Received: 24 April 2023 | Revised: 5 October 2023 | Accepted: 3 November 2023

DOI: 10.1111/mec.17208

EDITORIAL

MOLECULAR ECOLOGY WILEY

Insights into Ecological & Evolutionary Processes via community metabarcoding

This Special Issue brings together papers that highlight the power of high-throughput sequencing (HTS) data to address classic questions in ecology and evolution, particularly focused on metabarcoding (amplicon) datasets in conjunction with complementary -omics data types and/or models/theory to infer overall ecosystem processes. We highlight key papers that show the power of the new technology to address questions related to: (i) dynamics of community assembly and how these may change across environmental conditions, successional processes and extended evolutionary time; (ii) interaction networks, and how these can show predictable patterns over spatial and temporal gradients, providing insights into questions of biotic resilience. Studies also examined (iii) cross-scale interactions and host-microbiome associations, with critical developments demonstrating the ease of comparison and integration across scales of organismic complexity that allow insights at one scale to inform the other. These approaches are also amenable to (iv) studies of invasive species and biotic homogenization, providing insights on shifts in alpha- and beta-diversity across a wide range of spatial scales.

1 | INTRODUCTION

Biodiversity—the multiplicity of life, from microbes to macro-organisms and from genes to ecosystems—is in crisis, yet we have little understanding of factors that can sustain biodiversity and enhance its resilience to perturbations (IPBES, 2019; Oliver et al., 2015). Key questions that remain include the interplay between niche and neutral processes in shaping the assembly of communities (Mittelbach & McGill, 2019) and the associated role of stochastic and deterministic processes governing assembly (Menéndez-Serra et al., 2023); the complexity-stability paradox (Domínguez-García et al., 2019); metacommunity dynamics and the connection between local and regional diversity (Thompson et al., 2020); the extent to which a given community can exist in equilibrium or steady state (Qian & Akçay, 2020) and concepts of alternative stable states (Van Nes et al., 2016), among others. These questions have been the focus of much theoretical development in the past, but the ability to generate the data needed to validate these theories has been limited by the difficulty of sampling biological communities at the needed scale. However, without answers to these fundamental questions, we are left with major gaps in our understanding of biodiversity dynamics and questions of biotic resilience, ecosystem sustainability and strategies for restoration, which are all so critical for effective conservation and management of ecosystems.

The advance of molecular profiling methods (e.g. metabarcoding-marker gene amplicon-based community profiling metagenomics, and metatranscriptomics) has recently provided a remarkably effective toolkit for measuring biodiversity and presents the opportunity to answer the outstanding questions mentioned above. Moreover, because these approaches harness common tools across both macro- and micro-organisms, we have the ability to answer macroecological questions of shifts in community composition across scales (e.g. the work of Brown et al., 2020). These technological developments have initiated a dramatic shift in the ability to measure ecological metrics within entire macro- and micro-organismal communities, and how they change over space and time. In this Special Issue, as we outline below, authors use high throughput technologies to address classic questions in ecology and evolution and/or use models/theory to infer key ecological and evolutionary processes and make predictions.

1.1 | Community assembly processes

Describing the composition and structure of communities and their responses to perturbations and stressors has been a primary objective of ecological research since its inception. We still struggle to understand and predict the mechanisms shaping the dynamics of biological communities and how these accommodate or collapse in the face of change (Urban et al., 2016). Community profiling methods, by providing data on the diversity and abundance of the entire community of taxa across sites of different age, nutrient availability and so forth, are providing unprecedented insights into the processes of assembly. New modelling approaches (Overcast et al., 2019, 2021) are now being applied to these data to provide insights into the temporal and spatial components that govern the assembly process, and hence the factors that might dictate resilience. In this issue, Overcast et al. (2023) describe an eco-evolutionary simulation model that uses community-scale genetic data to study community assembly dynamics and show that there are detectable signatures of neutral and non-neutral processes in simulated community profiles. Applying the model to soil microarthropod metabarcoding data from Cyprus, they show that widespread low-elevation communities are structured by neutral

processes, while isolated high-elevation habitats are shaped by non-neutral processes.

Studies in this category included terrestrial and marine systems, macro- and micro-organism assembly, and comparisons of community assembly processes across scales of organismic complexity. For terrestrial communities, several papers focused on the respective roles of environmental filtering, niche conservatism/lability and spatial isolation in shaping animal species diversity at a given site. Noguerales et al. (2023) use whole organism bulk community DNA (Creedy et al., 2022) metabarcoding at both operational taxonomic unit (OTU) level and amplicon sequence variant (ASV) level to tease apart the role of environmental filtering and spatial isolation in metacommunity dynamics of soil microarthropods. The study showed that OTU (species) richness follows an altitudinal gradient, presumably associated with filtering and niche-based processes; the ASV diversity showed a contrasting pattern of decline in genetic diversity associated with anthropogenic disturbance. The paper by Andujar et al. (2022) uses the soil mesofauna in the Canary Islands to highlight the importance of environmental filtering and niche conservatism as a driver of insular community assembly, showing little evidence of niche lability, and strong geographic structure. Likewise, the paper by Arjona et al. (2022) focuses on soil arthropod communities at different depths, highlighting the diversity of species (many new species records), with the results supporting the hypothesis that deeper soil beetle communities are much more dispersal limited compared to those closer to the surface. Focusing on biodiversity loss in beetle communities in Gaoligongshan National Park in southwestern China, Li et al. (2022) use high-throughput community barcoding to compare scenarios of climate-change-induced biodiversity loss, by simulating local extinction of communities clustered by season, elevation or latitude. The expectation was that close relatives (as inferred from phylogenetic affinities) would be buffered against loss of evolutionary history; that is, if one species went extinct, the clade would still be represented by other members. However, they find that regional biodiversity was not adequately buffered by the shared evolutionary history remaining after extinction. The overall promise of whole community metabarcoding is presented in Emerson et al. (2022) who highlight the potential to complement such high throughput barcode sequencing with deep learning image recognition workflows to advance the way we study terrestrial arthropod biodiversity as a whole.

Considering marine systems, Macheriotou et al. (2023) use a community phylogenetics approach with metabarcoding data to assess the dynamics of nematode diversity across an ocean depth gradient. They showed that nematode ASV richness increases with depth up to the bathyal zone (200–4000 m), then decreases; moreover, strong phylogenetic clustering of ASVs suggests that communities have been assembled through environmental filtering. Kiemel et al. (2022) again use DNA metabarcoding (cytochrome oxidase, COI, and 18S ribosomal RNA) to ask (i) how zooplankton communities are spatially and temporally connected, (ii) what are the environmental factors influencing local communities, and (iii) what are the underlying metacommunity dynamics in this system. There was no difference between ephemeral and permanent kettle holes (ponds formed by retreating glaciers) and overall the results suggest that communities are mainly structured by environmental filtering based on pH, water temperature, kettle hole size and hydroperiod. Species sorting is a dominant driver in community assembly in the studied kettle hole zooplankton metacommunity. Likewise Govender et al. (2022) use a metabarcoding approach to highlight the point that, while sheltered marine bights around South Africa have lower pelagic zooplankton diversity due to structural homogeneity, they actually represent important fish spawning grounds (with key ramifications for fisheries and higher-level consumers). In this case, diversity measures could thus not be used as a proxy for ecological importance. Finally, Ip, Chang, Oh, et al. (2022) combine standardised sampling using Autonomous Reef Monitoring Structures (ARMS) and high-throughput sequencing to test whether coral cover shapes diversity patterns among organisms inhabiting hidden spaces within the reef matrix (the "cryptobiome"). They showed that, while marine fungi, bacteria, phytoplankton and other planktonic organisms were impacted primarily by abiotic factors (depth, temperature, level of particles in the water column and distance from the mainland), diversity patterns in larger-sized metazoans were associated with coral cover.

A number of studies focused explicitly on microbial communities. For example, Pino et al. (2023) use 16S rRNA and ITS metabarcoding of soil microbiomes (bacteria and fungi) across large scale edaphic and climatic gradients in Australia to ask classic questions in soil science and macroecology: Are broad soil classifications sufficient to capture biological soil function, and what large-scale factors determine turnover in community composition? The authors find that soil classes are predictive of bacterial and fungal community composition regardless of spatial proximity, natural and cultivated soils are reliably distinct in their microbiomes, and the primary drivers of these microbiome community differences are soil pH and temperature cycles. Van der Loos et al. (2022) explore the interplay between environment and host genotype in shaping the stability and variability of microbial composition. Using seaweed-associated bacterial communities along a salinity gradient, they were able to identify a small group of core microbes possibly involved in salinity adaptation of the host. The experimental study by Nappi et al. (2022) tested the effects of two bacterial strains on the assembly and succession of microbial communities associated with the green macroalga *Ulva australis*. Both bacterial strains exert a priority effect, with one strain (D2) causing initially strong but temporary changes in the taxonomic profile of the microbial community, and the second strain (D323) causing weaker but consistent changes that were predominantly facilitatory and included taxa that may benefit the algal host. Priority effects do not appear to be a simple replacement of functionally equivalent taxa, but result in distinct differences in the functional potential of the community. Besides the implications for community ecology, this work provides insights on the development of new probiotics (e.g. for human health or agriculture).

Finally, there are several studies in which the authors examine processes across scales (macro- and micro-organisms). Wang

et al. (2022) compare community assembly processes across scales of organismic complexity showing that (i) small soil microorganisms (bacteria, fungi) were mostly influenced by stochastic processes while the community assembly of larger soil organisms (nematodes) was more deterministic; (ii) the independent effects of habitat (including soil and topographic variables) and its interaction with plant attributes for community structure significantly decreased with increasing body size; and (iii) plant leaf phosphorus directly influenced the spatial distribution of soil-available phosphorus, which indicates their indirect impact on the assembly of the soil communities. Data suggest that the assembly of multitrophic soil communities can be explained to some extent by changes in above-ground plant attributes. Guerrieri et al. (2022) use multi-locus metabarcoding to explore the development of successional communities in recently deglaciated soils, focusing on six groups (Eukaryota, Bacteria, Mycota, Collembola, Insecta and Oligochaeta) and asking how soil communities change through time following deglaciation, and how this change differs between different soil layers. They were able to show increasing diversity within, but also increasing biotic homogenization between, soil layers, with increasing time since deglaciation. The shifts were likely associated with the development of plant communities during succession.

1.2 | Interaction networks

Another major area of study examined interaction networks, and how the properties of the networks might reflect the health and functioning of both macro-organismal (Banerjee et al., 2022) and micro-organismal (Peixoto et al., 2022) communities. Metabarcoding provides an ideal opportunity to examine questions relating to interaction networks and can provide quantitative assessment of resilience to perturbation. Highlighting the promise and importance of metabarcoding for a holistic understanding of entire interacting assemblages of different trophic groups, Ficetola and Taberlet (2023) review approaches that can reveal biodiversity response to global change. Metabarcoding approaches provide information not only on species occurrences, but also on species interactions, with new approaches using species traits, phylogenetic information, and machine learning algorithms to infer multitrophic and multitaxa interactions. Moreover, metabarcoding can provide a means for detecting hidden diversity (e.g. Yin et al., 2022) and associated cryptic interactions (e.g. Sow et al., 2019). Using novel long-read metabarcoding approaches, Lu et al. (2022) focussed on cryptic diversity by comparing mycobiomes in marine, gut and soil samples; they found that, while soils have the highest diversity, the gut has the highest number of unknown fungal species, followed by marine sediments.

Recent developments in high throughput approaches have revealed entirely novel insights into plant-pollinator interactions. Bell et al. (2022) review the opportunities provided by these approaches to examine how plant-pollinator interactions change as a result of modification in land-use. They consider how the approach can be applied to understanding key questions in global change ecology, in particular, how interactions change through space and time, including the impacts of climate and other anthropogenic stressors. Similar studies have shown how environmental DNA (eDNA) from flowers can be used to identify the community of pollinating bumblebees and has the potential to reveal complex networks (Harper et al., 2023). The paper by Lowe et al. (2022) provides an empirical example in which they used pollen DNA metabarcoding of honey samples in the honeybee (*Apis mellifera*) to reveal seasonal changes in diet specialisation according to resource availability. Because the degree of specialisation is linked to network resilience, the study highlighted seasonal changes in network vulnerability. Along similar lines, the paper by Encinas-Viso et al. (2022) focuses on factors that might drive beta diversity in alpine plant-pollinator communities. By analysing insect pollen loads they showed that metabarcoding data generated networks that were more diverse but much less specialised compared to observational data. The results supported their hypothesis that niche specialisation of alpine taxa leads to fine-scale spatial turnover of phylogenetic diversity, species and interactions, of alpine plant-pollinator networks compared to low-elevation ecosystems. Finally, Tommasi et al. (2022) test the impact of anthropogenic habitat fragmentation on the complexity of plant-pollinator interaction networks. Using pollen metabarcoding, they analysed pollinator richness, plant-pollinator interactions and pollination efficiency in landscapes of different fragmentation levels on the Maldives Islands. Contrary to their expectations, they found that moderate levels of habitat fragmentation increase the local richness of pollinators, consistent with the intermediate disturbance hypothesis. Despite harbouring a high pollinator richness, fragmented landscapes resulted in less complex plant-pollinator networks, with detrimental effects on the pollination ecosystem service. A particularly concerning finding is a preference of native pollinators for invasive plant species, possibly additionally speeding up their spread.

Metabarcoding has now been used to look at dietary niche and questions of niche partitioning. Ando et al. (2022) use hundreds of faecal DNA metabarcoding samples from seven species of ducks to show strong niche partitioning of plant diet across species but opportunistic foraging when invertebrates were the available food source. Several studies examine how interaction networks change across gradients. The paper by Srivathsan et al. (2022) tests for the impact of human disturbance on fly-vertebrate communities and their interactions, to understand whether there is any specialisation. They sampled dung and carrion fly communities along a disturbance gradient in a swamp forest remnant in Singapore. While there was no evidence of specialisation in the interactions between fly and vertebrate species, they reveal the effect of roads on the presence of native and endangered rainforest vertebrate species, highlighting indirect eDNA monitoring as an important conservation tool. The paper by Pitteloud et al. (2022) uses DNA metabarcoding of insect faeces to test specific hypotheses regarding factors that might dictate interactions in plant–orthoptera bipartite networks along elevation gradients. The results showed that the structure of the ecological networks was governed by both (i) the phylogenetic position of the plant taxa, where herbivores feed on plants based on

their taxonomic identity and (ii) plant abundance, where herbivores feed on the plant species in proportion to the cover of the plant species. The results also highlighted other aspects of the environment that shape interactions, in particular leaf nitrogen content in warmer environments, and phenolics and terpenoids in colder environments. Dürrbaum et al. (2022) examine the impact of urbanisation on diversity and trophic interactions in arthropod communities at two trophic levels. By metabarcoding pollen from herbivorous bees and arthropod prey from wasp nests, they found contrasting responses to urbanisation of predator–prey and plant-pollinator interactions. While the available diet is impacted for both trophic levels, the negative effects of urbanisation are stronger for predators than herbivores, likely due to their increased requirement for larger, unfragmented habitat. The approach can also be used to address applied questions of biological control interactions as reviewed in Lue et al. (2022) who showed that it can allow not only identification of biological control interactions but also evidence of hyperparasitism or multiparasitism, which can disrupt biological control by introduced agents.

High-throughput data can also be used to infer changes in the overall set of interactions in a given biological community. Ip, Chang, Tun, et al. (2022) use multilocus eDNA metabarcoding in coral reefs to reveal parallel shifts in community composition and trophic structure of corals coral-associated fish species. A key finding was that inversion of the trophic pyramid in reefs was a common response to coral spawning events due to large numbers of predators (secondary and tertiary fish consumers) associated with the high predation on coral eggs by planktivorous fish.

Over evolutionary time, the study by Graham et al. (2022) uses the Hawaiian Island geological sequence to show how interactions among arthropod communities become progressively more specialised over the 5 million year time period. Using bipartite networks of arthropod-plant associations, they showed that the average number of interactions per species (linkage density), ratio of plant to arthropod species (vulnerability), and uniformity of energy flow (interaction evenness) increased significantly with community age, suggesting that the communities show a natural progression towards specialisation over extended time.

2 | CROSS-SCALE INTERACTIONS & MICROBIOMES

The widespread adoption of molecular profiling methods has provided unprecedented avenues for comparing processes across scales, with the approaches used for metabarcoding of whole communities of animals or plants sharing the same overall methods and being amenable to the analytical tools used for microbial community profiling. When applied to the same environmental samples, this suite of sequencing-based methodologies enables deep characterisation of organismal communities, ranging from macro–/micro-organismal community structure and ecosystem function down to traits associated with individual taxa. Thus, we now have the opportunity to conduct parallel analyses of macro- and micro-scale community structure across biological communities and assess the interplay between biotic and abiotic components of entire ecosystems. Highlighting these parallels, Câmara dos Reis et al. (2022) test the relative importance of stochastic and deterministic processes in shaping bacterial community dynamics associated with a widespread and ecologically important bloom-forming phytoplankton species. Through a combination of observational (field sampling) and experimental (microcosm) approaches to assess bacterial community assembly over bloom succession, they found that deterministic processes shape microbial communities within phytoplanktonic bloom conditions, whereas stochastic processes were more prevalent outside of blooms.

Several studies examined questions involved in the interaction between animals and their microbiome, looking at the effects of the microbiome on diet and niche. Michel et al. (2022) use metabarcoding methods to investigate the interplay between diet and gut microbiome in several geographically isolated and genetically differentiated populations of the critically endangered Grauer's gorilla. They showed marked differences in the composition (though not richness or evenness) of the diet and gut microbiome of genetically differentiated populations, associated with social, ecological, and geographic factors. Manthey et al. (2022) test the hypothesis that the holometabolous insect gut microbiota rapidly remoulds during metamorphosis, allowing exploration of novel niches during their ontogenesis. By measuring microbial community turnover during ontogeny, they showed that beta-diversity and hence microbiota turnover is much higher in holometabolous insects compared to hemimetabolous insects. The microbial shedding and turnover during ontogenesis of holometabolous insects could open novel ecological niches and explain the evolutionary success of holometabolous insects.

Several approaches considered the importance of high-throughput sequencing approaches for understanding how microbial communities can affect biogeochemical cycling and food web dynamics. Considering microbes and their viral infection dynamics, Merges et al. (2022) tested the hypothesis that the activity of bacteria and bacteriophages co-declines across an elevational gradient. They used transcriptome levels along an elevational transect in the Swiss Alps to show that metabolic activity of bacteria declined with increasing elevation, but activity of bacteriophages did not, highlighting a gap in our understanding of microbial predator–prey relationships and associated viral contributions to carbon, nitrogen and phosphorus cycling. The paper by Pereira et al. (2022) examined the microbiome of a marine tunicate and the potential role of the microbiomes in pelagic biogeochemical cycling and nutrient remineralisation. They showed that the trophic activity and faecal pellet processing of the tunicates may impact the structure of pelagic food webs and biogeochemical nitrogen, sulphur and carbon cycling. The paper by Hu et al. (2022) examines protistan communities across geographically separated deep-sea hydrothermal vent environments. Their results suggested that the diversity is shaped by the composition of bacteria and archaea, which in turn are shaped by the chemistry of the environment. The work highlights some of the mechanisms that may

influence food web interactions and selective pressures among microbial eukaryotic communities at hydrothermal vents.

The interactions between microbiomes and their host species can change across gradients, allowing fine scale adaptation. To understand these relationships, Molina et al. (2022) tested the role of climate, site, and host variables in structuring sapwood-inhabiting fungal communities across a gradient of climatic, seasonal and site factors in the North Patagonian *Nothofagus* forests. The results supported their hypothesis that host identity and site were the major drivers of fungal community structure. Remarkable insights are now showing the tight relationship between hosts and the different components of their microbiome. Rolshausen et al. (2022) measured predictability in the structuring of the different components of a multi taxon holobiont across environmental gradients. Using a combination of whole genome analysis and metabarcoding in fungal, algal and bacterial components of lichen holobionts along elevation gradients they showed that, while chemically and morphologically indistinguishable, these lichen holobionts exhibit pronounced compositional turnover with elevation. The turnover happens in a concerted fashion for the three taxonomic components, highlighting the importance of coadaptation of different components of complex holobionts in evolutionary diversification. The paper by Kivistik et al. (2022) examined the combined impact of diet and environmental disturbance (salinity and antibiotics) on the gastrointestinal microbiome of aquatic gastropods. The results showed that a transition to salinity led to lower gut community richness and higher host viability, but only when there was an increase in bacterial generalists in the gut. Brinker et al. (2022) tested the interplay between host population structure, environmental conditions and the presence of an endosymbiont on the bacterial community of an insect host. They simultaneously investigated the population structure of a parasitic wasp host and the spatial turnover in its microbiome, with high similarity among microbial communities in *Wolbachia* infected (asexually reproducing) hosts and marked host population structure in uninfected (sexually reproducing) hosts.

High throughput approaches have also provided insights into the role of microbiomes in imparting disease resilience. Navine et al. (2022) tested the effect of microbiome communities on resistance to avian malaria by comparing two birds species in Hawaii, one native, one introduced. Neither microbial alpha nor beta diversity covaried with infection, but 149 microbes showed positive associations with malaria survivors, highlighting possible candidates for probiotics to facilitate immunity to malaria in endangered birds.

A critical component in microbiome studies is to tease apart the relative importance of the host and the environment in shaping observed patterns, something that can be difficult. Perez-Lamarque and Morlon (2022) evaluated several widely used methods for inferring host-microbiome cophylogenetic processes that aim to differentiate between vertical transmission and host-switching. They used simulations to measure power and type-I error rate and find that there are trade-offs between computational and statistical performance among the methods. They conclude that no one current method is optimal and make recommendations for the scenarios under which different methods are most appropriate.

3 | INVASIVE SPECIES/ HOMOGENIZATION

Homogenization of landscapes and seascapes through the arrival of non-native species leads to loss of resilience, with subsequent erosion of the role of biodiversity in ecosystem services (Díaz et al., 2018) and buffering against tipping points and regime shifts (Nyström et al., 2019). However, detecting non-native species and teasing them out from natives can be a difficult task, especially for larger phyla (Essl et al., 2018). Perhaps because of this difficulty, some have argued that non-native species must be incorporated into conservation decisions (Sax et al., 2022), though the scientific rationale is difficult to establish and there is a substantial literature indicating that the co-evolved nature of species in a given area is critical to its resilience (Pauchard et al., 2018). High throughput approaches are now providing entirely novel avenues for the study of non-native species. First, the use of eDNA can provide unprecedented levels of detectability, both in aquatic and terrestrial systems (Valentin et al., 2020). In addition, an intriguing new analytical tool uses the genetic signature derived from metabarcoding studies to separate, bioinformatically, native from non-native species (Andersen et al., 2019); this method was employed in several studies in this special issue to provide insights into the impact of non-native species and the associated biotic homogenization (Graham et al., 2022; Kennedy et al., 2022).

The modelling approaches developed in the context of community assembly can equally be applied to understanding invasions and the impact of humans on species assemblages. Thus, Overcast et al. (2023) demonstrate how metabarcoding data can be used to identify the importance of neutral processes in disturbed communities. This study paves the way for applying high throughput data to measure attributes of biodiversity, and its resilience to anthropogenic modification. The paper by Hampel et al. (2022) showed that the presence of undersea "built habitats" (shipwrecks) causes increased microbial biodiversity and a predictable core microbiome in their surrounding deep-sea sediments (extending up to 300 m from the wrecks). Specific archaeal groups showed enrichment around shipwrecks, suggesting metabolic shifts towards chemolithoautotrophy in these proximate sediments. Similarly, Andrés et al. (2023) used eukaryotic environmental DNA (eDNA) to reveal the interplay between environmental factors in the homogenising effects of shipping, with route-based models of shipborne species showing that environmental dissimilarity, shipping, and their interaction reduce biological dissimilarity among commercial port habitats.

As in the previous sections, metabarcoding across gradients provides insights into processes of invasion and, in particular, the phenomenon of biotic resistance, or the reduction in invasion success

maintained by the resident community (Levine et al., 2004). Notably, the paper by Graham et al. (2022) used the geological age gradient of the Hawaiian Islands in which comparable sites of high elevation native forest show increasing diversity of native species over the 5 MY timeframe. Results from metabarcoding of entire arthropod communities demonstrate that, where species diversity is lowest (on the youngest island), infiltration of non-native species is highest. Likewise, Kennedy et al. (2022) used DNA metabarcoding and statistical modelling to survey community-wide arthropod richness, the proportion of native and non-native species, and the incursion of non-natives into primary habitats on three archipelagos in the Pacific. Focusing on one island from each of the three archipelagos that differ with respect to age, area, and proportion of native habitat, there were three alternative hypotheses defined by fundamental eco-evolutionary processes with associated predictions that were detectable from the high-throughput metabarcoding surveys. The study showed that older age and correspondingly higher taxonomic richness was associated with higher resistance to invasion, and that invasion did not lead to homogenization of arthropod assemblages across the different degraded forests on the three archipelagos.

3.1 | Recurring themes

Besides the insights made in each of the major theme areas above, there were several recurring themes that emerged from multiple studies:

3.1.1 | Importance of museum & associated reference collections

Museums play a key role in metabarcoding approaches. First, while many insights can be gained from molecular sequences alone, the availability of a reference collection (i.e. molecular barcodes for identified specimens) adds unprecedented dimensionality to the data. The availability of a reference collection allows us to identify the functional traits and morphological attributes of every taxon in a sample, its status as native or introduced, and its overall distribution and trophic relationships. Moreover, it is critical that the identity of the specimen has been thoroughly confirmed, as misidentification can lead to flawed interpretations. Thus, rather than diminishing any role of natural history museums in such approaches, the vast data that have been generated through molecular profiling approaches have increasingly highlighted the fundamental importance of barcodes from reliably identified species and populations (Valdivia-Carrillo et al., 2021). The importance of a reference collection is highlighted by Lue et al. (2022) who describe the importance of a vetted and curated reference library for biological control studies. Likewise, Lu et al. (2022) emphasise the limitations of inference without a reference database, and introduce a fungal rRNA operon database (FRODO) with 1116 sequences linked to taxonomically identified species.

A second role of museum specimens in these approaches is that they can provide historic samples of past environments. For example, metabarcoding of pollen loads from museum bee specimens has provided key insights into environmental change over decadal scales, both in the availability of plants, and changes in interaction networks (Bell et al., 2022; Gous et al., 2019). This work adds to the increasing body of research that shows how metabarcoding of museum specimens can provide information on changes in interactions through time, including diet and microbiome (Heindler et al., 2018) and parasite–host interactions (Greiman et al., 2018).

3.1.2 | Insights from clustering at different levels

Early metabarcoding studies used clustering approaches and generally grouped ASVs into Operational Taxonomic Units (OTUs), assumed to correspond to species. The purpose of this step was to remove the known noise in the data, while also grouping taxa into species. However, new denoising approaches have presented the opportunity for analysing ASVs directly and hence gaining insights into population-level patterns (Noguerales et al., 2023). The most important aspect of the ability to look at different levels of genetic clustering is that the comparison can be tremendously informative into the processes that govern species assembly.

3.1.3 | Incorporating machine learning and biodiversity big data

Large scale metabarcoding studies generate a tremendous amount of data, potentially including not only DNA sequence data, but also information about traits, phylogenetic relationships, and networks structures, as well as environmental data like remotely sensed bioclimatic variables. Moving beyond descriptive statistics and simple statistical correlations to understand biodiversity processes, using such massive datasets will require adopting more powerful modelling approaches and machine learning inference methods, such as many of the manuscripts in this Special Issue have exemplified. For example, machine learning visual processing approaches may be effectively applied to image recognition analysis to study arthropod biodiversity as in Emerson et al. (2022). Another supervised learning method was used to make predictions of sediment sample proximity to shipwrecks based on frequency of microbial taxa (Hampel et al., 2022). Machine learning inference methods paired with eco-evolutionary simulation models can additionally identify the ecological and evolutionary processes that interact to generate biodiversity patterns, as demonstrated by Overcast et al. (2023).

3.2 | Future outlook

The collection of papers in this Special Issue highlights the critical insights that can be gained using high-throughput approaches,

particularly in relation to biodiversity dynamics. We now have a tool for understanding how overall species composition changes across (i) spatial gradients, including gradients of habitat, elevation, precipitation, nutrients, or anthropogenically associated modifications. Moreover, we can also examine changes through (ii) time, whether using museum specimens, ancient sediments, or sub-fossils to show how diet, host-associations, parasitism, and other interactions have changed; and geological or ecological chronosequences that provide insights into how entire communities change over extended time periods. The set of papers includes a mixture of studies, with approximately half focusing on macro-organisms, and the other half on microorganisms. The critical point here is that we have a tool that allows comparison of processes across scales. Thus, concepts developed for understanding biodiversity in macro-organisms can be tested in real time using microorganisms, and dynamics that have been learned from microbial systems can provide insights into factors shaping communities of macro-organisms and their interaction with entire ecosystems. As the approaches become more robust, it will be easier to realise the potential of high-throughput analyses to answer some of the most intractable questions in biodiversity science.

AUTHOR CONTRIBUTIONS

All authors worked together to develop the Special Issue and served as editors of the manuscripts. HMB wrote a first draft of the manuscript, which was then developed by RGG, with all authors contributing to the final version.

FUNDING INFORMATION

The Special Issue was largely conceived through a working group sEcoEvo -Biodiversity Dynamics: The Nexus Between Space & Time, supported by sDiv, the Synthesis Centre of the German Centre for Integrative Biodiversity Research (iDiv), with additional insights through a workshop supported by the National Science Foundation DEB 2135502: Insights from Macro-Ecology and Macro-Evolution for Biodiversity Assessment (PI RGG) and DEB 1927510 A Rules Of Life (RoLE) Model to Uncover Fundamental Processes Governing Biodiversity (PI AJR).

CONFLICT OF INTEREST STATEMENT

The authors declare no conflict of interest.

DATA AVAILABILITY STATEMENT

Data sharing is not applicable to this article as no new data were created or analyzed in this study.

Rosemary G. Gillespie[1]
Holly M. Bik[2]
Michael J. Hickerson[3,4,5]
Henrik Krehenwinkel[6]
Isaac Overcast[7,8,9]
Andrew J. Rominger[7,10]

[1]*Department of Environmental Science, Policy, and Management, University of California, Berkeley, California, USA*
[2]*Department of Marine Sciences and Institute of Bioinformatics, University of Georgia, Athens, Georgia, USA*
[3]*Graduate Center of the City University of New York, New York City, New York, USA*
[4]*Biology Department, City College of New York, New York City, New York, USA*
[5]*Division of Invertebrate Zoology, American Museum of Natural History, New York City, New York, USA*
[6]*Department of Biogeography, Trier University, Trier, Germany*
[7]*School of Biology and Ecology, University of Maine, Orono, Maine, USA*
[8]*Department of Vertebrate Zoology, Division of Invertebrate Zoology, American Museum of Natural History, New York City, New York, USA*
[9]*California Academy of Sciences, San Francisco, California, USA*
[10]*School of Life Sciences, University of Hawai'i at Mānoa, Honolulu, Hawaii, USA*

Correspondence
Rosemary G. Gillespie, Department of Environmental Science, Policy, and Management, University of California, Berkeley, CA, USA.
Email: gillespie@berkeley.edu

Handling Editor: Benjamin Sibbett

ORCID

Rosemary G. Gillespie https://orcid.org/0000-0003-0086-7424
Holly M. Bik https://orcid.org/0000-0002-4356-3837
Michael J. Hickerson https://orcid.org/0000-0002-5802-406X
Henrik Krehenwinkel https://orcid.org/0000-0001-5069-8601
Isaac Overcast https://orcid.org/0000-0001-8614-6892
Andrew J. Rominger https://orcid.org/0000-0003-3755-4480

REFERENCES

Andersen, J. C., Oboyski, P., Davies, N., Charlat, S., Ewing, C., Meyer, C., Krehenwinkel, H., Lim, J. Y., Noriyuki, S., Ramage, T., Gillespie, R. G., & Roderick, G. K. (2019). Categorization of species as native or nonnative using DNA sequence signatures without a complete reference library. *Ecological Applications*, *29*(5), e01914.

Ando, H., Ikeno, S., Narita, A., Komura, T., Takada, A., Isagi, Y., Oguma, H., Inoue, T., & Takenaka, A. (2022). Temporal and interspecific dietary variation in wintering ducks in agricultural landscapes. *Molecular Ecology*, *32*(23), 6405–6417.

Andrés, J., Grey, E., Czechowski, P., Saebi, M., Andres, K., Brown, C., Chawla, N., Corbett, J. J., Brys, R., Cassey, P., Correa, N., Deveney, M. R., Egan, S. P., Fisher, J. P., Vanden Hooff, R., Knapp, C. R., Leong, S. C. Y., Neilson, B. J., Paolucci, E. M., … Lodge, D. (2023). Environment and shipping drive eDNA beta-diversity among commercial ports. *Molecular Ecology*, *32*(23), 6696–6709.

Andujar, C., Arribas, P., Lopez, H., Arjona, Y., Perez-Delgado, A., Oromi, P., Vogler, A. P., & Emerson, B. C. (2022). Community assembly

and metaphylogeography of soil biodiversity: Insights from haplotype-level community DNA metabarcoding within an oceanic Island. *Molecular Ecology*, *32*(23), 4078–4094.

Arjona, Y., Arribas, P., Salces-Castellano, A., López, H., Emerson, B. C., & Andújar, C. (2022). Metabarcoding for biodiversity inventory blind spots: A test case using the beetle fauna of an insular cloud forest. *Molecular Ecology*, *32*(23), 6130–6146.

Banerjee, P., Stewart, K. A., Antognazza, C. M., Bunholi, I. V., Deiner, K., Barnes, M. A., Saha, S., Verdier, H., Doi, H., Maity, J. P., & Chan, M. W. (2022). Plant–animal interactions in the era of environmental DNA (eDNA)—A review. *Environmental DNA*, *4*(5), 987–999.

Bell, K. L., Turo, K. J., Lowe, A., Nota, K., Keller, A., Encinas-Viso, F., Parducci, L., Richardson, R. T., Leggett, R. M., Brosi, B. J., Burgess, K. S., Suyama, Y., & de Vere, N. (2022). Plants, pollinators and their interactions under global ecological change: The role of pollen DNA metabarcoding. *Molecular Ecology*, *32*(23), 6345–6362.

Brinker, P., Chen, F., Chehida, Y. B., Beukeboom, L. W., Fontaine, M. C., & Salles, J. F. (2022). Microbiome composition is shaped by geography and population structure in the parasitic wasp *Asobara japonica*, but not in the presence of the endosymbiont Wolbachia. *Molecular Ecology*, *32*(23), 6644–6658.

Brown, J. J., Mihaljevic, J. R., Des Marteaux, L., & Hrček, J. (2020). Metacommunity theory for transmission of heritable symbionts within insect communities. *Ecology and Evolution*, *10*(3), 1703–1721.

Câmara dos Reis, M., Romac, S., Le Gall, F., Marie, D., Frada, M. J., Koplovitz, G., Cariou, T., Henry, N., de Vargas, C., & Jeanthon, C. (2022). Exploring the phycosphere of *Emiliania huxleyi*: From bloom dynamics to microbiome assembly experiments. *Molecular Ecology*, *32*(23), 6507–6522.

Creedy, T. J., Andújar, C., Meramveliotakis, E., Noguerales, V., Overcast, I., Papadopoulou, A., Morlon, H., Vogler, A. P., Emerson, B. C., & Arribas, P. (2022). Coming of age for COI metabarcoding of whole organism community DNA: Towards bioinformatic harmonisation. *Molecular Ecology Resources*, *22*, 847–861.

Díaz, S., Pascual, U., Stenseke, M., Martín-López, B., Watson, R. T., Molnár, Z., Hill, R., Chan, K. M. A., Baste, I. A., Brauman, K. A., & Polasky, S. (2018). Assessing nature's contributions to people. *Science*, *359*(6373), 270–272.

Domínguez-García, V., Dakos, V., & Kéfi, S. (2019). Unveiling dimensions of stability in complex ecological networks. *Proceedings of the National Academy of Sciences of the United States of America*, *116*(51), 25714–25720.

Dürrbaum, E., Fornoff, F., Scherber, C., Vesterinen, E. J., & Eitzinger, B. (2022). Metabarcoding of trap nests reveals differential impact of urbanization on cavity-nesting bee and wasp communities. *Molecular Ecology*, *32*(23), 6449–6460.

Emerson, B. C., Borges, P. A., Cardoso, P., Convey, P., de Waard, J. R., Economo, E. P., Gillespie, R. G., Kennedy, S., Krehenwinkel, H., Meier, R., Roderick, G. K., Strasberg, D., Thébaud, C., Traveset, A., Creedy, T. J., Meramveliotakis, E., Noguerales, V., Overcast, I., Morlon, H., … Meier, R. (2022). Collective and harmonized high throughput barcoding of insular arthropod biodiversity: Toward a genomic observatories network for islands. *Molecular Ecology*, *32*(23), 6161–6176.

Encinas-Viso, F., Bovill, J., Albrecht, D. E., Florez-Fernandez, J., Lessard, B., Lumbers, J., Rodriguez, J., Schmidt-Lebuhn, A., Zwick, A., & Milla, L. (2022). Pollen DNA metabarcoding reveals cryptic diversity and high spatial turnover in alpine plant–pollinator networks. *Molecular Ecology*, *32*(23), 6377–6393.

Essl, F., Bacher, S., Genovesi, P., Hulme, P. E., Jeschke, J. M., Katsanevakis, S., Kowarik, I., Kühn, I., Pyšek, P., Rabitsch, W., & Rabitsch, W. (2018). Which taxa are alien? Criteria, applications, and uncertainties. *Bioscience*, *68*(7), 496–509.

Ficetola, G. F., & Taberlet, P. (2023). Towards exhaustive community ecology via DNA metabarcoding. *Molecular Ecology*, *32*(23), 6320–6329.

Gous, A., Swanevelder, D. Z., Eardley, C. D., & Willows-Munro, S. (2019). Plant–pollinator interactions over time: Pollen metabarcoding from bees in a historic collection. *Evolutionary Applications*, *12*(2), 187–197.

Govender, A., Singh, S., Groeneveld, J., Pillay, S., & Willows-Munro, S. (2022). Metabarcoding analysis of marine zooplankton confirms the ecological role of a sheltered bight along an exposed continental shelf. *Molecular Ecology*, *32*(23), 6210–6222.

Graham, N. R., Krehenwinkel, H., Lim, J. Y., Staniczenko, P., Callaghan, J., Andersen, J. C., Gruner, D. S., & Gillespie, R. G. (2022). Ecological network structure in response to community assembly processes over evolutionary time. *Molecular Ecology*, *32*(23), 6489–6506.

Greiman, S. E., Cook, J. A., Tkach, V. V., Hoberg, E. P., Menning, D. M., Hope, A. G., Sonsthagen, S. A., & Talbot, S. L. (2018). Museum metabarcoding: A novel method revealing gut helminth communities of small mammals across space and time. *International Journal for Parasitology*, *48*(13), 1061–1070.

Guerrieri, A., Carteron, A., Bonin, A., Marta, S., Ambrosini, R., Caccianiga, M., Cantera, I., Compostella, C., Diolaiuti, G., Fontaneto, D., Gielly, L., Gili, F., Gobbi, M., Poulenard, J., Taberlet, P., Zerboni, A., Thuiller, W., & Ficetola, G. F. (2022). Metabarcoding data reveal vertical multitaxa variation in topsoil communities during the colonization of deglaciated forelands. *Molecular Ecology*, *32*(23), 6304–6319.

Hampel, J. J., Moseley, R. D., & Hamdan, L. J. (2022). Microbiomes respond predictably to built habitats on the seafloor. *Molecular Ecology*, *32*(23), 6686–6695.

Harper, L. R., Niemiller, M. L., Benito, J. B., Paddock, L. E., Knittle, E., Molano-Flores, B., & Davis, M. A. (2023). BeeDNA: Microfluidic environmental DNA metabarcoding as a tool for connecting plant and pollinator communities. *Environmental DNA*, *5*(1), 191–211.

Heindler, F. M., Christiansen, H., Frédérich, B., Dettaï, A., Lepoint, G., Maes, G. E., Van de Putte, A. P., & Volckaert, F. A. (2018). Historical DNA metabarcoding of the prey and microbiome of trematomid fishes using museum samples. *Frontiers in Ecology and Evolution*, *6*, 151.

Hu, S. K., Smith, A. R., Anderson, R. E., Sylva, S. P., Setzer, M., Steadmon, M., Frank, K. L., Chan, E. W., Lim, D. S., & German, C. R. (2022). Globally-distributed microbial eukaryotes exhibit endemism at deep-sea hydrothermal vents. *Molecular Ecology*, *32*(23), 6580–6598.

Ip, Y. C. A., Chang, J. J. M., Oh, R. M., Quek, Z. B. R., Chan, Y. K. S., Bauman, A. G., & Huang, D. (2022). Seq'and ARMS shall find: DNA (meta) barcoding of autonomous reef monitoring structures across the tree of life uncovers hidden cryptobiome of tropical urban coral reefs. *Molecular Ecology*, *32*(23), 6223–6242.

Ip, Y. C. A., Chang, J. J. M., Tun, K. P. P., Meier, R., & Huang, D. (2022). Multispecies environmental DNA metabarcoding sheds light on annual coral spawning events. *Molecular Ecology*, *32*(23), 6474–6488.

IPBES Secretariat (Ed.). (2019). *Summary for policymakers of the global assessment report on biodiversity and ecosystem Services of the Intergovernmental Science-Policy Platform on biodiversity and ecosystem services*. IPBES Secretariat.

Kennedy, S., Calaor, J., Zurápiti, Y., Hans, J., Yoshimura, M., Choo, J., Andersen, J. C., Callaghan, J., Roderick, G. K., & Krehenwinkel, H. (2022). Richness and resilience in the Pacific: DNA metabarcoding enables parallelized evaluation of biogeographic patterns. *Molecular Ecology*, *32*(23), 6710–6723.

Kiemel, K., Weithoff, G., & Tiedemann, R. (2022). DNA metabarcoding reveals impact of local recruitment, dispersal, and hydroperiod on assembly of a zooplankton metacommunity. *Molecular Ecology*, *32*(23), 6190–6209.

Kivistik, C., Tammert, H., Kisand, V., Käiro, K., & Herlemann, D. P. (2022). Impact of disturbance and dietary shift on gastrointestinal bacterial community and its invertebrate host system. *Molecular Ecology*, *32*(23), 6631–6643.

Levine, J. M., Peter, B., Adler, A. S. G., & Yelenik, S. G. (2004). A meta-analysis of biotic resistance to exotic plant invasions. *Ecology Letters*, *7*(10), 975–989.

Li, Z., Linard, B., Vogler, A. P., Yu, D. W., & Wang, Z. (2022). Phylogenetic diversity only weakly mitigates climate-change-driven biodiversity loss in insect communities. *Molecular Ecology*, *32*(23), 6147–6160.

Lowe, A., Jones, L., Brennan, G., Creer, S., Christie, L., & de Vere, N. (2022). Temporal change in floral availability leads to periods of resource limitation and affects diet specificity in a generalist pollinator. *Molecular Ecology*, *32*(23), 6363–6376.

Lu, J., Zhang, X., Zhang, X., Wang, L., Zhao, R., Liu, X. Y., Liu, X., Zhuang, W., & Chen, L. (2022). Nanopore sequencing of full rRNA operon improves resolution in mycobiome analysis and reveals high diversity in both human gut and environments. *Molecular Ecology*, *32*(23), 6330–6344.

Lue, C. H., Abram, P. K., Hrcek, J., Buffington, M. L., & Staniczenko, P. P. (2022). Metabarcoding and applied ecology with hyperdiverse organisms: Recommendations for biological control research. *Molecular Ecology*, *32*(23), 6461–6473.

Macheriotou, L., Derycke, S., & Vanreusel, A. (2023). Drivers of bathymetric gradients of diversity and phylogenetic community structure in free-living nematodes: A metabarcoding meta-analysis. *Molecular Ecology*, *32*(23), 6177–6189.

Manthey, C., Johnston, P. R., Nakagawa, S., & Rolff, J. (2022). Complete metamorphosis and microbiota turnover in insects. *Molecular Ecology*, *32*(23), 6543–6551.

Menéndez-Serra, M., Ontiveros, V. J., Cáliz, J., Alonso, D., & Casamayor, E. O. (2023). Understanding stochastic and deterministic assembly processes in microbial communities along temporal, spatial and environmental scales. *Molecular Ecology*, *32*(23), 1629–1638.

Merges, D., Schmidt, A., Schmitt, I., Neuschulz, E. L., Dal Grande, F., & Bálint, M. (2022). Metatranscriptomics reveals contrasting effects of elevation on the activity of bacteria and bacterial viruses in soil. *Molecular Ecology*, *32*(23), 6552–6563.

Michel, A., Minocher, R., Niehoff, P. P., Li, Y., Nota, K., Gadhvi, M. A., Su, J., Iyer, N., Porter, A., & Ngobobo-As-Ibungu, U. (2022). Isolated Grauer's gorilla populations differ in diet and gut microbiome. *Molecular Ecology*, *32*(23), 6523–6542.

Mittelbach, G. G., & McGill, B. J. (2019). *Community ecology*. Oxford University Press.

Molina, L., Rajchenberg, M., de Errasti, A., Vogel, B., Coetzee, M. P., Aime, M. C., & Pildain, M. B. (2022). Sapwood mycobiome varies across host, plant compartment and environments in Nothofagus forests from northern Patagonia. *Molecular Ecology*, *32*(23), 6599–6618.

Nappi, J., Goncalves, P., Khan, T., Majzoub, M. E., Grobler, A. S., Marzinelli, E. M., Thomas, T., & Egan, S. (2022). Differential priority effects impact taxonomy and functionality of host-associated microbiomes. *Molecular Ecology*, *32*(23), 6728–6293.

Navine, A. K., Paxton, K. L., Paxton, E. H., Hart, P. J., Foster, J. T., McInerney, N., Fleischer, R. C., & Videvall, E. (2022). Microbiomes associated with avian malaria survival differ between susceptible Hawaiian honeycreepers and sympatric malaria-resistant introduced birds. *Molecular Ecology*, *32*(23), 6659–6670.

Noguerales, V., Meramveliotakis, E., Castro-Insua, A., Andujar, C., Arribas, P., Creedy, T., Overcast, I., Morlon, H., Emerson, B. C., Vogler, A. P., & Papadopoulou, A. (2023). Community metabarcoding reveals the relative role of environmental filtering and spatial processes in metacommunity dynamics of soil microarthropods across a mosaic of montane forests. *Molecular Ecology*, *32*(23), 6110–6128.

Nyström, M., Jouffray, J.-B., Norström, A. V., Crona, B., Jørgensen, P. S., Carpenter, S. R., Bodin, Ö., Galaz, V., & Folke, C. (2019). Anatomy and resilience of the global production ecosystem. *Nature*, *575*(7781), 98–108.

Oliver, T. H., Heard, M. S., Isaac, N. J., Roy, D. B., Procter, D., Eigenbrod, F., Freckleton, R., Hector, A., Orme, C. D., & Petchey, O. L. (2015). Biodiversity and resilience of ecosystem functions. *Trends in Ecology & Evolution*, *30*(11), 673–684.

Overcast, I., Emerson, B. C., & Hickerson, M. J. (2019). An integrated model of population genetics and community ecology. *Journal of Biogeography*, *46*(4), 816–829.

Overcast, I., Noguerales, V., Meramveliotakis, E., Andujar, C., Arribas, P., Creedy, T., Emerson, B. C., Vogler, A. P., Papadopoulou, A., & Morlon, H. (2023). Inferring the ecological and evolutionary determinants of community genetic diversity. *Molecular Ecology*, *32*(23), 6093–6109.

Overcast, I., Ruffley, M., Rosindell, J., Harmon, L., Borges, P. A., Emerson, B. C., Etienne, R. S., Gillespie, R., Krehenwinkel, H., Mahler, D. L., & Mahler, D. L. (2021). A unified model of species abundance, genetic diversity, and functional diversity reveals the mechanisms structuring ecological communities. *Molecular Ecology Resources*, *21*(8), 2782–2800.

Pauchard, A., Meyerson, L. A., Bacher, S., Blackburn, T. M., Brundu, G., Cadotte, M. W., Courchamp, F., Essl, F., Genovesi, P., Haider, S., & Holmes, N. D. (2018). Biodiversity assessments: Origin matters. *PLoS Biology*, *16*(11), e2006686.

Peixoto, R. S., Voolstra, C. R., Sweet, M., Duarte, C. M., Carvalho, S., Villela, H., Lunshof, J. E., Gram, L., Woodhams, D. C., Walter, J., & Roik, A. (2022). Harnessing the microbiome to prevent global biodiversity loss. *Nature Microbiology*, *7*(11), 1726–1735.

Pereira, T. J., Walters, T. L., El-Shaffey, H. M., Bik, H. M., & Frischer, M. E. (2022). The microbiome of the pelagic tunicate Dolioletta gegenbauri: A potential link between the grazing and microbial food web. *Molecular Ecology*, *32*(23), 6564–6579.

Perez-Lamarque, B., & Morlon, H. (2022). Comparing different computational approaches for detecting long-term vertical transmission in host-associated microbiota. *Molecular Ecology*, *32*(23), 6671–6685.

Pino, V., Fajardo, M., McBratney, A., Minasny, B., Wilson, N., & Baldock, C. (2023). Australian soil microbiome: A first sightseeing regional prediction driven by cycles of soil temperature and pedogenic variations. *Molecular Ecology*, *32*(23), 6243–6259.

Pitteloud, C., Defossez, E., Albouy, C., Descombes, P., Rasmann, S., & Pellissier, L. (2022). DNA-based networks reveal the ecological determinants of plant–herbivore interactions along environmental gradients. *Molecular Ecology*, *32*(23), 6436–6448.

Qian, J. J., & Akçay, E. (2020). The balance of interaction types determines the assembly and stability of ecological communities. *Nature Ecology & Evolution*, *4*(3), 356–365.

Rolshausen, G., Dal Grande, F., Otte, J., & Schmitt, I. (2022). Lichen holobionts show compositional structure along elevation. *Molecular Ecology*, *32*(23), 6619–6630.

Sax, D. F., Schlaepfer, M. A., & Olden, J. D. (2022). Valuing the contributions of non-native species to people and nature. *Trends in Ecology & Evolution*, *37*, 1058–1066.

Sow, A., Brévault, T., Benoit, L., Chapuis, M.-P., Galan, M., Coeur d'acier, A., Delvare, G., Sembène, M., & Haran, J. (2019). Deciphering host-parasitoid interactions and parasitism rates of crop pests using DNA metabarcoding. *Scientific Reports*, *9*(1), 3646.

Srivathsan, A., Loh, R. K., Ong, E. J., Lee, L., Ang, Y., Kutty, S. N., & Meier, R. (2022). Network analysis with either Illumina or MinION reveals that detecting vertebrate species requires metabarcoding of iDNA from a diverse fly community. *Molecular Ecology*, *32*(23), 6418–6435.

Thompson, P. L., Guzman, L. M., De Meester, L., Horváth, Z., Ptacnik, R., Vanschoenwinkel, B., Viana, D. S., & Chase, J. M. (2020). A process-based metacommunity framework linking local and regional scale community ecology. *Ecology Letters*, *23*(9), 1314–1329.

Tommasi, N., Biella, P., Maggioni, D., Fallati, L., Agostinetto, G., Labra, M., Galli, P., & Galimberti, A. (2022). DNA metabarcoding unveils the effects of habitat fragmentation on pollinator diversity, plant-pollinator interactions, and pollination efficiency in Maldive islands. *Molecular Ecology*, *32*(23), 6394–6404.

Urban, M. C., Bocedi, G., Hendry, A. P., Mihoub, J.-B., Pe'er, G., Singer, A., Bridle, J. R., Crozier, L. G., De Meester, L., & Godsoe, W. (2016). Improving the forecast for biodiversity under climate change. *Science*, *353*(6304), aad8466.

Valdivia-Carrillo, T., Rocha-Olivares, A., Reyes-Bonilla, H., Domínguez-Contreras, J. F., & Munguia-Vega, A. (2021). Integrating eDNA metabarcoding and simultaneous underwater visual surveys to describe complex fish communities in a marine biodiversity hotspot. *Molecular Ecology Resources*, *21*(5), 1558–1574.

Valentin, R. E., Fonseca, D. M., Gable, S., Kyle, K. E., Hamilton, G. C., Nielsen, A. L., & Lockwood, J. L. (2020). Moving eDNA surveys onto land: Strategies for active eDNA aggregation to detect invasive forest insects. *Molecular Ecology Resources*, *20*(3), 746–755.

Van der Loos, L. M., D'hondt, S., Engelen, A. H., Pavia, H., Toth, G. B., Willems, A., Weinberger, F., De Clerck, O., & Steinhagen, S. (2022). Salinity and host drive Ulva-associated bacterial communities across the Atlantic–Baltic Sea gradient. *Molecular Ecology*, *32*(23), 6260–6277.

Van Nes, E. H., Arani, B. M., Staal, A., van der Bolt, B., Flores, B. M., Bathiany, S., & Scheffer, M. (2016). What do you mean,'tipping point'? *Trends in Ecology & Evolution*, *31*(12), 902–904.

Wang, W., Sun, Z., Mishra, S., Xia, S., Lin, L., & Yang, X. (2022). Body size determines multitrophic soil microbiota community assembly associated with soil and plant attributes in a tropical seasonal rainforest. *Molecular Ecology*, *32*(23), 6294–6303.

Yin, Y., Yao, L. F., Hu, Y., Shao, Z. K., Hong, X. Y., Hebert, P. D., & Xue, X. F. (2022). DNA barcoding uncovers cryptic diversity in minute herbivorous mites (Acari, Eriophyoidea). *Molecular Ecology Resources*, *22*(5), 1986–1998.