Title: Microbial Diversity - Exploration of Natural Ecosystems and Microbiomes

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Abstract

Microorganisms are the pillars of life on Earth. Over billions of years, they have evolved into every conceivable niche on the planet. Microbes reshaped the oceans and atmosphere and gave rise to conditions conducive to multicellular organisms. Only in the past decade have we started to peer deeply into the microbial cosmos, and what we have found is amazing. Microbial ecosystems behave, in many ways, like large-scale ecosystems, although there are important exceptions. We review recent advances in our understanding of how microbial diversity is distributed across environments, how microbes influence the ecosystems in which they live, and how these nano-machines might be harnessed to advance our understanding of the natural world.

The turn of the 21st century saw the rise of a new kind of natural historian, focused on the invisible life that permeates our planet [1]. Unlike earlier naturalists, like Alexander von Humboldt or Alfred Russell Wallace, who documented the "…endless forms most beautiful…", recognized by Darwin as the fruits of natural selection, these new explorers confronted a strange and unfathomably vast world of imperceptible single-celled organisms [2]. This world was largely inaccessible and underestimated prior to the advent of molecular fingerprinting and high-throughput sequencing technologies, which now allow us to circumvent culture-based approaches [2,3].

The excitement in this new era of exploration is palpable, as molecular toolsets help crack open the microbial "dark matter" [4] responsible for driving global biogeochemical cycles [5], maintaining the health of multicellular organisms [6], and ensuring the longevity of our ~3.8 billion-year-old biosphere [7]. At first, each sequencing survey seemed like another *Voyage of the Beagle*. However, unlike Victorian naturalists, microbial ecologists had the tools of modern genetics and molecular biology at their fingertips. Consequently, the transition from a descriptive phase to a more quantitative, mechanistic understanding of how diverse microbial communities assemble, fluctuate through time, and achieve biological and ecological functionality was rapid. Although microbial ecology is still a young field with many unanswered questions, we explore recent advances in our understanding of how natural environments shape and maintain microbial diversity over time and space, and how the diversity of microbial communities influences the environment. We briefly discuss how microbial ecology fits into the larger body of established theory underlying traditional ecology. Finally, we look toward the future and suggest how the study of microbial ecology will influence other disciplines and how it might change the course of human history.

Quantifying Diversity

What are the units of microbial diversity? The answer to this question is not as straightforward as for plant and animal species, though these definitions are often arbitrary as well. We cannot rely upon morphological or functional features, as most microorganisms are indistinguishable under the microscope [3], and distantly related organisms can fill equivalent ecological roles [8]. We are often fooled by molecular phylogenies because microbes can swap genes across vast phylogenetic distances [9]. Thus, we rely on phylogenetic inference derived from highly conserved genes that are vertically inherited (e.g. 16S rRNA gene sequences), or on concatenations of multiple housekeeping genes [10]. The most common unit of diversity in microbial ecology is what we call the “operational taxonomic unit” (OTU; or, equivalently, “phylotype”), which clusters environmentally derived sequences based upon nucleotide similarity. For example, 97% sequence similarity of the 16S rRNA gene is often used as a rough estimation of species clusters in bacteria, based on a species definition established using DNA-DNA hybridization [11]. However, many researchers advocate for finer-scale distinction of diversity using single base pair differences in marker genes [12], genomes-scale alignments [10,13], and/or contextual information regarding the environment (e.g. ecotypes) [13,14]. These higher resolution methods can reveal interesting patterns that would be obscured by traditional approaches [15,16]. However, higher resolution is not always desirable, especially when the dominant mechanisms underlying shifts in community composition are due to functional pathways that are deeply rooted within lineages (e.g. oxygenic photosynthesis in cyanobacteria; see **Figure 1**). In this case, strain-level variation could be noisy, and might wash out subtle differences that are only apparent when correlated organismal abundances are grouped at higher taxonomic levels [8,17]. Thus, we should not assume a one-size-fits-all heuristic for assessing microbial diversity.

What governs the distribution of microbial diversity?

For the last few decades, microbial ecologists have used a wide array of molecular tools to characterize microbial communities, enabling the observation of particular organismal assemblages or community characteristics. However, as each method has its own set of biases, it is often difficult to compare between studies, reducing the potential for meta-analysis. There have been a few within-study global surveys of microbial diversity, which have revealed dominant physicochemical drivers of microbial community structure using consistent methodologies [18-22]. However, only recently have multi-study consortia begun to standardize their data collection and analysis workflows to build large intra-comparable databases [6,23]. The largest global survey of microbial diversity to date, carried out by the Earth Microbiome Project (http://www.earthmicrobiome.org/), revealed the existence of 5.6 million OTUs (97% similarity at the V4 region of the 16S gene; not including singleton OTUs) in the first 15,000 samples, which set a new lower-bound on the number of bacterial and archaeal phylotypes on Earth [24]. In addition, as sampling efforts increase, the number of novel phylotypes discovered continues to rise beyond prior estimates, and far beyond estimates for multicellular organismal diversity [25].

We have just begun to negotiate the complex interactions within and between biological and physicochemical parameters that determine how microbial communities assemble in natural ecosystems. An initial step in this journey has been to characterize the environmental axes that are important for filtering diversity. For example, we know that salinity is a strong driver of community structure in aquatic environments, pH is a dominant force in soil systems, and host-associated and environmental communities are very distinct from one another [18,22,26]. Microorganisms carry out a diverse array of metabolisms, using everything from sunlight, to organic carbon and inorganic minerals as energy sources, and are often able to switch between these metabolic modes. Microbes can make a living under a staggering array of physicochemical conditions, from boiling thermal springs to acid mine drainage [27]. In addition, they are able to produce and consume innumerable metabolites, including complex carbohydrates, antibiotics, peptides, and lipids, which allow microbes to cross-feed one another and carve out highly specific niches and different life history strategies [28,29]. Furthermore, rapid evolution and speciation in microorganisms can contribute significantly to diversity on ecological timescales [29,30].

Beyond fine-scale niche partitioning, microbial diversity is also influenced by stochastic forces, like extremely high rates of dispersal, coupled with the ability of many microorganisms to become dormant when conditions are not conducive to growth [31,32]. These processes appear to give rise to a persistent seed bank of scarce but viable microbes [32,33], often referred to as the “rare biosphere” [34], with almost endless phylogenetic and functional potential for populating emerging or transient niches [35]. However, despite high rates of dispersal and dormancy, there is evidence that microorganisms encounter barriers to dispersal that gave rise to temporarily isolated populations, which can result in allopatric differentiation of ecotypes at the genomic level [15,36].

The balance between niche (e.g. pH or temperature driving changes in microbial dominance) and neutral (e.g. stochastic dispersal and dormancy) processes will influence the diversity of microbial ecosystems [37]. Recent work has suggested that increasing environmental heterogeneity or noise disrupts the deterministic coupling between ecosystem properties and ecological diversity, which results in neutrally assembled communities [37]. The magnitude of alpha diversity in neutrally assembled communities is partially determined by the composition of the metapopulation from which the local species pool is drawn [38]. If the local species pool is drawn from multiple source populations of varying composition at a high enough rate of dispersal, then the diversity of the local population will be greater than any of the individual source populations (i.e. the apparent meta-community will be a mixture of the source communities; see **Figure 2**). The magnitude of alpha diversity in niche-structured systems will depend upon the volume of niche space and how finely this space can be partitioned. Over evolutionary time, as novel ecotypes arise, there will be a rapid saturation of niche-volume, with a small number of taxa dominating most of the available resources. Due to the diminishing return of invading smaller and smaller pockets of resource-space, there will be an asymptotic approach to some maximal alpha diversity as low-abundance species are able to pack into ever-shrinking interstitial niches [39].

Does microbial diversity matter for the environment?

From oceanic weather patterns [7], to the oxidation of Earth’s atmosphere [40], and the health of multi-cellular hosts [6], microbes engineer their environments [5]. In fact, human civilization would soon collapse in the absence of microorganisms, followed soon thereafter by the remaining life on Earth [41]. The following section details a few examples of how microbial communities alter their surroundings.

Climate scientists are beginning to recognize a sleeping giant beneath the Arctic tundra. Permafrost locks away around half of global soil carbon, but these regions are beginning to thaw due to anthropogenic climate change, which is having a disproportionate impact on the poles. Soil warming has been shown to alter the diversity and function of microbial communities [42,43]. Thawing of permafrost soils will likely result in large-scale losses in soil carbon in the form of methane and carbon dioxide as a result of microbial activity [44]. Depending on the rate of temperature increase, permafrost soils would account for an 8-18% increase in anthropogenic carbon emissions over the next 100 years [45]. This positive biological feedback on climate change could reshape the structure of the entire biosphere.

Another fascinating way that microbes engineer their physical environments comes from early in Earth's history, when bacterial communities gave rise to naturally occurring nuclear fission reactors [46]. Certain bacteria are able to respire uranium (i.e. use oxidized uranium as an electron acceptor). However, the early Earth had an anoxic, reducing atmosphere, and uranium, which is insoluble in its reduced form, remained locked away in rock and sediment. The rise of cyanobacteria resulted in the steady production of O_2, which began to weather the Earth's crust and accumulate in the atmosphere over hundreds of millions of years [40]. Uranium deposits were slowly oxidized, which allowed uranium to dissolve in water and be carried into lakes. This process led to the enrichment for uranium-respiring microbes in these bodies of water. These microbes reduced the uranium, which made it fall out of solution and settle to the bottom of the lakes. Over time, uranium was enriched and deposited on lakebeds until critical mass was achieved, and the lakes became natural fission reactors [46]. This process was only possible early in Earth’s history, when the radioactive isotope of uranium was still at high enough abundance.

Gut-associated microbial communities can also influence their mammalian hosts. Host diet and activity can have large effects on the gut microbiome composition and function, even on daily timescales [47-49]. However, we also know that gut microbiota are integral to maintaining the health of their hosts. For example, we are accumulating a large body of evidence showing that microbes are crucial for our developing immune systems and help protect us from allergies and autoimmune disorders [50,51]. Gut microbes are also implicated in driving obesity and a number of metabolic disorders [52]. Additionally, there is a subset of the human population that, when they contract a streptococcal infection, develop obsessive-compulsive disorder [53]. In fact, microbial dysbioses have been implicated in a number of behavioral disorders [54].

The future of microbial ecology

As our appreciation of the extent and complexity of microbial ecosystems grows, we can begin to extrapolate how our new understanding could shape our future. It is clear that microbes can alter their environments, and it is possible that they could be harnessed to engineer our planet and our health. While our current knowledge of the metabolic mechanisms and evolutionary processes that underpin most microbial ecosystem dynamics is extremely limited, rapid advances in technologies that help elucidate these processes are set to drastically increase the current rate of knowledge acquisition. Microbial ecology is changing the way we practice medicine, so that instead of trying to deal with the one-disease-one-pathogen paradigm, clinical practice is adopting ecological approaches to diagnose and treat complex conditions [48,52,55,56]. Similarly, industrial processes that once relied on biotechnology derived from a single organism are starting to embrace complexity and explore ways to standardize metabolic interactions within complex communities to elicit reproducible biochemical transformations [57]. Indeed, even agriculture and ecosystem restoration, which have long had a deep appreciation of the role of bacteria in shaping the relevant environments, are starting to use systems biology, molecular analysis, and modeling to elucidate the mechanism of action for improving crop productivity, disease suppression, and stress tolerance [58].

Several research fields have come to appreciate how microbial communities can serve as tractable models. The enormous population sizes and rapid growth rates of microorganisms mean that microbial ecology may transform the fields of ecology and evolution by providing a biological system that is easily manipulated to test specific hypotheses. For example, we have seen the rise of long-term evolution experiments, which have captured speciation in action [59]. Also, the complex process of community assembly, or community response to environmental perturbations, can now be followed under controlled, replicated conditions in microbial meso- and microcosms [60-63]. Perhaps the largest contribution of microbial communities to the Darwinian Sciences so far is to establish stronger empirical links between ecological and evolutionary processes, because microbial evolution is rapid enough to quickly feedback on ecological phenomena [64]. This has led to experiments aimed at asking Stephen Jay Gould's classic question about what would happen if we tried "replaying the tape of life" [65]. Such experiments have shown us how ecological communities can stabilize themselves through division of labor [29], show signs of collapse prior to a critical transition - just like dynamic physical phenomena [66], exhibit different eco-evolutionary dynamics depending on timescale [64], and that multiple ecological steady-states can evolve from the same initial conditions [67].

Together, these microbiome-enabled experimental approaches will help transform biology into a more quantitative discipline. With the ability to replicate and test eco-evolutionary processes, we can start to ask about the forces underlying these levels of biological organization [68]. The boundaries between physics, chemistry, and biology have become increasingly perforated, and new fields are emerging at the frontiers. This newfound potential is leading us back to the beginning, with "origins of life" research and astrobiology gaining traction and funding.

In summary, we have entered an exciting era of discovery. Our new understanding of microbial diversity will allow us to cure disease, engineer and conserve our environment, manufacture better products, grow more food, colonize other worlds, and so much more. In both practical and scientific terms, microbes have given us the power to ask new questions and solve previously intractable problems.

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References

1. Stahl D: **The natural history of microorganisms**. *ASM News* 1993, **59**:609-613.

2*. Whitman WB, Coleman DC, Wiebe WJ: **Prokaryotes: The unseen majority**. *P Natl Acad Sci USA* 1998, **95**:6578-6583.

This review article describes how microbial communities, although invisible to the naked eye, are essential components of the Earth's biota. They provide estimates of the total number of prokaryotes living in various environments and suggest that most of the biomass and diversity present in the biosphere is bound up in the microbial world.

3. Fierer N, Lennon JT: **The generation and maintenance of diversity in microbial communities**. *Am J Bot* 2011, **98**:439-448.
4. Rinke C, Schwientek P, Sczyrba A, Ivanova NN, Anderson IJ, Cheng J-F, Darling A, Malfatti S, Swan BK, Gies EA: **Insights into the phylogeny and coding potential of microbial dark matter**. *Nature* 2013.

5*. Falkowski PG, Fenchel T, Delong EF: **The Microbial Engines That Drive Earth's Biogeochemical Cycles**. *Science* 2008, **320**:1034-1039.

This review article describes the intimate connection between geochemistry and microbial life, and how microbial metabolism maintains the redox state of Earth's oceans and atmosphere.

6**. Turnbaugh PJ, Ley RE, Hamady M, Fraser-Liggett CM, Knight R, Gordon JI: **The Human Microbiome Project**. *Nature* 2007, **449**:804-810.

This Feature piece in Nature described the Human Microbiome Project (HMP). The HMP was a massive collaborative effort to characterize the microbes living in and on healthy humans, to establish a baseline for future microbiome research. This work has spawned a new field of medicine that views humans and their microbiota as complex 'supra-organisms'.

7. Lovelock JE, Margulis L: **Atmospheric homeostasis by and for the biosphere: the gaia hypothesis**. *Tellus* 1974, **26**:2-10.

8**. Martiny AC, Treseder K, Pusch G: **Phylogenetic conservatism of functional traits in microorganisms**. *ISME J* 2012.

The authors show how functional traits in bacteria show different levels of phylogenetic rootedness. They find a positive correlation between the number of genes that encode a functional trait and how deeply rooted that trait is in phylogeny. Traits encoded by a single gene are labile and can move horizontally through the tree of life due to lateral gene transfer. Complex multi-gene traits are less likely to be transferred laterally and are more phylogenetically constrained. These results have broad implications for linking phylogeny and function in microbial ecosystems.

9. Fraser C, Alm EJ, Polz MF, Spratt BG, Hanage WP: **The bacterial species challenge: making sense of genetic and ecological diversity**. *Science* 2009, **323**:741-746.
10. Eisen JA: **Phylogenomics: improving functional predictions for uncharacterized genes by evolutionary analysis**. *Genome Res* 1998, **8**:163-167.
11. Stackebrandt E, Goebel B: **Taxonomic note: a place for DNA-DNA reassociation and 16S rRNA sequence analysis in the present species definition in bacteriology**. *Int J Syst Bacteriol* 1994, **44**:846-849.
12. Eren AM, Borisy GG, Huse SM, Welch JLM: **Oligotyping analysis of the human oral microbiome**. *P Natl Acad Sci USA* 2014, **111**:E2875-E2884.

13**. Shapiro BJ, Friedman J, Cordero OX, Preheim SP, Timberlake SC, Szabó G, Polz MF, Alm EJ: **Population genomics of early events in the ecological differentiation of bacteria**. *Science* 2012, **336**:48-51.

The authors show that advantageous mutations can sweep through bacterial populations without necessarily selecting for clonal genomes, similar to how beneficial mutations sweep through sexual eukaryotes. These results resolve contradictory empirical observations in microbial genetics and suggest unified mechanisms by which both sexual and non-sexual populations evolve.

14. Hunt DE, David LA, Gevers D, Preheim SP, Alm EJ, Polz MF: **Resource partitioning and sympatric differentiation among closely related bacterioplankton**. *Science* 2008, **320**:1081-1085.

15[**]. Coleman ML, Chisholm SW: **Ecosystem-specific selection pressures revealed through comparative population genomics**. *P Natl Acad Sci USA* 2010, **107**:18634-18639.

The authors demonstrate a genomic enrichment of phosphate-acquisition genes in *Prochlorococcus* and SAR11 populations in the Atlantic Ocean, relative to populations of these species in the Pacific Ocean. These phosphate acquisition genes also cluster together phylogenetically, suggesting recent horizontal transfer. These results suggest that phosphate availability is driving geographic divergence of population genomes for these abundant marine microbes.

16. Eren AM, Zozaya M, Taylor CM, Dowd SE, Martin DH, Ferris MJ: **Exploring the diversity of Gardnerella vaginalis in the genitourinary tract microbiota of monogamous couples through subtle nucleotide variation**. *PLoS One* 2011, **6**:e26732.

17. Lekberg Y, Gibbons SM, Rosendahl S: **Will different OTU delineation methods change interpretation of arbuscular mycorrhizal fungal community patterns?** *New Phytol* 2014, **202**:1101-1104.

18. Caporaso JG, Lauber CL, Walters WA, Berg-Lyons D, Lozupone CA, Turnbaugh PJ, Fierer N, Knight R: **Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample**. *P Natl Acad Sci USA* 2011, **108**:4516-4522.

19. Fierer N, Leff JW, Adams BJ, Nielsen UN, Bates ST, Lauber CL, Owens S, Gilbert JA, Wall DH, Caporaso JG: **Cross-biome metagenomic analyses of soil microbial communities and their functional attributes**. *P Natl Acad Sci USA* 2012, **109**:21390-21395.

20. Tedersoo L, Bahram M, Põlme S, Kõljalg U, Yorou NS, Wijesundera R, Ruiz LV, Vasco-Palacios AM, Thu PQ, Suija A: **Global diversity and geography of soil fungi**. *Science* 2014, **346**:1256688.

21. Ghiglione J-F, Galand PE, Pommier T, Pedrós-Alió C, Maas EW, Bakker K, Bertilson S, Kirchman DL, Lovejoy C, Yager PL: **Pole-to-pole biogeography of surface and deep marine bacterial communities**. *P Natl Acad Sci USA* 2012, **109**:17633-17638.

22[*]. Lozupone CA, Knight R: **Global patterns in bacterial diversity**. *P Natl Acad Sci USA* 2007, **104**:11436-11440.

The authors present one of the first global surveys of microbial diveristy, and identify several environmental factors that appear to be most important for driving differential community composition (e.g., salinity).

23. Gilbert JA, Jansson JK, Knight R: **The Earth Microbiome project: successes and aspirations**. *BMC Biol* 2014, **12**:69.

24. Rideout JR, He Y, Navas-Molina JA, Walters WA, Ursell LK, Gibbons SM, Chase J, McDonald D, Gonzalez A, Robbins-Pianka A: **Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences**. *PeerJ* 2014, **2**:e545.

25. Scheffers BR, Joppa LN, Pimm SL, Laurance WF: **What we know and don’t know about Earth's missing biodiversity**. *Trends Ecol Evol* 2012, **27**:501-510.

26. Fierer N, Jackson RB: **The diversity and biogeography of soil bacterial communities**. *P Natl Acad Sci USA* 2006, **103**:626-631.

27. Grant WD: *Extremophiles: microbial life in extreme environments*, vol 20: Wiley-Liss; 1998.

28**. Giovannoni SJ, Thrash JC, Temperton B: **Implications of streamlining theory for microbial ecology**. *ISME J* 2014.

The authors review the current understanding of how minimal genomes evolve in free-living and host-associated microbes. They show how recent evidence suggests that, in many ecosystems, streamlined genomes are quite common. The discussion focuses on the implications for loss of coding potential in these minimal genomes for the ecology and evolution of microbial communities.

29**. Morris JJ, Papoulis SE, Lenski RE: **Coexistence of evolving bacteria stabilized by a shared black queen function**. *Evolution* 2014.

The authors present an exciting new evolutionary theory for how cooperation arises in microbial communities, called the Black Queen Hypothesis (BQH). The authors suggest that many microbial functions are 'leaky' and promote adaptive gene loss. Thus, over time, certain organisms get stuck with providing essential functions, while others are able to avoid the cost and increase their fitness. The BQH provides a selfish mechanism for the evolution of cooperation between unrelated organisms, and avoids the need to invoke controversial goup selection processes.

30. Raeside C, Gaffé J, Deatherage DE, Tenaillon O, Briska AM, Ptashkin RN, Cruveiller S, Médigue C, Lenski RE, Barrick JE: **Large Chromosomal Rearrangements during a Long-Term Evolution Experiment with Escherichia coli**. *mBio* 2014, **5**:e01377-01314.

31. Lennon JT, Jones SE: **Microbial seed banks: the ecological and evolutionary implications of dormancy**. *Nat Rev Micro* 2011, **9**:119-130.

32**. Gibbons SM, Caporaso JG, Pirrung M, Field D, Knight R, Gilbert JA: **Evidence for a persistent microbial seed bank throughout the global ocean**. *P Natl Acad Sci USA* 2013, **110**:4651-4655.

The authors show a large degree of microbial community overlap between a deeply-sequence site in the English Channel and several hundred spatially dispersed sites from around the globe. These results suggest the presence of a vast, spatially dispersed seed bank of rare microbial taxa in marine environments.

33. Caporaso JG, Paszkiewicz K, Field D, Knight R, Gilbert JA: **The Western English Channel contains a persistent microbial seed bank**. *ISME J* 2012, **6**:1089-1093.

34. Sogin ML, Morrison HG, Huber JA, Welch DM, Huse SM, Neal PR, Arrieta JM, Herndl GJ: **Microbial diversity in the deep sea and the underexplored “rare biosphere”**. *P Natl Acad Sci USA* 2006, **103**:12115-12120.

35**. Shade A, Gilbert JA: **Temporal patterns of rarity provide a more complete view of microbial diversity**. *Trends Microbiol* 2015.

In this paper, the authors show how much of the turnover in microbial community structure seen in time series is due to transient increases in the abundances of rare microbes. These results suggest that the 'rare biosphere' is dynamic and very important to the stability and structure of microbial communities.

36. Hellweger FL, van Sebille E, Fredrick ND: **Biogeographic patterns in ocean microbes emerge in a neutral agent-based model**. *Science* 2014, **345**:1346-1349.

37[**]. Fisher CK, Mehta P: **The transition between the niche and neutral regimes in ecology**. *P Natl Acad Sci USA* 2014, **111**:13111-13116.

The authors construct a unified model that combines ecological drift and ecological selection components. They show how there is a phase transition from niche to neutral community assembly as the amount of environemental noise or the strength of ecological interactions are modulated. Ultimately, the authors show how niche and neutral regimes both emerge from the same underlying ecological principles.

38. Hubbell SP: **Neutral theory in community ecology and the hypothesis of functional equivalence**. *Funct Ecol* 2005, **19**:166-172.

39. Chesson P: **Mechanisms of maintenance of species diversity**. *Annu Rev Ecol Syst* 2000, **31**:343-366.

40. David LA, Alm EJ: **Rapid evolutionary innovation during an Archaean genetic expansion**. *Nature* 2011, **469**:93-96.

41. Gilbert JA, Neufeld JD: **Life in a World without Microbes**. *PLoS Biol* 2014, **12**:e1002020.

42. Xiong J, Sun H, Peng F, Zhang H, Xue X, Gibbons SM, Gilbert JA, Chu H: **Characterizing changes in soil bacterial community structure in response to short- term warming**. *FEMS Microbiol Ecol* 2014.

43. Mackelprang R, Jacobsen CS, Jansson J, Tas N: **Permafrost Metagenomics and Climate Change**. *Annual Review of Earth and Planetary Sciences* 2015, **43**.

44. McCalley CK, Woodcroft BJ, Hodgkins SB, Wehr RA, Kim E-H, Mondav R, Crill PM, Chanton JP, Rich VI, Tyson GW, et al.: **Methane dynamics regulated by microbial community response to permafrost thaw**. *Nature* 2014, **514**:478-481.

45. Schuur E, Abbott B, Bowden W, Brovkin V, Camill P, Canadell J, Chanton J, Chapin III F, Christensen T, Ciais P: **Expert assessment of vulnerability of permafrost carbon to climate change**. *Climatic Change* 2013, **119**:359-374.

46. Gauthier-Lafaye F, Weber F: **Natural nuclear fission reactors: time constraints for occurrence, and their relation to uranium and manganese deposits and to the evolution of the atmosphere**. *Precambrian Res* 2003, **120**:81-100.

47. Thaiss CA, Zeevi D, Levy M, Zilberman-Schapira G, Suez J, Tengeler AC, Abramson L, Katz MN, Korem T, Zmora N: **Transkingdom control of microbiota diurnal oscillations promotes metabolic homeostasis**. *Cell* 2014, **159**:514-529.

48[**]. Leone V, Gibbons Sean M, Martinez K, Hutchison Alan L, Huang Edmond Y, Cham Candace M, Pierre Joseph F, Heneghan Aaron F, Nadimpalli A, Hubert N, et al.: **Effects of Diurnal Variation of Gut Microbes and High-Fat Feeding on Host Circadian Clock Function and Metabolism**. *Cell Host Microbe* 2014, early online: http://www.cell.com/cell-host-microbe/abstract/S1931-3128%2815%2900123-7.

The authors show how mammalian circadian rhythms are inextricably linked to the dirurnal variation in gut microbial activity. They show that microbial abundances and metabolites oscilate in the gut on a 24 hr period, and that these oscillation are blunted by a high-fat diet. In particular, it seems that the oscillation in butyrate production is linked to healthy liver function. If microbial oscillations are disrupted, host circadian oscillations are also disrupted.

49. Zarrinpar A, Chaix A, Yooseph S, Panda S: **Diet and Feeding Pattern Affect the Diurnal Dynamics of the Gut Microbiome**. *Cell Metabol* 2014, **20**:1006-1017.
50. Stefka AT, Feehley T, Tripathi P, Qiu J, McCoy K, Mazmanian SK, Tjota MY, Seo G-Y, Cao S, Theriault BR: **Commensal bacteria protect against food allergen sensitization**. *P Natl Acad Sci USA* 2014, **111**:13145-13150.
51. Hooper LV, Littman DR, Macpherson AJ: **Interactions between the microbiota and the immune system**. *Science* 2012, **336**:1268-1273.
52. Ley RE, Turnbaugh PJ, Klein S, Gordon JI: **Microbial ecology: human gut microbes associated with obesity**. *Nature* 2006, **444**:1022-1023.
53. Swedo SE, Leonard HL, Garvey M, Mittleman B, Allen AJ, Perlmutter S, Lougee L, Dow S, Zamkoff J, Dubbert BK: **Pediatric autoimmune neuropsychiatric disorders associated with streptococcal infections**. *Am Psychiatric Assoc* 2014.

54[**]. Gilbert JA, Krajmalnik-Brown R, Porazinska DL, Weiss SJ, Knight R: **Toward effective probiotics for autism and other neurodevelopmental disorders**. *Cell* 2013, **155**:1446-1448.

The authors of this Preview article highlight a recent study showing a connection between autism and gut microbes in a mouse model and review recent advances in our understanding abou the interplay between the microbiome and neurodevelopmental disorders. The authors suggest that therapies targeting our microbiota may hold the key to making progress on treating historically recalcitrant psychological disorders.

55. Dethlefsen L, McFall-Ngai M, Relman DA: **An ecological and evolutionary perspective on human–microbe mutualism and disease**. *Nature* 2007, **449**:811-818.
56. Weingarden A, González A, Vázquez-Baeza Y, Weiss S, Humphry G, Berg-Lyons D, Knights D, Unno T, Bobr A, Kang J: **Dynamic changes in short-and long-term bacterial composition following fecal microbiota transplantation for recurrent Clostridium difficile infection**. *Microbiome* 2015, **3**:10.
57. Shurin JB, Abbott RL, Deal MS, Kwan GT, Litchman E, McBride RC, Mandal S, Smith VH: **Industrial‐ strength ecology: trade‐ offs and opportunities in algal biofuel production**. *Ecol Lett* 2013, **16**:1393-1404.
58. Philippot L, Raaijmakers JM, Lemanceau P, van der Putten WH: **Going back to the roots: the microbial ecology of the rhizosphere**. *Nat Rev Microbiol* 2013, **11**:789-799.
59. Cooper VS, Lenski RE: **The population genetics of ecological specialization in evolving Escherichia coli populations**. *Nature* 2000, **407**:736-739.
60. Zhou J, Deng Y, Zhang P, Xue K, Liang Y, Van Nostrand JD, Yang Y, He Z, Wu L, Stahl DA: **Stochasticity, succession, and environmental perturbations in a fluidic ecosystem**. *P Natl Acad Sci USA* 2014, **111**:E836-E845.

61. Hall AR, Miller AD, Leggett HC, Roxburgh SH, Buckling A, Shea K: **Diversity–disturbance relationships: frequency and intensity interact**. *Biol Lett* 2012, **8**:768-771.
62. Gibbons SM, Schwartz T, Fouquier J, Mitchell M, Sangwan N, Gilbert JA, Kelley ST: **Ecological succession and viability of human-associated microbiota on restroom surfaces**. *Appl Environ Microbiol* 2014.
63. Roy A-S, Gibbons S, Schunck H, Owens S, Caporaso J, Sperling M, Nissimov J, Romac S, Bittner L, Mühling M: **Ocean acidification shows negligible impacts on high-latitude bacterial community structure in coastal pelagic mesocosms**. *Biogeosciences* 2013, **10**:555-566.
64**. Levy SF, Blundell JR, Venkataram S, Petrov DA, Fisher DS, Sherlock G: **Quantitative evolutionary dynamics using high-resolution lineage tracking**. *Nature* 2015.
The authors present an impressive study that tracked half a million isogenic lineages of yeast, evolving for over a hundred generations. The authors showed what fraction of mutations led to fitness increases and were able to characterize the distribution of the magnitudes of fitness increases due to point mutations. The authors validate their fitness calculations by competing evolved lineages against the ancestral strain. This is the most quantitative emperical study of population genetics ever carried out, and suggests a suble interplay between deterministic and stochastic effects for shaping evolutionary trajectories of populations.
65. Lobkovsky AE, Koonin EV: **Replaying the tape of life: quantification of the predictability of evolution**. *Front Genet* 2012, **3**.
66. Dai L, Vorselen D, Korolev KS, Gore J: **Generic Indicators for Loss of Resilience Before a Tipping Point Leading to Population Collapse**. *Science* 2012, **336**:1175-1177.
67**. Celiker H, Gore J: **Clustering in community structure across replicate ecosystems following a long-term bacterial evolution experiment**. *Nat Comm* 2014, **5**.
The authors construct synthetic microbial communities, composed of seven culturable isolates, and evolve them in replicate for 400 generations. Initially, the community composition was the same across all replicates. However, after 400 generations, the authors found that four discrete community clusters arose. Each cluster was defined by a single strain that had become dominant, which likely reflects some beneficial mutation in that organism. These results show that evolving communities converge on discrete sets of potential community configurations after a few hundred generations.
68. England JL: **Statistical physics of self-replication**. *J Chem Phys* 2013, **139**:121923.

Figure Captions

Figure 1. The hypothetical tree pictured above shows the phylogenetic distribution of two arbitrary functional traits across bacterial genera. The colored symbols denote the identity and origin of each function (see key). Both functions originated within a single clade. However, ‘oxygenic photosynthesis’ remained confined to a deeply-rooted group, while ‘galactose metabolism’ has been passed around via horizontal gene transfer. If phylotypes were assigned at the phylum level (red inner circle), the distribution of

of phylotypes across light and dark environments would yield a clear pattern, with a single phylotype enriched by the light. However, if response to galactose concentration were assessed at the phylum level, the result might be unclear, as many phylotypes would contain a mixture of taxa with and without galactose genes. If phylotypes were assigned at the family level (red outer circle), the changing abundances of phylotypes along a galactose gradient would yield more coherent patterns. However, there would be a variety of behaviors in response to galactose in the photosynthetic clade due to horizontal gene transfer and gene loss.

Figure 2. Both deterministic and stochastic processes are important for shaping microbial diversity. Each environment selects for a particular set of taxa (e.g., 3 'mesophiles' in the lake and 3 'thermophiles' in the hot spring). These different sets of taxa inhabit incompatible ecological niches that are widely separated along an environmental gradient (i.e., temperature). The structure of each community (i.e., the relative abundances of species) is determined by competition for niche space, unless environmental noise is too high or ecological interactions are too weak, in which case no species will have an advantage (see phase diagrams, modeled after Fig. 2 in Fisher and Mehta, 2014). As such, niche-structured communities will tend to have a highly uneven rank-abundance pattern (i.e., there will be winners and losers in the competition for niche-space), while neutral communities should, on average, have a more even rank-abundance distribution (i.e., no species has an advantage). When the two communities are forced to mix along an environmental gradient (see the 'stream' above), ecological diversity is increased – both in terms of community richness and evenness – independent of niche/neutral dynamics. This maximum in diversity has been described before in many systems (e.g., the Intermediate Disturbance Hypothesis). The diversity maximum in the stream is a non-equilibrium state that would dissipate if the environmental mixing were to stop. The above picture can be further complicated by further dispersal from outside the system (i.e. meta- communities and island biogeography models), speciation, and extinction.

Figure 1

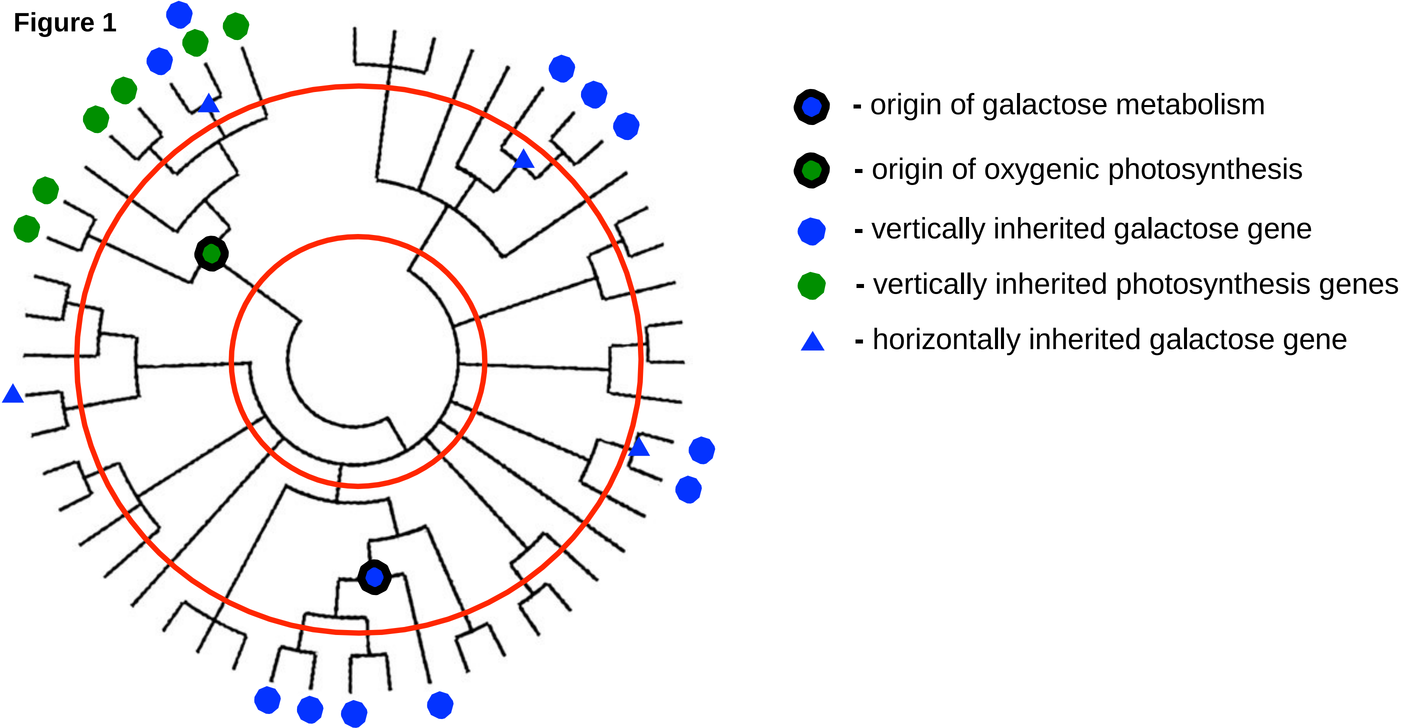
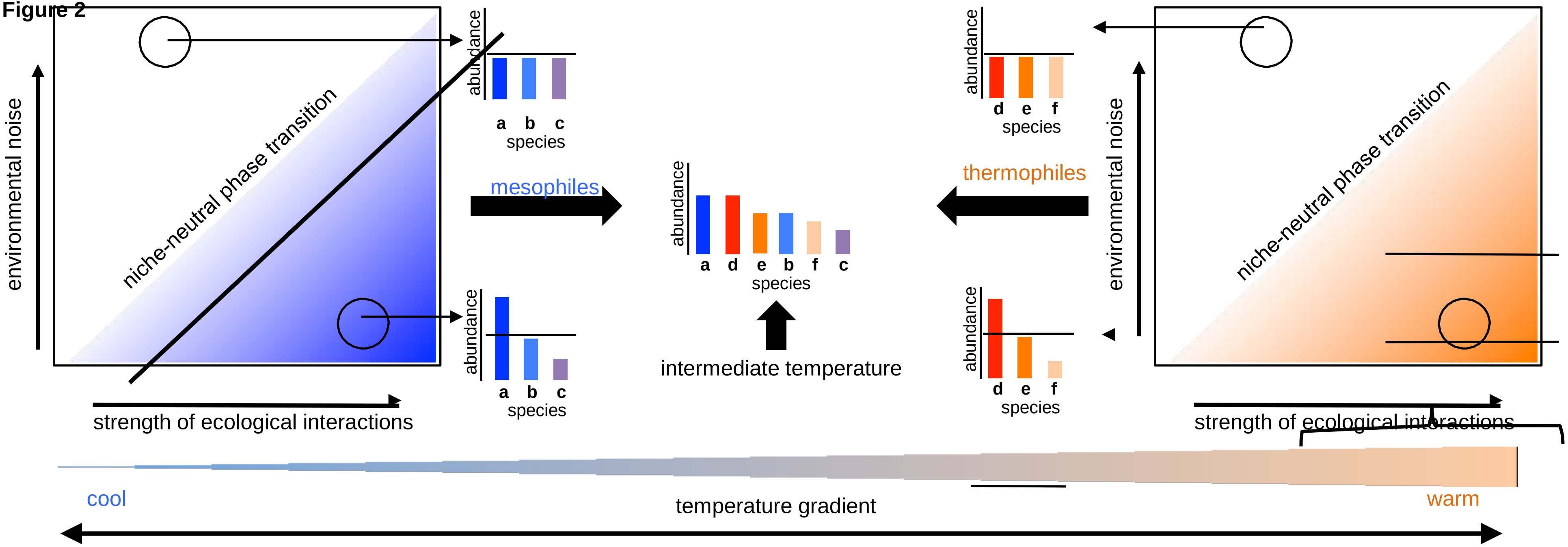
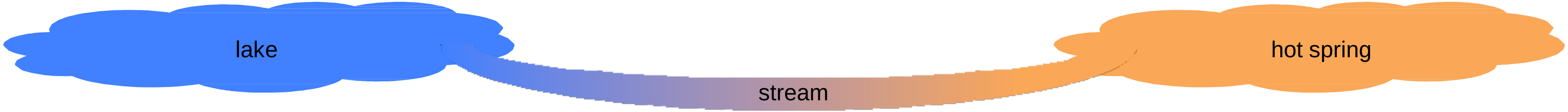
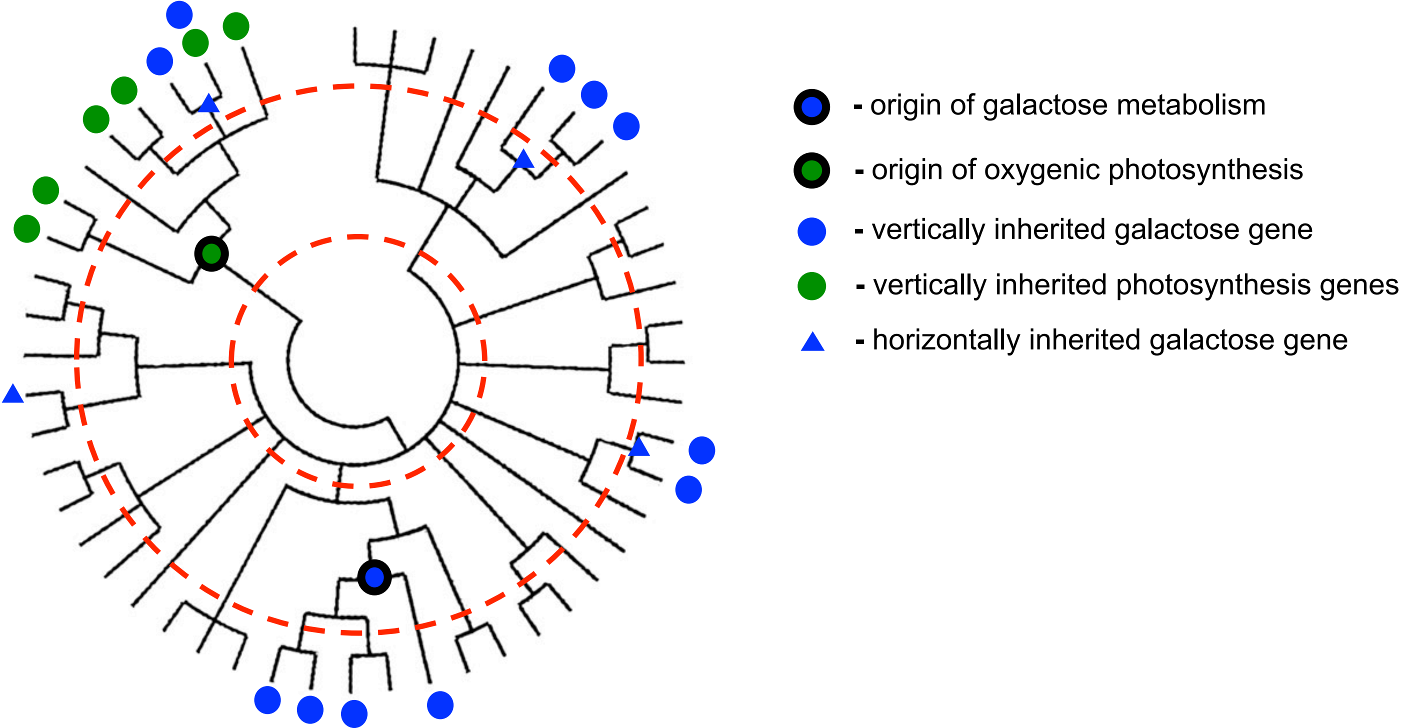
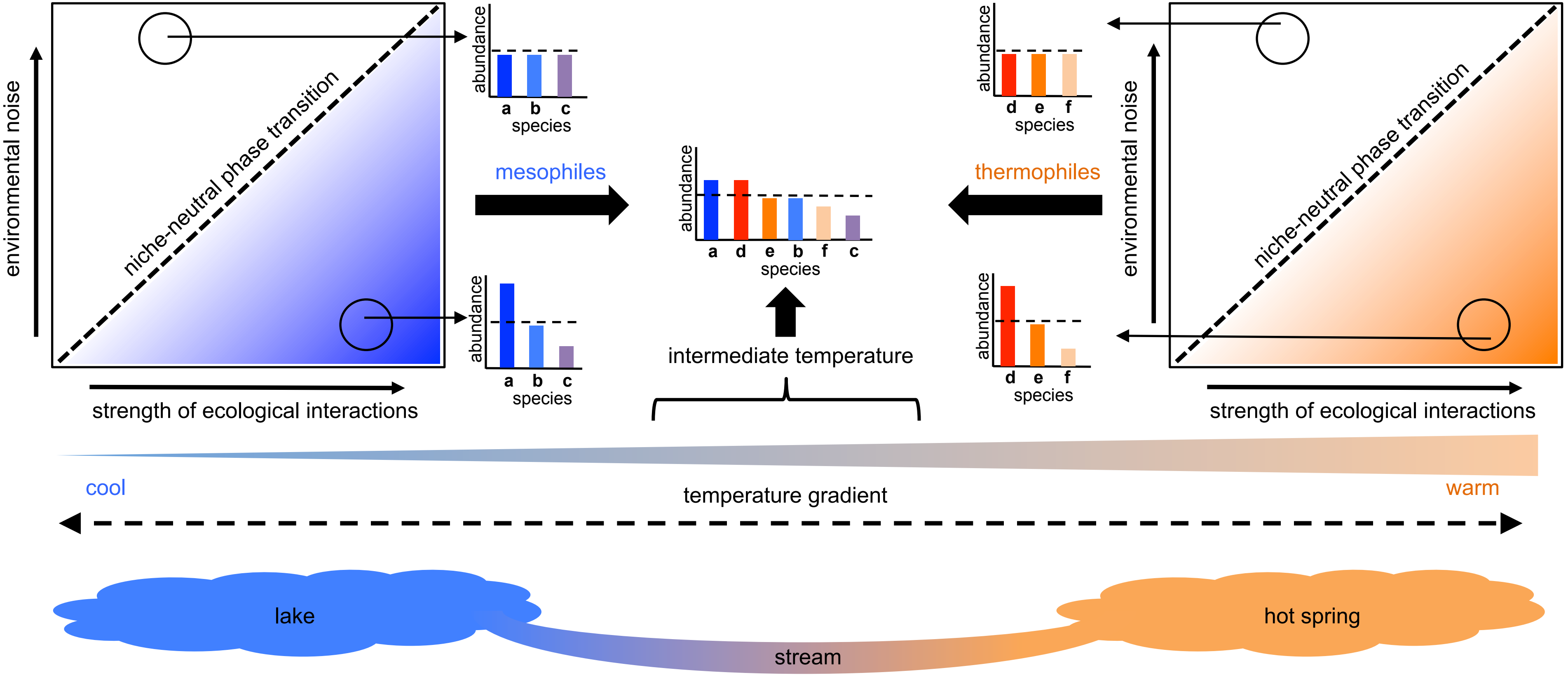

- origin of galactose metabolism
- origin of oxygenic photosynthesis
- vertically inherited galactose gene
- vertically inherited photosynthesis genes
- horizontally inherited galactose gene

Figure 2


environmental noise
niche-neutral phase transition
strength of ecological interactions
abundance
a b c
species
abundance
a b c
species
mesophiles
abundance
a d e b f c
species
intermediate temperature
thermophiles
abundance
d e f
species
abundance
d e f
species
environmental noise
niche-neutral phase transition
strength of ecological interactions
cool
temperature gradient
warm


lake
stream
hot spring


◉ - origin of galactose metabolism
◉ - origin of oxygenic photosynthesis
● - vertically inherited galactose gene
● - vertically inherited photosynthesis genes
▲ - horizontally inherited galactose gene


environmental noise
niche-neutral phase transition
strength of ecological interactions
abundance
a b c
species
abundance
a b c
species
mesophiles
abundance
a d e b f c
species
intermediate temperature
thermophiles
abundance
d e f
species
abundance
d e f
species
environmental noise
niche-neutral phase transition
strength of ecological interactions
cool
temperature gradient
warm
lake
stream
hot spring