Epibionts associated with floating *Sargassum horneri* in the Korea Strait

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Floating seaweed rafts are a surface-pelagic habitat that serve as substrates for benthic flora and fauna. Since 2008, *Sargassum horneri* clumps have periodically invaded the Korea Strait. In this study, the polymerase chain reaction–free small-organelles enriched metagenomics method was adopted to identify the species of epibiotic eukaryotes present in floating *S. horneri* fronds. A total of 185 species were identified, of which about 63% were previously undetected or unreported in Korean waters. The rafts harbor a diverse assemblage of eukaryotic species, including 39 Alveolata, 4 Archaeplastida, 95 Opisthokonts, 4 Rhizaria, and 43 Stramenopiles. Of these 185 taxa, 48 species were found at both *Sargassum* rafts collection stations and included 24 Stramenopiles, 17 Alveolata, and 7 Opisthokonts. Among these, the highest proportion (50%) of species was photo-autotrophic in basic trophic modes, while the proportion of phagotrophic, osmo- or saprotrophic, and parasitic modes were 43.8%, 4.2%, and 2.1%, respectively. This study demonstrates the contribution of floating *Sargassum* rafts as dispersal vectors that facilitate the spread of alien species.

**Key Words:** alien species; floating seaweed; Korea Strait; *Sargassum horneri*; small-organelles enriched metagenomics (SoEM); trophic mode

**INTRODUCTION**

*Sargassum horneri* rafts, which were sparsely detected in the open ocean in the past century, have periodically invaded the Korea Strait since 2008 (Kim et al. 2019). They now comprise the vast majority of marine debris in the Korea Strait, Yellow Sea, and East China Sea. These large biotic rafts that can support an extensive pelagic habitat are far from uncommon but few studies have focused on these and there exist no insights on the diversity of their epibiotic organisms. The most common floating brown alga, *S. muticum* (Yendo) Fensholt, has high fecundity but cannot reproduce vegetatively. Therefore, the presence of conceptacles bearing antheridia and oogonia as well as air-bladders in this monoecious species has proven to be a great advantage for its successful dispersal to appropriate habitats (Strong et al. 2006). In contrast, *S. horneri* (Turner) C. Agardh can propagate through both germlings and vegetative reproduction and branches separated from a shoot will continue to grow into a new fronds (Uchida 1993).

*S. horneri* (hereafter *Sargassum*) is distinct from other...
The surveys of seaweed-associated assemblages that have been conducted so far have been geographically restricted and did not provide for a wide range of taxonomic groups. A wide range of eukaryotic taxa in the pelagic rafting assemblages, particularly *Sargassum*-associated, remains unexplored, and fungi, macroalgae, protists and invertebrates may be present. A newly established polymerase chain reaction (PCR)-free small-organelles enriched metagenomics (SoEM) method is an effective and accurate tool for identifying species across all taxonomic groups of eukaryotes from the smallest unicellular protists (>0.2 micrometers) to small animals that are a few millimeters long (Jo et al. 2019). This method would be a useful alternative approach in evaluating the biodiversity and community structure of both plankton and benthos in marine ecosystems.

In this study, we aimed to identify the eukaryotic epibiont community found on floating *Sargassum* fronds. We summarized the species diversity by analyzing an innovative SoEM method and discussed the ecological implications of epibionts associated with this specialized habitat in the Korea Strait. Although only epibionts associated with floating rafts are reported, this result will help fill the knowledge gap regarding the ecological roles of floating algae.

**MATERIALS AND METHODS**

**Sample collection and filtration**

Floating *Sargassum* rafts were collected from two off-
shore stations in the Korea Strait during cruises of the National Institute of Fisheries Science (NIFS) research vessel TAMGU8 from Apr 16 to 20, 2017 (Fig. 1). The sampling of rafts was performed using a landing net and conducted as near as possible to the stations 205-05 (33°37’18.1” N, 128°09’11.9” E) and 314-01 (33°00’00.0” N, 127°42’00.0” E) of the NIFS monitoring program. At the same time, an approximately 10 L sample of surface seawater was collected at each station.

Floating fronds over 100 cm in length, with holdfast regions, were immediately transferred into a plastic bag with 4 L of the surface seawater. Any organisms that fell off the thallus were quickly collected and added into the bag. All contents of the bag were immediately transported to the shipboard laboratory, and were shaken violently for several minutes to remove all mobile associated taxa and scraped to remove as many sessile invertebrates as possible. After shaking, *Sargassum* fronds were discarded from the plastic bag, and the remaining seawater was filtered using the cellulose acetate (CA) filter with a pore size of 0.45 µm. The surface seawater was also filtered using the same filter to provide control plankton communities, to exclude plankton species that were observed in *Sargassum* fronds. All CA filters were placed separately into sterile screw-cap tubes, and were frozen in liquid nitrogen. Before they were delivered to the laboratory, they were stored at -80°C until needed.

Subsequently, macroscopic specimens on all flora and fauna associated with the *Sargassum* rafts were identified under a dissecting microscope to the lowest possible identification levels using the available identification keys. The subsamples were preserved in 5% formalin for later identification.

**DNA extraction, SoEM library preparation, and sequencing**

To profile eukaryotic biodiversity of *Sargassum* rafts hitchhikers, we utilized a previously developed metagenomics method, SoEM, with slight modification (Jo et al. 2019). The CA filter contained trapped environmental samples that were subsequently chopped into tiny pieces with sterile scissors on ice, and then resuspended in 10 mL of ice-chilled homogenizing buffer (250 mM sucrose, 30 mM Tris-HCl, 10 mM EDTA, and pH 7.5). Chopped filter papers within the buffer were homogenized using an IKA-T10 tissue homogenizer (IKA, Staufen, Germany) at maximum RPM on ice for five cycles of 15 s and 15 s off ice. The homogenate was firstly centrifuged at 4°C at 1,300 xg for 10 min to remove nuclei, cellular debris, and filter paper pieces, and then the supernatant was transferred to a fresh tube. It was then centrifuged at 4°C at 17,000 xg for 30 min to enrich small organelles. The supernatant was discarded, and small-organelles enriched DNA was extracted from the pellet using the Qiagen DNeasy Blood/Tissue Kit (Qiagen, Hilden, Germany) following the manufacturer’s protocol. The DNA was quantified and qualified using the Qubit 3.0 fluorometer (Thermo Fisher, Waltham, MA, USA) and an Agilent 2100 bioanalyzer (Agilent Technologies, Palo Alto, CA, USA). Preparation of SoEM libraries and sequencing were carried out following the same procedures followed in the previous study (Jo et al. 2019).

**Bioinformatics analysis**

To remove sequencing adaptors and low-quality sequences, all paired-end sequences of SoEM libraries were preprocessed using Trimmmomatic (v0.36) (Bolger et al. 2014). To extend the sequence length in further taxonomy-assignment processes, the preprocessed read-pairs were merged to one read by overlapped sequences using PEAR (Paired-End reAd mergeR, v0.9.10) (Zhang et al. 2014) with a minimum length `-n 400,’ and minimum overlap ‘-v 10’ options. To assign taxonomic information of the merged reads, a BLAST search was performed against the NCBI NT database (download date: Jun 7, 2017) with queries of the merged reads. After the BLAST search, the results were filtered according to the following criteria, (1) E-value < 1e-10, (2) aligned length ≥ 400 bp, and (3) pick the top one result based on the bit-score. And, NCBI GenBank accession numbers were converted to NCBI taxonomy IDs of the results that satisfied above criteria using ‘nucl_gb.accession2taxid’ file in NCBI taxonomy FTP (ftp://ftp.ncbi.nih.gov/pub/taxonomy/accession2taxid/), and an in-house python script. To eliminate false positive results in this process, accession numbers with less than five distinct assigned reads were discarded in further steps.

**Taxonomy assignment of eukaryotic plankton and epibionts**

To profile hierarchical taxonomic information of taxonomy IDs obtained in the previous step (e.g., Phylum, Class, Order, Genus, and Species levels), we utilized the ‘taxize’ tool, a package of R program (Chamberlain and Szocs 2013). After this assignment, we first excluded results that assigned taxonomic IDs to superkingdoms of ‘Bacteria,’ ‘Virus,’ ‘Archaea,’ and ‘Unclassified’ groups.
to investigate eukaryotic biodiversity. Results following cases of ambiguous assignments were discarded or combined in further steps: (1) taxonomy IDs with unavailable taxonomic information at the genus level were discarded; (2) environmental entries in the NCBI taxonomy database, such as ‘283062; eukaryotic picoplankton environmental sample,’ ‘212038; Copepoda environmental sample,’ and ‘693772; invertebrate environmental sample,’ were discarded; (3) uncultured entries in the database, such as ‘175278; uncultured metazoan’ and ‘100272; uncultured eukaryote’ were discarded; and (4) to avoid duplicate species assignments, ambiguous results in species level, such as ‘Cyclotella sp. WC03_2,’ and ‘Cyclotella sp. L04_2,’ were combined into same species as ‘Cyclotella sp.’ Finally, to investigate the biodiversity of marine eukaryotes within the data, we manually curated the taxonomic hierarchy of the remaining taxonomic IDs by matching them with the World Register of Marine Species (WoRMS; http://www.marinespecies.org, accessed on Nov 19, 2019) database and the Korea National List of Marine Species (KNLMS; https://www.mbris.kr/pub/marine/natilist/nationalist.do, accessed on Aug 1, 2019) from Marine Bio Resource Information System (MBRIS) of Republic of Korea. Here, the species that was recorded in at least one database between both databases (i.e., WoRMS or KNLMS) was regarded as a marine eukaryotic species in this study.

For Sargassum-specific epibiotic species, we determined the trophic mode of each taxon from our own biological knowledge and from reference to the literature as necessary (e.g., Adl et al. 2019). When the feeding ecology of a specific taxon was unknown, we assigned it to the most probable feeding type.

### Chlorophyll-a fluorometry

The photosynthetic activity of Sargassum was measured via chlorophyll-a fluorescence using a Diving-PAM fluorometer (Walz GmbH, Effeltrich, Germany). The maximum efficiency of PSII photochemistry \( (F_v / F_m) \) was determined for all fronds after being acclimatized to darkness for 10 min using leaf clips (Diving-LC; Walz), where \( F_v \) represents the variable fluorescence calculated as the maximum \( (F_m) \) minus the minimum \( (F_o) \) fluorescence (Genty et al. 1989). To compare these results with those of the floating fronds, the benthic Sargassum was collected on Apr 15, 2003 from the low intertidal to shallow subtidal zone of Wando (34°18’ N, 126°41’ E) along the southwestern coast of Korea.

### RESULTS

#### Environments in the study area

To understand the mean surface circulation in the Korean Strait, mean surface current vectors were calculated in each lattice with 0.25° grid spacing using the velocity data of surface drifters that passed through the Korean Strait from 1991 to 2017 (Fig. 1B). The Tsushima Warm Current flowing northeast through the Korean Strait is a branch of the Kuroshio Current (Lie and Cho 2016). The Cheju Warm Current flows clockwise around Jeju-do and transports warm and saline seawater into the Jeju Strait. Annual mean current speeds estimated from the surface drifter observations were 18-20 cm s\(^{-1}\) at station 205-05 and 12-13 cm s\(^{-1}\) at station 314-01 (Park et al. 2019). The

### Table 1. Sampling date and geographic position of two floating rafts in the Korea Strait

<table>
<thead>
<tr>
<th>Station</th>
<th>Date</th>
<th>Latitude</th>
<th>Longitude</th>
<th>SST</th>
<th>SSS</th>
<th>( F_v / F_m )</th>
</tr>
</thead>
<tbody>
<tr>
<td>205-05</td>
<td>Apr 16, 2017</td>
<td>33°37’18.1” N</td>
<td>128°09’11.9” E</td>
<td>16.5</td>
<td>34.5</td>
<td>0.636 ± 0.011</td>
</tr>
<tr>
<td>314-01</td>
<td>Apr 20, 2017</td>
<td>33°00’00.0” N</td>
<td>127°42’00.0” E</td>
<td>18.4</td>
<td>34.7</td>
<td>0.644 ± 0.009</td>
</tr>
</tbody>
</table>

Sea surface temperature (SST, °C), sea surface salinity (SSS), and maximum quantum yield \( (F_v / F_m) \) for floating fronds of Sargassum homeri (mean ± standard error, n = 25).

### Table 2. Summary of sequencing statistics for samples used in the SoEM method using Trimmomatic (v0.35) and PEAR (v0.9.10)

<table>
<thead>
<tr>
<th>Station</th>
<th>Total reads (raw data)</th>
<th>Total read bases pairs (raw data)</th>
<th>Total read (trimmed data)</th>
<th>PEAR-assembled read pairs to single-end</th>
<th>Assembled reads (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>205-05 Water</td>
<td>45,155,648</td>
<td>13,195,601,272</td>
<td>41,839,682</td>
<td>6,458,940</td>
<td>30.9</td>
</tr>
<tr>
<td>205-05 Sargassum</td>
<td>34,396,480</td>
<td>10,015,710,427</td>
<td>32,786,872</td>
<td>4,927,012</td>
<td>30.0</td>
</tr>
<tr>
<td>314-01 Water</td>
<td>41,694,760</td>
<td>12,249,347,061</td>
<td>39,224,952</td>
<td>5,999,949</td>
<td>30.6</td>
</tr>
<tr>
<td>314-01 Sargassum</td>
<td>38,910,710</td>
<td>11,337,831,984</td>
<td>36,281,754</td>
<td>6,621,541</td>
<td>36.5</td>
</tr>
</tbody>
</table>

SoEM, small-organels enriched metagenomics; PEAR, Paired-End reAd mergeR.
current is faster at station 205-05 than at station 314-01 because the flows from the Jeju Strait and the south converge at this juncture. In April, the water column is not yet vertically stratified and there is a surface meridional temperature gradient in the Korea Strait. The sea surface temperature data in Fig. 1 were obtained from the Operational Sea Surface Temperature and the Sea Ice Analysis (OSTIA) dataset was generated by the UK Met Office.

**Photosynthetic performance of floating Sargassum**

Twenty-five fronds from each raft and a benthic habitat were selected at random and the maximum quantum yield ($F_v / F_m$), which is an indicator of photosynthetic activity, was measured with a Diving-PAM. The $F_v / F_m$ of the benthic fronds was $0.704 \pm 0.011$ (mean ± standard error, $n = 25$), which is normal for the natural vegetative fronds, whereas the $F_v / F_m$ values of the floating fronds from stations 205-05 and 314-01 were approximately 0.636 and 0.644, respectively (Table 1). As a result, floating fronds $F_v / F_m$ values exhibited negligible differences between the two stations at which they were sampled and were only about 10% lower than those of benthic vegetation fronds.

**Eukaryotic plankton and epibiont diversity**

To profile eukaryotic biodiversity of plankton and epibionts at stations 205-05 and 314-01, small-organelles enriched DNAs from the four samples (two seawater and two Sargassum samples) were sequenced using an Illumina Miseq (v2, 301-cycle). A total of 34.4-45.1 million raw data reads (10.0-13.2 Giga bases) were obtained from each sample. After trimming and filtering adapter and low-quality reads, a range of 32.8-41.8 million high-quality reads per sample remained. To obtain longer sequences with more than 400 bp, paired-end reads were merged to single-end read, and 4.9-6.6 million read-pairs were merged (i.e., 30.0-36.5% of paired-end reads were merged) (Table 2). A BLAST search was performed on the NCBI nt database in May 2018 with an e-value option of 1e-10. We first obtained a total of 2,243 NCBI Taxonomy IDs by taxonomic profiling, and 609 eukaryote IDs were extracted by hierarchical taxonomy status using the “taxize” package in R.

The SoEM output showed that a total of 366 eukaryotic operational taxonomic units (OTUs) were identified at the species level. These eukaryotes taxa comprised 7 supergroups, 25 phyla (8 not available [NA]), 62 classes (11 NA), 128 orders (10 NA), 196 families (6 NA), and 280 genera, including the “not available (NA)” taxa. Of these 366 OTUs, 201 (54.9%) taxa that had been previously unreported in Korean waters were detected at the species level and were compared with the integrated database from KNLMS. The information of the taxon-assigned OTUs is presented in Supplementary Table S1.

To determine the Sargassum epibiotic species, eukaryotic plankton communities that were not associated with floating rafts were excluded from a complete OTUs list. This clarified whether the epibiotic species specifically inhabited the floating Sargassum or had floated on by chance from the surrounding seawater.

There were obvious differences in the diversity of specimens obtained from the four different samples. For the seawater and floating Sargassum samples, the highest number of eukaryotic OTUs were observed from the Sargassum of station 314-01, followed by those from the seawater and the Sargassum of station 205-05. The lowest number of OTUs (108) was obtained from the seawater sample from station 314-01 (Fig. 2).

**Sargassum-specific epibionts**

We identified 185 taxa associated with floating Sargassum, with representatives of nearly all supergroups, including 95 (51.4%) Opisthokonts, 43 (23.2%) Strameno-
DISCUSSION

Although it was difficult to determine the exact origin of the Sargassum rafts collected from the South Sea of Korea (the Korea Strait) during the last several years, there have been reports of different origins and pathways from those in the main Kuroshio Current, East China Sea, northwestern East China Sea, and southern Yellow Sea (Chang and Isobe 2003, Abé et al. 2013, Komatsu et al. 2014a, 2014b, Qi et al. 2017). Considering the direction of flow of the Kuroshio Current, however, we do not argue the origin of our samples as most of the floating Sargassum rafts possibly originated somewhere in the southern part of East China Sea. The Tsushima Warm Current flowing northeast through the Korea Strait is a branch of the Kuroshio Current (see Fig. 1B).

It has been shown that certain hitchhikers on the seaweed rafts (e.g., stalked barnacles of the genus Lepas) can help determine the time period for which the host rafts have been floating as well as their origin and path they traversed during the time spent in the water. Free-floating or detached seaweeds that are just beginning to float in surface waters are immediately colonized by stalked barnacles. Therefore, the sizes of these barnacles can be used as a proxy of floating duration because they only adhere to buoyant objects, and their size provides a good estimate of the duration for which a hitchhiker has been afloat (Thiel and Gutow 2005b, Fraser et al. 2011, Macaya et al. 2016). However, contrary to our expectations, these species were not found in epibiotic communities of Sargassum rafts during the present study.
Floating *Sargassum* was found to harbor a diverse epibiotic assemblage with 185 species, belonging to 18 different phyla and 35 classes from only two rafts sampled in the Korea Strait (Fig. 3, Supplementary Table S1). It is difficult to determine whether the *Sargassum* epibionts are truly endemic or nonindigenous species to Korean waters due to incomplete knowledge of their taxonomy and as the many geographical areas and habitats where they originate are not well studied.

The taxonomic classification of not only protists but also many other groups of eukaryotes is continuously changing due to small differences in the taxonomic criteria used. Thus, many species described as new for an area, later turn up as synonyms to previously described species. This makes it difficult to judge whether they have existed in a particular region earlier or not. Furthermore, many eukaryotic species have not been detected or properly identified before now due to the lack of taxonomists in this country. These taxonomical changes are likely to shift even more in the future, when molecular tools will be used more frequently than they are today. In particular, the use of the SoEM method for species identification across the whole taxonomic group of eukaryotes from an environmental sample has greatly contributed towards the better understanding and the extension of marine biodiversity considerations.

Approximately two-thirds of the species found in our studies are newly recorded from Korean waters. Many epibionts may have been originally living on the *Sargassum* fronds or have colonized it before it became a floating raft. This study demonstrates some further evidence that floating *Sargassum* rafts are an important pelagic habitat that provides vital resources for a diverse epibiotic assemblage.

![Fig. 4. Schematic phylogeny and trophic mode of *Sargassum*-specific epibionts.](http://e-algae.org)

The 48 species, *Sargassum*-specific epibionts, belong to 3 supergroups. Each species has four broad ecological traits. The trophic modes were expressed as parasitic (red line), osmo- or saprotrophic (blue line), photo-autotrophic (green line), and phagotrophic mode (black line). The majority of these taxa are photo-autotrophs (50% of the *Sargassum*-specific epibionts) and phagotrophs (44%). The circular phylogenetic tree was created using phylot (http://phylo.t.biobyte.de/) and the tree was visualized using iTOL (http://itol.embl.de/).
Although many of the large brown algae cannot propagate vegetatively, floating fertile parts can drift away and establish new populations. Whether floating Sargassum fronds are capable of releasing viable embryos is unknown, but mature fronds bearing reproductive conceptacles have been observed often in this study (throughout the Korea Strait in the spring of 2017). Moreover, photosynthetic activity determined by chlorophyll-a fluorescence measurements revealed normal or slightly decreased (ca. 90%) maximum quantum yields when compared with those collected from nearby natural rocky habitats (Table 1). Sargassum rafts sampled in this study may have been exposed to sunlight and air for a long period of time considering that their fronds had the potential to stay afloat. However, the complex interaction of abiotic and biotic stressors (temperature, irradiance, and grazig) on their floating persistence at the sea surface still remains poorly understood, although it is known that the persistence of seaweeds at the sea surface plays an important role in promoting long-distance dispersal and connectivity (Arroyo and Bonsdorff 2016, Rothäusler et al. 2018).

Chlorophyll-a fluorescence analysis has become one of the most powerful approaches for measuring photosynthetic activity of algae in vivo (Schreiber et al. 1994). It is particularly useful for measuring the impact of environmental stress on the physiological state of photosynthesis (e.g., Kang et al. 2016). Maximum quantum yield \( (F_v / F_m) \) can be used to reflect the photosynthetic activity and stress levels of both floating and benthic vegetative fronds. When values decline, this can reflect the development of mechanisms either for photoprotection or photodamage. Benthic fresh fronds from natural Sargassum habitats had negligible impact on the photosynthetic performance and had no detectable impact on health. However, the \( F_v / F_m \) values were about 0.64 for all floating Sargassum fronds. It indicates that in the spring, the floating Sargassum fronds in the Korea Strait are under exposed to adverse conditions that are not conductive to their growth.

An important role of the seaweeds in temperate waters is their architectural structure, which provides shelter for the mobile epifauna and an increased surface area for epibionts (Wallentinus 2002). The richness of epibiotic species associated with the floating seaweeds was strongly influenced by the raft size, weight or volume and age, and varied according to seasonal and geographical changes (Stoner and Greening 1984, Thiel and Gutow 2005a, 2005b, Vandendriessche et al. 2007, Wichmann et al. 2012, Abé et al. 2013). The composition of these epibionts was also affected by physical environments such as temperature, salinity, ocean currents, and even weather conditions (Clarkin et al. 2012, Thiel and Fraser 2016). In addition, the health and physiological status of seaweed rafts are likely to play important roles in the development of epibiotic communities. Although we could not analyze the effects of frond age or floating times on the diversity of epibionts, in the floating Sargassum fronds, which presumably reached the senescence stage, the \( F_v / F_m \) remained relatively high at about 90% of that in control fronds.

The economic impact of these seaweed rafts on fisheries and aquaculture mainly occurs through clogging of fish nets and/or by creating a nuisance in aquaculture through fouling supporting structures and aquaculture target species (e.g., seaweeds, oysters, and mussels), clogging of cages, and, in extreme cases, by lifting and sailing away with free-living oysters and mussels. Massive rafts of floating seaweeds are both an economic and a recreational problem as they can hinder navigation of boats around aquaculture grounds and fishing ports. In Korea, great efforts have been made to clear Sargassum strandings to protect the biodiversity of an area or because they hinder shellfish and seaweed harvests, but often with limited success. Furthermore, other introduced species cause problems by fouling aquaculture structures and getting entangled in fishing tools and have to be cleared away.

The other side, Sargassum species are well-known ecosystem engineers of shallow hard-bottom ecosystems, forming extended canopies, structuring the algae and invertebrate communities, and attracting predators in the temperate areas of China, Japan, and Korea. Although S. horneri appears often as a free-floating object in temperate eastern Asia, it is capable of reproducing nearly year round in these countries, and is known to rapidly colonize new habitats, growing up to 5 m in height in dense forests and forming dense thickets on rocky shores that provide a habitat and spawning ground for a diverse assemblage of organisms (Choi et al. 2003, Sun et al. 2009).

In the eastern YS, large rafts of floating Sargassum were observed in March 2017 covering an area of 1,300 m\(^2\) (Kim et al. 2019). Seaweeds forming dense mats floating on the surface may be detrimental for the benthos habitats as they can drastically decrease the light penetration needed for the benthic plants and by reducing oxygen for aquatic animals by decreasing air exchange through the water surface. The problems with almost total Sargassum rafts are well-known, as are those that arise when such huge biomasses descend to the sea bottom and smother.
benthic communities and increase hypoxia conditions.

In conclusion, species dispersal and connectivity via seaweed rafts may be highly effective in some areas and limited in others. For this reason, studies of their biodiversity are important. The surveys conducted so far have been geographically restricted and have not account for the full range of taxonomic groups. To assess the diversity of eukaryotic epibionts, Sargassum fronds were collected from the Korea Strait, during which massive amounts of floating rafts invaded episodically. The recently established PCR-free SoEM method was adapted to assess eukaryotic diversity, ranging from the smallest unicellular eukaryotes (protists) to small animals a few millimeters long. Beyond taxonomic assignation, we inferred basic trophic modes to 48 Sargassum-specific epibionts on basis of their genetic affiliation to trophic group of reference. We explored the potential impacts of floating seaweeds and their role in the dispersal of alien eukaryotes into new habitats.

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**SUPPLEMENTARY MATERIALS**

**Supplementary Table S1.** A complete list of eukaryotic plankton and Sargassum epibionts in this study, with the Korea National List of Marine Species (KNLMS) (https://www.e-algae.org).

**REFERENCES**


