Variations in epifaunal assemblages among different algal species in the coastal waters of the Noto Peninsula, Japan

Variations in epifauna by algal species

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Abstract

Algal beds are biodiversity hotspots in coastal ecosystems, forming complex food webs based on seaweeds. Epifauna serve as important indicators of algal productivity and environmental change, interacting closely with their host seaweeds. This study compared the composition of epifaunal assemblages associated with different seaweed species in the Noto Peninsula, Japan, to elucidate their characteristics. A survey of epifaunal communities on 13 seaweed species around Tsukumo Bay revealed significant differences in abundance and composition among species. Epifaunal abundance was particularly high in *Sargassum siliquastrum* and *S. patens*. Differences in assemblage structures were observed among seaweed species and sampling sites, with flow velocity, salinity, and water depth identified as key environmental factors. Fucales seaweeds harbored more diverse epifaunal communities compared to Laminariales species. Variations in epifaunal composition among taxa suggest that interactions with host seaweed species play a crucial role in shaping community structure.

Keywords: algal beds, *Sargassum* seaweeds, epifaunal community, Sea of Japan

Introduction

Algal beds serve as biodiversity hotspots in coastal ecosystems, offering habitat and food resources for a wide range of marine organisms. As primary producers, seaweeds support complex food webs that sustain various invertebrates and fish (Fuse, 1962; Mukai, 1978). These ecosystems also contribute to carbon sequestration and water purification, enhancing coastal environmental stability (Akeda *et al*., 2010; Filbee-Dexter *et al*., 2024).

Epifauna, small invertebrates residing on or near seaweed surfaces, act as key indicators of ecosystem health and productivity. Primary composed of crustaceans and gastropods, these communities are shaped by environmental conditions, seasonal changes, and structural characteristics of their host seaweed (Mukai, 1978; Yamamoto *et al*., 1999). Factors such as structural complexity, food availability, wave action and interaction with other algal species contribute to seasonal variations in faunal communities (Hirst, 2007; Machado *et al*., 2015; Winkler *et al*., 2017). Epifauna benefit seaweeds by controlling competitive epiphytes and facilitating fertilization, but can also negatively impact hosts through direct grazing (Duffy, 1990; Mancinelli & Rossi, 2001; Kamermans *et al*., 2002; Poore *et al*., 2014; Lavaut *et al*., 2022). These findings highlight the multifunctional role of epifaunal communities in algal ecosystems.

Previous studies have examined the effects of specific seaweed species and their morphology on epifaunal assemblages (e.g. Mukai, 1971; Imada *et al*., 1981; Ito *et al*., 2019; Kodama *et al*., 2020). However, how different seaweed species share epifaunal communities and form distinct assemblages remains unclear, with regional and environmental factors influencing outcomes (Saito *et al*., 2002; Yatsuya *et al*., 2008). Understanding these interactions is particularly important in Japan's coastal regions, known for their high biodiversity and complex environmental conditions. This study investigates epifaunal assemblages across multiple seaweed species in the Noto Peninsula, a central region of the Sea of Japan. By comparing epifaunal diversity and abundance among different host seaweeds, we aim to clarify the influence of seaweed species and environmental factors on community structure. These findings provide insights into coastal ecosystem dynamics and species interactions in algal beds.

Materials and Methods

Seaweeds were randomly collected from *Sargassum* beds at depths shallower than 1 m around Tsukumo Bay on the Noto Peninsula in February and March 2023. Sampling sites included six locations: Hime port (HP), Ogi port (OP), Noto Isaribi Youth Hostel (NIYH), Hotel Notokinpura (HN), Noto Marine Center (NMC), Shiromaru (S) (Fig. 1). Individual seaweeds were manually collected from the holdfast while wearing a long body suit and stored in plastic bags. Environmental parameters, including illuminance (lux), air temperature (°C), water temperature (°C), salinity (‰), depth (cm), and flow velocity (cm/s; VR-401, Kenek, Japan), were measured at each site. Collected seaweeds were stored at -20°C.

Defrosted seaweeds were washed three times in a water-filled bucket by rubbing. This method recovers over 99% of total epifaunal abundance in *S. fusiforme* (Kondo *et al.*, 2019). Organisms detached from seaweeds were collected using a 1.0 mm sieve and classified into 11 taxa, based on Ito *et al.* (2019) and Ministry of Environment (accessed online 2 January 2025), plus three Decapoda taxa: Nematoda, Mollusca, Gastropoda, Bivalvia, Annelida, Arthropoda, Gammaridea, Caprellidea, Isopoda, Caridea, Anomura and Brachyura. Taxa such as Foraminifera, Acarina, Ostracoda, Tanaidacea, Cumacea, and Harpacticoida were excluded as they were not found in this study. Ito *et al.* (2019) and Ministry of Environment (accessed online 2 January 2025) included Polychaeta, but as it is now considered non-monophyletic, Annelida was used instead (Kobayashi, 2021). The suborder Caprellidea was reclassfied into Senticaudata along with some Gammaridea taxa, invalidating both suborders (Lowry & Myers, 2013, 2017). However, following Kodama *et al.* (2020), we treated the historical suborders Gammaridea and Caprellidea separately. The wet weight of seaweeds, after removing organisms, was measured using a digital scale with 0.1 g accuracy.

Epifaunal abundance was normalized to individuals per 100 g of seaweed. All subsequent analyses were based on standardized abundances. Cluster analysis using Ward's method (ward.D2) grouped samples at 50% similarity. PERMANOVA assessed the effects of host seaweed species, location, and their interaction on community structure. Non-metric multidimensional scaling (nMDS) based on Bray-Curtis distance visualized faunal community similarities. Species significantly influencing community structure were identified at the 5% level, while environmental factors were analyzed at the 10% level. Renyi's diversity profiles were calculated for each sample and averaged for each seaweed species. Community prosperity was calculated by multiplying total abundance by the number of effective species as determined from Renyi's diversity profile. All statistical analyses were performed in R (version 4.3.2), using the 'vegan' package (version 2.6.4) (Oksanen *et al.*, accessed online 7 February 2025) for ordination and the 'adonis2' function for PERMANOVA, the 'metaMDS' function for nMDS, and the 'renyi' function for Renyi's diversity profiles. These results were output by the 'ggplot2' package (version 3.5.1) (Wickham *et al.*, accessed online 7 February 2025).

Results

A total of 13 species (39 individuals) were collected from six sites around Tsukumo Bay (Table 1). These included 10 species of Fucales (*Myagropsis myagroides*, *Sargassum autumnale*, *S. confusum*, *S. horneri*, *S. macrocarpum*, *S. microceratium*, *S. patens*, *S. piluliferum*, *S. siliquastrum*, and *S. thunbergii*), two Laminariales species (*Ecklonia cava* and *Undaria pinnatifida*), and one red algal species, Gracilariales (*Gracilaria textorii*). The average wet weight of each seaweed (Fig. 2) exceeded 300 g for *M. myagroides*, *S. horneri*, *S. microceratium*, and *S. piluliferum*, while *S. macrocarpum*, *S.*

patens, and *S. siliquastrum* averaged around 200 g. *Sargassum autumnale*, *S. confusum*, *S. thunbergii*, *E. cava*, and *U. pinnatifida* had average weights of approximately 100 g, with *G. textorii* being the lightest at about 20 g.

Epifaunal abundance (Fig. 2) was highest in *S. siliquastrum* (403 individuals), approximately 1.5 times higher than in *S. patens* (241 individuals). *Sargassum autumnale* and *S. macrocarpum* had 141 individuals each. Other species, including *M. myagroides*, *S. confusum*, *S. microceratium*, and *S. piluliferum*, harbored around 100 individuals, while *S. horneri*, *S. thunbergii*, *E. cava*, *U. pinnatifida*, and *G. textorii* supported fewer than 50 individuals.

Cluster analysis (Fig. 3) revealed five distinct clusters: (1) *S. thunbergii*, *E. cava*, *U. pinnatifida*, and *G. textorii*; (2) *S. horneri*, *S. macrocarpum*, *S. thunbergii*, *E. cava*, and *U. pinnatifida*; (3) *S. macrocarpum*, *S. patens*, and *S. siliquastrum*; (4) *S. autumnale*, *S. macrocarpum*, and *S. patens*; (5) *M. myagroides*, *S. autumnale*, *S. confusum*, *S. horneri*, *S. microceratium*, *S. patens*, *S. piluliferum*, *S. thunbergii*, and *G. textorii*. Cluster 1 and 2 formed a sister group, as did clusters 4 and 5. Clusters 3, 4, and 5 formed a higher-level sister group. Additionally, samples clustered partly by collection site. Half of cluster 2 consisted of Laminariales species from HP and OP, cluster 3 composed mostly Fucales in HP, and half of cluster 5 included seaweeds from NMC. Community structure significantly differed among host seaweed species and collections (PERMANOVA, p = 0.001 for both), with interactions between these factors (p = 0.006).

The nMDS plots (Fig. 4) exhibited an acceptable stress value (0.121), supporting adequate ordination of samples. Environmental factors contributing to sample similarity (10% significance level) included flow velocity, salinity, and water depth, while water temperature, air temperature, and illumination were not significant. Significant taxa contributing to community differences (5% significance level) were Annelida, Caprellidea, Caridea, Gammaridea, Gastropoda, and Isopoda. Renyi's diversity profiles (Fig. 5A) indicated that the 10 Fucales species showed a marked decline from q = 0 to q = 2, whereas *E. cava*, *U. pinnatifida*, and *G. textorii* exhibited little variation. The top three species in epifaunal richness (q = 0) were *M. myagroides*, *S. siliquastrum*, and *S. patens*, while the lowest were *U. pinnatifida*, *G. textorii*, and *E. cava*. Shannon's diversity index (q = 1) ranked *S. confusum*, *M. myagroides*, and *S. siliquastrum* highest, with *U. pinnatifida*, *S. microceratium*, and *G. textorii* lowest. The inverse of Simpson's diversity index (q = 2) ranked *S. confusum*, *M. myagroides*, and *E. cava* highest, while *U. pinnatifida*, *S. microceratium*, and *S. piluliferum* were lowest. Similarity, *E. cava*, *S. confusum*, and *M. myagroides* exhibited the highest inverse dominance values (q = Inf), whereas *U. pinnatifida*, *S. microceratium*, and *S. piluliferum* had the lowest. *Undaria pinnatifida* showed the lowest diversity across all q values. Community prosperity (Fig. 5B) was highest for *S. siliquastrum* across all q values, followed by *S. patens* and *S. macrocarpum*. Conversely, *U. pinnatifida* consistently showed the lowest values, followed by *E. cava* and *G. textorii*. In terms of epifaunal composition (Fig. 6), Gastropoda accounted for over 50% of the abundance in *S. autumnale*, *S.*

microceratium, *S. piluliferum*, *S. thunbergii*, and *G. textorii*, while Gammaridea dominated in *S. horneri*, *S. patens*, and *S. siliquastrum*. Caprellidea made up 50% of the epifauna in *Ecklonia cava* and *U. pinnatifida*. In al seaweed species except *S. confusum*, Caprellidea, Gammaridea, and Gastropoda collectively represented over 85% of total epifauna. In *S. confusum*, these groups accounted for about 60%, with Isopoda contributing around 35%. Other taxa, such as Annelida in *S. thunbergii* and *E. cava*, comprised about 10%, while all remaining taxa were under 5%.

Discussion

This study examined how epifaunal communities varied by location and host seaweed species. Wet weights of *S. autumnale*, *S. confusum*, *S. thunbergii*, *E. cava*, and *U. pinnatifida* were similar. However, epifaunal abundance varied, with *S. autumnale* and *S. confusum* supporting 140 and 100 individuals, respectively, whereas *S. thunbergii*, *E. cava*, and *U. pinnatifida* had fewer than 50 individuals. These differences may be attributed to seaweed morphology and ecology. *Sargassum thunbergii* has smaller leaves and pneumatocytes than other *Sargassum* species (Yoshida, 1983), providing fewer food resources and hiding places. It also inhabits shallower water (Yatsuya et al., 2006), making it more susceptible to environmental fluctuations (Inoue, 1977; Ito et al., 2019). *Ecklonia cava* and *U. pinnatifida*, both Laminariales, have simpler morphologies than Fucales, potentially explain their lower epifaunal abundance. Dotsu *et al*. (2010) found that epifaunal abundance correlates with seaweed complexity, a trend supported by this study. The nMDS plot also suggested that *S. thunbergii*, *E. cava*, and *U. pinnatifida* were associated with fewer key epifaunal taxa, including Annelida, Caprellidea, Caridea, Gammaridea, Gastropoda, and Isopoda. *Gracilaria textorii* had low epifaunal abundance and occupied an nMDS position opposite the depth vector, suggesting its simple morphology and shallow habitat contribute to low epifaunal density. *Sargassum horneri*, despite its large wet weight, had the lowest epifaunal abundance among Fucales. Ito et al. (2019) reported that its epifaunal assemblage primarily consists small bivalve spats and harpacticoid copepods, which may have been underrepresented in this study due to the use of a 1 mm sieve instead of a 100 μm sieve.

Cluster analysis categorized the samples into two primary groups: Laminariales-dominated clusters (clusters 1 and 2) and Fucales-dominated clusters (clusters 3, 4, and 5). Renyi's diversity profile also distinguished these groups, with Fucales exhibiting greater species richness and diversity. Fucales hosted more rare species and had higher community prosperity values, likely due to their complex structures providing abundant niches. *Myagropsis* and *Sargassum*, both in the family Sargassaceae, did not form distinct epifaunal communities, suggesting structural complexity rather than taxonomy is the primary determinant of epifaunal diversity. *Gracilaria textorii* appeared in clusters 1 and 5, indicating inconsistent similarity. As the only red alga in this study, its epifaunal community remains insufficiently understood, necessitating further research.

Community structure also varied significantly by site, likely due to differences in environmental conditions such as flow velocity and salinity. Site facing the open ocean (NIYH, NMC, S) exhibited high flow velocity and suspended sediments, while inner bay sites (HP, OP, HN) had slower currents and higher sediment deposition (Tamaki, 1981). These conditions affect seaweeds function as habitat and food source, shaping distinct community structures at each location.

Across all seaweed species, Caprellidea, Gammaridea, and Gastropoda dominated the epifaunal communities, consistent with previous studies (Yamamoto *et al*., 1999; Yatsuya *et al*., 2008; Dotsu *et al*., 2010; Shinohara & Shimooka, 2024). Caprellids were abundant only on two Laminariales species, possibly due to their ability to mimic seaweed and evade predation (Goto, published online 2023).

The Noto Peninsula Earthquake on January 1, 2024, severely impacted the Tsukumo Bay area, leading tsunamis, sediment deposition, and seafloor alterations. Among the surveyed sites, Shiromaru (S) was particularly affected by the tsunami, which caused severe coastal disturbances. This disturbance likely affected not only Sargassum species but the entire seaweed assemblage, potentially leading to shifts in species composition and structural complexity. Given the role of diverse seaweeds in maintaining epifaunal biodiversity, future surveys should assess long-term ecological impacts and recovery processes. Similar effects were observed following the 2011 Tohoku Earthquake, which significantly altered benthic habitats and community structures in coastal Japan (e.g. Kanaya *et al*., 2012; Abe *et al*., 2015; Noda & Iwasaki, 2017; Sugiura *et al*., 2024). The ecological data from this study will serve as a critical baseline for evaluating post-earthquake changes in small invertebrate communities in the Noto Peninsula coastal region. Long-term monitoring will be crucial for assessing ecosystem resilience and recovery following seismic disturbances.

This study revealed variations in epifaunal abundance and composition across 13 seaweed species. Future research should monitor seasonal changes to better understand epifaunal life cycles in relation to seaweed phenology.

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Author contributions

Keito Tsunoda: conceptualization, investigation, analysis, writing of first draft; Yukimasa Higashide: species identification of seaweed; Kenji Toyota: conceptualization, investigation, writing.

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Competing interest

The authors declare none.

Data availability

All research data are available upon request to Kenji Toyota (toyotak@hiroshima-u.ac.jp).

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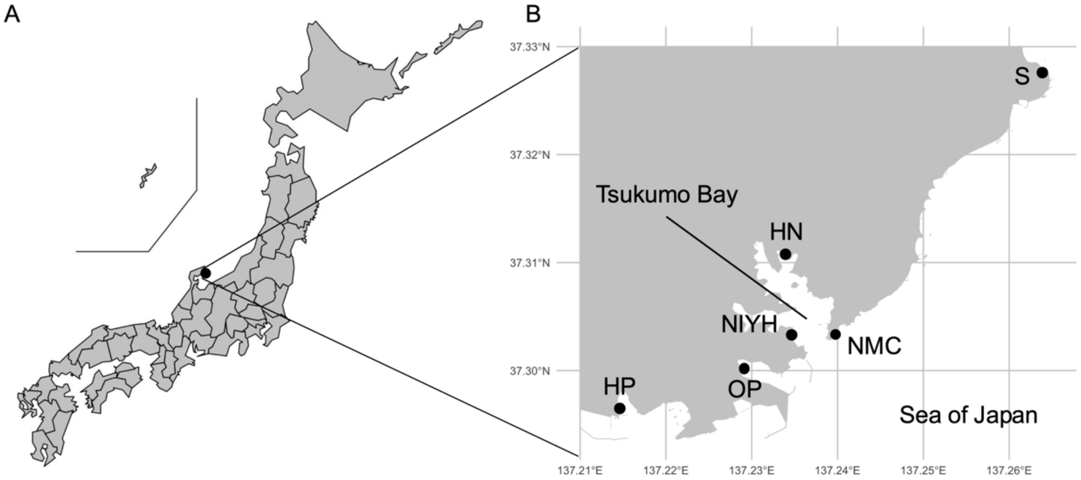

Fig. 1. Sampling site of this study around Tsukumo Bay, Noto Peninsula, Japan. Abbreviation is the name of seaweed collection sites. HN: Hotel Notokinpura, HP: Hime port, NIYH: Noto Isaribi Youth Hostel, NMC: Noto Marine Center, OP: Ogi port, S: Shiromaru.

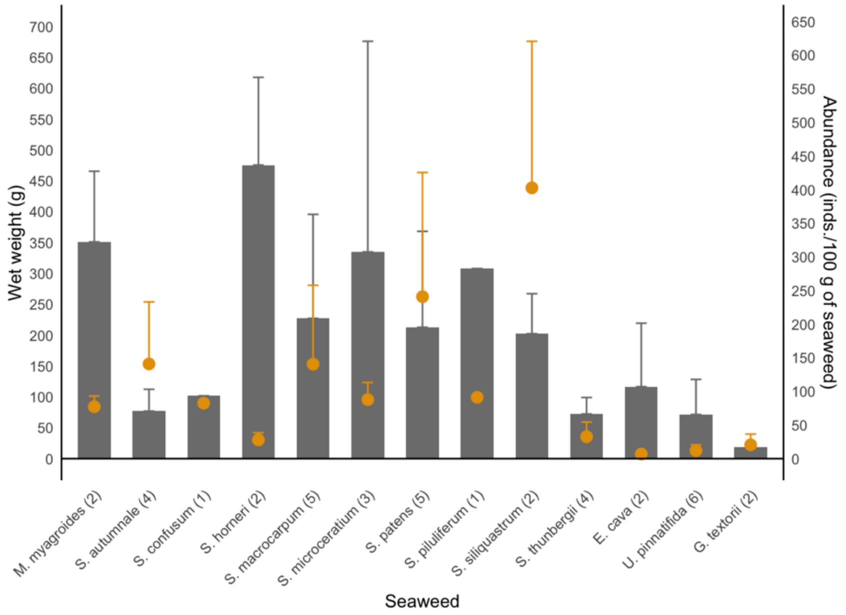

Fig. 2. Wet weight of seaweed species and epifaunal abundance. The bars represent seaweed wet weight, and the plots represent epifaunal abundance. Error bars are expressed as mean + standard deviation. The number after the scientific name indicates the number of samples.

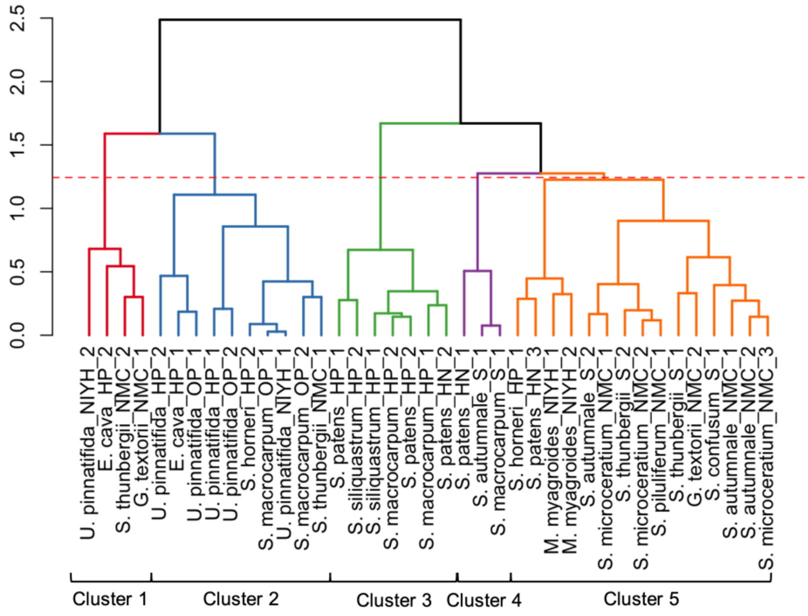

Fig. 3. Cluster analysis of epifauna in each seaweed sample. Sample names were represented by "the scientific name_collection location_ seaweed replication number". The red dashed line represents the position of the 50% similarity, and each color corresponds to each cluster.

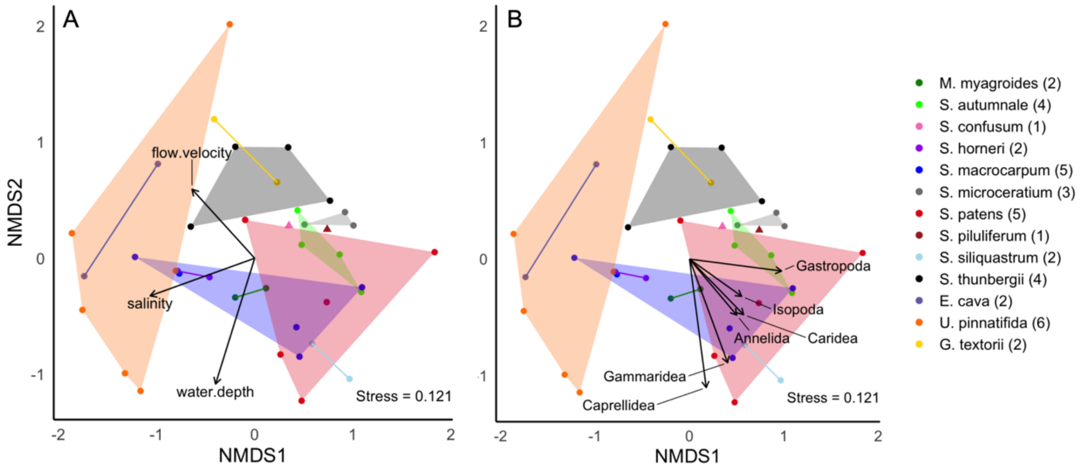

Fig. 4. Non-metric multidimensional scaling grouped by seaweed species. nMDS plot with environmental information selected at the 10% significance level (A), and with the taxon selected at the 5% significance level (B). The number after the scientific name indicates the number of samples.

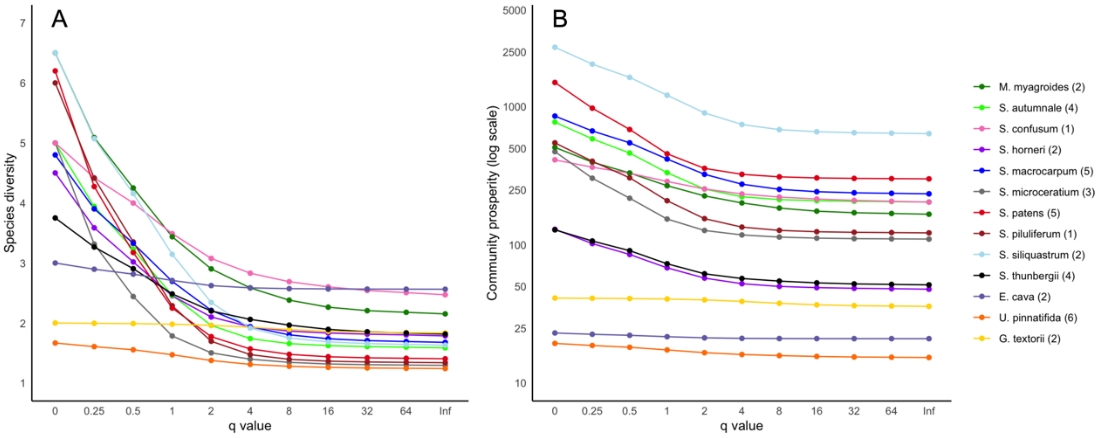

Fig. 5. Renyi's diversity profiles by seaweed species (A) and community prosperity by seaweed species (B). The vertical axis is expressed on a log scale (B). The number after the scientific name indicates the number of samples.

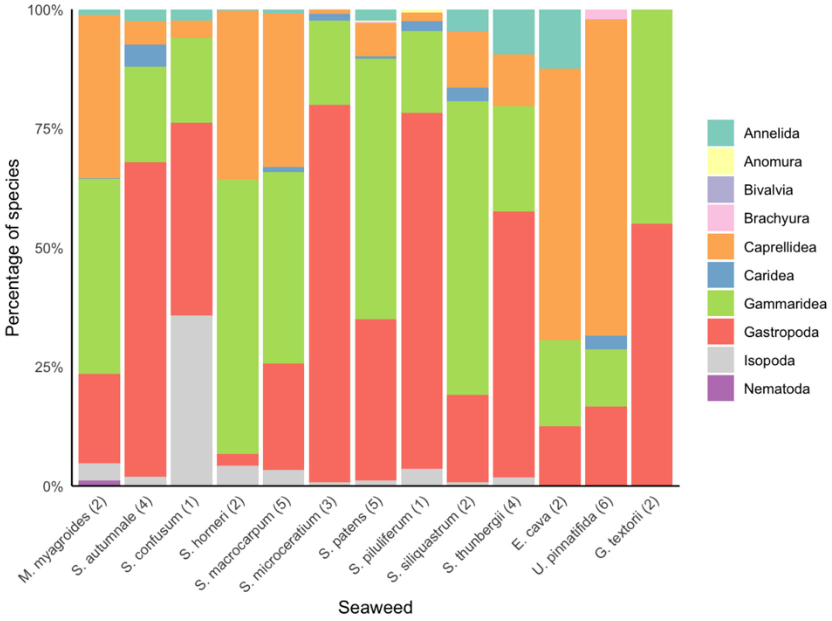

Fig. 6. Percentage of epifauna by seaweed species. The number after the scientific name indicates the number of samples.

Table 1. Collected seaweed.

Order	Species	Number of samples	Site
Fucales	*M. myagroides*	2	NIYH
	S. autumnale	4	NMC, S
	S. confusum	1	S
	S. horneri	2	HP
	S. macrocarpum	5	HP, OP, S
	S. microceratium	3	NMC
	S. patens	5	HP, HN
	S. piluliferum	1	NMC
	S. siliquastrum	2	HP
	S. thunbergii	4	NMC, S
Laminariales	*E. cava*	2	HP
	U. pinnatifida	6	HP, NIYH, OP
Gracilariales	*G. textorii*	2	NMC

HN: Hotel Notokinpura, HP: Hime port, NIYH: Noto Isaribi Youth Hostel, NMC: Noto Marine Center, OP: Ogi port, S: Shiromaru.