

Biogeochemical cycling and fate of PAHs in coral reef ecosystem: Associations with coral holobiont microbial functional profiles

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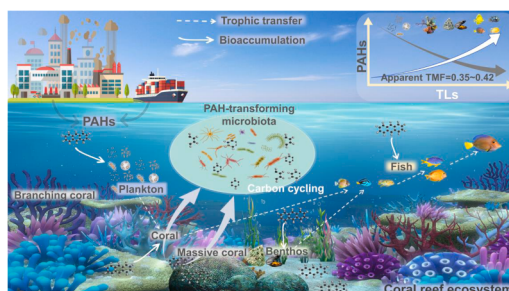
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HIGHLIGHTS

- Plankton/coral are the major reservoirs of PAHs in coral reef ecosystem.
- PAHs showed an apparent trophic dilution trend in reef ecological compartments.
- Coral species differed in predicted PAH-related microbial functional potential.
- Predicted microbial functional potential was associated with PAH accumulation.

GRAPHICAL ABSTRACT



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ABSTRACT

Current understanding of the distribution, bioaccumulation, and trophic transfer patterns of polycyclic aromatic hydrocarbons (PAHs) in coral reef ecosystem remains limited, particularly regarding their potential associations with coral-associated microbial communities. This study investigated PAH occurrence, bioaccumulation, and apparent trophic distribution patterns across ecological compartments within the coral reef ecosystem of the Weizhou Island, northern South China Sea (SCS). PAHs were detected in multiple environmental and biological compartments, with zooplankton and coral tissue exhibiting relatively high PAH concentrations, and *Turbinaria peltata* (*T. peltata*; massive coral) showing the greatest PAH burdens among the investigated coral species. Bio-water accumulation factors (BWAFs) varied substantially among reef organisms, and a significant positive relationship between log BWAFs and log K_{OW} indicated that hydrophobicity was an important determinant of PAH accumulation. Apparent trophic magnification analysis revealed an overall tendency toward trophic dilution of PAHs across the coral reef ecosystem, indicating limited biomagnification potential under the investigated conditions. Comparative analysis of coral-associated microbial communities from 16S rRNA datasets revealed distinct microbial community composition and higher predicted PAH-related metabolic potential in *T. peltata*. The predicted enrichment of PAH-related metabolic pathways suggests that PAH transformation products may potentially enter microbial carbon metabolic pathways, where the transformed carbon could be utilized by microorganisms or contribute to carbon cycling within coral reef ecosystems, although direct functional validation is still required. Further studies integrating paired chemical and microbial measurements are required to

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determine whether these microbial processes contribute directly to PAH transformation and trophic transfer. Overall, this study provides new insights into PAH distribution and trophic behavior in coral reef ecosystems and offers an exploratory perspective on the potential role of coral-associated microbial communities in PAH fate under anthropogenic stress.

1. Introduction

Polycyclic aromatic hydrocarbons (PAHs) are a class of ubiquitous semi-volatile organic pollutants that are widely distributed in marine environments. Due to their carcinogenic, mutagenic and teratogenic properties, PAHs have attracted considerable attention as priority pollutants of global concern (Armstrong et al., 2004; Peng et al., 2023; Zhang et al., 2012). As persistent hydrophobic compounds, PAHs can accumulate in marine organisms and be transferred through food webs, posing potential risks to ecosystem functioning and human health. Increasing environmental burden of PAHs are primarily associated with anthropogenic activities, including incomplete combustion of fossil fuels and biomass, petroleum extraction and transportation, and industrial emissions (Dai et al., 2025; Zhu et al., 2024).

Coral reefs are among the most biodiverse and ecologically important marine ecosystems worldwide. However, their proximity to densely populated coastal regions makes them particularly vulnerable to contaminant inputs from both land-based and marine sources. Previous studies have documented the occurrence and accumulation of PAHs in various coral reef compartments, including seawater, sediments, corals, fish, and other reef-associated organisms (Ashok et al., 2022, 2020; Han et al., 2019). These studies have demonstrated that the environmental fate of PAHs in reef ecosystems is influenced by multiple factors, such as geographical location, contamination sources, food-web structure, and species-specific ecological characteristics. Nevertheless, most existing studies have focused on contaminant occurrence and bioaccumulation in individual environmental matrices or organisms, whereas investigations of PAH trophodynamics across complete coral reef ecosystems remain relatively limited. In addition to trophic interactions, coral-associated microorganisms may represent an important but understudied driver of PAH fate in reef ecosystems. As integral components of the coral holobiont, microbial communities contribute to nutrient cycling, host health maintenance, and environmental stress responses. Coral-associated microbes are capable of degrading hydrocarbons and participating in pollutant detoxification processes (Cao et al., 2025). However, despite their potential importance, the extent to which microbial functional characteristics influence PAH bioaccumulation and trophic transfer within coral reef ecosystems remain largely unknown. To date, studies integrating contaminant trophodynamics with coral-associated microbial functions are still scarce.

The South China Sea (SCS) contains one of the world's most important coral reef regions but has experienced increasing environmental pressure from climate change and anthropogenic activities during recent decades (Han et al., 2023; Yu, 2012; Zhao et al., 2012). Elevated PAH contamination has been reported in several coastal areas of the SCS, particularly in regions affected by urbanization, industrial development, maritime transportation, and petroleum-related activities (Han et al., 2023, 2019; Zhang et al., 2021). In coastal reef ecosystems, PAHs can enter marine environments through multiple pathways, including marine-based inputs such as shipping activities and offshore petroleum operations, as well as land-based inputs associated with terrestrial runoff, wastewater discharge, coastal development, and atmospheric deposition (Han et al., 2023). Weizhou Island, located in the northern SCS, represents a typical tropical coral reef ecosystem subjected to multiple anthropogenic pressures, including land-based pollution, offshore oil exploitation, maritime transportation, and increasing coastal human activities (Feng et al., 2024; Yu et al., 2019). These stressors may increase the exposure risk of local coral reef organisms to persistent organic contaminants and potentially threaten ecosystem

stability (Ding et al., 2020; Pan et al., 2021; Zhu et al., 2024). Despite the high biodiversity and complex trophic structure of the coral reefs surrounding Weizhou Island (Liao et al., 2019; Yu et al., 2020), the mechanisms governing PAH trophodynamic behavior within complex coral reef ecosystems remain poorly understood, particularly regarding how species-specific ecological traits and coral-associated microbial functions may contribute to variations in contaminant fate across trophic levels (TLs).

To address these knowledge gaps, this study provides an integrated assessment of PAH fate across a coral reef ecosystem by linking contaminant distribution, trophic transfer patterns, and coral-associated microbial functional characteristics. Specifically, we investigated PAH distributions in multiple environmental and biological compartments of the coral reef ecosystem surrounding Weizhou Island, evaluated PAH bioaccumulation and trophic transfer patterns across the reef food web, and explored the potential influence of coral-associated microbial functional divergence on PAH trophodynamics. Compared with previous studies that focused primarily on contaminant occurrence or bioaccumulation alone, this study integrates food-web and microbial perspectives to provide new insights into the ecological processes governing PAH fate in coral reef ecosystems.

Accordingly, the objectives of this study were to: (1) characterize PAHs contamination levels in environmental media and representative organisms from the coral reef ecosystem of Weizhou Island; (2) assess PAH bioaccumulation patterns among different coral reef organisms; (3) elucidate the trophodynamic characteristics of PAHs within the coral reef ecological compartments; and (4) conduct an exploratory synthesis of coral-associated microbial characteristics and PAH distribution patterns to identify potential microbial-related factors associated with PAH fate. The findings provide new evidence critical for understanding the environmental fate of PAHs in coral reef ecosystems and contribute to ecological risk assessment and management of coral reefs under increasing anthropogenic and climate-related pressures.

2. Materials and methods

2.1. Sampling and sample pretreatment

A field survey was conducted around Weizhou Island in August 2024. Three sampling sites were selected to represent the regional coral reef ecosystem. Because this study aimed to characterize the overall PAH contamination status and trophic transfer patterns of the Weizhou Island coral reef ecosystem rather than to investigate spatial heterogeneity among individual sites, samples collected from the three sites were pooled for subsequent analyses. Forty samples in total were collected, comprising 3 phytoplankton, 3 zooplankton, 3 reef macroalgae, 12 reef fish, 9 benthos, 4 coral tissues and 3 sediment samples. Algae collected in this study refer specifically to reef-associated macroalgae (*Sargassum* spp.), which were collected from coral reef habitats. Unlike phytoplankton, which are suspended microscopic primary producers in the water column, *Sargassum* spp. are attached macroalgae with distinct ecological function. Detailed sampling and species information is provided Figure S1 and Tables S1. For coral samples, *Turbinaria peltata* (*T. peltata*) and *Acropora pruinosa* (*A. pruinosa*) were selected for the cross-dataset comparison because the previously published 16S rRNA datasets used in this study were derived from the same two coral species. Plankton samples were collected by repeated vertical net tows. Phytoplankton were collected using a No 13 plankton net, and zooplankton with a No 25 plankton net. Samples were placed in 500 mL brown glass

bottles pre-treated with 50 mL of 75% ethanol and 20 mL of Lugol's iodine solution for fixation. the potential underestimation of PAH concentrations in plankton due to solvent-induced loss. Other coral reef organisms and sediments were collected via SCUBA diving. Plankton samples were refrigerated and transported to the laboratory for sieving through a 200 μm mesh. Phytoplankton fixed in ethanol were collected from the filtrate via sieve cloth, while zooplankton fixed in Lugol's solution were retained on the sieve cloth. Samples were filtered using pre-weighed, purified glass fiber filters (GFFs). Biological and sediment samples were sealed in aluminum bags and transported on dry ice to the laboratory. All GFFs, biological samples, and sediments were stored at $-20\text{ }^{\circ}\text{C}$ in sealed bags.

2.2. PAH analysis

The 16 US EPA priority PAHs were selected as target compounds (Table S2). Coral tissue was extracted via liquid-liquid extraction using a hexane/dichloromethane (1:1, v/v) mixture (15 mL per extraction, repeated three times). Other organisms were extracted ultrasonically using a hexane/acetone (1:1, v/v) mixture (15 mL per extraction, repeated three times). Detailed methods are provided in Text S2. Lipid contents of organisms were determined gravimetrically by evaporating an aliquot of the extract to complete dryness and weighing the residual lipid mass. For coral tissue, fish and benthos invertebrates (samples with sufficient biomass), one-quarter of the total extract volume was subsampled to quantify lipid content via gravimetric weight loss. Due to the limited biomass of zooplankton, phytoplankton, and zooxanthellae, no aliquots of their extracts were reserved for lipid measurement to maximize the extract volume available for PAH detection and quantification. Analysis of the 16 target PAHs was performed using an Agilent 7890B gas chromatograph coupled with a 7000C triple quadrupole mass spectrometer (GC-MS/MS).

2.3. Estimation of bioaccumulation and apparent trophic magnification

Bioaccumulation is an important process governing the migration, transformation, and ecological exposure of persistent contaminants within aquatic ecosystems (Sun et al., 2020). Bioaccumulation factors (BAFs, L/kg) integrate the contribution of contaminants acquired from both environmental media and dietary sources (Arnot and Gobas, 2006). In this study, bio-water accumulation factors (BWAfFs) and bio-sediment accumulation factors (BSAafFs) were calculated to evaluate the relative accumulation potential of PAHs in coral reef organisms from Weizhou Island. Detailed calculation method can be found in Text S3. According to the European Chemicals Agency, chemical with log BAF values >3.7 are considered bioaccumulative, whereas values between 3.3 and 3.7 indicate potentially bioaccumulative (European Chemicals Agency, 2023; Arnot and Gobas, 2006).

Conventional trophic magnification factors (TMFs) are generally applied to well-resolved food webs with validated trophic relationships. In this study, because the sampled organisms represented ecological compartments rather than a fully resolved food web, regression-based trophic metrics were interpreted as apparent TMFs. Relative TLs were estimated using stable nitrogen isotope ratios ($\delta^{15}\text{N}$), while stable carbon isotope ratios ($\delta^{13}\text{C}$) were used to provide information on potential carbon sources. Apparent TMFs were calculated from the regression relationship between $\delta^{15}\text{N}$ -derived relative trophic positions and lipid-normalized PAH concentrations (ng/g lw) (Text S3).

2.4. Coral-associated microbial community analysis

The 16S rRNA amplicon sequencing data analyzed in this study were retrieved from the NCBI Sequence Read Archive (SRA) from previously published datasets of the *T. peltata* and *A. pruinosa* and represent the whole coral holobiont rather than separately analyzed coral tissue and zooxanthellae. The datasets were reanalyzed using the workflow

described in Text S6. The corresponding BioProject accession number PRJNA687610 and PRJNA639237, and original references are provided below (Chen et al., 2021; Yu et al., 2021).

Raw sequencing reads were quality-filtered and processed using fastp and QIIME2 with the DADA2 pipeline to generate amplicon sequence variants (ASVs). Taxonomic classification was performed using the SILVA database. Microbial community characteristics were evaluated based on α -diversity indices (ACE, Chao1, Shannon, and Simpson), β -diversity analysis using principal coordinate analysis (PCoA), and genus-level community composition profiling. Community assembly processes were assessed using a phylogeny-based null model framework based on β -nearest taxon index (βNTI) and Bray-Curtis-based Raup-Crick metric (RCbray), while the contribution of stochastic processes was further evaluated using Sloan's neutral community model (NCM). Ecological niche characteristics and persistent microbial members were evaluated using niche breadth and core microbiome analyses, respectively. Differentially enriched microbial taxa were identified using LEfSe combined with Kruskal-Wallis tests, and correlations between microbial taxa and coral tissue PAH concentrations were assessed using Spearman correlation analysis. Predicted microbial functional potential was inferred using PICRUSt2 and Tax4Fun based on 16S rRNA gene data.

Importantly, the PAH dataset and the microbial datasets were not collected synchronously and do not originate from paired samples. The PAH measurements were conducted on coral samples collected in 2024, whereas the 16S rRNA datasets were derived from previously published studies (Chen et al., 2021; Yu et al., 2021). Therefore, the two datasets differ in sampling period and sample resolution, and their integration in this study is intended for exploratory ecological comparison rather than for establishing mechanistic relationships.

2.5. Quality assurance and quality control

Experimental blanks, reagent blanks, procedural blanks and duplicate samples were added during the PAHs extraction process. Five deuterium-labeled PAHs of a known concentration were added prior to ultrasonic extraction in order to monitor the recovery rates at specific concentrations. During data analysis, it was found that the recovery rates of the other four deuterium-labelled PAHs ranged from 71 to 113% (anthracene-D10: $79 \pm 8\%$; phenanthrene-D10: $82 \pm 12\%$; pyrene-D12: $92 \pm 13\%$; pyrene-D12: $91 \pm 21\%$), except for naphthalene-D8 $< 30\%$. Due to naphthalene's high volatility, the actual measured concentration data were significantly lower than its true concentration in the sample. Therefore, naphthalene was not reported in this study. Instrument detection limits (IDLs) were based on the signal-to-noise ratio (SNR) of the lowest standard. Method detection limits (MDLs) were calculated as three times the IDL divided by the sample mass. Relative standard deviations for all replicates remained 3.0 – 15%. The concentrations of the target PAHs in all the blanks were either below the IDLs or not detected. MDLs ranged from 0.14 to 3.09 ng/g for organisms and 0.07 to 1.55 ng/g for sediments.

2.6. Statistical analysis

Data were analyzed using Excel 2019, Origin 2024, and IBM SPSS Statistics 24.0. Normality was assessed using the Shapiro-Wilk test. For normally distributed data, independent *t*-tests were used; otherwise, non-parametric tests were applied. Significance was set at $p < 0.05$, and high significance at $p < 0.01$. Pearson's correlation was used for normally distributed data; otherwise, Spearman's correlation was applied. Because TMF regressions were performed using mean PAH concentrations of representative ecological groups rather than individual biological replicates, sensitivity analyses were conducted at the ecological-group level. Cook's distance was calculated to identify potentially influential groups, and leave-one-group-out analyses were performed by sequentially removing each ecological group and recalculating

regression slopes.

3. Result and discussion

3.1. Occurrence of PAHs in coral reef ecosystem

Planktons. All 15 PAHs were detected in planktons, with detection rates ranging from 50% to 100%. The $\Sigma_{15}\text{PAHs}$ (total concentration of 15 US EPA priority controlled PAHs excluding naphthalene) in the planktons were 5252–11,302 ng/g dw (7895 ± 2077 ng/g dw), with 3- and 4-ring PAHs accounting for $31\% \pm 5\%$ and $35\% \pm 12\%$ of the $\Sigma_{15}\text{PAHs}$, respectively (Fig. 1). The $\Sigma_{15}\text{PAHs}$ in zooplankton (9413 ± 1428 ng/g dw) was significantly higher than that in phytoplankton (6377 ± 1407 ng/g dw) (t -test, $p < 0.05$). This phenomenon may be attributed to the substantial ingestion of PAHs by zooplankton through their consumption of phytoplankton, and their higher lipid content increases their ability to accumulate PAHs. Furthermore, the composition of PAHs also exhibits significant differences, the proportion of 4-ring PAHs in zooplankton is significantly higher than that in phytoplankton (Fig. 1). PAH concentrations in zooplankton of the Weizhou Island is higher than that in the Pearl River Estuary (Qari and Hassan, 2017), but lower than that in the Wujiang River, Guangzhou (Long et al., 2024).

Algae. All 15 PAHs were widely detected in algae, with detection

rates ranging from 50% to 100%. The $\Sigma_{15}\text{PAHs}$ in the algae were 319–567 ng/g dw (513 ± 141 ng/g dw), with 3- and 4-ring PAHs accounting for $> 70\%$ of the $\Sigma_{15}\text{PAHs}$, respectively (Fig. 1). PAH concentrations in algae in the coral reef region of Weizhou Island is higher than that in the Mediterranean Sea (El-Maradny et al., 2022), the Red Sea (Qari and Hassan, 2017), but lower than that in the Pearl River Estuary (Qari and Hassan, 2017).

Benthos. All 15 PAHs were commonly detected in benthos, with detection rates ranging from 11% to 100%. The $\Sigma_{15}\text{PAHs}$ in benthos were 668–1188 ng/g dw (830 ± 160 ng/g dw). Among them, 3-ring PAHs ($39\% \pm 5\%$) accounted for the highest proportion. The concentrations of PAHs in different species also varied slightly, with $\Sigma_{15}\text{PAHs}$ in *Ostrea gigas* tnunb (*O. gigas* tnunb; 983 ± 171 ng/g dw) slightly higher than those in *Trochus niloticus* (*T. niloticus*; 761 ± 198.3 ng/g dw) and *Perna viridis* (*P. viridis*; 747 ± 57.0 ng/g dw) (Fig. 1). The bio-accumulation capacity of these benthic organisms for PAHs is primarily influenced by similar habitats and feeding habits, resulting in no significant heterogeneity in PAH concentrations among species. Overall, PAH concentrations in benthos in the coral reef region of Weizhou Island is higher than that in the Mexican Gulf (Pie et al., 2015), the Virgin Island (Bargar et al., 2013) and the SCS (Han et al., 2022).

Fish. All target PAHs were detected in coral reef fish, with detection rates ranging from 33% to 100%. The $\Sigma_{15}\text{PAHs}$ in fish were 624–1188 ng/g dw (849 ± 151 ng/g dw), with 3-ring PAHs accounting

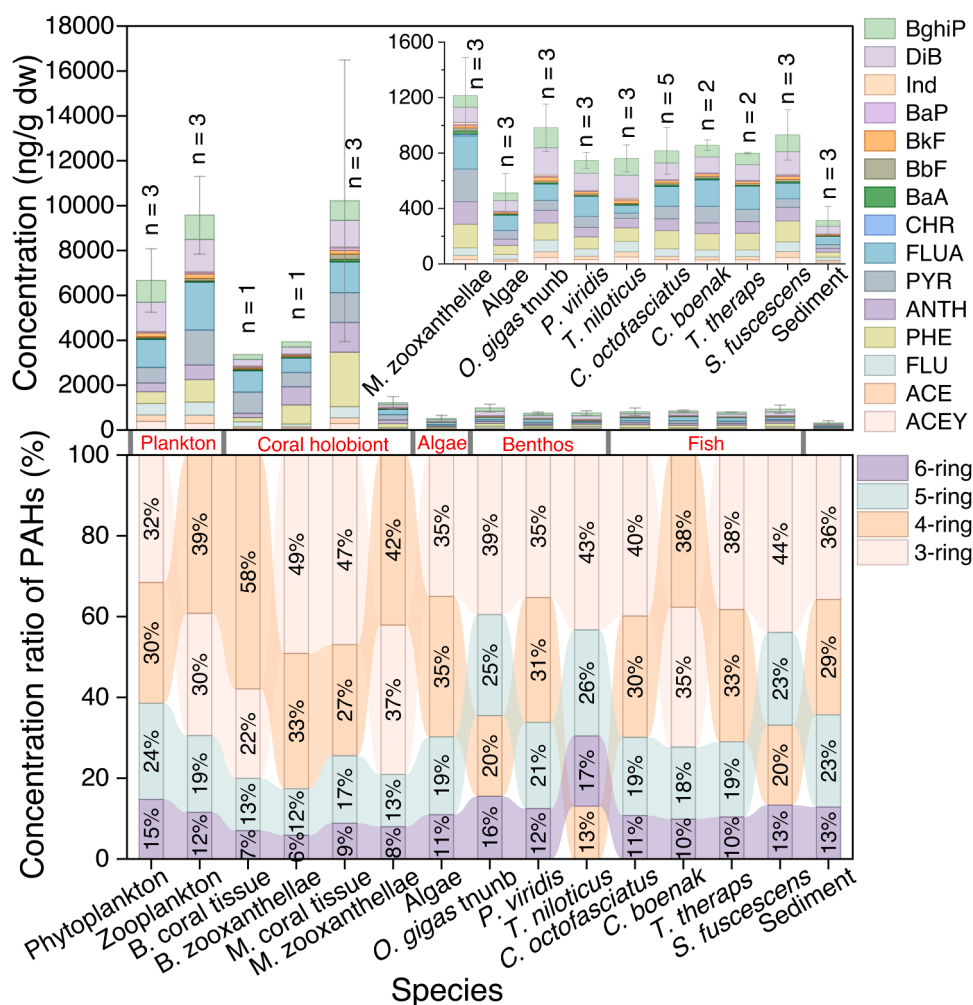


Fig. 1. Concentration and composition characteristics of PAHs in various media of the coral reefs from Weizhou Island. Note: B. coral tissue, B. zooxanthellae, M. coral tissue, M. zooxanthellae represent branching coral tissue, branching coral zooxanthellae, massive coral tissue, massive coral zooxanthellae, respectively. *O. gigas* tnunb, *P. viridis*, *T. niloticus*, *C. octofasciatus*, *C. boenak*, *T. theraps*, *S. fuscescens* represent *Ostrea gigas* tnunb, *Perna viridis*, *Trochus niloticus*, *Chaetodon octofasciatus*, *Cephalopholis boenak*, *Terapon theraps* and *Siganus fuscescens*, respectively.

for $40\% \pm 6\%$. The $\Sigma_{15}\text{PAHs}$ exhibited no significant disparities among the coral reef fish species: *Chaetodon octofasciatus* (*C. octofasciatus*; 816 ± 169 ng/g dw), *Cephalopholis boenak* (*C. boenak*; 857 ± 37.8 ng/g dw), *Terapon theraps* (*T. theraps*; 799 ± 6.01 ng/g dw) and *Siganus fuscus* (*S. fuscus*; 931 ± 181 ng/g dw) (Fig. 1). The $\Sigma_{15}\text{PAHs}$ in this study were relatively high compared with those reported in the Pearl River Estuary and Hainan Island (Li et al., 2021), the SCS (Han et al., 2022), Haizhou Bay (Zhang et al., 2020).

Coral. All 15 target PAHs were detected in both coral tissue and zooxanthellae, with detection rates ranging from 25% to 100%. $\Sigma_{15}\text{PAHs}$ were significantly higher in coral tissue (8789 ± 5969 ng/g dw) than in zooxanthellae (1894 ± 1202 ng/g dw) (nonparametric test, $p < 0.05$). PAH concentrations exhibited significant heterogeneity across different coral morphologies, with higher $\Sigma_{15}\text{PAHs}$ observed in massive coral tissue ($10,216 \pm 6273$ ng/g dw) compared to branching coral tissue (4508 ng/g dw), and significantly higher $\Sigma_{15}\text{PAHs}$ recorded in branching coral zooxanthellae (3934 ng/g dw) compared to massive coral zooxanthellae (1214.21 ± 276.52 ng/g dw) (nonparametric test, $p < 0.05$) (Fig. 1). Massive corals have a larger specific surface area, allowing organic pollutants such as PAHs to adsorb onto suspended particles, which can then enter coral tissue through sedimentation processes or coral predation. These PAH-laden suspended particles are more likely to remain on the larger surface area of massive corals, resulting in a significant increase in PAH concentrations within their tissues. In addition, this study found that massive corals secreted much more mucus than branching corals during sample pretreatment, and the presence of large amounts of coral mucus further enhanced the PAHs enrichment capacity of massive corals. In contrast, the differences in PAH concentrations observed in zooxanthellae between coral morphologies remain less clear. These patterns may reflect differences in internal partitioning, physiological characteristics, or exposure pathways within the coral holobiont. However, the underlying mechanisms are uncertain, and no direct measurements of zooxanthellae abundance or metabolic activity were conducted in this study. Therefore, these results should be interpreted cautiously, and further investigations are needed to clarify the processes governing PAH distribution between coral tissue and symbiotic zooxanthellae. In coral tissue, the $\Sigma_{15}\text{PAHs}$ in study area are relatively high, exceeding those in other coral reef regions worldwide, including the Southwestern Atlantic (Menezes et al., 2024), the Persian Gulf (Ranjbar Jafarabadi et al., 2018), and the Kenting coral reefs (Ko et al., 2014). This study further confirms that PAHs pollution in the SCS is intensifying (Han et al., 2023; Zhang et al., 2021). However, the $\Sigma_{15}\text{PAHs}$ in zooxanthellae are low compared to the Persian Gulf (Ranjbar Jafarabadi et al., 2018).

Sediment. A total of 14 PAHs were detected in the sediment, with a detection rate ranging from 67% to 100%. The $\Sigma_{15}\text{PAHs}$ in sediment were $169\text{--}397$ ng/g dw (313 ± 102 ng/g dw), with 3-ring PAHs accounting for $36\% \pm 2\%$. The $\Sigma_{15}\text{PAHs}$ in the sediment of Weizhou Island are relatively low compared to the Fernando de Noronha (Mello et al., 2025) and the Persian Gulf (Ranjbar Jafarabadi et al., 2020), but higher than that in the Hainan Island (Cao et al., 2024), Dazhou Island (Yang et al., 2019) and the west coast of Havana, Cuba (Martins et al., 2018).

In summary, PAHs are widely distributed in various coral reef organisms within the coral reef ecosystem of Weizhou Island. The substantial accumulation of PAHs in foundation species (especially corals and zooplankton) poses considerable ecological risks, chronic exposure to high PAH levels may disrupt coral physiology, impair reproductive health, and weaken stress resilience, potentially compromising reef structure and function.

3.2. Bioaccumulation of PAHs by coral reef organisms

BWAFs were estimated using previously reported PAH concentrations in seawater from the Weizhou Island region (Shi et al., 2023). Because these water samples were not obtained simultaneously with the

biological samples collected in August 2024, the calculated BWAF values should be interpreted as comparative estimates of relative accumulation potential rather than precise organism–water partition coefficients. As shown in Fig. 2a, the estimated log BWAFs indicated that most detected PAHs exhibited relatively high accumulation potential in reef organisms. Zooplankton exhibited the highest apparent accumulation potential, with log BWAFs ranging from 3.58 ± 0.15 for ACEY to 7.05 ± 0.15 for BkF. Notably, High-molecular-weight PAHs (HMW-PAHs, 5–6 rings) generally exhibited higher accumulation potential than low-molecular-weight PAHs (LMW-PAHs, 3–4 rings), consistent with their greater hydrophobicity and persistence. Among coral holobionts, coral tissue showed higher estimated log BWAFs (3.01–6.70) than zooxanthellae (2.27–6.04) (*t*-test, $p < 0.01$), which may be related to differences in tissue composition, exposure pathways, and physiological characteristics (Fig. 2a). BSAFs were further calculated to evaluate the relative contribution of sediment-associated exposure pathways (Fig. 2b). The estimated log BSAFs for fish (1.40–1.99), benthos (1.80–2.75), and coral holobionts (2.05–3.52) suggested limited sediment-associated accumulation potential for most PAHs. However, coral tissue showed relatively higher accumulation potential for several PAHs, including Ind, indicating that sediment-associated exposure may contribute to PAH burdens in corals. Therefore, these findings suggest that corals may represent sensitive receptors for sediment-derived PAH exposure in reef ecosystems. It should be noted that uncertainty exists in the calculated accumulation factors due to several methodological limitations. In particular, phytoplankton samples were preserved using ethanol prior to chemical analysis, which may influence PAH retention and lipid composition. In addition, the BWAF calculations relied on previously reported seawater concentrations rather than synchronous organism–water measurements. Therefore, BWAF and BSAF values should primarily be interpreted as comparative indicators among biological groups rather than absolute quantitative estimates of accumulation potential.

The octanol–water partition coefficient (K_{OW}) is an important physicochemical parameter reflecting the hydrophobicity of organic contaminants, whereas BWAF represents their observed accumulation patterns in organisms (Berrojalbiz et al., 2009; Han et al., 2019). Although biotransformation and molecular weight may cause discrepancies between the observed BAF values and those predictions derived from K_{OW} , PAHs (hydrophobic organics) show a strong K_{OW} –BAF correlation (Han et al., 2019; Long et al., 2024), and BAFs can be accurately estimated by K_{OW} (Berrojalbiz et al., 2009). In this study, significant positive correlation were observed between log K_{OW} values of PAHs and log BWAFs across coral reef organisms (Fig. 2c–j). This relationship indicates that PAHs with higher hydrophobicity generally exhibit greater apparent accumulation potential in reef organisms, suggesting that hydrophobicity is an important factor influencing PAH distribution. However, the present results do not directly demonstrate that lipid-dependent partitioning is the dominant accumulation mechanism, as species-specific physiology, exposure pathways, and biotransformation may also contribute to the observed accumulation patterns. Nevertheless, the observed relationship between PAH hydrophobicity and accumulation provides useful information for understanding the environmental fate and ecological exposure potential of PAHs in coral reef ecosystems under changing environmental conditions, including future ocean warming.

3.3. Trophic transfer of PAHs in coral reef ecosystems

Coral reef ecosystems are characterised by high biodiversity, strong species interactions, and multiple coexisting exposure and nutritional pathways. In the present study, the sampled organisms (plankton, corals, fish, benthos, and corals) were considered as representative ecological compartments of a coral reef assemblage rather than as components of a fully resolved and strictly linear food chain or food web. Stable nitrogen isotopes ($\delta^{15}\text{N}$) were used as an integrative proxy to

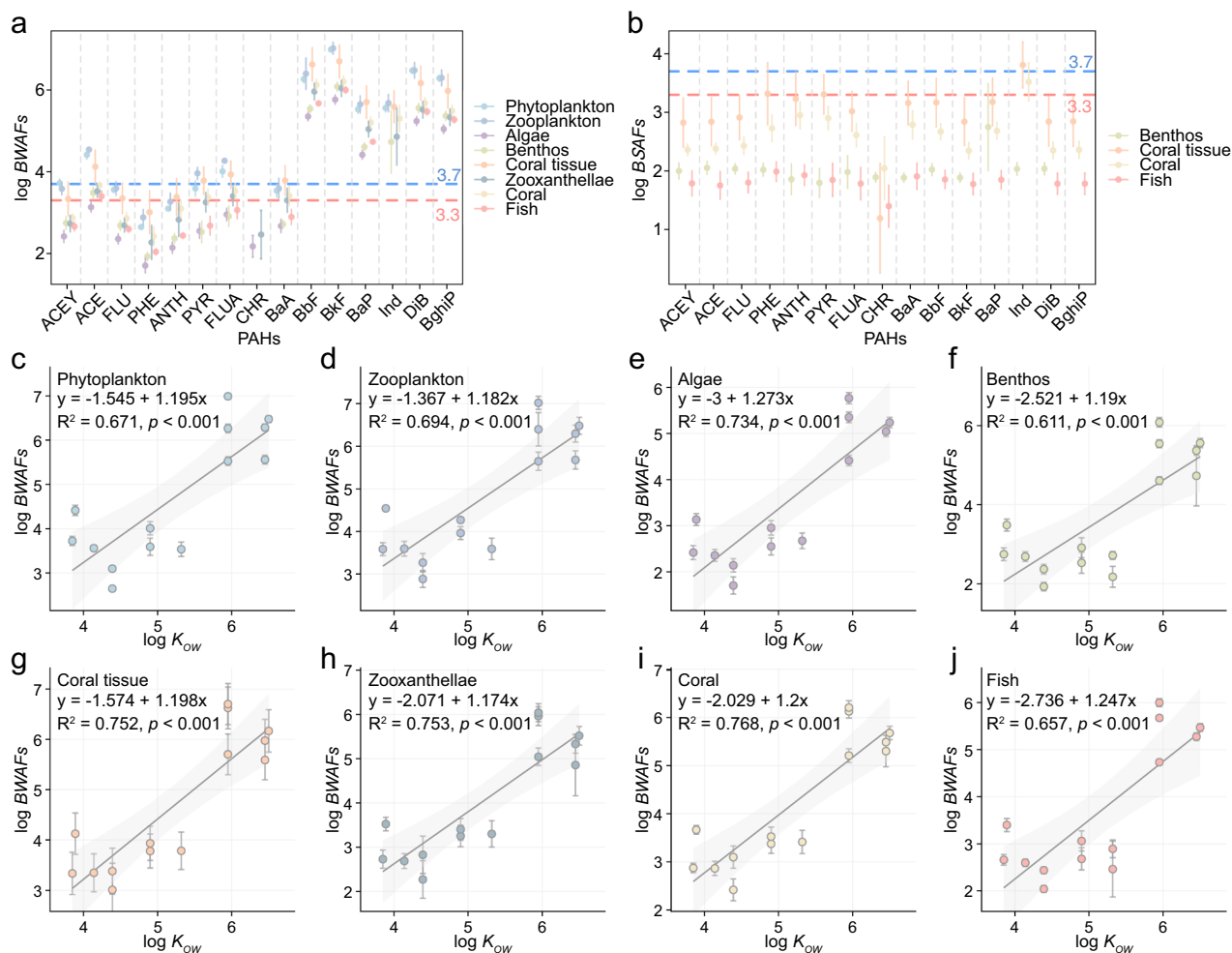


Fig. 2. The log BAFs and log BSAFs of PAHs (a-b), and relationship between the log BAFs of detected PAHs and their log K_{ow} (c-j), in the coral reef organisms from Weizhou Island.

describe the relative isotopic gradient among organisms, which reflects combined influences of dietary sources and ecological positioning. Accordingly, TLs derived from $\delta^{15}\text{N}$ values in this study should be interpreted as relative isotopic positions. Based on this framework, the energy transfer and flow patterns of the coral reef ecosystem were preliminarily constructed. Corals were considered as symbiotic functional units (holobiont) rather than conventional single trophic consumers. Because coral nutrition involves both autotrophic input from zooxanthellae and heterotrophic feeding by the host, the $\delta^{15}\text{N}$ -derived values for coral tissue and zooxanthellae were interpreted as relative isotopic positions of holobiont compartments rather than fixed TLs. Zooxanthellae were not treated as independent consumers in a conventional food-chain sense. Instead, they were considered a symbiotic component of the coral holobiont. Their inclusion was intended to compare PAH partitioning between coral host tissue and symbiotic algae, rather than to define a separate trophic node. Similarly, coral tissue and whole-coral compartments were used to explore compartment-specific accumulation patterns within the coral holobiont.

The $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ are widely used in studies to infer dietary sources and relative trophic positioning within aquatic ecosystems (Ding et al., 2020; Hou et al., 2022; Wei et al., 2024). In particular, $\delta^{15}\text{N}$ is commonly applied as an integrative proxy for estimating relative TLs among organisms. Measurements of $\delta^{15}\text{N}$ values in coral reef organisms ranged from 9.06‰ in phytoplankton to 16.1‰ in *C. boenak*. Using the $\delta^{15}\text{N}$ of reef organisms, the relative positions of organisms were as follows: phytoplankton (2.0)→zooxanthellae (2.10 ± 0.20)→coral tissue

(2.37 ± 0.73)→*P. viridis* (2.39 ± 0.05)→zooplankton (2.40)→*T. niloticus* (2.58 ± 0.18)→*O. gigas* (2.80 ± 0.13)→*S. fuscescens* (3.19 ± 0.18)→*T. theraps* (3.42 ± 0.13)→*C. octofasciatus* (3.64 ± 0.06)→*C. boenak* (3.84 ± 0.02) (Fig. 3a). However, these trophic positions should be interpreted cautiously because these groups differ in exposure routes, including direct water exposure, sediment contact, filter feeding, predation, and symbiosis. Organisms at different TLs in reef ecosystems often exhibit predation and competitive relationships, characterised by the transfer of nutrients and energy, as well as the migration of PAHs. For species with analogous TLs, competitive relationships may not only involve the acquisition of food sources but also competition for the bioaccumulation of PAHs (Tao et al., 2018). As shown in Fig. 3c-f, the TLs of organisms in the coral reef ecosystem of Weizhou Island exhibit a negative correlation with the logarithmically transformed PAH concentrations for most PAHs. This suggests that the capacity of coral reef organisms to bioaccumulate PAHs likely decreases as TLs increase. High-TL organisms in coral reefs may possess higher metabolic detoxification capabilities for PAHs, enabling them to rapidly convert absorbed or ingested PAHs into excretable forms (Hou et al., 2022; Walters et al., 2016). Conversely, organisms at lower TLs have weaker metabolic capabilities and primarily accumulate PAHs through direct contact with PAHs-rich water and sediments, resulting in higher accumulation within their bodies. Furthermore, the high productivity of coral reefs is accompanied by rapid material cycling and energy flow, and TLs transmission is associated with significant energy loss, which may further reinforce this trend.

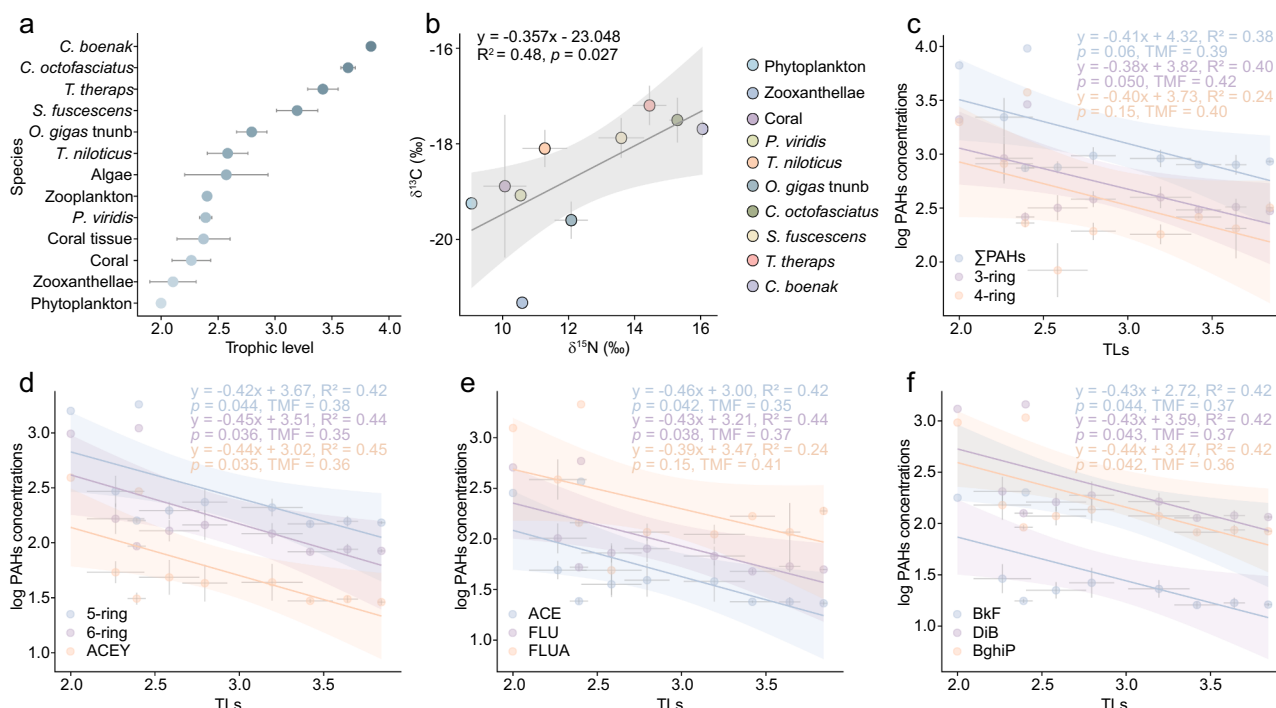


Fig. 3. Trophic levels (TLs) of coral reef organisms on Weizhou Island (a), the correlations between $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ of reef organisms (b), and regressions between TLs of coral reef organisms and log-transformed PAHs concentrations (c-f). Note: *O. gigas tnunb*, *P. viridis*, *T. niloticus*, *C. octofasciatus*, *C. boenak*, *T. theraps*, *S. fuscescens* represent *Ostrea gigas tnunb*, *Perna viridis*, *Trochus niloticus*, *Chaetodon octofasciatus*, *Cephalopholis boenak*, *Terapon theraps* and *Signanus fuscescens*, respectively.

The $\delta^{13}\text{C}$ are typically employed to identify the dietary sources of organisms and the origin of dietary carbon within ecosystems (de la Vega et al., 2019). Measurements of $\delta^{13}\text{C}$ values in coral reef organisms ranged from -21.3‰ in zooplankton to -12.1‰ in *Sargassum* spp. The $\delta^{13}\text{C}$ values of algae were over 29% higher than those of other reef organisms, whereas most other reef organisms exhibited narrower $\delta^{13}\text{C}$ variation (-17.1‰ to -21.3‰), suggesting partially overlapping carbon sources (Dong et al., 2025; Wei et al., 2024). Nevertheless, because $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values alone cannot fully resolve predator-prey relationships in such a complex coral reef ecosystem, the isotope results were used only to support a relative trophic gradient rather than to reconstruct a complete food web. As shown in Fig. 3b, there is a significant correlation ($R^2 = 0.48$, $p < 0.05$) between the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of various coral reef organisms.

In this study, the apparent TMF was calculated to evaluate the relationship between PAH concentrations and $\delta^{15}\text{N}$ -derived relative TLs. This study employed a 95% confidence interval and utilised a logarithmic transformation of PAH concentrations in reef organisms and their corresponding TL values. Based on this trophic gradient, we further evaluated the apparent relationship between PAH concentrations and trophic position using linear regression (Fig. 3c-f). The regression analyses showed negative associations between PAH concentrations and TL for all evaluated PAH groups. However, the strength of statistical support varied among ring classes. Significant negative relationships were observed for 5-ring ($R^2 = 0.42$, $p = 0.04$) and 6-ring PAHs ($R^2 = 0.44$, $p = 0.04$), whereas the relationship was marginal for 3-ring PAHs ($R^2 = 0.40$, $p = 0.05$) and non-significant for 4-ring PAHs ($R^2 = 0.24$, $p = 0.15$). The relationship for Σ_{15} PAHs was also negative but did not reach the conventional significance threshold ($R^2 = 0.38$, $p = 0.06$). These results therefore support an overall tendency toward trophic dilution, particularly for 5- and 6-ring PAHs, rather than a statistically significant dilution pattern across all PAH classes. (Fig. 3c-d). For individual PAHs, the log-transformed concentrations of ACEY, ACE, FLU, BkF, DiB, and BghiP still showed a significant negative correlation with the TLs of reef organisms, further supporting the tendency for lower-

trophic or basal ecological compartments to retain higher PAH burdens (Fig. 3c-f). Because the apparent TMF analysis was based on mean PAH concentrations of ecological groups, regression robustness was further evaluated using group-level influence diagnostics. Cook's distance analysis indicated that no single ecological group disproportionately affected the major trophic trends. Leave-one-group-out analyses confirmed that regression slopes remained negative after exclusion of individual groups (Table S8). Similar trophic dilution patterns have been reported in several aquatic food webs, including Dianchi Lake (Fan et al., 2017), Laizhou Bay, China (Liu et al., 2023), and urban riverine food web (Goutte et al., 2020). However, trophic magnification of certain PAHs has also been observed in other aquatic systems (Wan et al., 2007; Wu et al., 2025), indicating that PAH trophodynamics may vary with ecosystem structure, temperature, productivity, species composition, and metabolic capacity.

The apparent trophic dilution observed in this study may be partly related to the relatively high productivity and rapid material cycling of coral reef ecosystems, as well as the stronger metabolic transformation capacity of higher-TL fish. Overall, the results indicate an apparent decline in PAH concentrations with increasing $\delta^{15}\text{N}$ -derived trophic position across coral reef functional groups. Given the limited number of observations and the heterogeneity in exposure routes among functional groups, these relationships should be interpreted as apparent trophic trends at the functional-group level rather than definitive evidence of food-web-wide trophic magnification or dilution. Importantly, the observed dilution trend does not imply reduced ecological risk for corals. Coral tissue still exhibited strong PAH accumulation, likely associated with lipid-rich tissues, mucus-mediated adsorption, and sediment-related exposure pathways, highlighting the potential vulnerability of corals and other low-TL organisms in PAH sequestration.

3.4. Potential impact of coral-associated microorganisms on trophic transfer of PAHs

3.4.1. Morphological differences in coral-associated microbial community structure and niche assembly

High-throughput 16S rRNA gene sequencing of *T. peltata* and *A. pruinosa* revealed pronounced differences in their associated microbial community structures. Phylogenetic analysis of the 500 most abundant amplicon sequence variants (ASVs) showed distinct phylum-level clustering, with no taxonomic overlap between the two types of coral (Fig. 4a). Consistently, no shared ASVs were detected, and *A. pruinosa* harbored more unique ASVs than *T. peltata* (1636 vs. 546; Fig. 4f). The *A. pruinosa* also exhibited significantly higher α -diversity (ACE, Chao1, Shannon, and Simpson; Fig. 4b-e). principal coordinate analysis (PCoA) further confirmed the strong separation of microbial communities between the two types of coral (Fig. 4g). At the genus level, *Prosthecochloris* exhibited a higher relative abundance in *A. pruinosa* than in *T. peltata*. In contrast, several genera closely associated with PAHs degradation (*Sphingobacterium*, *Acinetobacter*, *Novosphingobium*, *Sphingomonas*, and *Stenotrophomonas*) (Lu et al., 2011; Meng et al., 2025) were significantly enriched in *T. peltata*, which may be linked to the higher PAHs accumulation observed in their tissues, although direct causal relationships cannot be established due to differences in sampling timing (Fig. 4h).

To further evaluate the relative contributions of deterministic versus stochastic processes in microbial community assembly, we employed null model analysis (999 randomizations) to calculate beta-nearest taxon index (β NTI). The results indicated that microbial community assembly in both *T. peltata* and *A. pruinosa* were predominantly governed by stochastic processes, particularly homogeneous dispersal (HD)

and drift (DR) (Fig. 5a). Consistently, neutral community model (NCM) analysis showed that community assembly in both coral types was strongly influenced by stochastic processes ($R^2 = 0.5164$, $m = 0.0097$) (Fig. 5b). Niche-breadth analysis further showed that *T. peltata* contained fewer specialists but significantly more generalists than *A. pruinosa* (Fig. 5c), suggesting lower sensitivity of *T. peltata* microbiomes to environmental fluctuations. Consistently, *T. peltata* harbored a higher fraction of persistent taxa in the core community (Fig. 5d). In addition, the mean relative abundance of microbial ASVs was positively correlated with their occurrence frequency in both coral types (Fig. 5e-f). This common ecological pattern supports a dominant role of stochastic processes in community assembly. However, environmental factors, including pollutant exposure history and host-associated ecological characteristics, may contribute to the distribution of specific microbial functional groups.

3.4.2. Differences in microbial functional potential associated with PAH accumulation patterns in *T. peltata*

Linear discriminant analysis effect size (LEfSe) analysis revealed marked differences in dominant taxa between *A. pruinosa* and *T. peltata*. The *A. pruinosa* were dominated by *Prosthecochloris*, BD1–7 clade, *Ruegeria*, *Marinifilum*, *Synechococcus*, BD2–11 terrestrial group, *Arcobacter*, and *Acanthopleuribacter*, whereas *T. peltata* were significantly enriched with high-efficiency PAH degraders, including *Sphingobacterium*, *Novosphingobium*, *Sphingomonas*, *Acinetobacter*, and *Stenotrophomonas* (Fig. 6a) (Lu et al., 2011; Meng et al., 2025). Kruskal-Wallis tests and differential abundance (DA) analysis consistently supported significant enrichment of these genera in *T. peltata* ($p < 0.05$; Fig. 6b-c), identifying them as microbial taxa previously associated with hydrocarbon transformation potential. Consistent with this pattern, the relative

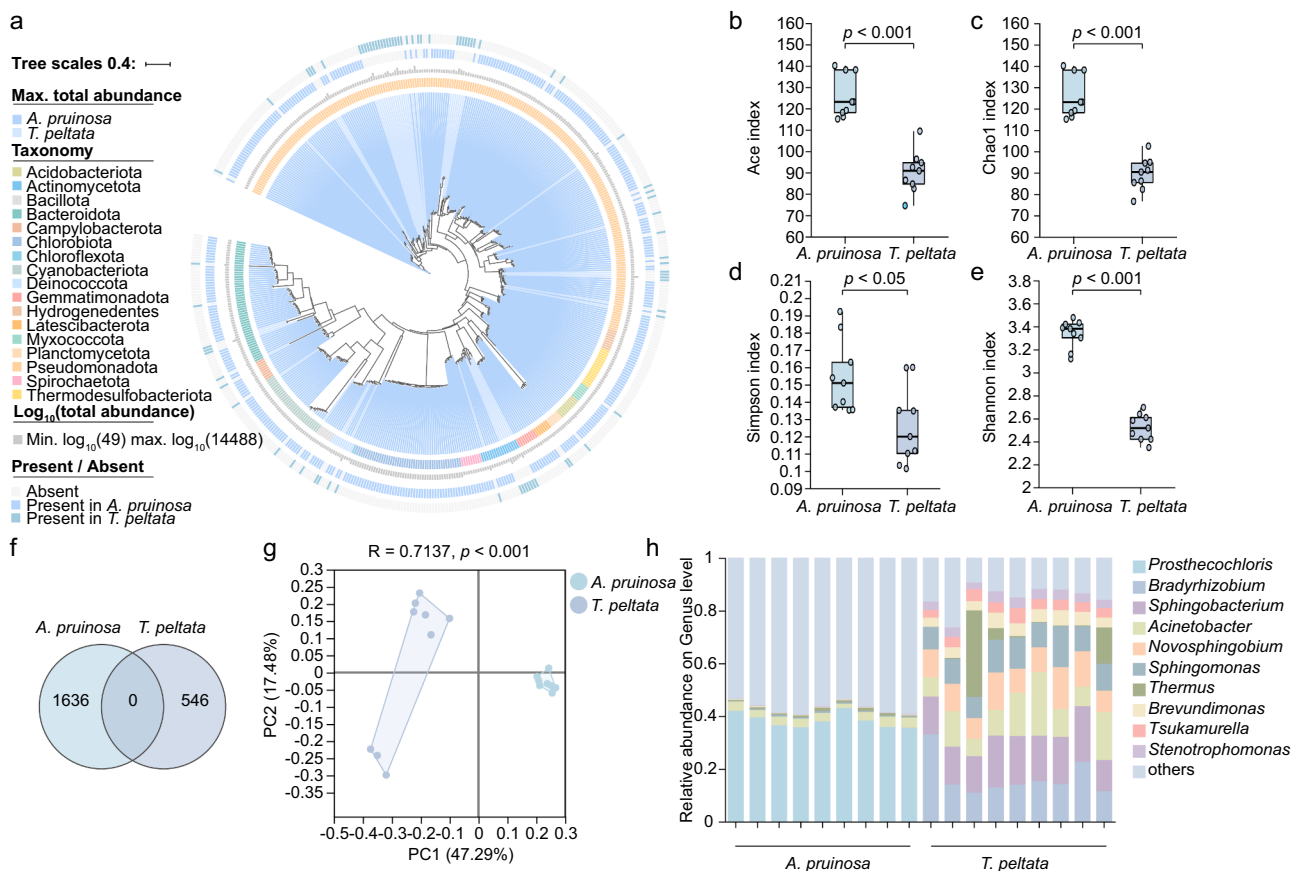


Fig. 4. Distinct microbial community structures and diversity patterns between *T. peltata* and *A. pruinosa*. Phylogenetic tree of the 500 most abundant ASVs (a). α -diversity comparison between *T. peltata* and *A. pruinosa*: ACE (b), Chao1 (c), Simpson (d), Shannon (e). Venn diagram of unique/shared ASVs (f). PCoA plot based on unweighted UniFrac distances (g). Relative abundance of the top 10 genera (and others) (h).

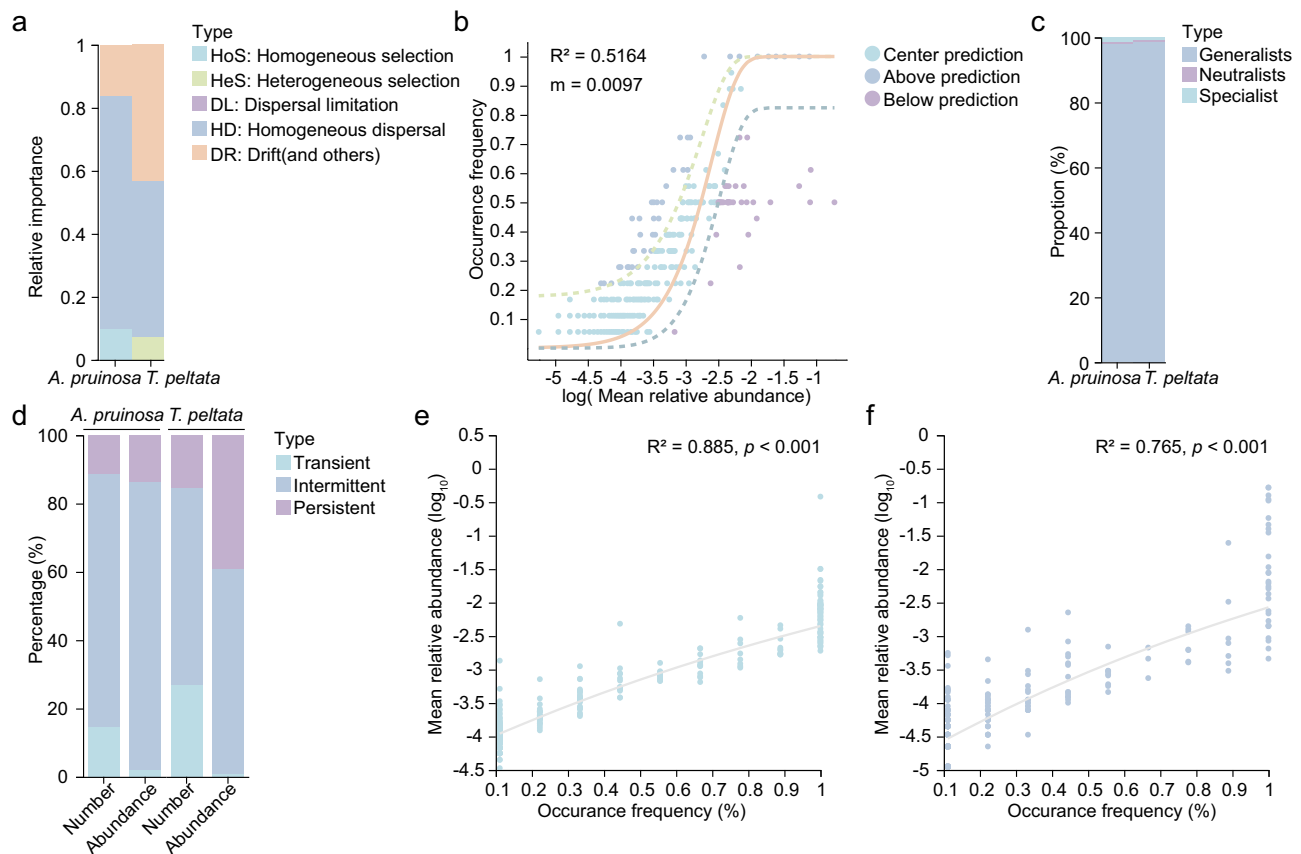


Fig. 5. Ecological assembly mechanisms and niche characteristics of microbial communities in *T. peltata* and *A. pruinosa*. Null model analysis of community assembly processes (a). NCM fit for coral-associated microbiomes (b). Niche breadth comparison between *T. peltata* and *A. pruinosa* (c). Fractions of transient, intermittent, and persistent taxa in each coral type (d). Relationship between ASV mean relative abundance and occurrence frequency in *A. pruinosa* (e), and *T. peltata* (f).

abundances of these five genera were positively associated with the concentrations of 3–6-ring PAHs and total PAHs in the tissues of *T. peltata* and *A. pruinosa* (Fig. 6d), suggesting a potential association between the distribution of microbial taxa with hydrocarbon transformation potential and long-term PAH accumulation patterns. Because the coral-associated microbial datasets were derived from previously published 16S rRNA sequencing studies (2019–2020), whereas PAH concentrations were measured from coral samples collected in 2024, these associations should be interpreted as exploratory historical comparisons rather than direct contemporaneous responses. Consistently, functional prediction indicated a higher abundance of PAH-related metabolic pathways in the *T. peltata*-associated microbial community (Fig. 6e), suggesting a greater predicted functional potential for PAH transformation. Microbial communities may contribute to pollutant transformation processes through their predicted PAH-related metabolic potential, while coral hosts may provide ecological niches that support the persistence of specific microbial taxa, which aligns with the predicted enhancement of carbon metabolism pathways in *T. peltata* (Fig. 6e). However, these potential interactions require validation through direct functional measurements. Predicted metabolic profiles suggested the potential involvement of PAH-related compounds in microbial carbon transformation pathways. The carbon derived from PAHs can either be directly utilized by PAH-degrading microorganisms themselves, or promote trophic transfer within the food web through biogeochemical cycling. Specifically, the predicted relative abundances of key PAH-degrading enzymes (Haritash and Kaushik, 2009; Ricketts and Dean, 1999) such as Catechol 1,2-dioxygenase, Catechol 2,3-dioxygenase, Protocatechuate 3,4-dioxygenase, Protocatechuate 4,5-dioxygenase, Unspecific monooxygenase, Biphenyl-2,3-diol 1,2-dioxygenase, Phenol 2-monooxygenase, Salicylate hydroxylase, Chlorocatechol 1,

2-dioxygenase, and p-cumate 2,3-dioxygenase subunit alpha were significantly higher in *T. peltata* than in *A. pruinosa* (Fig. 6f). This suggests that microbial communities associated with *T. peltata* possess higher predicted potential for PAH-related metabolic pathways, representing a functional adaptive response to sustained pollutant stress. However, due to the lack of synchronous chemical and microbial measurements, whether this pattern represents an adaptive response to pollutant exposure remains uncertain and requires validation using functional genomic, transcriptomic, or physiological approaches.

Despite this elevated predicted metabolic potential, *T. peltata* accumulated substantially higher total PAHs in host tissue ($10,216 \pm 6273$ ng/g dw) than branching coral tissue (4508 ng/g dw), suggesting PAHs influx/retention exceeds microbial transformation capacity under sustained exposure. Collectively, these results support a “high exposure-high transformation potential” pattern in *T. peltata*: host morphology promotes PAHs accumulation (e.g., larger surface area and mucus adsorption), while the microbiome shifts functionally toward PAH-degrading taxa and pathways. This host-microbiome differentiation may shape PAH burdens in coral tissue and influence pollutant transfer among coral reef ecological compartments.

Our findings provide preliminary evidence suggesting that differences in coral-associated microbial functional potential may be associated with variations in PAH accumulation patterns among coral holobionts. The enrichment of bacterial genera previously reported to possess PAH degradation (e.g., *Sphingobacterium*, *Novosphingobium*, *Sphingomonas*, *Acinetobacter*, *Stenotrophomonas*) in *T. peltata*, together with higher predicted abundances of PAH-related metabolic pathways, suggests that its associated microbial communities may have greater potential for involvement in PAH transformation processes. However, because the microbial datasets were obtained from previously published

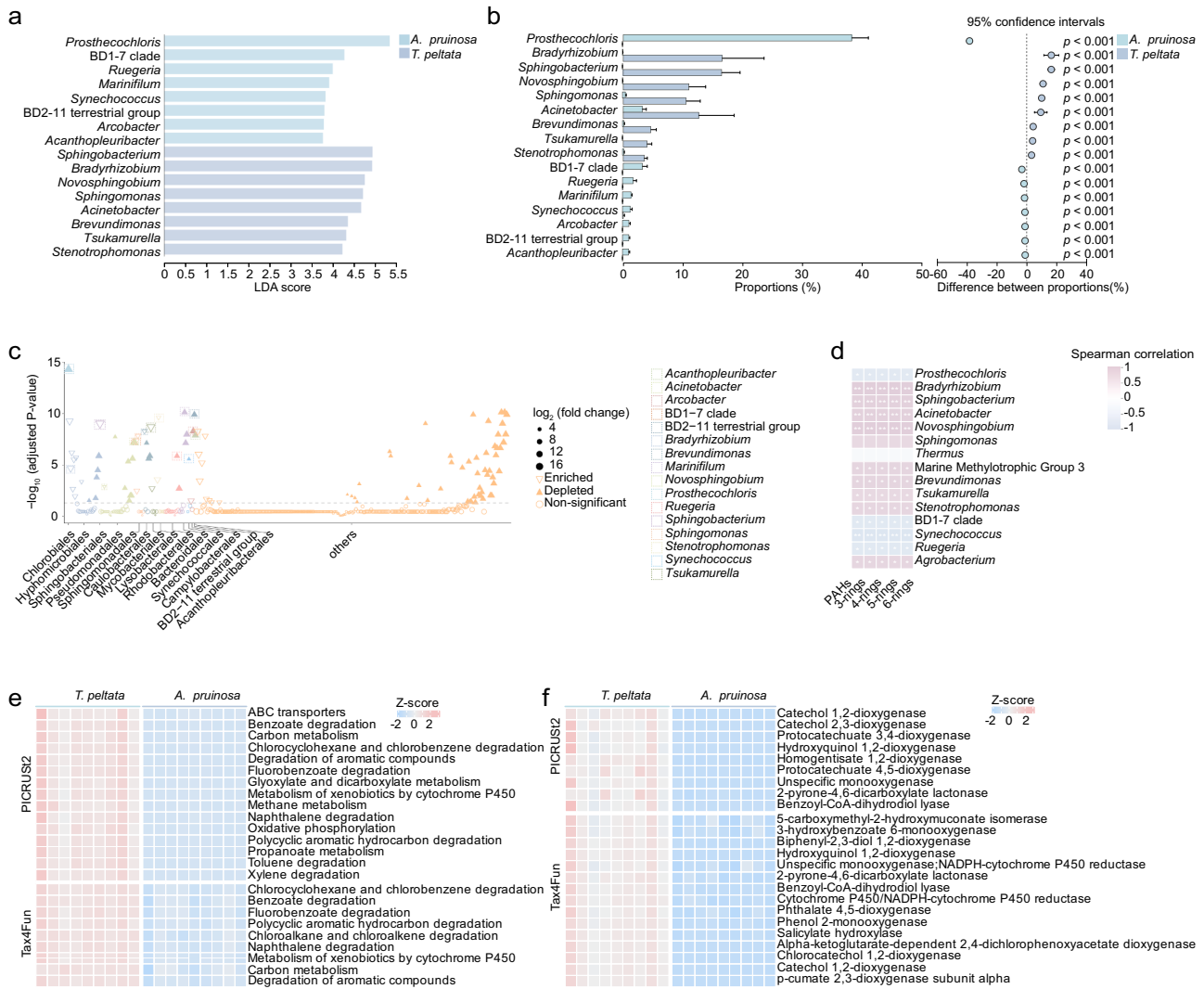


Fig. 6. Functional differentiation of microbial communities and their response to PAHs stress in *T. peltata* and *A. pruinosa*. LEfSe identifies taxonomic biomarkers ($p < 0.05$) (a). Key PAH-degrading genera differ between *T. peltata* and *A. pruinosa* ($p < 0.001$) (b). DA analysis shows genera enriched in each coral type (c). Correlations between genus-level relative abundance and tissue PAHs (d), color denotes correlation strength (* $p < 0.05$, ** $p < 0.01$). Enrichment of PAH-related metabolic pathways in both coral types (e). Relative abundance of key enzymes involved in PAHs degradation (f).

non-synchronous and non-paired studies, these patterns should be interpreted as exploratory associations rather than direct evidence of active microbial degradation or detoxification. The higher PAH concentrations observed in *T. peltata* compared with *A. pruinosa* suggest that enhanced predicted microbial transformation potential may not necessarily translate into reduced tissue PAH burdens under sustained exposure conditions. Instead, host morphological characteristics, pollutant exposure history, and microbial community composition may jointly influence PAH accumulation patterns. The lower PAH concentrations observed at higher trophic positions indicate an apparent decreasing trend along the $\delta^{15}\text{N}$ -derived trophic gradient, although the contribution of microbial processes to this pattern remains uncertain.

Overall, differences in coral-associated microbial functional potential may provide a possible ecological explanation for variations in PAH accumulation patterns among coral holobionts. Nevertheless, direct measurements of microbial activity, paired chemical-microbial sampling, and controlled degradation experiments are required to determine whether and to what extent coral-associated microorganisms contribute to PAH transformation and contaminant fate.

3.5. Limitations of this study

Several limitations of this study should be acknowledged. First, the present investigation was based on a single field survey conducted in August 2024. Therefore, the observed PAH distribution patterns and microbial-related interpretations represent the ecological conditions during the sampling period rather than long-term temporal trends. Seasonal variations in environmental conditions, anthropogenic inputs, organismal physiology, and microbial community dynamics may influence PAH fate in coral reef ecosystems. Long-term and multi-seasonal monitoring is therefore required to further resolve temporal variability in PAH contamination and microbial-mediated transformation processes. Second, the PAH measurements and coral-associated microbial datasets were not collected synchronously and were not derived from paired samples. PAH concentrations were measured in coral samples collected in 2024, whereas the 16S rRNA amplicon sequencing datasets were derived from previously published studies of the same coral species (Chen et al., 2021; Yu et al., 2021). Although the use of consistent host species enabled exploratory species-level comparisons, differences in sampling year, individual colonies, environmental conditions, sample composition, and analytical resolution may have introduced uncertainty into the cross-dataset associations. Accordingly, the observed

associations between microbial community characteristics and tissue PAH concentrations may indicate a potential contribution of coral-associated microorganisms to PAH fate, including bioaccumulation, transformation, and trophic transfer. However, these associations should not be interpreted as direct evidence of causal microbial regulation. Third, phytoplankton samples were preserved using 75% ethanol prior to filtration and chemical analysis to maintain sample integrity during field collection and transportation. Although ethanol may potentially extract a fraction of hydrophobic organic contaminants and influence the measured PAH concentrations, the magnitude of this effect could not be directly quantified in the present study due to the lack of parallel preservation recovery experiments. Nevertheless, the trophic transfer analysis was conducted based on multiple ecological groups rather than phytoplankton alone, and the observed overall trophic dilution tendency was unlikely to be determined solely by potential PAH losses from phytoplankton samples. Future studies should incorporate preservation recovery experiments or alternative preservation strategies to better constrain this uncertainty.

Future studies should incorporate multi-seasonal sampling and concurrently collect paired chemical and microbial samples from the same coral colonies. Absolute quantification of microbial taxa, functional genomic or transcriptomic analyses, and controlled degradation experiments will be required to determine whether and how coral-associated microorganisms contribute to PAH transformation and fate in coral reef ecosystems.

4. Conclusion and outlook

This study provides an ecosystem-level assessment of PAH occurrence, bioaccumulation, and potential trophic transfer characteristics across the coral reef ecosystem of Weizhou Island, northern SCS. PAHs were detected in multiple environmental and biological compartments, with phytoplankton and coral tissues exhibiting relatively high concentrations, particularly in *T. peltata*. The positive relationship between log *BWAFs* and log *K_{OW}* ($R^2 > 0.6$) indicated that hydrophobicity was an important physicochemical factor associated with PAH accumulation among coral reef organisms. Apparent trophic magnification analysis further indicated an overall tendency toward trophic dilution of PAHs across the sampled coral reef ecological compartments, suggesting limited biomagnification potential under the investigated conditions. Comparative analysis of previously published coral-associated 16S rRNA datasets revealed distinct microbial community characteristics between coral species, with *T. peltata* exhibiting higher predicted functional potential for PAH-related metabolic pathways and enrichment of microbial taxa previously associated with hydrocarbon transformation. Exploratory comparison suggested that these microbial characteristics were associated with differences in PAH accumulation patterns among coral holobionts, although causal relationships cannot be established because the chemical and microbial datasets were not collected synchronously. The predicted enrichment of PAH-related metabolic pathways further suggests that PAH transformation products may potentially enter microbial carbon metabolic pathways, where the transformed carbon could be utilized by microorganisms or contribute to carbon cycling within coral holobionts and coral reef ecosystems.

Future studies integrating synchronously collected contaminant and microbiome datasets, isotope tracing, metagenomic and transcriptomic analyses, and experimental validation of microbial transformation processes to determine whether and to what extent coral-associated microorganisms contribute to PAH transformation and trophic transfer. Such efforts will improve our understanding of contaminant–microbiome interactions and support ecological risk assessment and conservation of coral reef ecosystems under increasing anthropogenic pressures.

CRediT authorship contribution statement

Mei Xiong: Writing – original draft, Data curation, Conceptualization. **Minwei Han:** Writing – review & editing, Validation, Supervision, Investigation, Formal analysis, Data curation. **Kefu Yu:** Writing – review & editing, Supervision, Resources. **Xuejiao Lin:** Writing – review & editing, Formal analysis. **Xiangrong Xu:** Writing – review & editing, Supervision, Formal analysis.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at [doi:10.1016/j.watres.2026.126844](https://doi.org/10.1016/j.watres.2026.126844).

Data availability

Data will be made available on request.

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