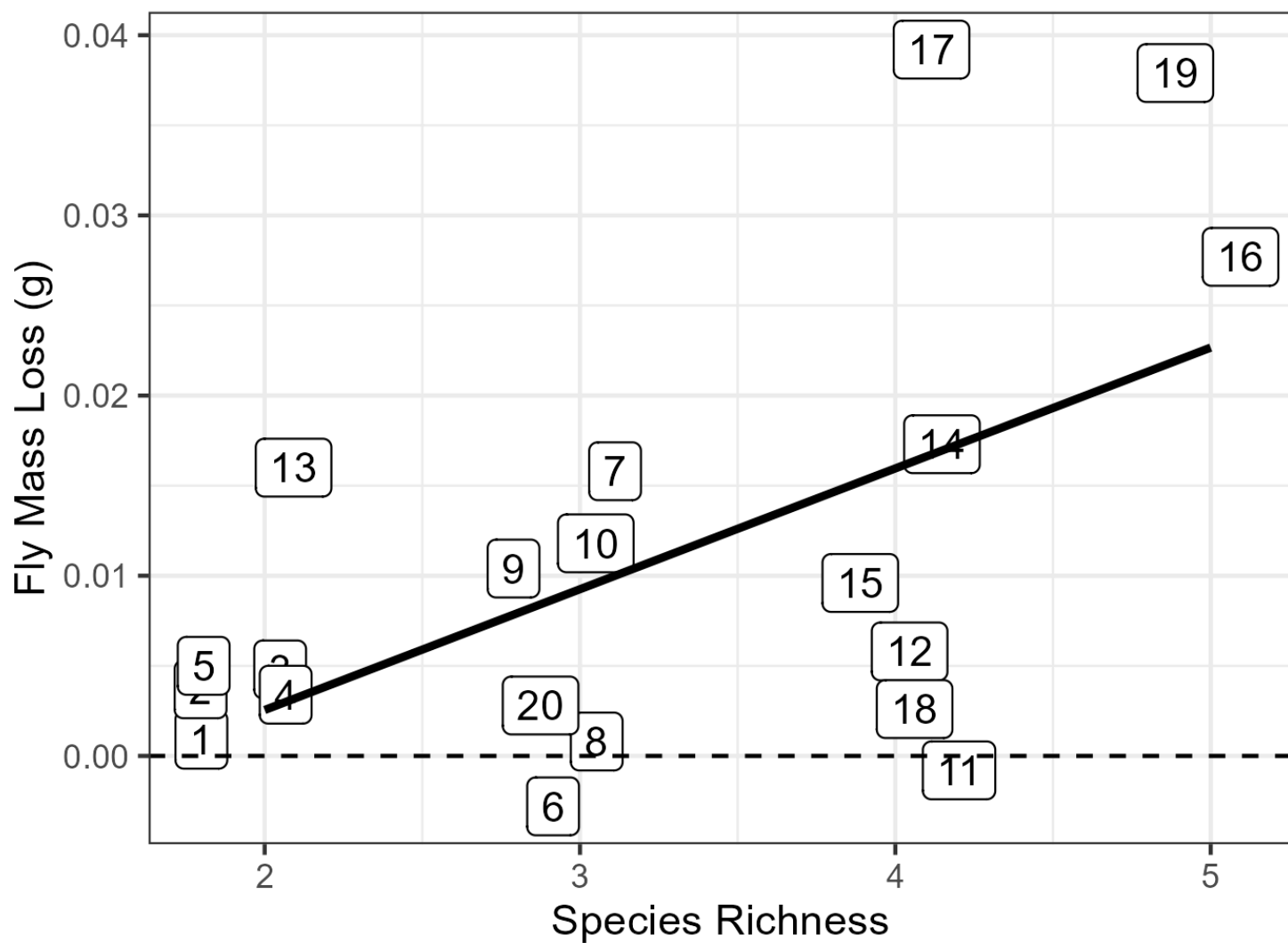


Figure 3

Mixed culture degradation rate vs. species richness.

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