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Current Status of *Sargassum* DNA Barcoding over the Last Three Decades from 1995-2025

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Abstract

Sargassum (Phaeophyceae) is a cosmopolitan macroalgae with great industrial and economic potential. Despite this, identification of *Sargassum* species with traditional taxonomy – morphological traits, often led to ambiguity since it is known that *Sargassum* has high phenotypic plasticity. Modern identification of *Sargassum*, DNA barcoding, is relatively new compared to the traditional means. This systematic review (1995-2025) aimed to provide an updated overview of the current climate of *Sargassum* DNA barcoding globally. The literature determination of this systematic review followed PRISMA framework, which started from literature search procured from major databases, Scopus, ResearchGate (RG), and Google Scholar (GS). After going through the criteria for duplicate, title-abstract, and full-text screening, 89 studies that were included for extraction and analysis. This review revealed that *Sargassum* DNA barcoding studies have been done with 38 different genetic markers from the nuclear, chloroplast, and mitochondria gene which are used 90, 47, and 83 times respectively. The most frequently used marker is the nuclear ribosomal marker, ITS2, which had been used 41 times across 89 studies. *Sargassum* DNA barcoding studies have also been done on 109 out of 356 taxonomically accepted *Sargassum* species, forms, and varieties, in 55 different locations around the world. This review provides an up-to-date and comprehensive overview of the global status of DNA barcoding studies on *Sargassum* as well as identifies knowledge gaps and areas for further research, which can expand the DNA sequence database of *Sargassum* and shed light on the taxonomic status of *Sargassum* species.

1. Introduction

Sargassum is a cosmopolitan genus of brown macroalgae (Phaeophyceae) that can be found across three oceans, namely the Atlantic, Pacific, and Indian Ocean, spanning from temperate, subtropical, and tropical waters (Yip et al., 2020). *Sargassum* have a lot of prospective and utilization in various industries (Puspita et al., 2020) due to the diverse bioactive compounds (Yende et al., 2014) and high nutritional values (Wahyuningtyas et al., 2020) they possessed.

Despite the wide usage and distribution, species identification of *Sargassum* from the early 19th century (Agardh, 1821) has been done by their morphological characteristics, while molecular identification did not start gaining attention until the early 21st century (Mattio & Payri, 2010). Molecular identification of *Sargassum* species resulted in taxonomical revisions (Mattio et al., 2009, 2010; Mattio, Payri, & Stiger-Pouvreau, 2008; Mattio & Payri, 2009), hence more accurate than morphological identification of *Sargassum* species (Bringloe & Saunders, 2019). This is in line with the fact that *Sargassum* is a type of macroalgae, a lower plant with simple morphology, high polymorphic nature, and phenotypic plasticity that make morphological identification a challenge (Cheang et al., 2008; Du et al., 2014; Saunders, 2005).

In addition to a more accurate way of identifying *Sargassum* species, molecular identification using the DNA barcoding technique also has several other advantages, including finding cryptic species and confirming new distribution records (Ali Alshehri et al., 2019; du Plessis,

2020), identifying and mitigating invasive species (Zhan et al., 2021), etc. Further studies and analyses of the DNA obtained from this technique could also develop accurate predictions of economically beneficial traits that can be inherited in the plant breeding process (Bhat et al., 2021; Hwang et al., 2019).

DNA barcoding studies of *Sargassum* species have developed worldwide over the past three decades. It is important to identify gaps from existing researches, since *Sargassum* DNA barcoding studies are still quite niche and not well studied yet, compared to the traditional way using morphological characteristics for identification and taxonomy that has been done for three centuries. Several prominent gaps include: the uneven geographic coverage, marker inconsistency in delineating closely related species, and limited species representation. The objective of this review is to provide an overview of the current status of DNA barcoding research on *Sargassum*, specifically to map the usage and performance of markers as well as the species and the location of the studies. Furthermore, this review also aimed to to assess the distribution, adaptation, and ecological role of *Sargassum* as well as clarify research gaps for future research direction.

2. Material and methods

2.1 Review objective

This review has the following primary review question:

- What literature and data are available on *Sargassum* DNA barcoding research worldwide?

The secondary review questions are:

- Which *Sargassum* species are most studied and vice versa?
- What different parameters that are used in these studies?
- Where are these studies conducted?
- What are the gaps in these studies?

2.2 Review scope

This systematic review focuses on *Sargassum* DNA barcoding studies reported in papers in English or *Bahasa Indonesia*. Data were gathered from published literatures through several bibliographic databases, including Scopus, Research Gate, and Google Scholar. The scope of this review is determined using a globally accepted standard approach to systematic review, which is done by determining the Population, Intervention, Comparator, and Outcome (PICO framework) of the review (Basyuni et al., 2024; Illian et al., 2021; Methley et al., 2014; Sasmito et al., 2023). The detailed description of PICO used for this review is as follows:

- *Population*: *Sargassum* DNA barcoding worldwide.
- *Intervention*: Any primers or DNA barcodes used for *Sargassum* DNA barcoding.
- *Comparator*: Any indicators used to monitor the success of DNA barcoding process.
- *Outcome*: Acquired DNA sequence data of *Sargassum* for further studies.

Most of the methodological steps in this systematic review follow previous systematic reviews in environmental science (Mengist et al., 2020). This systematic review adhered to the PRISMA guideline for reporting systematic reviewers in this discipline (Mengist et al., 2020; Page et al., 2021).

2.3 Literature search

Strings are created by identifying relevant keywords per the PICO definitions before the literature search is conducted. Only the terms from the Population and Intervention categories are used to avoid limited search results. Literature searches in Scopus and Research Gate (RG) are done in English, while searches in Google Scholar (GS) are done in both English and Bahasa Indonesia (Tables 1 and 2 and Fig 1). Only the first 50 results in both English GS and Bahasa Indonesia were selected to prevent irrelevant studies being included.

Table 1. Search string composition adapted from defined PICO with desired focus on studies both in English and Bahasa Indonesia

Language	Population search terms	Intervention search terms
English	*Sargassum*	DNA barcoding
Bahasa Indonesia	*Sargassum*	*Pemarkaan DNA*

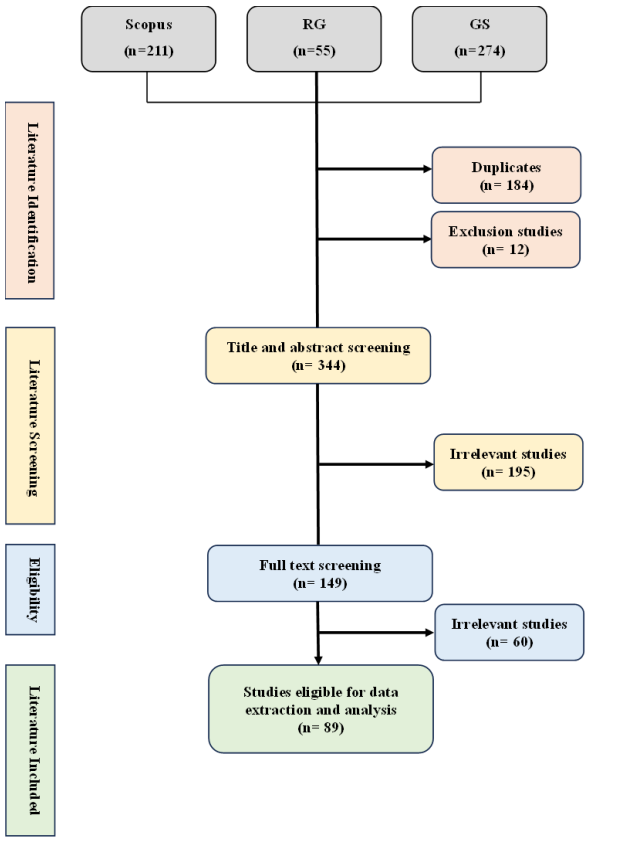

Figure 1. PRISMA flow diagram showing the process of literature determination of *Sargassum* DNA barcoding studies

Table 2. Literature search record

No	Database	Search string	Date of literature search	Search results
1	Scopus	(*Sargassum* AND DNA) AND (barcoding OR	27/06/2025	212
2	Research Gate	barcode) OR (marker OR molecular) OR	27/06/2025	55
3	Google Scholar English	(phylogenetic OR taxonomic revision)	27/06/2025	235
4	Google Scholar Indonesia	(*Sargassum* AND DNA) AND (*pemarkaan* OR *barkode*) OR (*marka* OR *molekuler*) OR (*filogenetik* OR *revisi taksonomi*)	27/06/2025	39

2.4 Literature screening

The inclusion criteria used to determine the relevance of the literature search result is listed in Table 3. To be included in this review, studies must satisfy the requirements of PICO (population, intervention, comparator, and outcome of interest). Furthermore, duplicates are removed, and the studies are screened through their title and abstract. Questions formulated from the PICO model are used in the screening process to choose studies that met the scope of this review.

2.5 Reporting and presentation

The reporting and presentation of the results of this review are written according to the standardized reporting approach for the systematic review of environmental science studies (Basyuni et al., 2024). Additionally, a database consisting of the results of the systematic review is provided.

3. Results

3.1 Publication screening

The publication screening process is shown in the PRISMA flow diagram (Fig 1). Initially, 540 papers were retrieved using the systematic literature search phrases listed in Table 2. Subsequently, after literature screening that included title, abstract, and full-text screening, 89 final papers were selected for further data extraction. Overall, 16% of the initially recognized publications in publication databases (Scopus, ResearchGate, and Google Scholar) were included in the extraction and analyses process. Quite a few publications were registered in more than one database, hence counted as duplicates (Fig 1). The cutoff date for the literature search was June 27, 2025.

In 1995, 1998, and 1999, the publications on *Sargassum* DNA barcoding research were one each year. From year 2000 onwards, the number of publications trend upwards with eight as the most publications in 2024 (Fig 2). Almost all of the publications consist of journal articles. Out of the 89 publications, there are only two review papers and dissertations, respectively.

3.2 Genetic markers used in *Sargassum* DNA barcoding studies

This review identified the markers that were used in *Sargassum* DNA barcoding studies worldwide (Fig 3).

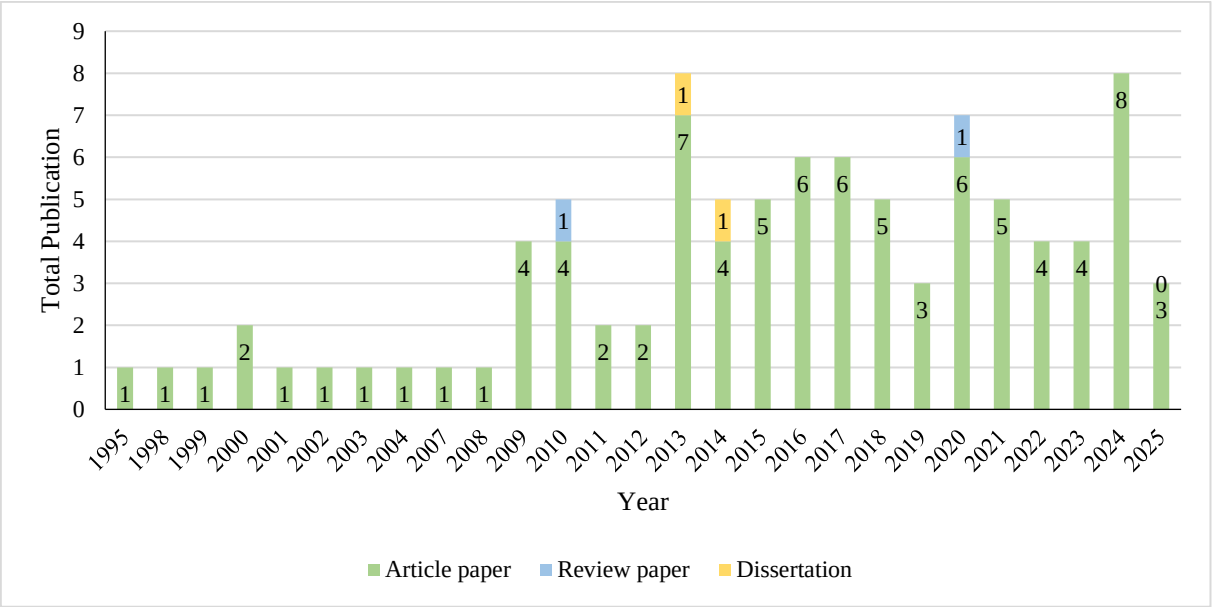

Figure 2. Publication trend of studies on *Sargassum* DNA barcoding (year vs number and type of publication)

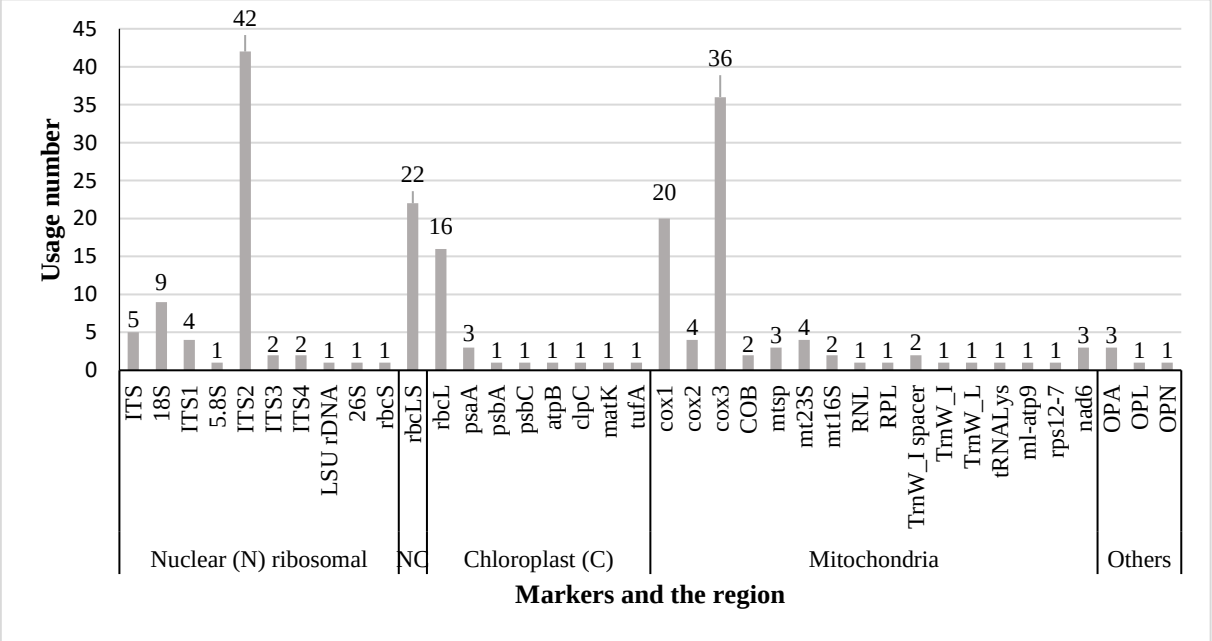

Figure 3. Various markers and the number of times they are being used in *Sargassum* DNA barcoding studies.

The markers can be categorized into several regions, mainly from nuclear, mitochondrial, and chloroplast DNA. Nuclear markers are used the most from the three regions. Among the nuclear, mitochondria, and chloroplast markers, ITS2 (nuclear ribosomal), rbcL and rbcLS (chloroplast), as well as cox1 and cox3 (mitochondria), were significantly used more in *Sargassum* DNA barcoding than the other markers. Several studies revealed low genetic variability for ITS2 and rbcL compared to mitochondrial markers like cox1 or cox3 in some closely related *Sargassum* species, such as with the species belonging to the *Sargassum* subgenus *Sargassum* (Álvarez-Canali et al., 2024; Mattio & Payri, 2010), namely *S. aquifolium* (Chan et al., 2014), *S. glaucescens* (Shimabukuro et al., 2015), as well as species belonging to the *Sargassum* subgenus *Bactrophycus* (Stiger et al., 2003), namely *S. horneri* (low variability for cox3) (Zhuang et al., 2021), and *S. hemiphyllum* (Chen et al., 2025). Lin et al. (2024) and Z. Hu et al. (2017) noted that mitochondrial markers, cox1 as well as tRNA W- L spacer (trnW- L) and cox3 markers respectively, were able to distinguished cryptic species. However, several studies noted that ITS2, rbcL, and cox3 is suitable for inferring species diversity and phylogenetic analyses within the genus (Stiger et al., 2000; Yip et al., 2018) as intraspecific variability of markers depend on each species (Andrade-Sorcia et al., 2014; Bae et al., 2013; Chan et al., 2014; Chen et al., 2025; Ng et al., 2019; Want et al., 2023).

3.3 Geographical locations of *Sargassum* DNA barcoding studies

Sargassum DNA barcoding studies has been done in 55 locations worldwide (Fig 4). *Sargassum* DNA barcoding are mostly carried out in Asia, especially in China, Japan, and South Korea, which had 21, 25, and 12 studies respectively. Only one study is done in as much as 22 places from 55 (40%) of the locations. However, several studies were done in specific location to reevaluate or assess the diversity, estimate distributional range, and/or carry out comprehensive taxonomic revisions of *Sargassum* species, namely in French Polynesia (Mattio, Payri, & Stiger-Pouvreau, 2008), Madagascar (Mattio, Bolton, et al., 2015), western and central Pacific Islands (Mattio et al., 2009), Mauritius and Réunion islands (Mattio et al., 2013), South Africa (Mattio, Anderson, et al., 2015), Arabian Gulf of Kuwait (Hasan et al., 2023), New Caledonia (Mattio & Payri, 2009), South Korea (Cho et al., 2012), Caribbean Colombia (Camacho et al., 2015), and Atlantic Ocean (Siuda et al., 2024). Two barcoding studies were also done in Brazilian and Caribbean shores, as well as in the Atlantic Ocean, confirming that the *Sargassum* species that was stranded on those shores did not originate from the Sargasso Sea (Sissini et al., 2017) and was a form of holopelagic *Sargassum* species that was previously rare, namely *S. natans VIII* (Amaral-Zettler et al., 2017).

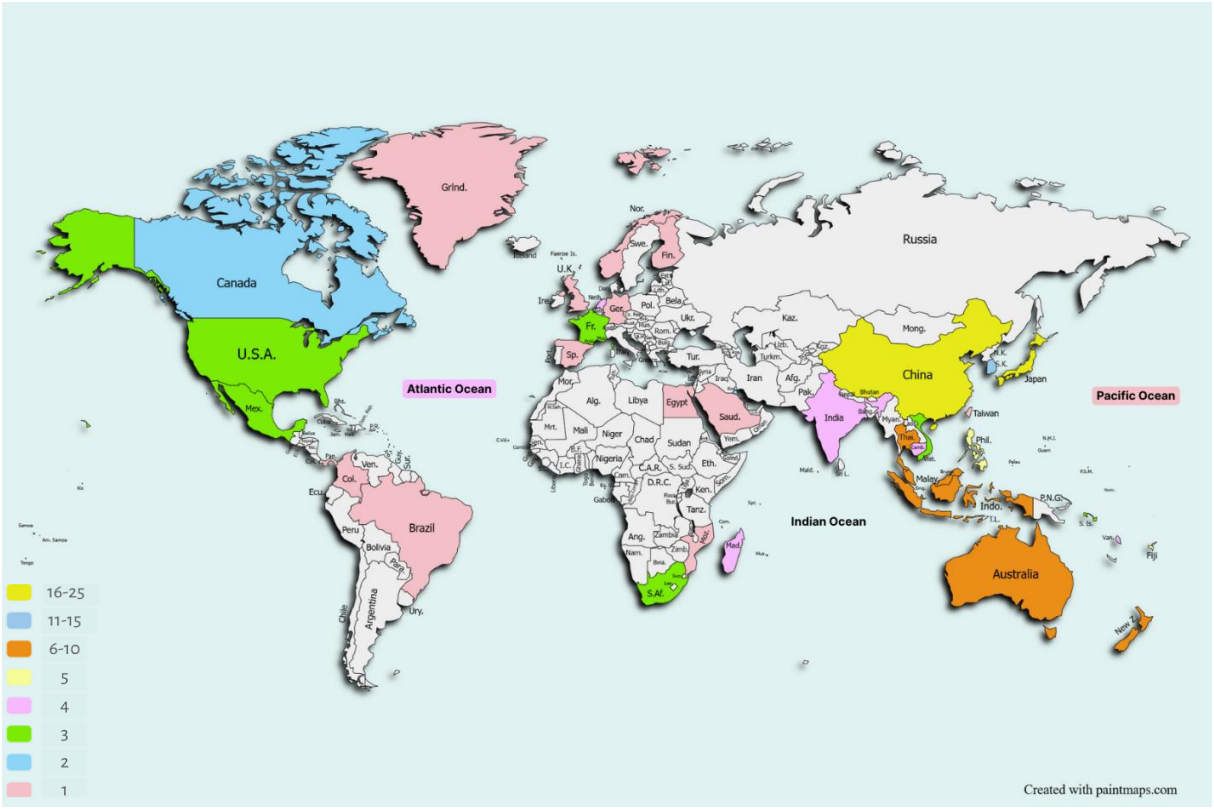

Figure 4. Location where *Sargassum* DNA barcoding studies have been conducted

3.4 *Sargassum* species studied on *Sargassum* DNA barcoding studies

From 89 *Sargassum* DNA barcoding studies, five most studied species are *S. polycystum* C. Agardh (Chan et al., 2013; Cho et al., 2012; Dixon et al., 2012, 2014; Dumilag et al., 2022; Ho et al., 1995; Z. Hu et al., 2018; Kantachumpoo et al., 2014, 2015; Mattio et al., 2009, 2013; Mattio, Anderson, et al., 2015; Mattio, Bolton, et al., 2015; Mattio & Payri, 2010, 2009; Phillips & Fredericq, 2000; Prasanthi et al., 2020; Santiañez et al., 2023; Saraswati et al., 2024; Stiger et al., 2000, 2003; Sulistiyani et al., 2022; C.-L. Wong et al., 2004; C. L. Wong et al., 2007; Yap-Dejeto et al., 2022; Yip et al., 2018), *S. horneri* (Turner) C. Agardh (Akita et al., 2020; Byeon et al., 2019; Cho et al., 2012; Dixon et al., 2014; Draisma et al., 2010; Hamaguchi et al., 2022; Horiguchi & Yoshida, 1998; Z. M. Hu et al., 2011; Huang et al., 2017; Lee et al., 2011; J. Li et al., 2020; Liu et al., 2018; Nakano et al., 2017; Oak et al., 2002; Stiger et al., 2000, 2003; Uwai et al.,

2009; Wang et al., 2024; Watanabe et al., 2019; Xia et al., 2023; Zhang et al., 2019; Zhuang et al., 2021), *S. muticum* Yendo (Fensholt) (Akita et al., 2020; Ali Alshehri et al., 2019; Bae et al., 2013; Cheang, Chu, Fujita, et al., 2010; Cho et al., 2012; Dixon et al., 2014; Draisma et al., 2001, 2010; Hamaguchi et al., 2022; Huang et al., 2017; Lee et al., 2011; Liu et al., 2013; McDevit & Saunders, 2009; Oak et al., 2002; Ortega et al., 2020; Phillips & Fredericq, 2000; Rousseau & De Reviers, 1999; Stiger et al., 2003; Want et al., 2023), *S. ilicifolium* (Turner) C. Agardh (Al-Adilah et al., 2020; Cho et al., 2012; Dixon et al., 2012, 2014; Draisma et al., 2010; Kantachumpoo et al., 2015; Mattio, Anderson, et al., 2015; Mattio, Bolton, et al., 2015; Mattio et al., 2009, 2010; Mattio & Payri, 2010, 2009; Ng et al., 2019; Ortega et al., 2020; Santiañez et al., 2023; Senggagau et al., 2025; Vieira et al., 2021; Yip et al., 2018), and *S. aquifolium* (Turner) C. Agardh (Al-Adilah et al., 2020; Chan et al., 2014; Cho et al., 2012; Dixon et al., 2012, 2014; Draisma et al., 2010; Hasan et al., 2023; Kantachumpoo et al., 2015; Mattio et al., 2009, 2010; Mattio & Payri, 2010, 2009; Rani, 2014; Santiañez et al., 2023; Saraswati et al., 2024; Wantania et al., 2025; Yip et al., 2018), which were recorded in 26, 22, 19, 18, and 17 studies respectively.

As the highest recorded *Sargassum* species, *S. polycystum*, has a wide distribution, spanning from warm tropical to temperate waters, ranging from the Indo-Pacific region to the Atlantic, Indian, and Pacific Ocean (Soe-Htun et al., 2012). Additionally, *S. ilicifolium* (Guiry & Guiry, 2021) and *S. aquifolium* (Guiry & Guiry, 2022b) also have wide distributions. *S. ilicifolium* is widely distributed from the cool-temperate locations in the Indo-West Pacific to tropical waters, which range from the very northern limit at southern Japan, Australia, and the Pacific Islands, Southeast and Southwest Asia, to Indian Ocean Islands, and to the eastern coasts of Africa (Ng et al., 2019). *S. aquifolium* can be found throughout the Indo-Pacific region, in both the tropical and subtropical regions (Chan et al., 2014; Mattio et al., 2009).

S. horneri can be found in the temperate waters of East Asia (Watanabe et al., 2019). *S. horneri* is well studied since it is the dominant species in the "golden tide" happening in Yellow Sea and East China Sea (Byeon et al., 2019; Z. M. Hu et al., 2011; Huang et al., 2017; J. Li et al., 2020; Liu et al., 2018; Wang et al., 2024; Watanabe et al., 2019; Xia et al., 2023; Zhang et al., 2019; Zhuang et al., 2021). *S. muticum* is native to East Asia, but is invasive to North America and Europe due to its high adaptability to diverse temperature and salinities (Bae et al., 2013; Want et al., 2023). In general, those studies shown that *Sargassum* species have a wide distribution, even though there are also endemic *Sargassum* species, such as *S. schnetteri* and *S. giganteum*, which can be found in the Tayrona National Natural Park in the northern coast of Caribbean Colombia (Camacho et al., 2015).

In total, there are 143 *Sargassum* species, forms, and varieties recorded across 89 *Sargassum* DNA barcoding studies (supplementary material), of which, only 109 are currently accepted taxonomically. A total of 25 species (17%) were unaccepted taxonomically, regarded as a synonym for another *Sargassum* species or genus. There are some species regarded as unsure from the study itself, unclear (still recorded as *Sargassum* sp.), uncertain (species name with "cf." or confer/ compare with), and unresolved (*S. vulgare*), all of which needed further investigation and study.

4. Discussion

There are two different periods in *Sargassum* taxonomy (Mattio & Payri, 2011), with the first one being the traditional taxonomy that uses morphological characteristics to distinguished between species, while the second one are the modern taxonomy that utilizes DNA markers. The earliest *Sargassum* molecular identification began with the usage of random amplified polymorphic DNA (RAPD) primers by Ho et al. (1995) that demonstrated the usefulness of RAPD-PCR in developing species-specific fingerprints, which is also confirmed by Yao et al. (2019) in a more recent study. While RAPD was also used in establishing *Sargassum* genetic structure (Zhao et al., 2007) and species identification (Wong et al., 2004, 2007), they had limited reproducibility and phylogenetic applications. Studies then utilized other markers (e.g., 18S, LSU, and SSU rDNA) to infer *Sargassum* phylogenetic relationships (Horiguchi & Yoshida, 1998; Phillips & Fredericq, 2000; Rousseau & De Reviers, 1999; Stiger et al., 2000), with the study by Stiger et al. (2000) resulted in a taxonomic revision of the section *Phyllocystae*. These early approaches influenced the transition toward modern DNA barcoding markers. *Sargassum* DNA barcoding studies became more popular as time went by, since it is an accurate and reliable method of identifying the otherwise phenotypically plastic *Sargassum*, with the total studies recorded from 1995-2025 amounted to 89 publications.

A diverse usage of markers in *Sargassum* DNA barcoding studies is likely because of the low genetic divergence of *Sargassum* species. For example, Bae et al. (2013) noted that cox3 is a more suitable marker than ITS2, trnW-I, and rubisco spacer, in understanding the haplotypic diversity of *S. muticum*. On the other hand, Hasan et al. (2023) confirmed that ITS2 marker were able to elucidate the phylogenetic relationship of the family *Sargassaceae*, including *Sargassum* species. However, Amaral-Zettler et al. (2017) noted that the usage of standard popular markers in *Sargassum* DNA barcoding, such as, ITS2, rbcLS, cox3, mtsp, etc., were not enough to resolve the phylogenetic relationships between the closely related holopelagic *Sargassum* species. Instead, the novel cox2 and cox3 primer sets designed by Amaral-Zettler et al. (2017) were able to differentiate between the closely related species.

With varying divergence in different species, studies begin to combine the usage of nuclear ITS2, chloroplastic partial rubisco, and mitochondrial cox3 and 23S to obtain better comparative datasets (Mattio et al., 2013). With that method, Mattio, Bolton, et al. (2015) were able to delineate 11 taxa including seven new records of *Sargassum* species in Madagascar. Chloroplast marker, namely rbcL were able to elucidate cryptic species of Japanese red algae, *Polysiphonia harveyi* (McIvor et al., 2001). Although, the study by Cheang, Chu, Fujita, et al. (2010) using rbcL did not identify cryptic species in native or introduced population of the invasive *Sargassum muticum*. Rather, it was mitochondrial markers, namely cox1 as well as tRNA W- L spacer (trnW- L) and cox3 markers, that were able to distinguished cryptic species in *Sargassum* (Z. Hu et al., 2017; Lin et al., 2024). In summary, the fixed polymorphism in mitochondrial markers (Amaral-Zettler et al., 2017) made the mitochondrial markers (e.g., cox1, cox2, cox3, tRNA W-L spacer) better in elucidating closely related *Sargassum* species and distinguishing cryptic species, compared to nuclear (e.g. ITS2) and chloroplast (e.g. rbcL). Nevertheless, a multigene approach might be better in inferring phylogeographic pattern and delineating *Sargassum* species, since different marker works differently for each species.

Studies applied the phylogenetic/ molecular analyses from various DNA markers (e.g., ITS2, rbcLS, cox3, mt23s) along with morphological examinations to challenge

the traditional classification and phylogenetic relationships of *Sargassum* species, which resulted in various taxonomic revisions (Mattio & Payri, 2011). Two major outcomes were the synonymization trend of *Sargassum* species (Huang et al., 2017; Mattio et al., 2009; Mattio, Anderson, et al., 2015; Mattio, Payri, & Stiger-Pouvreau, 2008; Mattio & Payri, 2009) and subgenus/ section restructuring (Dixon et al., 2014; Mattio et al., 2009, 2010).

Aside from taxonomic revisions, most *Sargassum* DNA barcoding studies yielded phylogenetic trees showing the taxonomic relationships between (Ali Alshehri et al., 2019; Álvarez-Canali et al., 2024; Amaral-Zettler et al., 2017; Andrade-Sorcia et al., 2014; Bast et al., 2016; Bhushan, 2013; Camacho et al., 2015; Chan et al., 2014, 2013; Cheang, Chu, & Ang, 2010; Cheang, Chu, Fujita, et al., 2010; Chen et al., 2025; Cho et al., 2012; Dibner et al., 2022; du Preez et al., 2021; Dumilag et al., 2022; Z. Hu et al., 2017; Kang & Nam, 2016; Kantachumpoo et al., 2015; Lee et al., 2011; J. Li et al., 2020; Liu et al., 2018; Mattio et al., 2013; Mattio, Bolton, et al., 2015; Mattio & Payri, 2010; Ng et al., 2019; Oak et al., 2002; Phillips & Fredericq, 2000; Rani, 2014; Santiañez et al., 2023; Saraswati et al., 2024; Shimabukuro et al., 2015; Sissini et al., 2017; Siuda et al., 2024; Stiger et al., 2000; Sulistiyani et al., 2022; Wang et al., 2024; Wantania et al., 2025; C.-L. Wong et al., 2004; C. L. Wong et al., 2007; Xia et al., 2023; Yap-Dejeto et al., 2022; Yip et al., 2018, 2020; Zhang et al., 2019) and beyond (Dixon et al., 2012; Draisma et al., 2001, 2010; Hasan et al., 2023; Horiguchi & Yoshida, 1998; McDevit & Saunders, 2009; Ortega et al., 2020; Prasanthi et al., 2020; Rousseau & De Reviers, 1999; Stiger et al., 2003; Yap-Dejeto et al., 2022) the *Sargassum* species itself, while others only identified the *Sargassum* species (Akita et al., 2020; Al-Adilah et al., 2020; Bae et al., 2013; Hamaguchi et al., 2022; Z.-M. Hu et al., 2013; Z. Hu et al., 2018; Z. M. Hu et al., 2011; Kantachumpoo et al., 2014; Kouduka et al., 2017; J.-J. Li et al., 2017; J. Li et al., 2017; Lin et al., 2024; Liu et al., 2013; Nakano et al., 2017; Peoples et al., 2024; Senggagau et al., 2025; Soliman & Tawfik, 2021; Uwai et al., 2009; Want et al., 2023; Watanabe et al., 2019; Weng et al., 2024; Yu et al., 2024; Zhuang et al., 2021). Papers that provided phylogenetic tree that showed taxonomic relationship between *Sargassum* species were the studies that were conducted on one or more species of *Sargassum*. On the other hand, those that showed taxonomic relationship beyond *Sargassum* species were done with *Sargassum* species and other macroalgae species, mostly still under Phaeophyceae. Single *Sargassum* species studies that provided phylogenetic tree often provided information and analyses on haplotypes clades and/or phylogeographic analyses of the certain species on certain areas (Bae et al., 2013; Chan et al., 2013, 2014; Cheang, Chu, & Ang, 2010; Cheang, Chu, Fujita, et al., 2010; Chen et al., 2025; Dumilag et al., 2022; Z.-M. Hu et al., 2013; Z. Hu et al., 2017, 2018; Z. M. Hu et al., 2011; Kantachumpoo et al., 2014; J.-J. Li et al., 2017; J. Li et al., 2017, 2020; Lin et al., 2024; Liu et al., 2018; Ng et al., 2019; Uwai et al., 2009; Wang et al., 2024; Watanabe et al., 2019; Zhang et al., 2019; Zhuang et al., 2021).

Alternately, studies that only identifies the species of *Sargassum* itself are often either trying to identify *Sargassum* diversity from certain areas, or from other interesting studies. For example, *Sargassum* species were identified via metabarcoding (Weng et al., 2024) in seagull's diet (Yu et al., 2024), in the guts of both the deep sea isopod, *Bathyopsurus nybelini* (Peoples et al., 2024) and the sea urchin, *Hemicentrotus pulcherrimus* (Nakano et al., 2017), from the shell surface of the limpet, *Niveotectura pallida* (Akita et al., 2020), and from the late Pleistocene marine sediments (Kouduka et al., 2017).

As mentioned before, the advancements of *Sargassum* DNA barcoding studies resulted in a more accurate species identification as well as taxonomy revisions. Such taxonomic resolutions ensure proper identification, leading to ecological applications, such as tracking invasive species and blooming events, detecting and confirming range shifts, as well as monitoring holopelagic *Sargassum* species. For example, *Sargassum polyporum* Montagne has been recorded in South Korea waters for the first time after previously only reported in several east Asian countries such as China and Japan (Kang & Nam, 2016). A study confirming the presence of *S. muticum*, which was a non-native species, in the north of Scotland, suggesting invasiveness and the trends of this *Sargassum* species spreading northwards due to global warming (Want et al., 2023).

In 2015, accumulations of *Sargassum*, "golden tide" happening in coastal regions of Brazil, Caribbean islands, and western Africa prompted investigation and research on whether it originated from floating *Sargassum* masses in the Sargasso Sea. Research shown that the golden tide in the Gulf of Mexico did not come from the Sargasso Sea, based on seven consecutive years of satellite imaging on pelagic *Sargassum* (Sissini et al., 2017). As mentioned before, the study by Amaral-Zettler et al. (2017) successfully delineate two *S. natans* forms (*I* and *VIII*) from each other and both from *S. fluitans III*, all of which constitute as the holopelagic *Sargassum* species found in the Sargasso Sea. *S. natans* and *S. fluitans* are the only recognized holopelagic species that drift and did not attach to substrates, creating floating pelagic biome in minimal substrate and low nutrient open ocean waters (in the North Atlantic Ocean subtropical gyre; North Equatorial Recirculation Region – NERR) that supports more than 100 species of invertebrates and fishes, including ten endemic species (Amaral-Zettler et al., 2017; Laffoley et al., 2011).

Just as the holopelagic *Sargassum* species in the Sargasso Sea, *Sargassum* species in general have important ecological role, especially in forming seaweed beds and underwater forests that acted as habitats and food sources of various numerous organisms, including local carbon sequestration (Chen et al., 2025; Cheung-Wong et al., 2022; Jung et al., 2020; Matsui et al., 2025; Sun et al., 2025). However, *Sargassum* species could also pose as an ecological threat for biodiversity, especially through introduction events for invasive *Sargassum* species like *S. muticum* (Mattio et al., 2009). *S. muticum* is a well-known invasive species that originated from the northwest Pacific region (Ali Alshehri et al., 2019) and found introduced to the northwestern Pacific of North America in 1944 (Critchley et al., 1990) and on the Atlantic coasts of Europe in 1973 (Critchley et al., 1983). The distribution of *S. muticum* in the UK waters continued to spread westward and northward (Davison, 2009), and recorded in Scotland by 2004 (Want et al., 2023). Recently, a study recorded the existence of *S. muticum* in the northern coast of Scotland (Want et al., 2023). The introduction of *S. muticum* through the oceans, for North America and Europe respectively, was most possibly through the farmed Pacific oyster, *Crassostrea gigas* (Critchley et al., 1990) that was imported from Japan (Critchley et al., 1983; Mineur et al., 2007) and both Japan and British Columbia, Canada (Farnham et al., 1973; Grizel & Héral, 1991).

Establishment of *S. muticum* in new habitats harm existing dominant seaweed (Engelen et al., 2015) and may

reduce/ lower ecosystem complexity along with local biodiversity (Engelen et al., 2015; Stæhr et al., 2000). *S. muticum* has been a focus of study (Ali Alshehri et al., 2019; Bae et al., 2013; Cheang, Chu, Fujita, et al., 2010; Want et al., 2023) because of their anthropogenic dispersal and range that extend in the northeast Pacific and/or Atlantic Ocean (Cho et al., 2012), and was reported to be able to reproduce in a temperature as low as 7˚C (Steen, 2003). Moreover, *S. muticum* has the potential to become a golden tide species under the right circumstances (Yan et al., 2021). Nevertheless, a study by Rossi et al. (2019) showed that even though *S. muticum* had negative impact on the native species – in terms of reduced carbon storage capacity – the contribution of *S. muticum* itself counterbalanced such impact. The world is losing its "lungs" for carbon sinks due to global warming events, even though these "lungs" are needed to combat the said climate change. Therefore, as an organism that can sequester carbon and has high adaptive ability, we propose *S. muticum* as a model organism to be studied for its wide adaptability despite climate change and global warming.

In summary, the progression of *Sargassum* taxonomy from morphology-based classification to DNA-based approaches has substantially improved species identification and phylogenetic resolution in this highly phenotypically plastic genus. Even though studies indicated that mitochondrial markers are often superior in delineating between closely related *Sargassum* species, no single marker is universally effective across all *Sargassum* species, emphasizing a methodological limitation and the need of a multigene approach for a more robust species delimitation and phylogeographic inference. These molecular advances lead to taxonomic revisions, including synonymization, subgenera restructuring, as well as ecological applications. Future research should prioritize multimarker barcoding with expanded geographic sampling to refine taxonomic resolution and better link *Sargassum* systematics with its ecological and biogeochemical significance under ongoing climate change.

5. Conclusions

As of this review, a data compilation of the geographical locations, primers used, and species studied from 89 *Sargassum* DNA barcoding researches has been made. *Sargassum* DNA barcoding studies have been done in 55 locations, with only one study done in each 22 (40%) of those locations. It frequently used five genetic markers, ITS2, cox1, cox3, rbcL, and rbcLS, out of 38 recorded markers. The species studied only reached 109 (30.6%) out of 356 taxonomically accepted *Sargassum* species. Without *Sargassum* DNA barcoding researches that are evenly carried out, several applications such as taxonomic resolutions, biodiversity assessment, and other ecological applications (e.g., invasive species detection and monitoring) would not be accurate and bias-free. Hence, it is important for future *Sargassum* DNA barcoding studies to expand and cover previously understudied geographical locations, conduct barcoding studies with multi-marker approach to ensure accurate species delimitation, as well as integration with ecological and invasion studies to improve understanding whether proper invasive species control can combat global warming and climate change. This review contributes to the advancement of *Sargassum* systematics by providing an overview of the current status of *Sargassum* DNA barcoding studies and clarifying research gaps for future research directions and efforts.

Ethics approval

No permits were required.

Data availability statement

The database consisting of the results of this review can be accessed through the supplementary materials.

Author contributions

AC was responsible for conceptualization, data curation, methodology, resources, software visualization, as well as writing and editing. SRA and MUKA contributed to conceptualization, supervision, validation, formal analysis, as well as review & editing.

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Declaration of competing Interest

None

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