Reframing marine host-microbe symbioses: from taxonomic inventories to functional convergence

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Abstract

In October 2025, the Trends in Host-Microbe Symbioses Symposium at the University of Padova (Italy) brought together a global community of researchers, with the aim of taking stock of the current trajectory of marine host-microbiome research. Integrating perspectives from ecology, evolution, biogeochemistry, and biotechnology, the symposium documented a clear transition from descriptive surveys of microbial diversity toward a mechanistic understanding of host–microbe interactions. Across an unusually broad taxonomic spectrum – corals, sponges, fishes, molluscs, algae and seagrasses, cnidarians, acoels, arthropods and mammals - microbiomes were consistently framed as integral components of host biology, shaping nutrient cycling, development, immunity, and ecosystem function. Despite phylogenetic diversity across host groups, convergent functional processes (notably N and C cycling, stress buffering, immune priming, and metabolic complementation) emerged as a unifying framework, even though their taxonomic underpinnings remained system-specific. Advances in multi-omics, spatially resolved imaging (MALDI-MSI, NanoSIMS, FISH/CARD-FISH) and experimental microbiome manipulation are increasingly linking microbial identity to activity and function, enabling early predictive frameworks across scales. Collectively, the symposium laid the groundwork for microbiome-based interventions to enhance host resilience and support ecosystem conservation in a rapidly changing ocean.

Sustainability statement.

The manuscript directly contributes to United Nations Sustainable Development Goal 14: Life Below Water by synthesizing knowledge that supports the conservation and sustainable use of marine biodiversity and ecosystem services. By identifying research priorities and fostering interdisciplinary collaboration, this Perspective promotes scientific advances that can inform strategies to protect marine ecosystems from climate change and anthropogenic pressures. The article also aligns with SDG 13: Climate Action, as many of the highlighted research directions focus on understanding and enhancing the resilience of marine holobionts to warming, bleaching, disease outbreaks, and other climate-related stressors.

Introduction: a field in transition

Marine microbiome research is in the middle of a generational shift. What was, only a decade ago, largely a descriptive cataloguing exercise — driven by accessible 16S rRNA amplicon surveys — is now reorganising itself around questions of function, causation and intervention. The Trends in Host-Microbe Symbioses Symposium, held at the University of Padova botanical garden in October 2025, was conceived to take a snapshot of this transition. Eleven invited keynotes and 54 contributed talks and posters, with participants from 19 countries, spanned a wide range of marine hosts, including corals, sponges, fish, algae, seagrasses and their phycosphere, acoels, annelids, arthropods and even marine mammals, and combined perspectives from ecology, evolution, biogeochemistry, biotechnology and microbiome engineering.

The conference was explicitly designed to move marine microbiome research beyond the descriptive cataloguing of microbial diversity and toward a mechanistic understanding of host-microbe interactions. In line with broader efforts in the field, discussions emphasized the need to integrate ecological and evolutionary (Foster et al., 2017; Theis et al., 2016) theory with emerging molecular tools (Knight et al., 2018; Liu et al., 2021), and to explore how microbiomes can be harnessed to enhance host resilience and ecosystem function under rapid environmental change (Gilbert et al., 2025; Humanes et al., 2026). Across keynote and contributed presentations alike, three shared questions recurred regardless of host taxonomy: (i) how do microbiomes shape host physiology, development and immunity?; (ii) how are microbial functions regulated by environmental context?, and (iii) how do these interactions scale to ecosystem processes and translate into management-relevant outcomes? Around these questions, the meeting documented a clear movement of the field: from taxonomy-driven descriptions toward function-driven mechanistic frameworks.

To complement the narrative synthesis, we performed a contribution-level coding of the symposium programme and associated abstract content. We included 65 biological conference contributions (11 keynote lectures and 54 contributed talks or posters), excluding non-biological context material such as opening remarks and panel discussions. Each contribution was coded according to taxonomic anchor, host or model system, conceptual theme, evidence type, methodological family, origin context, sequencing depth, and host/model-resolution category. This synthesis is not intended as a systematic review of the marine microbiome literature, nor as a species-level meta-analysis. Rather, it provides a structured snapshot of the conceptual and methodological landscape represented at the meeting, allowing us to identify which host systems, themes, evidence types, and approaches were most prominently represented, where patterns of functional convergence emerged across taxa, and where evidence remains sparse or uneven.

The coded set spans broad taxonomic coverage, but is non-uniform across host systems (Fig. 1A). Mixed-host or ecosystem-level contributions (20%), scleractinian corals (17%), sponges (12%), fishes (11%), molluscs, non-scleractinian cnidarians (9% each) account for ~87% of the meeting.

Algae/seagrass-associated systems, alongside annelids, arthropods, mammals and acoels make up the long tail, with environmental microbiomes represented by a single contribution.

Historically, marine biology has been organised around what is visible: organisms, communities and ecosystems defined by macroscopic structure. Yet, this view is now rapidly absorbed into a wider framework – holobiont biology – in which host and microbes together constitute the unit of biological organisation (Bordenstein and The Holobiont Biology Network 2024; Bordenstein and Theis 2015). We believe that this shift is more than semantic: it changes which questions are considered fundamental (function over inventory), which methods are considered sufficient (causation over correlation), and which scales must be integrated (molecular, organismal, ecosystemic). The symposium provided a useful cross-section of how far this reorganisation has progressed in marine systems.

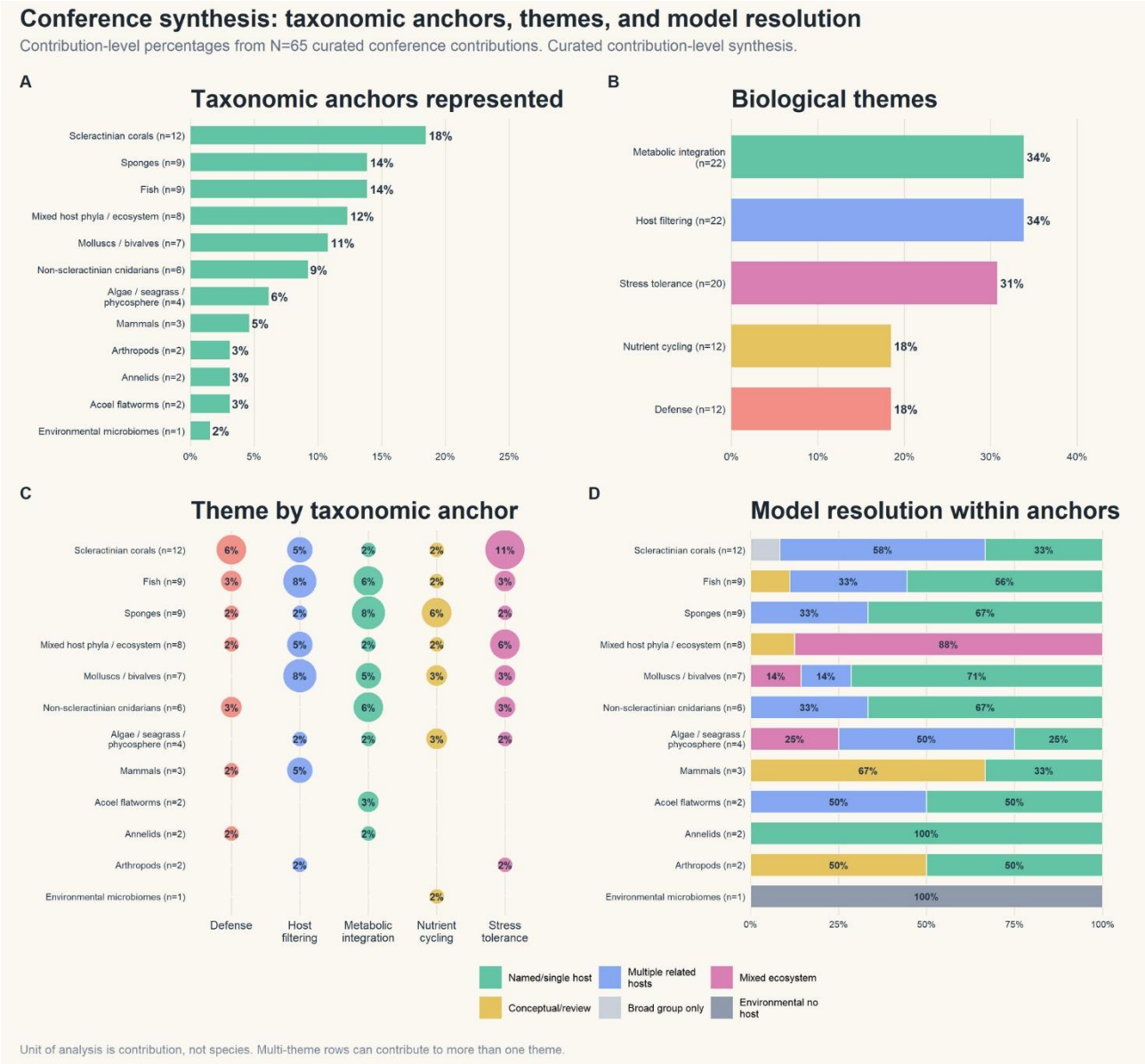

Figure 1 ***Conference landscape of marine host-microbe symbiosis research:*** *Presentation-level synthesis of 65 included symposium contributions.* ***(A)*** *Taxonomic anchors represented across the meeting (proportion of*

contributions). ***(B)*** *Main biological themes (union of primary and secondary themes; contributions may contribute to more than one theme).* ***(C)*** *Distribution of primary themes across taxonomic anchors.* ***(D)*** *Host/model resolution within each anchor. Percentages refer to contributions, not to species or publications.*

Together, these patterns frame the central argument of this Perspective. Marine host-microbe research is moving from asking primarily "who is there?" toward a broader framework centered on which microbial functions recur across hosts, under which ecological contexts they operate, and when they can be linked to prediction or intervention. In this sense, taxonomic diversity remains essential, but it is increasingly being interpreted through the lens of functional convergence, environmental contingency, and experimental tractability.

Holobionts as functional units

The meeting opened with the holobiont as its conceptual anchor. In the framing keynote, Seth Bordenstein argued for holobiont biology as the appropriate organising principle of 21st-century life sciences — a 'unified view of life' integrating microbiology and host macrobiology — and several keynotes built on this premise. Morten Limborg (University of Copenhagen) applied the hologenome concept to farmed salmon, showing that host genotype (CRISPR-edited tyrosinase in zebrafish) and host epigenetic state both shape the gut microbiota, and that a *Mycoplasma* species correlates with fitness traits including growth rate and disease resilience (Kale et al., 2025; Winther-Have et al., 2025). Mónica Medina (University of California, UCLA) demonstrated the same principle developmentally, showing that algal carotenoids from Symbiodiniaceae trigger the retinoic-acid pathway in *Cassiopea xamachana*, with different photosymbionts producing different strobilation outcomes — a textbook example of microbially encoded host development (Kerwin et al., 2025; Montesanto et al., 2026; Sharp et al., 2024).

Contributed talks pushed this conceptual frame into mechanistic territory. Emily Darin (San Diego State University) provided the first functional connection between innate immunity and metamorphosis: in the tubeworm *Hydroides elegans*, the immune adaptor MyD88 — canonical for TLR/IL signalling — is necessary both for bacteria-induced metamorphosis (in response to *Pseudoalteromonas luteoviolacea*) and for survival against *Pseudomonas aeruginosa*, dissolving the conventional boundary between immunity and developmental symbiosis (Darin et al., 2025). Francesca Pinton (Friedrich Schiller University Jena) reinforced the message from a comparative angle by showing that, in acoel flatworms, immune signalling pathways that are downregulated during cnidaria–dinoflagellate symbiosis are altogether absent, and their loss predates the origin of photosymbiosis in this clade - a striking case of immune evolution shaped by symbiotic history (Pinton et al., 2026). Grace Zhong (Stanford University) added a spatial dimension: dinoflagellate symbionts in the acoel *Waminoa* sp. are actively transported through host actin networks, travelling more than fifty times their body length within the host's peripheral parenchyma, overturning the long-standing assumption that established intracellular symbionts are static (Zhong et al., 2025). Vertebrate systems share the same logic. Beyond the salmon work already discussed, Marco Graziano (University of Padova) and Davide Piazza (University of Padova) used the

guppy *Poecilia reticulata* to disentangle host behaviour from environmental transmission of microbes, showing that physical contact between fish drives sex- and tissue-specific microbiome convergence and that proximity time quantitatively predicts microbial similarity (unpublished data). Andrea Quagliariello (University of Florence) repositioned parrotfish microbiomes inside the reef-bioerosion paradigm, isolating two novel bacterial strains (*Kocuria palustris* and a novel *Rossellomorea*) capable of $CaCO_3$ precipitation and dissolution - a direct microbial contribution to coral-sediment formation (unpublished data). Dave Rojas (Norwegian University of Life Sciences) presented genome-resolved resources (Salmon Microbial Genome Atlas) that operationalise the hologenome for breeding and aquaculture (Rojas Clderón et al., 2026). Together these contributions illustrate the bidirectional, context-dependent nature of the hologenome, but also expose how unevenly developed mechanistic evidence still is across taxa..

Microbial function across hosts: convergence beneath diversity

Across the 65 contributions, biochemical functions recurred across taxonomically unrelated hosts, even though the dominant research questions remained system-specific (Fig. 1C). Sponges provided the cleanest illustration of metabolic integration: Laura Steindler (University of Haifa) showed that sponge symbionts produce methane aerobically from dissolved methylphosphonate under phosphate limitation, with potentially climate-relevant fluxes as reefs shift from coral- to sponge-dominated states (Humanes et al., 2026; Montesanto et al., 2026); Torsten Thomas (UNSW) reported sponge-mediated N_2O production via either nitrification, denitrification or both, and CO_2 fixation by ammonia-oxidising archaea (AOA) in deep-sea sponges (Thomas & Garritano, 2026); Alessandro Garritano (University of New South Wales) used 16S amplicon sequencing on 72 South Atlantic deep-sea sponges and isotope labelling to show that microbial autotrophy in *Calyx* sp. fixes the equivalent of ~20% of host biomass annually (Garritano et al., 2026). At the cellular scale, Bettina Glasl (University of Vienna) used NanoSIMS plus FISH to demonstrate mixotrophy in sponge-associated AOA, with branched-chain amino acid uptake potentially modulating mTOR signalling in the host (Glasl et al., 2025). In seagrass ecosystems, Ulisse Cardini (Stazione Zoologica Anton Dohrn Genoa) showed that sulfur-oxidising lucinid symbionts shape DMS fluxes in *Cymodocea nodosa* meadows and that sponge–seagrass interkingdom associations modulate N and CH_4 cycling - pushing the holobiont concept to multi-partner 'nested' systems (Berlinghof et al., 2025; Cardini et al., 2024). Lone Gram (DTU Copenhagen) and Valeria Di Dato (Stazione Zoologica Anton Dohrn) extended the same logic to the phycosphere, showing that algal-associated bacteria suppress fish pathogens and produce novel polyketides, antibiotics and ectoine pathways relevant to biotechnology. These contributions together support a more nuanced reading than is sometimes offered for marine symbioses: at the biochemical level, microbial communities consistently extend host metabolic capabilities — N cycling, C fixation, sulfide oxidation, methane and DMS production, polyketide synthesis — and the specific microbial taxa carrying out these functions are largely interchangeable across host phyla. However, Fig. 1C shows that the questions asked of each system remain strongly taxon-specific: corals are studied predominantly through the lens of stress and defense, mammals

through host filtering, sponges through nutrient cycling, and fish through host filtering and metabolic integration. The field is therefore converging at the level of microbial functions but not yet at the level of integrated research programmes — a gap that the next generation of cross-system, mechanistic studies will need to close.

Context-dependent microbiomes

A recurring message from the symposium was that microbial function cannot be understood in isolation. Instead, it emerges from a complex web of interactions among microbes, between microbes and hosts and within the broader environmental context. Marie Vasse (CNRS, University of Bordeaux) articulated this most explicitly in a conceptual talk drawing on her work on microbial predation: even apparently directional interactions can reverse depending on ecological context, and individual strain metabolism is heavily modulated by community composition — strong cautions against inferring function from monoculture or from taxonomy alone (Vasse & Velicer, 2026). Coral-focused contributions provided the most direct experimental support for this view. Christian Voolstra (University of Konstanz) presented a standardised platform for functional screening of thermal-tolerance-modulating microbes in cnidarian holobionts (Voolstra & Ziegler, 2020); Taissa Damasceno (University of Perpignan) and Matteo Monti (King Abdullah University of Science and Technology, KAUST) used microbial consortia to accelerate recovery and prime immunity in deep-sea and shallow corals, respectively (Monti et al., 2026); Ty Roach (Duke University) framed phage-guided microbiome engineering and precision probiotics as actionable tools for reef restoration (unpublished data, Roach et al., 2021). At the evolutionary scale, Nicole Dubilier (Max Planck Institute for Marine Microbiology, Bremen) closed the keynote series by showing that up to sixteen co-existing endosymbiont strains in deep-sea *Bathymodiolus* mussels, together with horizontal gene transfer and mobile genetic elements, accelerate adaptation in chemosynthetic symbioses (Porras et al., 2024) - a striking demonstration that microbiome function is shaped not only by ecology but by within-host evolutionary processes that are largely decoupled from higher-level taxonomy. This context dependency has direct methodological consequences. Several contributions made the point concretely: Tina Keller-Costa (Instituto Superior Técnico, University of Lisbon) showed that two phylogenetically close Endozoicomonadaceae chitinases (GeuChi18, GleChi18) display divergent responses to salinity and temperature, indicating niche specialisation within a single bacterial family (da Silva et al., 2023; Meunier et al., 2025); Brooke Travis (Harvard University) reported that two co-occurring *Lucinoma* species in oxygen minimum zones show substantially different symbiont gene expression in nitrogen, methylotrophy and motility pathways despite hosting the same Candidatus Thiodiazotropha symbiont (unpublished data). Carlotta Kück (Max Planck Institute for Marine Microbiology, Bremen) provided the cleanest formal test: in three Caribbean lucinid hosts harbouring the same chemosynthetic symbiont, host species identity drove symbiont gene expression for carbon fixation, cell division and sulfide oxidation (Kück et al., 2026). Together these results argue that 16S-level taxonomy is necessary but no longer sufficient — function must be inferred from genome- and expression-resolved data tied to ecological context.

From description to mechanism: a methodological shift

The methodological signature of the symposium (Figs 1B and 3) was the combination of three previously separate toolkits. First, sequencing remained the workhorse — 48% of contributions used amplicon sequencing and 43% used deep sequencing or meta-omics (Fig. 3C) — but increasingly as a starting point rather than an endpoint. Second, spatially resolved chemical and microbial imaging emerged as a defining capability: Berta Pintó (University of Barcelona - Institut de Ciències del Mar-CSIC) and Marie Rutsch (University of Vienna) used MALDI mass-spectrometry imaging to map bastadins and other secondary metabolites onto sponge mesohyl and co-localise them with CARD-FISH–identified symbionts; Bettina Glasl (University of Vienna) and Laura Bulson (École Polytechnique Fédérale de Lausanne) used NanoSIMS coupled to FISH to quantify carbon and nitrogen flux at the single-cell level in AOA and *Endozoicomonas* symbionts respectively (Glasl et al., 2025, unpublished data). Third, experimental manipulation came of age: Amanda Alker (University of Rhode Island) presented adaptation of CRISPR-associated transposase (CAST) systems for species-specific in-community editing of marine gammaproteobacteria (Gotze et al., 2025; Shikuma& Alker, 2026); Laura Bulson used suicide-plasmid transposon tagging of *Endozoicomonas* combined with isotope labelling for reintroduction into native hosts; Sofia Sizikov (University of Haifa) expressed sponge-symbiont GPP34 in *E. coli* to test its role in evading phagolysosome maturation in macrophage assays (unpublished data). Activity tracing (isotope-based; 6% of contributions) and proteomics (2%) remain comparatively under-used, suggesting clear methodological growth points for the field (Fig. 3C). Together, these approaches are shifting the field from correlation to causation, enabling a mechanistic understanding of host-microbe interactions that was previously out of reach.

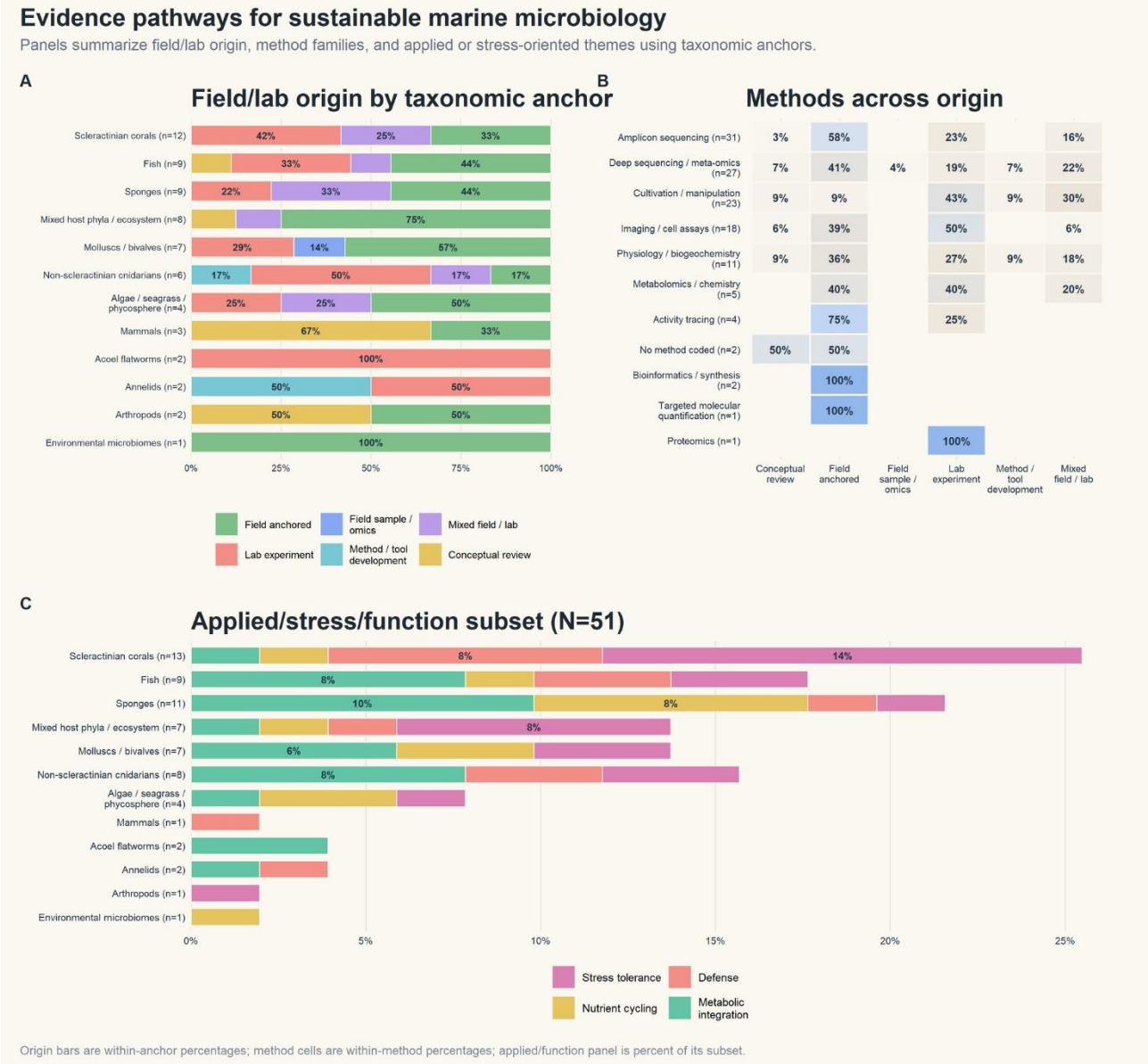

Figure 2. ***Evidence pathways from context to application.*** *Contribution-level synthesis of origin context, method families, and applied/stress/function themes across curated symposium contributions (N=65).* ***(A)*** *Origin context by taxonomic anchor.* ***(B)*** *Technique families across origin contexts; multi-method contributions can appear in more than one family.* ***(C)*** *Applied, stress, defense, and ecosystem-function subset by taxonomic anchor (N=51). Percentages refer to contributions within the relevant panel.*

The evidence and origin coding suggests that this transition is underway, but not yet complete (Fig. 2). Field-anchored contributions represented the largest origin category (28 of 65; 43%), followed by laboratory experiments (19 of 65; 29%) and mixed field/lab studies (10 of 65; 15%); conceptual reviews (5 of 65; 8%), method/tool development (2 of 65; 3%), and field-sampled omics-focused contributions (1 of 65; 2%) were less frequent. In parallel, evidence types spanned mechanistic (32 of 65; 49%), observational (19 of 65; 29%), experimental (9 of 65; 14%), and review-oriented contributions (5 of 65; 8%). This mixture shows that marine host-microbe research is increasingly

linking environmental realism with experimental control, while field observation, field-sampled omics,laboratory validation, and causal manipulation remain unevenly integrated across host systems.

The methodological coding reinforces this interpretation (Fig. 3). Method information could be assigned for nearly all curated contributions (63 of 65; 97%). Sequencing remained central but was not the only methodological axis: amplicon sequencing appeared in 48% of contributions and deep sequencing or meta-omics in 42%, while cultivation/manipulation (35%), imaging or cell assays (28%), and physiology or biogeochemistry approaches (17%) were also widely represented. Activity tracing (6%; e.g. NanoSIMS, isotope-based approaches), metabolomics/chemistry (8%), proteomics (2%), and targeted molecular quantification (2%) were less frequent, highlighting growth areas for linking microbial identity to in situ function. Overall, the pattern supports a shift beyond compositional cataloguing toward studies that combine community profiling with experimental, spatial, physiological, and biochemical evidence.

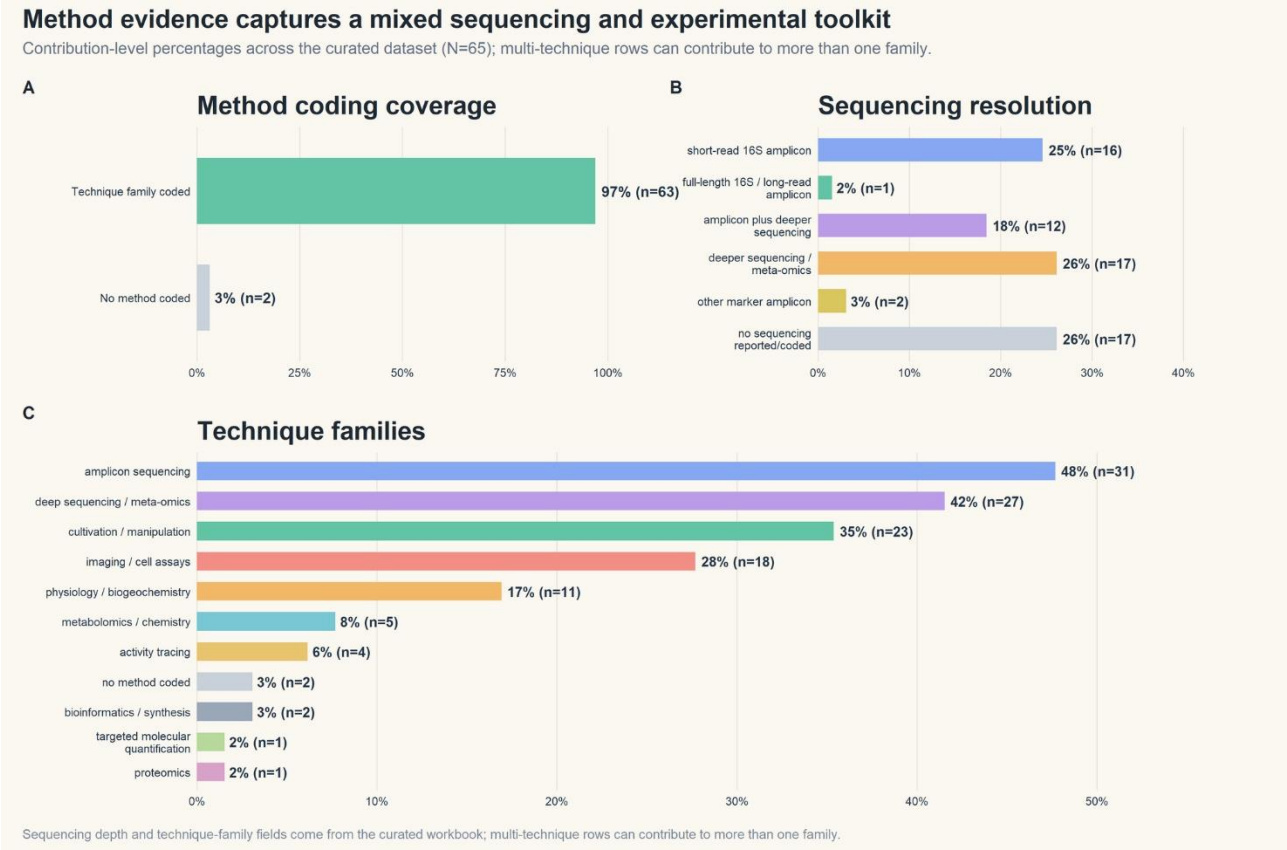

Figure 3. ***Methodological breadth and sequencing resolution across curated symposium contributions.*** *Contribution-level synthesis of methodological information extracted from the curated dataset (N=65).* ***(A)*** *Method coding coverage.* ***(B)*** *Sequencing-resolution categories.* ***(C)*** *Major technique families, with multi-method contributions allowed to contribute to more than one category. Percentages refer to conference contributions, not independent studies or publications.*

Sequencing depth should also be interpreted in light of the uneven infrastructures that shape microbiome research. Human and biomedical microbiome studies increasingly benefit from large

cohorts, clinical motivation, extensive reference databases, and substantial funding, enabling routine use of deep metagenomic, metatranscriptomic, strain-resolved, and long-read approaches. Marine host-microbe studies face a different reality: difficult and often opportunistic field sampling, non-model hosts, limited reference resources, and smaller budgets. In the curated symposium dataset, short-read 16S amplicon sequencing, deeper sequencing/meta-omics, and combined amplicon-plus-deeper approaches were all represented, while 26% of contributions had no sequencing reported or coded. This should not be read as a deficit alone, because several of these contributions used metabolomics, NanoSIMS, CARD-FISH, enzyme assays, growth experiments, physiology, or interaction assays. Rather, it shows that functional inference in marine symbiosis is being built through a mixed toolkit, while broader access to deeper sequencing and host-specific reference resources remains an important structural challenge.

Toward prediction and intervention

A central translational outcome of the symposium was the consolidation of microbial intervention as a credible, if early-stage, strategy for marine host resilience. The intervention subset is small but informative (N=10 of 65 contributions; Fig. 4). Within thissubset, the cnidarian bias was quantitatively explicit: 7 of 10 intervention contributions (70%) targeted scleractinian corals or other cnidarians (Voolstra; Roach; Damjanovic/Høj; Damasceno; Monti; Scribano; Høj), while molluscs (Nai, microbiome thermal priming in Manila clams), algae/phycosphere (Gram, phycosphere-mediated pathogen suppression) and mammalian gut (Walter, ecological framing of live microbial intervention (Walter et al., 2018) are each represented by a single contribution. . This taxonomic skew is itself a finding: the intervention agenda is currently driven by coral-reef conservation, with other marine systems following at distance. Two specific results stood out. Ilaria Nai (University of Padova) showed that transplanting a thermally-primed microbiome into naïve Manila clams (*Ruditapes philippinarum*) increased antioxidant enzyme activity (catalase, SOD) and reduced mortality under marine heatwave conditions - a direct demonstration that microbiome priming is sufficient (not merely necessary) for thermal tolerance in a commercially important bivalve (Martino et al., 2026). Katarina Damjanovic and Lone Høj (Australian Institute of Marine Science) inoculated newly settled *Acropora juveniles* with eight pre-screened native strains and documented the first microscopic observation of *Endozoicomonas*-induced coral-associated microbial aggregates (CAMAs) under controlled manipulation, a methodological milestone for probiotic R&D in cnidarians (Thatcher et al., 2025).

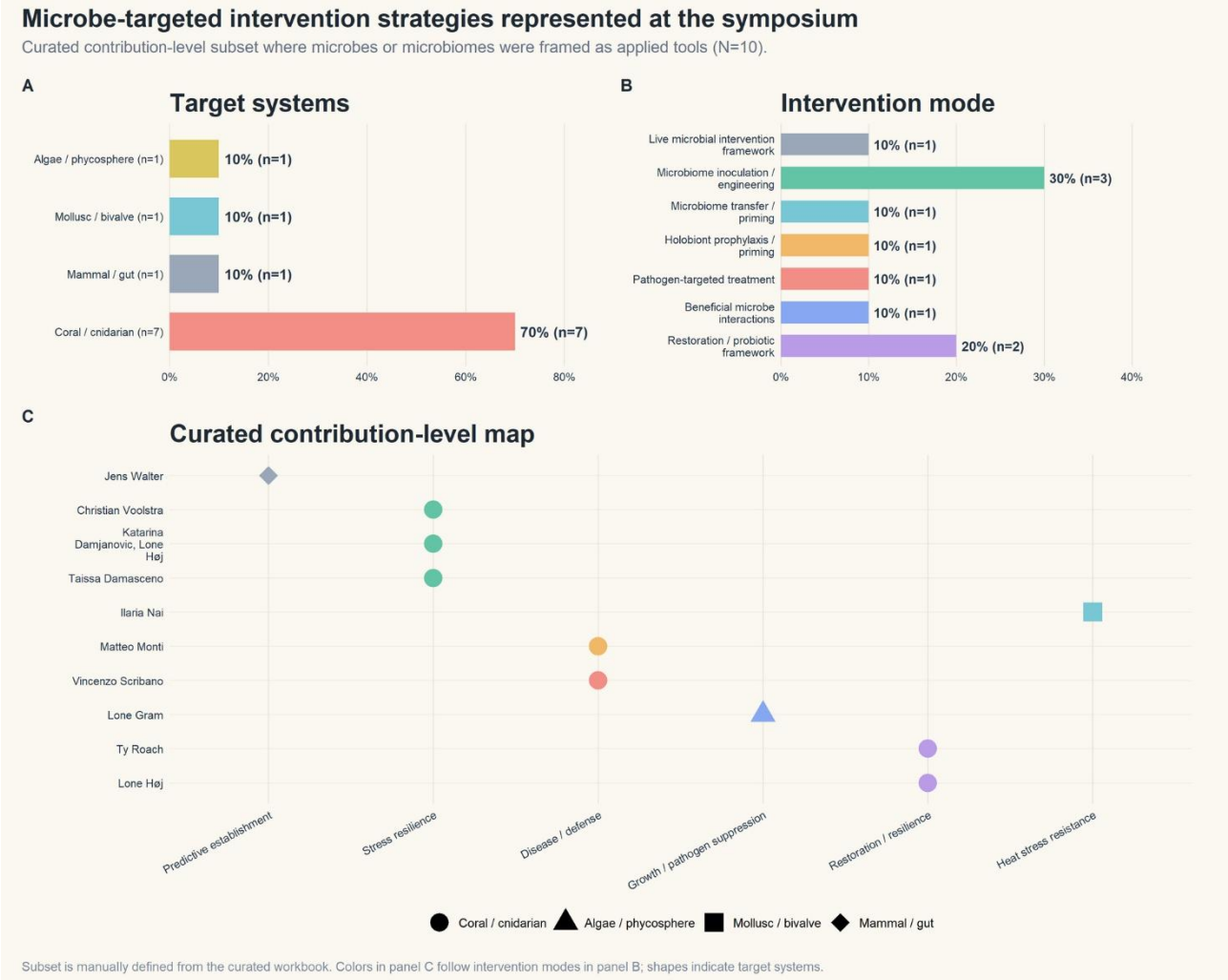

Figure 4. ***Microbe-targeted intervention strategies represented in the curated symposium dataset.*** *Manually curated subset of conference contributions in which microbes or microbiomes were framed as applied tools (N=10).* ***(A)*** *Target host or ecosystem systems represented in the intervention-oriented subset.* ***(B)*** *Intervention modes, including microbiome inoculation or engineering, microbiome transfer or priming, holobiont prophylaxis, pathogen-targeted treatment, beneficial microbe interactions, restoration/probiotic frameworks, and live microbial intervention frameworks.* ***(C)*** *Contribution-level map linking presenters, target outcomes, intervention modes, and target systems. Percentages refer to contributions within this curated subset, not to the full symposium dataset.*

Contributions on the phycosphere further reinforced this perspective, showing that host-associated microbial communities can enhance algal growth and suppress pathogens, thereby linking microbial interactions to measurable host or ecosystem-relevant outcomes (Roager et al., 2026). Together with coral intervention studies, these findings establish a quantitative input-output relationship: a defined microbial perturbation produces a measurable, reproducible host phenotype under defined environmental conditions. That is the operational definition of mechanism, and it is what distinguishes the current generation of marine microbiome work from the descriptive amplicon-survey era.

At the same time, applied and intervention-oriented themes were not evenly distributed across host groups (Fig. 1C, Fig. 2C). Stress tolerance dominates scleractinian-coral and mixed-ecosystem

contributions (55% and 46% of their primary themes, respectively); defense is a strong secondary theme in corals (27%), nutrient cycling anchors sponge and seagrass work (50% and 50%), and manipulation-focused contributions were especially prominent in coral and sponge systems. The taxonomic groups with the smallest contribution counts — annelids, acoel flatworms, arthropods, mammals, and environmental microbiomes - should be interpreted cautiously: they point to promising conceptual extensions, but not yet to equally mature evidence bases across host systems. The advanced state of coral intervention research is therefore as much an artefact of where conservation pressure has concentrated as it is a sign that coral systems are intrinsically tractable. Whether the same principles transfer to bivalves, fish, algae and seagrasses — taxa with substantially different ecology, immunity and life history — is one of the most important open questions in applied marine microbiome science.

Prediction and intervention, however, cannot be decoupled from ecological and evolutionary context. Jens Walter (University College Cork) made this point most forcefully in his keynote: live microbial interventions in the human gut — probiotics, live biotherapeutics, FMTs — fail or vary unpredictably because three ecological principles are typically ignored (evolutionary history of the introduced strains, priority effects, niche structure of the recipient community). The same principles will determine whether marine interventions succeed at scale. Likewise, Cameron Thrash (University of Southern California) emphasised that microbial spatio-temporal niche partitioning must be modelled explicitly if we are to forecast microbial activity under climate scenarios. Nicola Segata (University of Trento) added an evolutionary anchor by showing how primate–microbiome coevolution informs biomedical applications (Labisa-Morais et al., 2025), a useful counterpoint reminding the marine community that mature, interventional microbiome science requires deep evolutionary calibration. Taken together, these contributions argue for a hybrid agenda: mechanistic, single-system experiments to establish causal microbiome-host links; combined with ecological/evolutionary modelling to scale those links to natural communities and environmental change.

Priorities for a function-first marine symbiosis framework

Four operational priorities emerge from the symposium. (1) **Broaden the methodological stack**. Activity tracing (6% of contributions, Fig. 3C; e.g. NanoSIMS, isotope-FISH) and proteomics (3%) remain under-used despite providing the most direct bridges between sequence-resolved community structure and in situ function; spatial chemical imaging (MALDI-MSI) and genome-resolved metatranscriptomics also deserve expanded application. (2) **Broaden the taxonomic stack**. More than 70% of microbiome-intervention contributions targeted corals or cnidarians (Fig. 4A); expanding mechanistic and intervention work into bivalves, fishes, algae/seagrasses and other under-represented hosts is the single most important corrective. (3) **Build shared frameworks**. The field will benefit from comparable experimental designs, standardised intervention protocols and openly shared genome-resolved reference resources — exemplified at the symposium by the Salmon Microbial Genome Atlas (Rojas) and the expanded Tara Pacific coral microbiome dataset (Mayer,

revising global reef microbiome diversity upwards by ~3×). (4) **Evaluate interventions within ecological and evolutionary context.** Following Walter's keynote, the persistence, specificity, reversibility and unintended consequences of any deliberate microbiome manipulation must be assessed before translation to natural systems.

Conclusions: a converging field

The Trends in Host-Microbe Symbioses Symposium captured a field at an inflection point. Marine microbiome research has visibly outgrown the descriptive, taxonomy-driven phase and is consolidating around function, mechanism and intervention as its organising questions. Convergent biochemical themes — nitrogen and carbon cycling, sulfide and methane metabolism, immune priming and stress buffering — recur across taxonomically unrelated hosts, even where the research programmes themselves remain strongly system-specific (Fig. 1C). Acting on the four priorities set out above will determine whether the next decade of marine microbiome research delivers on its promise: not only redefining how we understand life in the ocean but contributing actionably to the conservation and management challenges of the Anthropocene.

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Author contributions

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Conflicts of interest

None declared.

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Data availability

All relevant data are contained within this manuscript.

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