Understanding How Microbiomes Influence The Systems They Inhabit: moving from a correlative to a causal research framework

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Abstract

Translating the ever-increasing wealth of information on microbiomes (environment, host, or built environment) to advance the understanding of system-level processes is proving to be an exceptional research challenge. One reason for this challenge is that relationships between characteristics of microbiomes and the system-level processes they influence are often evaluated in the absence of a robust conceptual framework and reported without elucidating the underlying causal mechanisms. The reliance on correlative approaches limits the potential to expand the inference of a single relationship to additional systems and advance the field. In this perspective piece we propose that research focused on how microbiomes influence the systems they inhabit should work within a common framework and target known microbial processes that contribute to the system-level process of interest. Here we identify three distinct categories of microbiome characteristics (microbial processes, microbial community properties, and microbial membership) and propose a framework to empirically link each of these categories to each other and the broader system level processes they affect. We posit that it is particularly important to distinguish microbial community properties that can be predicted from constituent taxa (community aggregated traits, CATs) from those properties that are currently unable to be predicted from constituent taxa (emergent properties, EPs). We discuss how a series of existing methods in microbial ecology can be applied to more explicitly elucidate properties within each of these categories and connect these three categories of microbial characteristics with each other. We view this proposed framework, gleaned from a breadth of research on environmental microbiomes and ecosystem processes, as a promising pathway with the potential to advance microbiome science across a broad range of disciplines.

Current Approaches Linking Microbial Characteristics and Ecosystem Processes

In all ecosystems, virtually all processes are influenced by microorganisms and many processes are carried out primarily/exclusively by microorganisms. This has sometimes led to the assumption that a better description of the microbiome (including its associated transcripts, proteins, and metabolic products) should lead to a better understanding and predictions of system level processes. However, such justifications assume that measureable characteristics of the microbiome (e.g. 16S rRNA gene libraries, metagenomes, enzymatic activities) can inform our ability to better understand and predict system-level processes. Unfortunately, additional information about the microbiome does not always provide a clearer understanding of ecosystem processes beyond what can be predicted by environmental factors alone[1,2] .

Two recent meta-analyses[3,4] suggest that research at the intersection of ecosystem science and microbial ecology often rely on assumed correlations between microbiome characteristics and ecosystem processes and less frequently test to see if those correlations are present. The first, an examination of 415 studies, found little evidence that protein-encoding genes (sometimes referred to as "functional genes") or gene transcripts correlate with associated biogeochemical processes[3]. Although all studies attempted (or presumed) to link microbial genes or transcripts with function, only 14% measured both the copy number of genes or transcripts and the corresponding process (n = 59 studies, comprising 224 individual effects as most studies had measured multiple gene-function relationships). Of the 224 effects where both characteristics were measured, only 38% exhibited a positive relationship between molecular and process measurements that many assume to

exist. The effect size for the relationship between gene copy number and process rate had an approximately normal distribution with a mean near zero[3]. This result was consistent whether functional gene or transcript abundance was used as the response variable. The second study, compiled a separate dataset of 148 studies that examined microbial membership and ecosystem processes in response to experimental manipulations[4]. Whereas 40% of included studies reported concomitant changes in microbial membership and an ecosystem process, only one third of those cases reported the relationship between microbial membership and an ecosystem process. Interestingly, of the 53 studies that posed a hypothesis or objective about links between microbial membership and ecosystem processes, more than half (53%) did not test for a statistical structure-function link[4].

Microbiomes are the engines that power system-level processes[5]. However the meta-analyses described above illustrate that the current approach to study the links between microbiome characteristics and ecosystem processes are not well formulated and relationships between microbiome characteristics and system level processes are rarely tested. When linkages are explicitly tested, significant correlations between microbiome characteristics and ecosystem processes are sometimes present, but more frequently not present [3,4]. One reason for the ambiguity between microbiome characteristics and system level processes is that many studies are conducted in the absence of a conceptual framework that illustrates how different measurable microbial characteristics relate to one another and to the system level process of interest.

Microbial characteristics can range in resolution from cellular abundance to the entire genetic potential of a species-rich community (i.e., a metagenome). Because all measureable microbial characteristics do not exist within the same plane of detail,

a conceptual structure is required to clarify how various microbial characteristics are related to each other and to the processes they affect. Identifying correlations between a microbial characteristic and an ecosystem process in the absence a broader conceptual underpinning creates the potential for correlations to be mediated by a third (or more) unaccounted variable(s). The absence of an underlying mechanism also limits the potential for each result to be applied to additional systems or to expand to broader spatial and temporal scales, for additional testing, replication, and confirmation.

Challenges in Linking Microbial Characteristics and Ecosystem Processes

A key challenge in linking microbial information to a system-level process is that conceptual research frameworks often do not effectively align with the methods being applied or the data those methods generate. For example, environmental factors act on the physiology of individual organisms, which alters their competitive ability, abundance, collective physiology, and ultimately their contribution to an ecosystem process. However, designing an observational study or experiment from this framework assumes that environmental and microbial characteristics are measurable across multiple categories of ecological organization (i.e., individuals, populations, and communities) at the temporal and spatial scales at which they influence microorganisms (Figure 1a). In addition, the relationships between environmental variables and microbial characteristics can be decoupled in both time and space[4], and are often non-linear[6]. Recent immigration, phenotypic plasticity, disequilibrium between the environment and the extant microbiome at the time of sampling, functional redundancy, and dormancy can all mask the relationship between measurable microbial characteristics and the processes microorganisms influence (Figure 1b).[4,7,8,9] As micrometer scale characteristics of microbiomes (10^{-6}

m) are scaled to the level of ecosystems (m to km), we assume that our conceptual understanding is also scalable. However, each of the aforementioned confounding factors aggregate over multiple orders of magnitude often masking the very relationships we seek to elucidate (Figure 1b). To formalize how measureable microbiome characteristics are linked with system-level processes we have conceptually defined the intersection of microbial and ecosystem ecology and identified three categories of microbial characteristics that illustrate the relationship among each category of microbial characteristics and how they may contribute to an ecosystem process (Figure 2).

Mapping Ecosystem Processes to Microbial Characteristics

Ecosystem processes are defined as a qualitative change in a pool or a flux from one pool to another (e.g. NH_4^+ to NO_3^-, or dissolved organic matter to CO_2). The first step to understand how the microbiome influences an ecosystem process, is to define the ecosystem process of interest and each sub-process that contributes to it (i.e., the set of constituent reactions that combine to determine net flux). Few, if any ecosystem processes involve a single metabolic pathway, or are carried out by a single organism (e.g., a notable exception being the recent discovery of commamox which can independently carry out nitrification, the conversion of NH_4^+ to NO_3^-)[10,11]. Rather, ecosystem processes are composites of complementary or antagonistic sub-processes, carried out by phylogenetically and metabolically diverse microorganisms[12]. For example, net ecosystem productivity (NEP) is the balance between antagonistic processes of C-fixation and C-mineralization. Each sub-process of NEP can be further partitioned into a series of metabolic pathways (e.g., chemoautotrophic nitrification and photoautotrophic C-fixation or heterotrophic fermentation and aerobic respiration). Partitioning each ecosystem process in this

hierarchical manner can continue until the sub-processes maps directly to specific microbial metabolic pathways (e.g., acetoclastic methanogenesis). Subsequently each of these metabolic pathways can be categorized as either phylogenetically broad or narrow[13]. Broad processes are phylogenetically common (i.e., widely distributed among taxa), whereas narrow processes are phylogenetically conserved (i.e., limited to a specific subset of taxa). For example, denitrification and photosynthesis are phylogenetically broad processes, while both methanogenesis and methanotrophy are phylogenetically narrow processes (with at least one notable exception[14]).

The second step is to identify, the controls or constraints on each constituent sub-process. For example, the kinetics of a single metabolic pathway in a model organism may help us understand the rate limiting steps of a narrow process, but insights from model organisms are much less likely to capture the full spectrum of responses of a broad process where phenotypic variation among phylogenetically diverse organisms is likely to be much greater[15,16]. Defining the ecosystem process, its critical sub-processes, and the known phylogenetic distribution of the metabolic pathways that drive those sub-processes creates an explicit conceptual pathway that links the ecosystem process to the microorganisms that contribute to it. Once the ecosystem process has been conceptually partitioned into its component parts and their primary controls, a concerted approach can be applied to investigate how characteristics of the microbiome influence the ecosystem process of interest within the complexity of a natural environment.

Categories of Microbial Characteristics

We propose that attempts to elucidate the microbial contribution to system-level processes needs to explicitly identify three distinct categories of microbial

151 characteristics: 1) microbial processes, 2) microbial community properties, and 3)
152 microbial membership (Figure 2). The contribution of the microbiome to ecosystem
153 processes is exerted through aggregate community properties that are shaped by
154 both microbial membership and environmental factors. This proposed framework
155 allows the researcher to clearly identify how different measurements used to
156 characterize a microbiome interact with each other and identify the potential of each
157 characteristic to elucidate the microbial contribution to the system level process.
158 These categories are hierarchically connected (Fig. 2), but they represent distinct
159 degrees of aggregation that are not simply an additive function of the previous
160 category. Furthermore, each category is potentially subject to different modes of
161 regulation, and, each category has different putative linkages to system-level
162 processes (Fig. 2). All measureable characteristics of microbial communities (e.g.,
163 abundance of cells, sequence of genes, transcripts, or proteins; enzyme expression
164 or activity) can be placed within one of the above categories, but most studies rarely
165 articulate how these measurements differ in their specificity (i.e., the level of
166 phylogenetic resolution at which they are applied), precision (i.e., the ability of the
167 method to repeatedly describe the characteristic of interest), or context (i.e., how a
168 characteristic relates to other characteristics or the ecosystem within which they
169 were measured). This conceptual structure that orientates each microbial category
170 within a broader context creates the opportunity to improve the design of
171 observational and experimental studies in micobiome research.
172 *Microbial Processes* - Microbial processes are the collective metabolism of the
173 microbiome that contribute to changes in pools and fluxes of elements or compounds
174 (i.e., Figure 2, Letter K). This is the level of microbial information that can most
175 readily be incorporated into system-level models because many microbial processes

represent the key sub-processes that contribute to a particular ecosystem process (e.g., methanogenesis + methanotrophy ≈ methane efflux). Commonly measured microbial processes in ecosystem science include nitrogen fixation, denitrification, nitrification, phosphorus uptake and immobilization, carbon fixation, and organic carbon mineralization. The rates of many microbial processes can be approximated through physiological assays (e.g., biological oxygen demand to estimate microbial community respiration), and while they do not open the "black box" of the microbial community, they do directly quantify the microbial contribution (or at least the potential contribution) to changes in resources moving through the box. Microbial processes can be distinguished from other microbial characteristics because they are all rates (i.e., have time in the denominator) and require a bioassay to estimate.

Assays used to estimate microbial processes are often logistically challenging, require manipulations that inevitably deviate from the *in situ* conditions, and often depend on the environment from which the microbiome was sampled. For example, the relationship between temperature and microbial processes such as enzyme activity and phosphorus use efficiency (PUE) vary across latitudinal gradients[17] and among seasons[18]. Thus, observations of the effect of temperature on either enzyme activity or PUE depend on where (e.g., at what latitude) and when (e.g., during which season) they were measured. In the absence of an understanding of the underlying physiological mechanism (e.g., the physiological change that allows a community to perform differently at different temperatures), the relationship between and environmental driver (e.g., temperature) and a microbial process must be measured through a direct assay at each location and at each time. This limits the inference possible from relying only on measurements of microbial processes alone.

Microbial Community Properties - Microbial community properties include a broad set of microbial characteristics such as community biomass or biomass elemental ratios (e.g., biomass C:N or C:P ratios) and the majority of phylogenetically undifferentiated aggregate sequence based measurements (e.g., gene abundance, metagenomes, transcriptomes). Microbial community properties (Figure 2) represent an integrated characteristic of the microbiome that has the potential to predict or at least constrain the estimates of microbial processes. For example, microbial community biomass C:N (a community property) indicates a microbiome's potential to mineralize or immobilize N.[19] Community biomass stoichiometry has been shown to be a useful predictor of nutrient immobilization or mineralization during litter decomposition[19], and in soils can predict both respiration and N-mineralization better than microbial biomass alone[20]. The power of biomass elemental ratios to explain nutrient cycling has also been shown in freshwater[21] and marine ecosystems[22] including the seminal paper that demonstrated the similarities between the stoichiometry of marine algal biomass and that of the dissolved fraction of nutrients in the ocean[23].

Microbial community properties can be separated into two categories, emergent properties (EPs) and community aggregated traits (CATs). Emergent properties have been used to refer to a variety of phenomena in ecology, however here we use emergent properties as it has been defined by Salt (1979)[24]: "An emergent property of an ecological unit is one which is wholly unpredictable from observation of the components of that unit", which is consistent with its contemporary use in microbial ecology.[25] For example, the potential importance of emergent properties to influence ecosystem processes has been demonstrated in a series of experimental flow-through flumes that mimicked development and metabolism of stream biofilms[26].

Transient storage (i.e., an increase in residence time of the water and its solutes near the biofilm relative to the flow around it) increased as the microbial biofilm density increased[26]. Microbial biofilm formation is an EP[27] that affects the important ecosystem process of hydrological transient storage[26]. Another example of an emergent property is the relative abundance of a certain traits within a microbiome. Trait based approaches have a rich history in ecology and have been increasingly applied to address questions in multiple areas of microbial ecology.[28] For example, specific functions (i.e. uptake of an individual organic substrate) are associated with traits which can involve multiple genes, among different taxa, all capable of performing the function albeit with differences in the underlying physiology and efficiency. The distribution and expression of these functional gene variants generates a trait structure among microbiomes, which determines the overall performance of the microbiome for that given function (i.e. uptake of a given organic substrate), but which cannot be predicted simply from the presence of the taxa that carry the genes conferring that trait.[29] While characterization of EPs may improve the understanding of microbial processes (Figure 2, Letter G) they cannot, in principle, be estimated or predicted on the basis of the constituent taxa (i.e. membership) alone (Figure 2, Letter F), and thus must remain as an intermediary between environmental drivers (Figure 2, Letter C) and microbial processes (Figure 2, Letter G).

Unlike EPs, CATs can potentially be estimated from characteristics of their constituents and provide a pathway to link microbial community membership to the community properties that drive microbial processes (Figure 2, Letter E)[30]. For example, CATs may include commonly measured community properties such as functional gene abundance as estimated from qPCR (e.g., pmoA which encodes a

subunit of the enzyme involved in methane oxidation, can be used to estimate potential for methanotrophy and as a phylogenetic marker for methanotrophs)[31]. A recent perspective article discussed the role of CATs in microbial ecology and noted a series of additional CATs (e.g., maximum growth rate, dormancy, osmoregulation) that could be inferred from metagenomic data of the extant community[30].

Understanding when, and which, community properties that shape microbial processes can be predicted by membership is a critical research question, and an important step in understanding how the microbiome contributes to system level processes. Whether or not a community property is an EP or a CAT is an exciting area of research and provides an important framework to advance research at the microbial-ecosystem nexus. New approaches, like studying higher-level interactions in ecological communities could help understand how a microbiome's constituents interact to from emergent properties.[32] This is not a trivial task, yet a suite of existing methods, discussed below, already provides the ability to directly pursue this challenge.

Microbial Community Membership **-** Although the now commonplace analysis of community membership by sequencing phylogenetic marker genes (e.g., regions of the 16S, 18S, or ITS genes) or suites of phylogenetically conserved protein sequences identifies constituent microbial taxa, the direct coupling of microbial phylogeny to physiology and ecology remains elusive (Figure 2, Letter H).[33,34,35] In general the paucity of associated physiological data or information on population phenotypes that accompany phylogenetic sequence data limits the system-level inference that is possible from analyses of community membership. This constrains our ability to attribute microbial processes to community membership of even relatively simple environmental consortia. Whereas it is clear that microbial

275 populations are not randomly distributed in space and time[35], and that some
276 microbial traits are conserved at coarse taxonomic scales [28,36,37], the physiological
277 mechanisms underlying non-random distributions of microbial taxa across
278 environmental gradients is often unknown. The limited understanding of the
279 metabolism of most bacterial phyla limits an explicit understanding between the
280 organism's abundance and its role in the microbial process that contributes to an
281 ecosystem process.

282 ***A Path Forward***

283 We suggest that a challenging but necessary step for microbiome science is to
284 move away from identifying correlative relationships between characteristics of the
285 microbiome and system level processes, and towards identifying more causative and
286 mechanistic relationships. The conceptual diagram (Figure 2) is a road map to
287 organize and link the diverse suite of measureable microbial characteristics that are
288 currently available to researchers. Figure 2 does not represent how these
289 components necessarily interact in the environment; rather it is a map that identifies
290 potential links between measureable microbial and system-level characteristics that
291 can help structure our exploration of how microorganisms influence the systems they
292 inhabit. Ecosystem ecology has traditionally been confined to interactions between
293 environmental parameters and ecosystem processes (depicted within the horizontal
294 arrow, Figure 2). Similarly, microbial ecology (depicted within the vertical arrow,
295 Figure 2) has historically focused on phylogenetically undefined aspects of microbial
296 communities (e.g., bacterial abundance) and microbial processes (e.g., bacterial
297 production) or on the physiology of microbial isolates (e.g., sulfate reducing bacteria)
298 or the collective physiology of highly reduced communities with known membership
299 (e.g., waste water treatment microbiome). The routine inclusion of sequence-based

approaches in studies of environmental microorganisms has lead to an increasingly detailed description of the world's microbiomes and an increasing interest in how constituents of those communities interact to influence the system as a whole.

The drive to include microbial characteristics into system-level science has led to a range of approaches for linking characteristics of the microbiome to ecosystem processes. Direct connections between microbial membership and ecosystem processes (Figure 2, Letter I), or community properties and ecosystem processes (Figure 2, Letter J), have proven consistently difficult to establish[3,4]. We propose 1) identifying which microbial processes are likely to contribute to ecosystem-level pools and fluxes *a priori* (Figure 2, Letter K), 2) determining which microbial community properties best describe and predict these microbial processes (Figure 2, Letter G), and 3) identifying whether the community properties that best describe each process are a CAT or an EP (Community Properties, Figure 2). If the community property is a CAT then exploring the link between microbial membership and community properties may lead to further understanding and perhaps an enhanced predictive power (Figure 2, Letter E). However, if the community property is an EP elucidating the microbial membership that contributes to the EP is unlikely to improve understanding of the drivers of that community property (Figure 2, Letter F) and understanding how environmental drivers structure the EP will be more insightful. Formalizing microbiome research into a structured, conceptual framework will allow the research community to better focus on potential links between microbiome characteristics and system-level processes that are most likely to be detected empirically. This approach will also allow researchers working in different systems to test the same pathways among defined microbiome characteristics and thus increase the possibility of understanding the casual mechanism (or absence of

causality) for observed correlations. Equally as important, we suggest that attempting to link community membership (Figure 2, Letter I) or community properties (Figure 2, Letter J) directly to ecosystem processes is by definition correlative and therefore a less powerful approach to integrating microbiome characteristics into system-level science. Thus future research endeavors will be most powerful if they focus on elucidating connections through the complete path of microbial ecology (Figure 2, blue arrow, Letters E, F, and G) and not direct connections between microbial membership or community properties and ecosystem processes (Figure 2, Letter I and J).

Applying and Testing the Proposed Framework

Applying and testing the proposed framework will depend on the ability to more robustly evaluate each category of microbial characteristics and to directly measure the arrows that connect each category (Figure 2). Both labeling/sorting approaches and phenotypic description of isolates provide an opportunity to better understand how microbial membership contributes to community properties (Figure 2, Letter E or F). Labeling and cell sorting approaches (e.g., fluorescent in situ hybridization (FISH) coupled with flow cytometry cell sorting[38], or immunocapture such as with bromodeosyuridine, BrdU)[39] provide powerful tools to constrain the complexity of the microbiome and directly test hypotheses that link membership to community properties or microbial processes. Labeling and sorting techniques allow the cells that can be targeted with a stain or other label to be separated from the broader community and then assayed for membership or phenotypes such as activity or biomass composition. For example, a study of an Arctic Ocean bacterial community labeled the actively growing component of the community using BrdU and then separated those populations from the rest of the community using an immunocapture

technique to better understand the portion of the microbiome that was driving community dynamics[39]. By simplifying the community, researchers were able to link membership to secondary production (a microbial process, Figure 2, Letter H) and begin to better understand which members of the community were contributing to secondary production.

In addition, physiological studies of isolates from a broader distribution of representative phyla are key to advancing our understanding of how membership contributes to community properties (Figure 2, Letter E). Finding isolates that are representative of important community properties has the potential to better understand phenotypic plasticity and how constituent populations do (CATs) or do not (EPs) contribute to a community property[15]. For example, work on the marine bacterioplankton SAR11 has led to an increased understanding of how this ubiquitous member of the marine microbiome interacts with elemental cycles in the open ocean[40]. Similarly, a rich body of work on multiple isolates of the comparably ubiquitous photoautotroph *Prochlorococcus* has advanced our understanding of the ecology and physiology of one of the most abundant phototrophs on the planet[41]. Detailed studies of isolates of common environmental OTUs have clearly demonstrated immense variation within a given OTU (i.e., “microdiversity”) that in part explains the challenge of linking membership to a community property[16]. For example, work on *Prochlorococcus has led to* a better understanding of how ecotypes within a single taxonomic unit (OTU) can lead to specialization in temperature and substrate affinity[41]. OTUs that form a substantial portion of the microbiome’s sequence abundance provide potential candidates for further investigation of possible phenotypic plasticity and or microdiversity[16]. For example, a single phylotype of the class *Spartobacteria* within the phyla *Verrucomicrobia* was

375 found to be present in a broad range of soil ecosystems and comprised as much as
376 31% of all 16S sequences returned from prairie soils[42], making it an excellent
377 candidate for targeted isolation and physiological studies. Whereas it is challenging
378 to isolate and culture many microorganisms from the environment, existing
379 approaches to isolation have been led to successful isolation of both abundant and
380 rare members of environmental microbiomes. A recent study isolated members of an
381 apple orchard soil microbiome where most isolates were from the least abundant
382 members of the community[43]. Previous studies have had success isolating members
383 of the pelagic marine microbiome by using filter-sterilized seawater with a dilution to
384 extinction approach[44]. Thus there is a potential to target both abundant[40,41] and rare[43]
385 members of diverse microbiomes to learn more about their influence on community
386 level properties. Studies of environmental isolates are essential in building a broader
387 understanding of how community membership does or does not contribute to
388 community properties (H2, Letter E and F).
389 The most commonly measured microbial characteristics can be associated with
390 one of the three categories of microbial characteristics defined here. However, the
391 key to moving from a correlative and descriptive approach to a causative and
392 mechanistic approach comes in measuring the arrows represented by letters in
393 Figure 2. There is a suite of powerful methods already being employed in microbial
394 ecology that can actively measure many of the arrows illustrated in Figure 2. These
395 include: stable isotope probing of mixed communities[45], single cell methods that can
396 assay cells in the physiological state they occur in in the environment[46], and labeling
397 individual cells with stable isotopes for single cell analyses[46]. Studies that use stable
398 isotope probing or any form of tracking stable isotopes into a population have been
399 successful in linking microbial membership to microbial processes (Figure 2, Letter

H). For example, a study of sulfate reduction in a Scottish peatland using SIP revealed that a single species of *Desulfosporosinus* was most likely responsible for the totality of sulfate reduction within the peatland even though it only comprised 0.006% of the retrieved 16S rRNA gene sequences[47]. In this case, the *Desulfosporosinus* species represented the only known sulfate reducer within the community and thus the kinetics of this organism seemingly defined the kinetics of sulfate reduction for the entire system. Whereas this is a single example of using SIP to link microbial membership to microbial processes (Figure 2, Letter H), there is a suite of culture-free techniques (such as Raman microspectroscopy (MS), NanoSIMS, or X-ray microanalysis, XRMA) that complement sequence-based microbiome analyses by reporting on the physiological and phenotypic characteristics of individual cells *in situ* [46,48,49]. For example, Raman MS has the ability to elucidate the macromolecular composition of uncultured individual cells *in situ*[46]. Incorporation of stable isotopes into a cell's macromolecules can be visualized as a shift in the Raman spectra. This provides information not only on which cells are incorporating the substrate but what macromolecular pool those substrates are being allocated to. Similarly, NanoSims allows for visualization of isotopes within a cell, and while it cannot be used to identify which macromolecule pool an isotopic label went into, it can visualize which cells are actively incorporating isotopically labeled substrates. Both Raman and NanoSims can be coupled with a range of *in situ* hybridization techniques (e.g., fluorescent in situ hybridization, FISH) to identify which populations are contributing to community properties (Figure 2, Letter E) or microbial processes (Figure 2, Letter H). For example, the study of a microbial consortia from the Sippewissett Salt Marsh on the coast of Massachusetts, USA used a combination of FISH and NanoSIMs to confirm a syntrophic association

between a population of autotrophic purple sulfur bacteria and heterotrophic sulfate reducing bacteria (SRB)[50]. Whereas several pieces of evidence pointed to a syntrophic association, the authors confirmed the association by first using FISH to visualize the physical association of each population. Further analysis with NanoSIMS after incubation with ^{34}S enriched sulfate and ^{14}C enriched bicarbonate confirmed the presence of carbon fixation by the purple photosynthetic bacteria with sulfide as the electron donor was coupled to the reduction of sulfate by the SRB. Using existing methods of confirmatory ecophysiology allows for direct measurements of the arrows connecting membership with microbial processes in a stable microbial consortia (in this case both carbon fixation and sulfate reduction, Figure 2, Letter H). These approaches applied in concert with sequence-based analyses have the potential to empirically link the categories of microbial information defined here (Figure 2), moving microbiome science from a descriptive and correlative approach to a mechanistic and causative approach.

These culture free approaches also create the potential to begin to determine which community properties are EPs, and which are CATs. For example, microbial community biomass stoichiometry (e.g., biomass C:N or C:P) cannot currently be predicted (or even constrained) from a list of it's constituent taxa (Figure 2, Letter F). However, microbial biomass stoichiometry is a community property with power to predict the microbial contribution to nutrient cycling (Figure 2, Letter G).[19-22] Independently, the biomass stoichiometry of microbial isolates grown on the same media has been shown to differ among different taxa suggesting a relationship between an organisms' identity and the elemental composition of its biomass.[51,52] However, there is an abundance of evidence that suggests that the biomass stoichiometry of many isolates is a function of the stoichiometry of the media they

were cultured on[52]. Electron dispersal spectroscopy (EDS) has the power to measure the C:N:P of individual bacterial cells growing *in situ* (i.e. not in culture)[49]. The potential to couple EDS analysis with a phylogenetic label presents the opportunity to assay mixed microbial communities and assess the link between phylogenetic identity and biomass stoichiometry under natural conditions[53]. Thus, community biomass stoichiometry can potentially be deconstructed into the biomass stoichiometry of its constituent taxa[53]. This approach would provide a direct link between community membership and a community property (e.g., biomass C:N, Figure 2, Letter E), that influences an important microbial process (i.e. nutrient recycling).

Designing microbiome research

It is critical that we recognize the influence of the taxonomic and functional composition of the microbiome is exerted through multiple pathways, some that are direct and can be readily identified, some that are indirect, and mediated by complex interactions at the community level. We must also recognize that the influence of microbiomes will vary depending on the system-level process in question, because analysis of microbial characteristics may simply not improve the environmentally-based prediction of certain processes (Figure 2, Letter A), whereas other system-level processes may indeed benefit from the inclusion of microbial characteristics including membership. For the latter, the challenge then is to determine which microbial category is the most relevant predictor of the system level process of interest: microbial processes, community properties, or microbial membership. Establishing the links between these microbial dimensions (Figure 2, Letters E, F, and G) further contributes to our understanding of the mechanistic underpinnings

474 that affect system level processes and thus will have greater explanatory power in a
475 broader range of systems.

476 The framework presented here provides one approach to formalize inquiry across
477 microbiome science and encourages empirical linkages between the presence of
478 organisms in a system and the processes that characterize that system. Whereas we
479 draw examples from environmental microbiomes and the ecosystems they inhabit,
480 this structured approach has the potential to benefit the analysis of microbiomes
481 associated with other systems such as host organisms and those of the built
482 environment. As important as establishing causal links among microbial
483 membership, community properties, microbial processes, and ecosystem processes,
484 is determining when these links are unlikely to be present. Research that
485 indiscriminately seeks to identify correlations, which does not recognize the
486 hierarchy of effects, and that places all metrics on an equal plane are susceptible to
487 confirmation bias and will continue to yield conflicting and ambiguous results that not
488 only fail to provide new insight into ecosystem processes, but also blurs the
489 connections that do exist. We suggest that rather than looking for linkages among
490 microbiome membership and system-level processes in every study, research efforts
491 would benefit from strategically targeting the linkages and processes for which an *a*
492 *priori* understanding of microbial physiology should allow us to improve our
493 understanding of the ecosystem process.

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501 preparation of this manuscript. She is one of a kind.

Figures

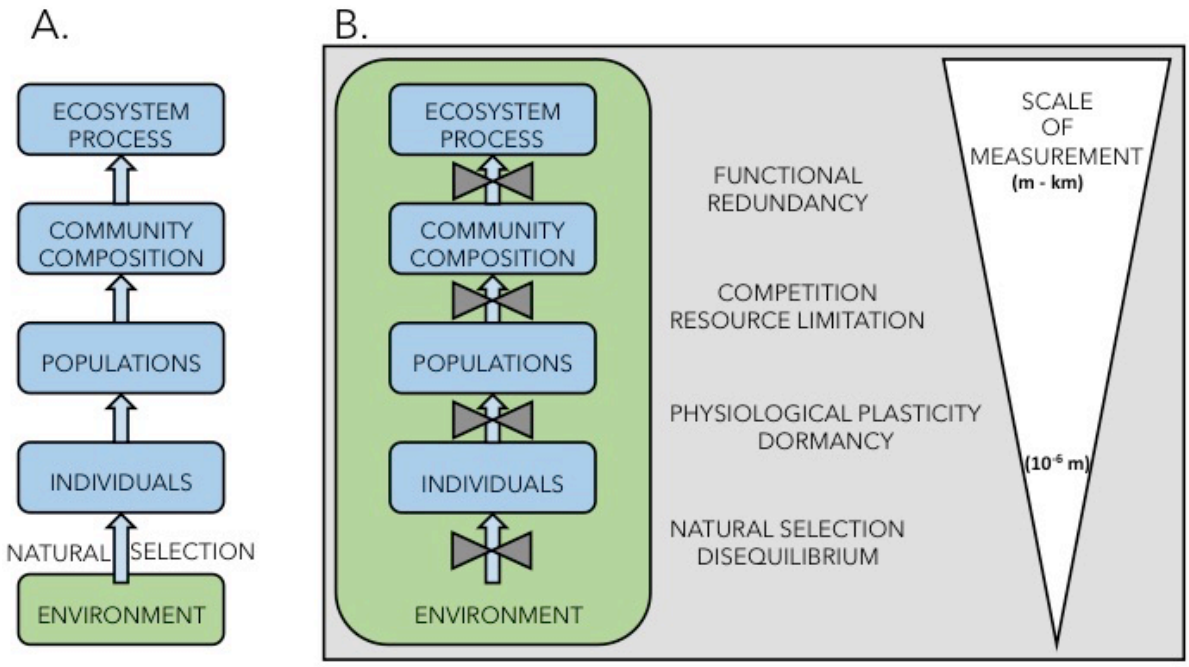

Figure 1 Diagram of microbial-ecosystem linkages A) how linkages are commonly conceptualized across levels of ecological organization and B) the series of ecological phenomena that create challenges when attempting to link metrics from one level of ecological organization to the other.

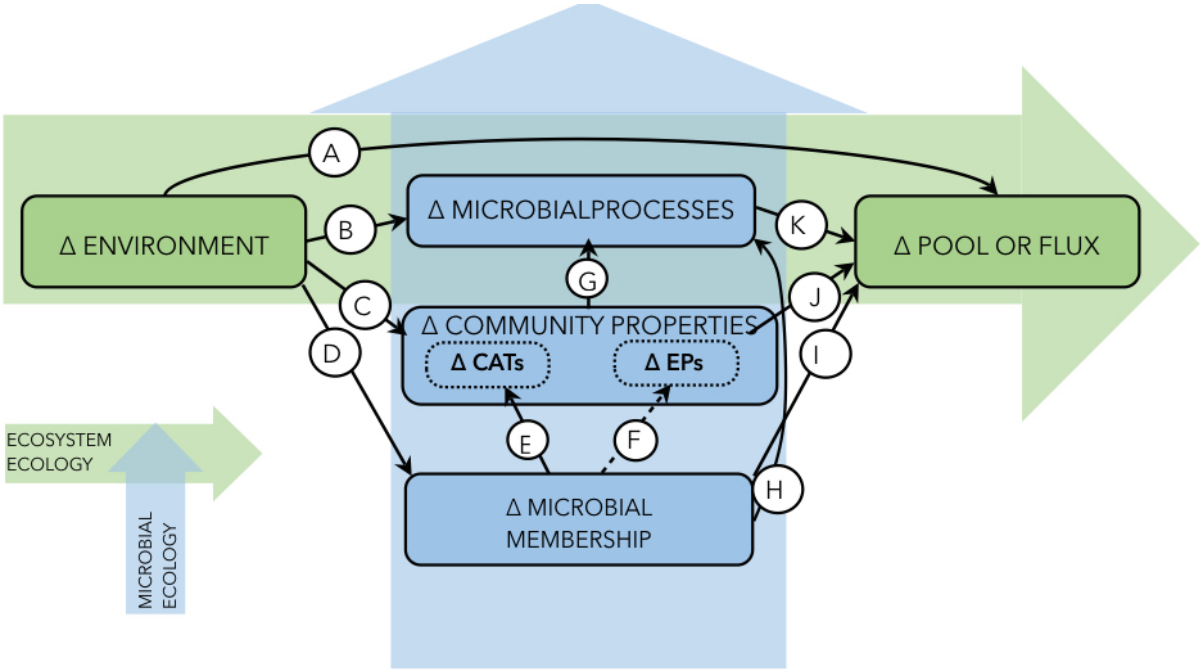

Figure 2 Shown is a conceptual map of the intersection between microbial (vertical) and ecosystem (horizontal) ecology with each of the three categories of microbial characteristics (microbial processes, community properties, and microbial membership) as defined in the text. We argue for an increased focus on studies that elucidate pathways E, F, and G. In addition, we note that pathways I and J are less likely to effectively incorporate microbiome characteristics into system-level science. The delta symbol in each category indicates an emphasis on how changes within a category may lead to a change in a connected category. The dotted arrow for letter F denotes that many emergent properties cannot currently be linked to membership and is an important area for active research.

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