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REVIEW

A review of autonomous reef monitoring structures (ARMS) for monitoring hard-bottom benthic biodiversity

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Abstract

1. Amid increasing anthropogenic pressures on ecosystems, standardised biodiversity monitoring is critical for assessing biodiversity change. Marine hard-bottom habitats, though ubiquitous and biodiverse, present challenges for biodiversity monitoring due to their complex structure and limited accessibility. Autonomous reef monitoring structures (ARMS) have been developed to standardise marine hard-bottom biodiversity monitoring across sites and research groups.
2. This review analyses the methodological approaches utilised to date, spatial distribution, and temporal coverage of ARMS research across 49 publications.
3. Variation in deployment, retrieval, replication strategy, and processing of ARMS was observed, presenting a barrier to study interoperability. Spatial coverage is biased to coral reef ecosystems and the Northern Hemisphere but is expanding globally. Irregular deployment timing and overall deployment durations constrain temporal coverage across sites and biogeographical regions, with few studies exploring the influence of deployment timing and duration on ARMS' community composition. Genetic methods, namely, DNA barcoding and metabarcoding, dominate community composition analyses but there is significant variation in methods of DNA extraction, PCR protocols, target genes, sequencing platforms, and bioinformatic pipelines. Furthermore, images of ARMS' plates are an underutilised resource for biodiversity investigations and rarely used in conjunction with genetic analyses.
4. This review highlights the need for greater standardisation and reporting consistency in ARMS research to improve study interoperability and reproducibility to enable global biodiversity monitoring in our changing world.

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KEYWORDS
autonomous reef monitoring structures, benthos, colonisation, hard substrata, marine biodiversity, metabarcoding, monitoring, standardisation

1 | INTRODUCTION

Human activity is driving unprecedented change in global biodiversity (IPBES, 2019). To inform policy and conservation, it is necessary to identify baseline spatial and temporal patterns of biodiversity and how they are changing (Dornelas et al., 2014). Marine benthic communities support rich biodiversity, are globally ubiquitous (Eddy et al., 2021; Waycott et al., 2009), and are of major socio-economic importance (Crespo & Pardal, 2022; Fitridge et al., 2012; Santavy et al., 2021). It is, therefore, vital that benthic biodiversity is monitored using accurate and standardised methods. While soft-bottom benthic communities have been widely surveyed, hard-bottom communities remain underrepresented in biodiversity research (David et al., 2019), which can be attributed to their complex three-dimensional structure and limited accessibility. These sampling difficulties have led to the implementation of less standardised monitoring methods for hard-bottom habitats relative to soft-bottom habitats (Bianchi et al., 2004).

Multiple methods have been developed for sampling marine hard-bottom biodiversity. One approach involves the collection of natural substrata and analysing associated biota (Keklikoglou et al., 2018). In coral reefs, for instance, dead corals have been retrieved and invertebrate diversity assessed as a proxy for reef diversity (Plaisance et al., 2009; Head et al., 2015). However, since dead corals (and other natural substrata) serve as important habitats for biodiversity, their removal from ecosystems is considered destructive and often undesirable (Horoszowski-Fridman et al., 2024). Another approach is the in situ collection of organisms from natural substrata. SCUBA divers, using brushes or suction devices, for example, can dislodge and collect marine organisms from rocks and debris (Coolen et al., 2018; Jørgensen & Gulliksen, 2001; Morley et al., 2022; Templado et al., 2010). However, these methods can damage soft-bodied organisms, preventing accurate morphological identification, and motile species may escape capture (Keklikoglou et al., 2018). Alternatively, divers can perform visual surveys or use cameras for image-based analyses, but these methods often miss cryptic biota which in coral reefs, for example, can account for the majority of biodiversity (Dennis & Aldhous, 2004; Knowlton et al., 2010; Plaisance et al., 2011b). Moreover, because the properties of natural substrata (including size, shape, material, and surface texture) influence biodiversity and are highly variable, visual surveys, in situ collection of biota, and the collection of natural substrata all lack standardisation (Gallucci et al., 2020; Romoth et al., 2023). In contrast, deploying artificial structures offers a non-destructive and standardised approach that can be used to sample hard-bottom biodiversity (Bowden et al., 2006; Leray & Knowlton, 2015; Obst et al., 2020).

Artificial structures are deployed on the seafloor, colonised by benthic biota over time, and retrieved for analyses of the biotic communities they support. They can be used to investigate biodiversity and/or to detect non-indigenous species. When implemented to a consistent design artificial structures promote the collection of standardised data within studies. However, this is often not the case across studies. For example, 3D-printed ceramic tiles with sculpted surfaces have been deployed in coral reefs in the Red Sea (Levy et al., 2023) while polyethylene artificial seaweed systems have been deployed in rocky reefs in Spain (Carreira-Flores et al., 2023). To address this issue, Autonomous reef monitoring structures (ARMS) have been developed with the aim to standardise marine hard-bottom biodiversity sampling across research groups (https://naturalhistory.si.edu/research/global-arms-program).

During their initial conception, in 2004, ARMS (at the time standing for 'Artificial Reef Matrix Structures') was constructed from polyvinyl chloride (PVC) pipes, concrete, nylon cleaning pads, and coral rubble (Zimmerman & Martin, 2004). However, these structures were not deemed suitable for large-scale applications (Knowlton et al., 2010). Subsequently, in 2006, during the international Census of Marine Life (CoML) initiative, an ARMS prototype was developed by the United States National Oceanic and Atmospheric Administration's (NOAA) Coral Reef Ecosystem Division and the Smithsonian Institution, USA. This prototype consisted of stacked PVC plates with openings of various sizes that allowed colonisation of both internal and external structures (Plaisance et al., 2011a; Yang et al., 2023). This original design has since been simplified to a stack of nine PVC plates (plates are 22.5 cm ×22.5 cm ×0.63 cm) with alternating 'open' and 'closed' layers (Yang et al., 2023; Figure 1). Although the standardised design consists of nine plates, some ARMS have been constructed with 10 plates but follow the same overall design principles (Leray & Knowlton, 2015). Open layers utilise nylon spacers to create a 1.27 cm space between plates, while closed layers consist of PVC crossbars (similarly 1.27 cm in height) that inhibit water flow through the layer. Although initially designed for use in coral reefs, the tiered ARMS design has been deployed across a range of marine ecosystems and has an increasingly global application (Figure 2).

Multiple protocols exist for the use of ARMS, but all follow broadly similar steps (Al-Rshaidat et al., 2016; Obst et al., 2020; Yang et al., 2023). Generally, ARMS are held in place on the seabed with weights or metal stakes. Following a period of colonisation and succession, ARMS are retrieved via SCUBA. During retrieval, the use of a cover lined with a fine mesh is recommended to prevent the escape of motile fauna. Once recovered, ARMS units are disassembled and motile fauna are separated from the ARMS' plates and filtered into three size classes (>2000, 500–2000, 100–500/106–500 μm). Both the upper and under sides of ARMS' plates

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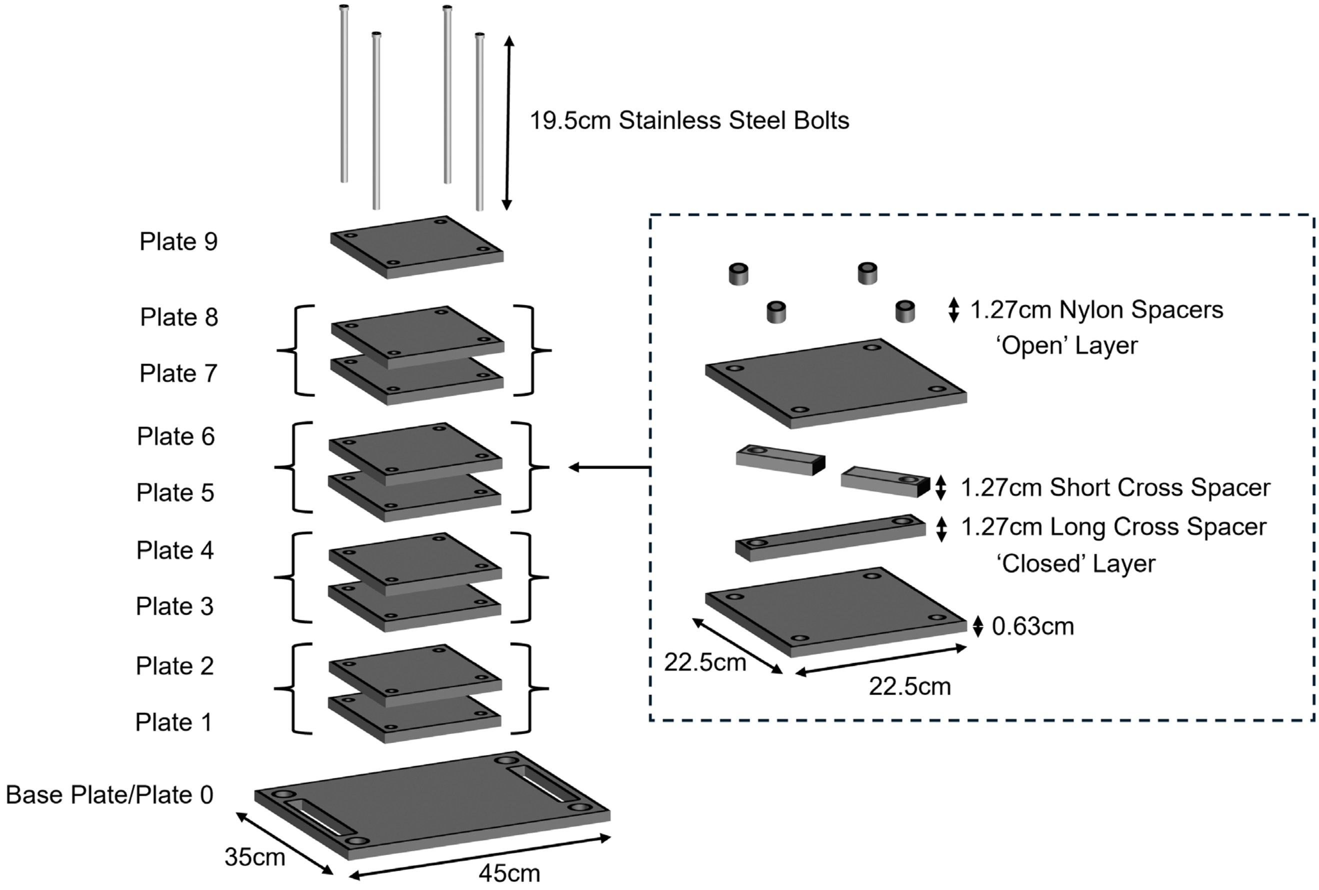

FIGURE 1 Construction of autonomous reef monitoring structures (ARMS; re-drawn from Smithsonian National Museum of Natural History, available at: https://naturalhistory.si.edu/research/global-arms-program/protocols). ARMS consist of alternating 'closed' and 'open' layers. Short and long cross-spacers form 'closed' layers that inhibit water flow, while nylon spacers create 'open' layers that allow water flow. Flat washers and nylon insert lock nuts are used with the stainless steel bolts, but these have not been illustrated for clarity.

are photographed and high-resolution photography of unique sessile individuals or colonies is recommended. ARMS' plates are then carefully scraped to remove the 'sessile fraction' which is homogenised for DNA metabarcoding, a genetic method for the simultaneous identification of multiple specimens in a single mixed sample using amplification and sequencing of a short DNA fragment widely conserved across multiple taxonomic groups. Motile fractions are similarly analysed via DNA metabarcoding, though some protocols recommend DNA barcoding, a genetic method for the identification of individual specimens using amplification and sequencing of a short DNA fragment, for specimens greater than 2000 μm. Alternatively, individual specimens may be identified morphologically. For DNA metabarcoding, both fragments of the mitochondrial cytochrome *c* oxidase subunit I gene (hereafter COI) and of the nuclear 18S rRNA gene (hereafter 18S) are most often targeted. Current recommendations for preservation, metabarcoding, and taxonomic assignment were shaped by Leray and Knowlton (2015) and Ransome et al. (2017) but differ between publications and ARMS protocols.

The ability to pair ARMS with genetic methods provides a major advantage over visual census methods in biodiversity research (Obst et al., 2020). Specifically, publications combining metabarcoding and visual analyses identify a greater range of phyla and have improved capacity for the identification of cryptic phyla (Pearman et al., 2016). Genetic methods can also enhance the detection of non-indigenous species, especially at the very earliest stages of colonisation (Comtet et al., 2015; Xiong et al., 2016). While ARMS and metabarcoding offer clear advantages for biodiversity research, both approaches also present logistical and methodological challenges: the deployment and retrieval of ARMS typically require SCUBA and repeated site visits; biotic communities that develop on artificial substrata, such as ARMS, can differ from those on natural substrata; and metabarcoding results can be affected by biases in primer design, gaps in reference databases (which limit the accuracy of taxonomic assignments), and bioinformatics pipelines applied.

When selecting a methodological approach for biodiversity monitoring, the advantages and disadvantages of each method must be carefully balanced. Standardised methodologies are critical for cross-study data integration, which is in turn critical for recognising patterns of biodiversity change on multiple spatial and temporal scales (Kissling et al., 2015). Accordingly, ARMS have been used to form the basis of international biodiversity monitoring programmes

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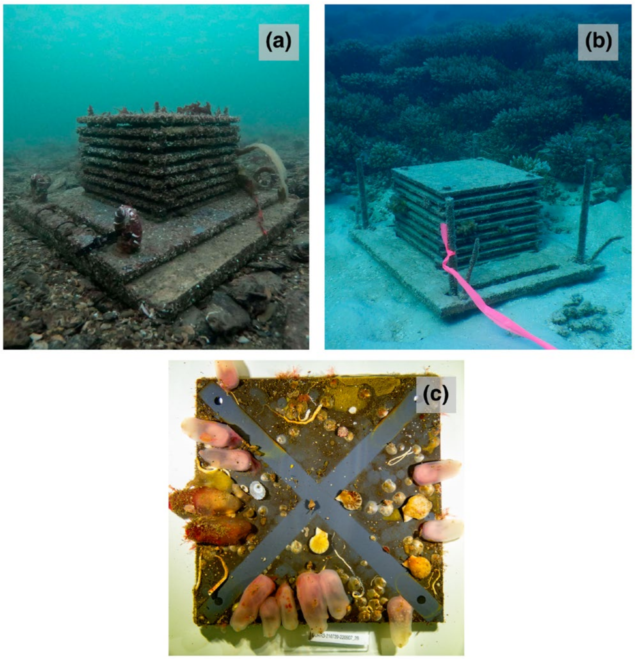

FIGURE 2 Autonomous reef monitoring structures (ARMS). (a) ARMS mounted on a concrete base plate, photographed after a 10-month deployment period in Plymouth Sound, United Kingdom. Photograph by A. Jessop (2024). (b) ARMS secured to seabed with metal stakes, photographed after a 3-year deployment period at Île du Coin, Peros Banhos Atoll, Chagos Archipelago. Photograph by M. Steyaert (2021). (c) ARMS' plate photographed after a 1-year deployment period in Galway, Ireland. Photograph by D. Nowak (2021).

(Obst et al., 2020). Nonetheless, there exists significant variation in the implementation of ARMS as biodiversity monitoring tools. In this review, we provide a comprehensive resource documenting the use of ARMS in biodiversity monitoring to date. We critically examine methodological approaches and offer recommendations for standardised protocols to enhance study interoperability with the aim of promoting more consistent global research efforts. Specifically, we address the research question: How have ARMS been implemented in biodiversity research to date and what methodological considerations are most critical for improving standardisation across studies?

2 | METHODS

2.1 | Literature search

To generate a list of relevant publications, we retrieved all peer-reviewed research articles listed on the Global ARMS Programme website (available at: https://naturalhistory.si.edu/research/global-arms-program; accessed 1 February 2025) and relevant publications returned by the Web of Science literary repository (available at: https://www.webofscience.com/wos/woscc/basic-search; accessed 1 February 2025) and Google Scholar (available at: https://scholar.google.com/; accessed 1 February 2025) when using the exact search phrase 'Autonomous Reef Monitoring Structures' ($n=70$). Publications that did not describe any novel ARMS research (e.g., were entirely prospective in nature; $n=6$), or that utilised ARMS as a tool for ecosystem restoration have been excluded from analyses ($n=4$). The Zimmerman and Martin (2004) publication describing Artificial Reef Matrix Structures and two publications utilising prototype ARMS have also been excluded. Thus, the initial starting sample size for this review was 57 publications, which were subsequently reduced to 49, as described below. A list of data sources used in this study is provided in the Data sources section.

2.2 | Data collation

All data were stored in five, interrelated datasets (publicly available at: https://doi.org/10.5281/zenodo.17226696). Each dataset contained metadata relevant to (i) the entire study; (ii) sites at which ARMS have been deployed; (iii) unique ARMS deployment events; (iv) where DNA barcoding or metabarcoding has been implemented, the distinct fractions of the biotic community being analysed; and (v) the molecular protocols used (Jessop et al., 2025). For all data fields, where multiple values were provided (e.g., a range of depths), the mean value was used to populate the dataset. As multiple publications have used data derived from the same sites or ARMS units, duplicate data entries have been merged.

2.2.1 | Methodological approach

As multiple ARMS designs have been implemented in the past, we recorded the dimensions of ARMS (number of plates and plate size) used in each publication. Personal communication was used to confirm ARMS design if not clearly stated in the text or visible in photographs. Only publications based on tiered nine or 10 plate ARMS (49 publications) were included in downstream analyses. In addition, each publication was categorised by its primary research objectives. The research objectives used for categorisation are biodiversity monitoring; non-indigenous species detection; methodological development; assessment of ecosystem function; and phylogenetic analysis.

To assess variation in methodological approach between publications, we recorded (i) the mode of attachment to the seafloor; (ii) whether ARMS or individual ARMS' plates were used as the unit of replication; (iii) the number of replicate ARMS; (iv) whether a cover was used to trap motile fauna during recovery; and (v) whether barcoding, metabarcoding, image analyses, morphological identification, or a combination of multiple approaches were used for analysing community composition. All unique coordinates given for the locations of ARMS deployments were considered to represent unique sites. ARMS were considered replicates if deployed at the same site with matching months of deployment and retrieval. Granularity to the day of deployment was not possible when defining replicates as timing was typically reported only to the month and year.

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For publications incorporating image-based analyses of plates, we recorded the method used (i.e., random point count or visual scanning) and noted the use of any automated software. For publications utilising genetic methods (either DNA barcoding or metabarcoding), we recorded the fraction type assessed (e.g., sessile and/or motile), and if appropriate, the size of the fraction (e.g., greater than 2000, 500–2000 or 100–500 μm) analysed. Additionally, we recorded the preservative used for storage of biological material; the storage temperature; and the commercial kit or method used for DNA extraction. Where DNA metabarcoding was used, we recorded the targeted marker gene(s); the specific primers used; and the sequencing platform. Primers are short single strands of DNA designed to highly conserved regions of the DNA across species, which are used to target the short DNA barcodes during polymerase chain reaction (PCR) amplification. Primers can be designed to be species-specific or 'universal' across groups of taxa, depending on the aims of the studies. Further, we have quantified the number of distinct PCR mixes and thermocycling protocols used for DNA metabarcoding of the COI and 18S genes. As only three publications targeted the nuclear 16S rRNA gene of prokaryotes (hereafter 16S), two publications targeted fragments of the internal transcribed spacer region (hereafter ITS), and a singular publication targeted the nuclear 23S rRNA gene (hereafter 23S), molecular methods for these genetic targets are not compared.

2.2.2 | Spatial, temporal, and taxonomic coverage of ARMS research

To develop an improved understanding of where and when ARMS have been deployed, we collated data on the spatial, temporal, and taxonomic coverage of published ARMS research. Namely, we collated data on the number of sites investigated; the coordinates and depth of those sites; the dates of deployment and retrieval; and the focal taxonomic group(s) of the investigation. Individual ARMS identified as lost or otherwise not retrieved have been omitted from analyses. To assess the global distribution of ARMS research in a biologically informative manner, we related site coordinates to the Marine Ecoregions of the World (MEOW) characterised by Spalding et al. (2007). The MEOW system divides coastal and shelf areas into nested realms, provinces, and ecoregions based on their biogeographic characteristics; 12 realms, 62 provinces, and 232 ecoregions are described (Spalding et al., 2007).

2.2.3 | Data management

For all publications, we noted the availability of sequence data, the availability of photographs of ARMS plates, and the data repositories used where applicable. Further, we recorded whether bioinformatic pipelines for DNA metabarcoding were reproducible considering the availability of code and in-text descriptions of the workflow.

3 | RESULTS

3.1 | Methodological approach

3.1.1 | Design of ARMS

Implementation of standardised ARMS, consisting of nine PVC plates and an individual plate size of 22.5 cm × 22.5 cm, was confirmed directly from publications for only 21 of 57 cases (Jessop et al., 2025, dataset on ARMS publications). Four publications used ARMS consisting of 10 plates and a further seven publications have utilised modified ARMS with three, four, or six plate designs (often, but not exclusively, contained in mesocosms). An additional, singular publication implemented both modified three-plate and standard nine-plate ARMS. Further, multiple publications referenced the artificial reef matrix structure (Zimmerman & Martin, 2004) as opposed to the autonomous reef monitoring structure (https://naturalhistory.si.edu/research/global-arms-program) when detailing ARMS units. Although these publications were likely to be based on the standardised ARMS described by the Smithsonian Institution this could not be confirmed from publications directly unless photographs or detailed text descriptions were also provided. Similarly, multiple publications referenced 10 plate ARMS designs despite having implemented nine plate ARMS (as confirmed via text descriptions, photographs, or personal communication). Personal communication confirmed that 45 of 57 publications implemented ARMS with nine plates. The reporting of individual plate size ranged from 22 cm × 22 cm to 23 cm × 23 cm. Discrepancies in plate size could be attributed to approximation and conversion between metric and imperial units. The difference in colonisable surface area per complete unit is 765 cm^2 between ARMS of 22 cm × 22 cm and 23 cm × 23 cm plate size, so not an inconsequential difference.

The seven publications based exclusively on modified three or four plate ARMS, and the three-plate ARMS of the singular publication implementing both three- and nine-plate ARMS, were not included in analyses beyond this point. An additional publication, for which ARMS design could not be confirmed, was also excluded from further analyses. Hence, the resulting data set retained for further interrogation comprised 49 publications.

3.1.2 | Replication

Across the 49 retained publications, 892 unique ARMS deployments were described (Jessop et al., 2025, dataset on ARMS deployments). For most publications, individual ARMS (45 publications) as opposed to individual plates (one publication) were treated as the unit of replication. Replication strategies were not implemented in three publications. Publications without replication evaluated target species' evolutionary history or presence/absence within a site. Despite most publications treating individual ARMS as the unit of replication, 179 ARMS deployments (20% of total) did not meet our criteria for replication (deployed in

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the same site, with matching months of deployment and retrieval). This result can be attributed to inconsistent spacing and variation in the timing of ARMS' deployment/recovery. Furthermore, due to insufficient reporting of metadata, it was not possible to confirm if there was any replication amongst 127 ARMS deployments (14% of total).

Triplicate ARMS have been deployed in 180 unique site and date combinations (540 ARMS or 61% of total). However, spacing between replicate ARMS was inconsistent. Distance between units deployed in the same site ranged from 2 to 10 m, but exact spacing was often not reported, was approximated, or was provided as a range of values. To date, no publications have comprehensively investigated the effects of distance between ARMS on ARMS' community composition.

3.1.3 | Deployment and recovery

ARMS have typically been held in place on the seabed via metal stakes or weights such that the baseplate is in direct contact with the seafloor. However, some ARMS have been deployed atop concrete or other structures that created a layer of separation between the ARMS' baseplate and the seafloor. Additionally, ARMS have occasionally been suspended mid-water above soft-bottom benthic habitats (e.g., hanging from pontoons) as part of a larger project (Obst et al., 2020). Specific deployment aims for these individual units have not been reported. One publication deployed ARMS in pelagic habitats, via attachment to offshore longlines (Villarino et al., 2025). However, only one of six deployed ARMS remained at target depth and was successfully retrieved. The pelagic ARMS supported a unique species assemblage when compared with ARMS deployed directly on the seabed (Villarino et al., 2025).

During recovery, the use of a mesh-lined crate to trap motile fauna was described in the methods of 18 publications (Jessop et al., 2025, dataset on ARMS publications; 37% of total). Four publications described the use of a crate, though whether a mesh was used in tandem is unknown. It is possible that these publications utilised solid covers with no routes of escape and thus a mesh cover was not necessary, but this remains unclear. Conversely, in five publications, only a mesh had been used to surround ARMS during recovery. Where mesh was used, the pore size was variable, ranging from 40 to 500 μm. The most common mesh pore sizes were 100 and 106 μm (equivalent to the sizes of the smallest motile fractions analysed), used in eight and seven papers, respectively. Mesh was used but pore size was not reported in four publications. Thus, the description of motile fauna was highly variable and inconsistent in methodology.

3.1.4 | Analysis of ARMS fractions

Morphological identification of organisms was employed in 35 of 49 publications but served as the sole source of biodiversity data in only seven publications (Jessop et al., 2025, dataset on ARMS publications). More often, morphological identification was integrated with photographic analyses of ARMS' plates and/or used to complement genetic methods (Table S1). Photographic records of ARMS' plates are reported for 32 of 49 publications, but image analyses were included in only 16 of these 32 publications (50%; Jessop et al., 2025, dataset on ARMS publications). Random point count was the most widely employed method for quantifying community composition from images (nine publications). Random point counts were semi-automated with CoralNet (https://coralnet.ucsd.edu/), Photoquad (Trygonis & Sini, 2012), and Coral Point Count with Excel extensions (Kohler & Gill, 2006). Estimates of percentage cover were reported in three publications and in one case supported using ImageJ (Schneider et al., 2012). In contrast, two publications relied on manual visual scanning by the investigator(s) to detect target taxa.

Metabarcoding approaches consistently captured greater biodiversity from ARMS than morphological or image-based methods, as demonstrated by six publications providing results suitable for cross-method comparisons (Jessop et al., 2025, dataset on ARMS publications). For example, at Close Encounters Reef, Bali, nine ARMS deployed across two sites and two sampling periods revealed 44 phyla with 18S metabarcoding, 32 phyla with COI metabarcoding, but only nine phyla via photo analysis of ARMS' plates (Casey et al., 2021). However, the reduced number of phyla detected from photo analysis in this publication reflects the use of predefined categories for taxonomic assignment (Casey et al., 2021). Nonetheless, analyses not constrained by the use of predefined categories showed similar patterns (Obst et al., 2020; Pearman et al., 2016; Thomasdotter et al., 2023). For instance, nine ARMS deployed at three sites in the Central Red Sea, yielded significantly greater diversity with 18S metabarcoding than photo analysis of ARMS plates (Pearman et al., 2016). Similarly, two ARMS from distinct European sites (Sweden and Greece) revealed much higher species richness from COI metabarcoding than photo analysis. Furthermore, there was little overlap in species observations between photo analysis and COI metabarcoding (8% and 4% species overlap respectively; Obst et al., 2020).

Although DNA metabarcoding of ARMS captured greater overall diversity, certain taxa were identified exclusively through morphological or image-based analyses. At Jeju Island, Korea, species of geniculate coralline algae, Mollusca, and Chordata were observed by photo analysis of ARMS' plates, but not detected through COI metabarcoding (Lee et al., 2024). Likewise, in a study of 27 ARMS deployed across nine sites in the Tyrrhenian and Northern Adriatic Seas, only one of 22 sessile species (*Ciona edwardsi*) identified from photo analysis of ARMS' plates was also detected by COI metabarcoding (Thomasdotter et al., 2023). Only one publication provided a direct comparison of species diversity captured by DNA barcoding versus morphological identification, but it is focused on Brachyuran and Anomuran crabs. DNA barcoding of specimens, targeting the COI gene, detected nine species, while morphological examination identified two additional taxa (Womacks & Janosik, 2023).

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3.1.5 | Genetic methods

Most publications used genetic methods to analyse ARMS' fractions (36 of 49 publications). Namely, 21 publications implemented DNA metabarcoding, 10 publications used DNA barcoding, and a further five publications combined DNA metabarcoding and barcoding (Jessop et al., 2025, dataset on ARMS publications).

Sample recovery and preservation

For genetic analyses, ARMS' biotic communities were typically divided into distinct fractions and analysed independently. Broadly, the biotic community was divided into motile and sessile fractions. Across the 36 publications to implement genetic methods, 1276 motile and 572 sessile fractions were described (Jessop et al., 2025, dataset on ARMS fractions). Some publications subdivided motile and sessile into unique subfractions, including Brachyuran and Anomuran crabs (18 fractions), exclusively Brachyuran crabs (three fractions), sponges (6 fractions), *Cirripectes* blennies (54 fractions), and the benthic photosynthetic community (considered in one publication to be the community occupying the top surface of the top ARMS' plate; 18 fractions). More commonly, motile fractions were split into three sizes: greater than 2000 μm (240 fractions), 500–2000 μm (326 fractions), and 100–500 μm (130 fractions) or 106–500 μm (318 fractions). Motile fractions have also been separated into 90–500 μm (five fractions), 125–500 μm (2 fractions), and 200–500 μm (one fraction) subfractions. Additionally, a greater than 500 μm subfraction (121 fractions) and a greater than 40 μm subfraction (3 fractions), have been used albeit not as commonly as the standard greater than 2000 μm subfraction.

DNA barcoding was widely used for analyses of greater than 2000 μm motile size fractions, while metabarcoding was used for smaller size fractions. Sessile fractions were not typically subdivided and were analysed via metabarcoding. However, for samples originating from ARMS-MBON (Obst et al., 2020), the sessile fraction was often passed through a 40 μm sieve prior to homogenisation with only the greater than 40 μm sample being retained for analysis (96 fractions). Sessile fractions have also been separated into greater than 38 μm (two fractions), 45 μm (four fractions), 48 μm (two fractions) and 50 μm (two fractions) subfractions. Two publications (based on the same ARMS units) subdivided the sessile fraction into greater than 2000 μm for barcoding, and less than 2000 μm for metabarcoding. Thus, although 73% of publications used molecular methods to characterise biodiversity, the methods were highly variable (Jessop et al., 2025, dataset on ARMS fractions).

Multiple preservatives and storage temperatures have been used to preserve fractions prior to DNA extraction. Ethanol was the most widely used preservative but dimethyl sulfoxide (DMSO), RNA*later*™, and a solution of dimethyl sulfoxide, ethylenediaminetetraacetic acid, and sodium chloride (DESS) have also been used. Sample storage temperatures have generally not been reported. Where this information was available, temperatures of −20°C and −80°C have been reported. Storage times to DNA extraction are often unknown but likely vary between publications and within publications (Jessop et al., 2025, dataset on ARMS fractions). Differences in storage times may be particularly pronounced in publications comprising multiple sampling sites but with centralised sample processing.

DNA extraction methods

The method of DNA extraction was dependent on whether DNA barcoding or metabarcoding analyses were employed (Jessop et al., 2025, dataset on ARMS fractions). For barcoding analyses, DNA extraction was most often performed with DNeasy® kits (Qiagen®), specifically the DNeasy® Blood and Tissue Extraction Kit (75 fractions from three publications), the DNeasy® PowerMax® Soil Kit (formerly the PowerMax® Soil DNA Isolation Kit, MO BIO®; nine fractions from one publication), and unspecified DNeasy® kits (Qiagen®; 113 fractions from three publications). The AutoGenPrep 965 (Autogen®) kit was used in four publications (for a total of 59 fractions), while the Animal Tissue Genomic DNA Extraction Kit (abGenix™) was used in two publications based on the same ARMS (24 fractions). The E-Z 96™ Tissue DNA Kit (Omega Bio-Tek®; six fractions), E.Z.N.A. MicroElute Kit (Omega Bio-Tek®; two fractions), Genomic DNA Mini Kit (GT100, Geneaid®; 48 fractions), and a custom phenol–chloroform protocol (42 fractions) were each utilised in singular publications.

DNA extraction prior to metabarcoding was most often performed with the DNeasy® PowerMax® Soil Kit (Qiagen®; 991 fractions, spanning 18 publications; Jessop et al., 2025, dataset on ARMS fractions). The DNeasy® PowerSoil® Kit (Qiagen®) was notably used for 349 fractions, but these originated from five publications that utilised the same ARMS units (originating from ARMS-MBON; Obst et al., 2020). The DNeasy® Blood and Tissue Kit (Qiagen®) and the NucleoSpin® Soil Kit (Macherey-Nagel®) are utilised in singular publications (36 and 27 fractions respectively). A custom methodology for DNA extraction was used in two publications (48 fractions), while DNA extraction kit/methodology was not clearly stated for 18 fractions spanning two publications.

DNA sequencing methodologies

DNA metabarcoding has been used to analyse most fractions described in current literature (1475 fractions, 80%; Jessop et al., 2025, dataset on ARMS publications). Of the 26 publications to implement DNA metabarcoding, 22 targeted the COI gene and 14 of these publications exclusively targeted COI (Table 2). 18S was targeted in 10 publications and was targeted exclusively in two of these publications. In contrast, 16S was targeted in three publications, ITS was targeted in two publications, and 23S was targeted by a singular publication. Nine publications targeted two or more genetic markers (Table 2).

Although multiple publications targeted the same genetic markers, the methods used for analyses were variable (Jessop et al., 2025, dataset on ARMS protocols). Four different primer pairs have been used for the amplification of the COI gene for DNA metabarcoding, with mlCOIintF (Leray et al., 2013) – jgHCO2198 (Geller et al., 2013) being the most widely employed (18 publications). The mlCOIintF (Leray et al., 2013)—LoboR1 (Lobo et al., 2013) primer pair was

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TABLE 2 Marker genes targeted in publications employing DNA metabarcoding to analyse the biotic communities of ARMS ($n = 26$).

Publication	COI	18S	16S	ITS	23S
Daraghmeh et al. (2025)	Y	Y		Y	
Pagnier et al. (2025)	Y	Y	N	N	N
Villarino et al. (2025)	Y	N	N	N	N
Williams et al. (2024)	N	N	Y	N	Y
Couëdel et al., 2024	Y	Y	N	N	N
McIlroy et al. (2024)	Y	N	N	N	N
Villalobos et al. (2024b)	Y	N	N	N	N
Lee et al., 2024	Y	N	N	N	N
Cecchetto et al., 2024	Y	N	N	N	N
Leite et al. (2023)	Y	Y	N	N	N
Thomasdotter et al., 2023	Y	N	N	N	N
Martaeng et al., (2023)	Y	N	N	N	N
Ip et al., 2023	Y	Y	Y	N	N
Reid et al. (2022)	N	Y	N	N	N
Nichols et al. (2022)	Y	N	N	N	N
Villalobos et al. (2022)	Y	N	N	N	N
Casey et al., 2021	Y	Y	N	N	N
Obst et al., 2020	Y	Y	N	Y	N
Pearman et al. (2020)	Y	N	N	N	N
Pearman et al. (2019)	N	N	Y	N	N
Carvalho et al. (2019)	Y	N	N	N	N
Pearman et al. (2018)	Y	Y	N	N	N
Ransome et al. (2017)	Y	N	N	N	N
Pearman et al., 2016	N	Y	N	N	N
Al-Rshaidat et al., 2016	Y	N	N	N	N
Leray and Knowlton (2015)	Y	N	N	N	N

Note: Green (Y) denotes that the corresponding gene was targeted while red (N) shows that the gene was not targeted for each respective publication.

used in two publications, while the IIICRrev–HBR2d (Thomasdotter et al., 2023) and LCO 1490–HCO 2198 (Sharma & Kobayashi, 2014) primer pairs were used in singular publications. Additionally, there is evidence of 12 unique PCR amplification mixes and thermocycling protocols having been implemented across 22 studies targeting the COI genetic marker. For amplification of the 18S gene, six different primer pairs have been implemented. The Tareuk454FWD1–TAReukREV3 (Stoeck et al., 2010) primer pair was used in three publications. The all18SF–all18SR (Hardy et al., 2010) primer pair was also used in three publications, but two are derivative works of the other. Primer pairs 1391F (Lane, 1991)–EukB (Medlin et al., 1988), 1F–2RC (Machida & Knowlton, 2012), Euk7F (Medlin et al., 1988)–Euk570R (Weekers et al., 1994), and v4_18SNext.For (Piredda et al., 2016)–V4_18SNext.Rev (Tragin et al., 2017) were utilised in singular publications. There is evidence for seven unique PCR amplification mixes and thermocycling protocols having been implemented across the 10 publications targeting the 18S genetic marker.

Sequencing platforms and bioinformatic analyses

Multiple platforms have been used for DNA high-throughput sequencing (HTS; Jessop et al., 2025, dataset on ARMS fractions). The most widely used HTS platform was the Illumina® MiSeq® (20 publications), followed by Ion Torrent® (Thermo-Fisher Scientific; three publications). Additionally, a singular publication used both the Illumina® MiSeq® and Illumina® HiSeq® 2500 Platforms for sequencing. Resulting sequences were predominantly clustered into operational taxonomic units (OTUs; 15 publications) or processed as amplicon sequence variants (ASVs; eight publications). ASVs represent unique DNA sequences that can differ by as little as a single nucleotide, whereas OTUs are clusters of highly similar ASVs. Grouping of ASVs into clusters is performed through different algorithms using custom similarity thresholds. A singular publication, utilising multiple genetic targets, clustered sequences into OTUs for both COI and 18S but analysed ASVs for 16S (Ip et al., 2023). In contrast, two publications utilising the PEMA pipeline (Zafeiropoulos et al., 2020) clustered sequences into OTUs for 18S but analysed ASVs for COI and ITS, although for the latter this was due to pipeline-specific terminology and represented sequence clusters (Daraghmeh et al., 2025; Obst et al., 2020). Notably, all publications to have analysed ASVs were published between 2019 and 2025. Conversely, publications that clustered sequences into OTUs have been published continuously since 2015. For ASV inference, DADA2 (first introduced in 2016; Callahan et al., 2016) was used in nine of 11 publications. The exceptions were the publication introducing the ARMS-MBON programme (Obst et al., 2020) and an ARMS-MBON derivative publication (Daraghmeh et al., 2025), where ASVs represented sequences clustered with Swarm v2 (Mahé et al., 2015). OTU clustering was performed with CROP (Hao et al., 2011; five publications), VSEARCH (Rognes et al., 2016; five publications), SWARM v3 (Mahé et al., 2021; three publications), USEARCH (Edgar, 2010; two publications), QIIME2 (Bolyen et al., 2019; one publication), a two-step process using both QIIME (Caporaso et al., 2010) and USEARCH (Edgar, 2010; one publication), and objective clustering (Ip et al., 2023; one publication).

Multiple reference databases have been used for taxonomic assignment in DNA metabarcoding bioinformatic pipelines (Jessop et al., 2025, dataset on ARMS publications). The Barcode of Life Data System (BOLD; Ratnasingham & Hebert, 2007) was the most frequently used reference database, reported in 14 publications that all targeted COI. National Centre for Biotechnology Information (NCBI; Sayers et al., 2020) databases are used in multiple publications, with GenBank (Clark et al., 2015) reported specifically in seven publications. Six of the seven publications utilising GenBank targeted COI and the other targeted 18S. Use of the NCBI Nucleotide database was reported by a singular publication that targeted COI. Three publications, that all targeted COI, reported the use of NCBI databases without specific reference to datasets.

The Protist Ribosomal Reference database (PR2; Guillou et al., 2013) was used in six publications that all targeted 18S. Use of the MIDORI database (Machida et al., 2017) was reported in four publications; three of these publications targeted COI and the other 18S. Use of the MIDORI 2 database (Leray et al., 2022) was

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reported in a further four publications; all four publications targeted COI. The Silva v128 database (Quast et al., 2013) was used in three publications; two of which targeted 18S and the other targeted 16S. Similarly, the SILVA v138 database was used in three publications; two of which targeted 18S and the other 16S. The SILVA SSU v138 and SILVA v132 databases were each used by singular publications that both targeted 18S. One publication, that targeted 18S, made use of the SILVAngs tool (https://ngs.arb-silva.de/silvangs/) that queries multiple databases provided by the SILVA project (Quast et al., 2013).

The Mo'orea Biocode project database (https://ocean.si.edu/ecosystems/coral-reefs/welcome-moorea-biocode-project) was notably queried in three publications that all targeted COI. The CO-ARBitrator database (Heller et al., 2018), GEOME (Deck et al., 2017), and a custom reference database of DNA barcodes generated from ARMS (Timmers et al., 2020), have been used singularly, each by publications that targeted COI. The Genome Taxonomy Database (GTDB; Parks et al., 2022), Unite (Nilsson et al., 2018), and μgreen-db (Djemiel et al., 2020) databases have also been used singularly by publications that targeted 16S, ITS, and 23S, respectively. Counts of reference databases cumulatively exceed the number of papers that have implemented DNA metabarcoding as 19 of 26 publications query sequences against multiple reference databases.

Fully reproducible bioinformatic pipelines for DNA metabarcoding (including statements of software and version used, detailed steps, and clearly defined code) were reported for 14 of 26 publications (Jessop et al., 2025, dataset on ARMS publications). R scripts facilitating reproduction of the applied bioinformatic pipeline are available on request for a singular publication. Code was not published, but there was a detailed in-text description of the workflow (including software used and version) for two publications. For the remaining nine publications, code has not been published and descriptions of the bioinformatic pipelines were either absent or brief.

3.2 | Spatial, taxonomic, and temporal coverage of ARMS research

3.2.1 | Spatial coverage

ARMS have been deployed in multiple ecosystems and across a range of anthropogenic pressure gradients (Jessop et al., 2025, dataset on ARMS study sites). Although exact coordinates were not stated for 122 of 892 ARMS deployments, it was possible to infer approximate coordinates and therefore ecoregions for all 892 ARMS from figures or site descriptions. ARMS deployments ranged from 74.69° South to 78.21° North, and 162.5° West to 164.1° East (Figure 3). 67% of realms, 37% of provinces, and 15% of ecoregions were covered by at least one ARMS unit (Jessop et al., 2025, dataset on ARMS deployments). No ARMS deployments are evidenced for the following four realms: Temperate Southern Africa, Temperate South America, Temperate Australasia, and the Tropical Eastern Pacific. Notably, no deployments are reported for South America, the Atlantic coast of Africa, or Australia.

ARMS deployments were biased to the Northern Hemisphere, with 722 of 892 deployments (81%) located north of the equator (Figure 3; Jessop et al., 2025, dataset on ARMS study sites). Additionally, ARMS deployments were concentrated around the Tropic of Cancer (mean latitude = 21.19°, interquartile range (IQR): 20.15–32.73°). Namely, 189 ARMS have been deployed in the Northern and Central Red Sea ecoregion and a further 33 ARMS have been deployed in the adjacent Southern Red Sea ecoregion, collectively comprising 25% of all deployments (Figure 3; Jessop et al., 2025, dataset on ARMS deployments). Conversely, only six ARMS have been deployed within the Arctic Circle and only 14 ARMS were reported for the Southern Ocean. Therefore only ~2% of total deployments were in the Polar Regions. Longitudinally, ARMS deployments were biased to the Eastern Hemisphere, with 665 of 892 deployments (75%) located east of the Prime Meridian (mean longitude = 20.32°, IQR: −2.23–55.24°).

ARMS have been deployed at depths ranging from one to 90 m (Jessop et al., 2025, dataset on ARMS study sites). However, deployments are concentrated at shallow-depth sites (mean site depth = 11 m, IQR = 5–12 m). The most common study site depth is 10 m (52 sites), and 84 of 255 sites (33%) have a reported depth between 10 and 12 m.

3.2.2 | Taxonomic coverage

Publications varied in taxonomic specificity, but most were non-specific (30 of 49 publications; Figure 4; Jessop et al., 2025, dataset on ARMS publications). In contrast, two publications targeted both the Brachyura and Anomura infraorders, a further two publications

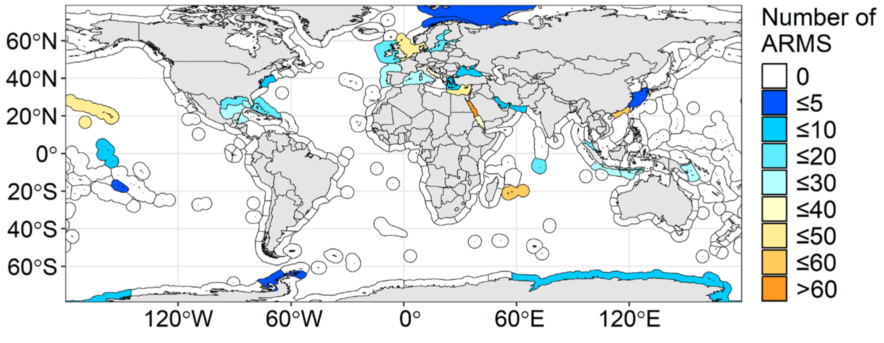

FIGURE 3 Distribution of autonomous reef monitoring structures (ARMS) across biogeographical ecoregions as described by Spalding et al. (2007) ($n = 892$).

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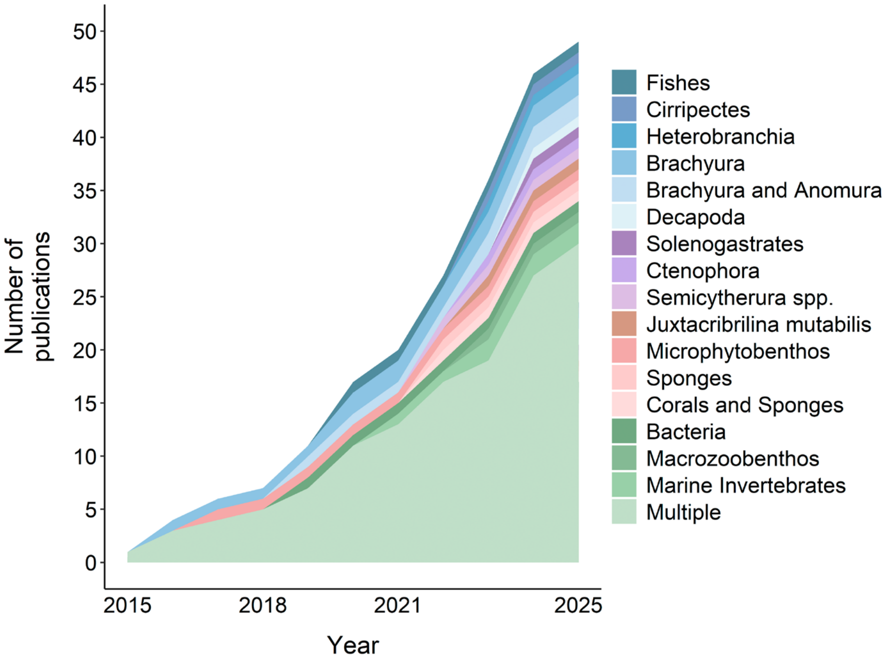

FIGURE 4 Stacked area chart showing the cumulative number of research publications that have used Autonomous Reef Monitoring Structures (ARMS) to monitor distinct taxonomic or ecological groups ($n=49$). Blue to purple shades represent primarily motile target groups, red shades indicate sessile target groups, and green shades identify target groups comprising both motile and sessile species.

targeted only the Brachyura infraorder, and one publication focused on the singular bryozoan species *Juxtacribrilina mutabilis* across its non-indigenous range (Martaeng et al., 2023). Varied taxonomic specificity reflects the broad applicability of ARMS to multiple research questions. Unfortunately, it was often unclear if the processing of ARMS was taxon-specific or if data for other taxa were generated but omitted from publications.

3.2.3 | Temporal coverage

Timing of deployment and retrieval is known to the month and year for 684 of 892 ARMS (77%; Jessop et al., 2025, dataset on ARMS deployments). Standardised ARMS units have been deployed continuously since April 2010. However, temporal coverage was highly variable per biogeographic realm (Figure 5). For example, ARMS deployments in the Eastern Indo-Pacific are limited to 2010, 2012, and 2016. Similarly, in the Tropical Atlantic there was a notable gap in ARMS deployments between 2014 and 2018. Furthermore, there were no ARMS deployments in the Arctic and Temperate Northern Pacific prior to 2018. In direct contrast, ARMS have been deployed regularly in the Western Indo-Pacific.

The timing of ARMS deployment and retrieval was variable within and between publications (Figure 5). The mean deployment duration was ~17 months but has ranged from 1 month to over 4 years. There was evidence of redeployment, with the deployment of ARMS at the same site at a later point in time, for 68 of 255 sites (27%). However, often the timing of redeployment contrasted with the initial deployment (i.e. occurs at a different time of the year) and overall immersion periods varied (i.e. the time from deployment to recovery).

The effects of deployment timing on ARMS biotic communities were directly addressed in three publications (Jessop et al., 2025, dataset on ARMS publications). Casey et al. (2021) found greater taxonomic overlap in ARMS communities between two sites separated by 100 m than within the same site sampled in two sequential years. Further, through the redeployment of ARMS in the Central Red Sea every 2 years, beginning in 2013, Villalobos et al. (2022) observed a major shift in ARMS' communities following the mass bleaching event of 2015. Additionally, significant temporal variation in alpha diversity was observed in the years following the bleaching event, with only 27% of OTUs being shared between the 2015–2017 and 2017–2019 sampling periods. Although other publications included ARMS with temporally staggered deployments, these data were typically pooled with the focus being placed on spatial patterns of biodiversity. For example, temporally staggered deployment periods have been used to maximise the capture of seasonally restricted species in spatial biodiversity investigations (McIlroy et al., 2024).

The effects of deployment duration on ARMS' biotic communities were directly addressed in seven publications. These publications provide strong evidence that taxonomic richness increases with deployment duration (Cecchetto et al., 2024; Sembiring et al., 2023; Womacks & Janosik, 2023). Further, the effects of deployment duration on abundance and richness are evidenced to be taxa-specific and site-dependent (Lee et al., 2024; Leite et al., 2023). Notably, differences in taxonomic richness and abundance were observable between ARMS that contrasted in deployment duration by 2 months (Sembiring et al., 2023). Although one publication reported that deployment duration does not significantly affect genetic and species-level alpha diversity, the authors acknowledge that the result is likely confounded by variable sequencing depth (Daraghmeh et al., 2025). The combined effects of deployment timing and deployment duration were simultaneously addressed by Couëdel et al. (2024) at a coral reef in the Southwest Indian Ocean. ARMS' community composition was dependent on both the time of deployment and

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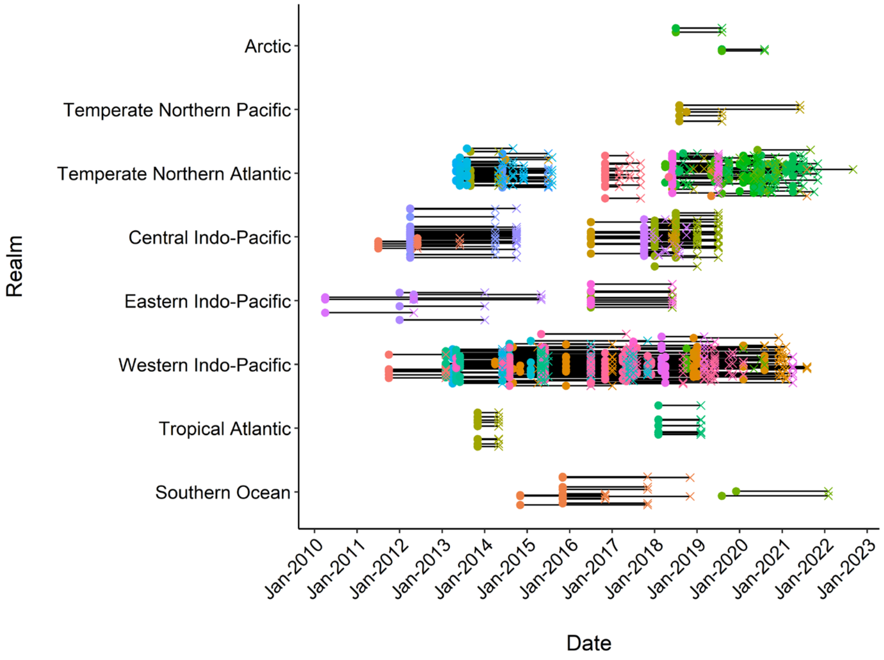
FIGURE 5 Timing of deployment and retrieval of autonomous reef monitoring structures (ARMS) across major biogeographic realms ($N=684$). Colours are representative of unique publications.



the overall deployment duration. However, per ARMS, OTU richness was independent of the time of deployment and deployment duration.

3.2.4 | Research objectives

The research objectives of publications using standardised ARMS units could be categorised into five broad themes: biodiversity monitoring, non-indigenous species detection, methodological development, assessment of ecosystem function, and phylogenetic analysis (Jessop et al., 2025, dataset on ARMS publications). Most studies focused exclusively on biodiversity monitoring (31 of 49). A further 13 publications combined biodiversity monitoring with an additional objective. Eight publications combined biodiversity monitoring with methodological development, two publications combined biodiversity monitoring with non-indigenous species detection, two combined biodiversity monitoring with assessment of ecosystem function, and one combined biodiversity monitoring with phylogenetic analyses. Of the five publications with research objectives other than biodiversity monitoring, three focused solely on non-indigenous species detection (a subset of biodiversity monitoring) and two publications focused on phylogenetic assessment of specific taxonomic groups captured by ARMS.

3.3 | Data management

Sequence data are publicly available for 34 of the 36 publications to have implemented DNA barcoding or metabarcoding and is available on request for the remaining two publications (Jessop et al., 2025, dataset on ARMS publications). Multiple repositories specifically designed to house sequence data have been used, including the NCBI databases, GenBank (Clark et al., 2015); the Sequence Read Archive (SRA; https://www.ncbi.nlm.nih.gov/sra; Leinonen et al., 2010); BOLD (Ratnasingham & Hebert, 2007); and the European Nucleotide Archive (ENA; https://www.ebi.ac.uk/ena; Burgin et al., 2022) hosted by the European Bioinformatics Institute (EBI). The NCBI SRA and GenBank were the most used repositories, housing sequence data for 11 publications each. Data repositories not specific to sequence data have also been used but to a lesser extent, and included Figshare (https://figshare.com/), Dryad (https://datadryad.org/stash), and Zenodo (https://zenodo.org/). There is no central, catered repository for ARMS' data across research groups.

In direct contrast to sequence data, images of ARMS plates were generally not accessible. Photographic records of ARMS plates are known for 32 of 49 publications but were publicly available for only five publications (Casey et al., 2021; Daraghmeh et al., 2025; Martaeng et al., 2023; Obst et al., 2020; Pagnier et al., 2025) and four of these publications are based on the same ARMS (Daraghmeh et al., 2025; Martaeng et al., 2023; Obst et al., 2020; Pagnier et al., 2025). Notably, ARMS-MBON has made plate photographs publicly available for 171 retrieved ARMS (as of 1 February 2025; Obst et al., 2020).

4 | DISCUSSION

Autonomous reef monitoring structures have been designed with the aim of standardising marine biodiversity monitoring across sites and research groups. Indeed, such standardisation is an essential prerequisite for interoperability and global approaches to biodiversity monitoring. However, it should be noted that the

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ARMS methodology is not without limitations. Namely, the use of PVC can bias the recruitment of key taxa (Mallela et al., 2017); the complexity of ARMS may not replicate natural complexity (O'Shaughnessy et al., 2023); and genetic investigations are limited by incomplete taxonomic reference databases (Hestetun et al., 2020; Meiklejohn et al., 2019; Weigand et al., 2019). Nonetheless, the standardisation of ARMS units may offset these disadvantages in large-scale biodiversity investigations (Obst et al., 2020). A key finding of our results is that even with the intent to standardise ARMS, there is widespread divergence in methodological approach, which is a barrier to interoperability. Importantly, this divergence cannot be explained solely by differences in research objectives as 90% of publications had biodiversity monitoring as a primary objective. Variability in the implementation of ARMS therefore reflects broad inconsistencies, rather than deliberate adaptations to study aims.

Divergence in ARMS methodological approach begins with the design of the units, which within current literature varies from three to 10 plates in each stack and variable sizes of the plates themselves. Although the reported discrepancies in plate size may initially seem minor, it should not be overlooked as variability in colonisable surface is evidenced to affect the results of biodiversity sampling in marine systems (Johnson et al., 2003). Lack of standardisation continues with the deployment of ARMS. Different anchoring methods and substratum types can influence community composition (Dafforn et al., 2009; Glasby, 2001). The influence of direct contact with the seabed (e.g. attachment via metal stakes), versus indirect contact via attachment to a weighted structure (e.g. concrete) warrants investigation in future research. It is also important to note that benthic habitats are often heterogeneous and may consist of patches of different substrata, and placement of ARMS within these microhabitats may influence community composition (Romoth et al., 2023). However, current ARMS research is focused on broader patterns of diversity across greater spatial scales. Targeted research into the effects of fine-scale placement within heterogeneous sites, particularly those with varying substrata or flow regimes, will facilitate more nuanced analyses of microhabitat effects on ARMS' community composition. Nonetheless, there is evidence that different communities develop on benthic versus suspended, pelagic ARMS (Villarino et al., 2025). This research aligns with previous artificial structure research that has demonstrated different sessile communities develop at different positions of the water column and on fixed versus moving structures (Dafforn et al., 2009; Glasby, 2001; Perkol-Finkel et al., 2006). As fixation to the seabed is the more common approach for ARMS, and more applicable to a broad range of ecosystems, this mode of deployment should be prioritised in future research. Nonetheless, suspended ARMS remain valuable for the detection of non-indigenous species.

Although eDNA (environmental DNA) sampling of water columns is increasingly being used to detect invasive species, there are still challenges with this technology (Beng & Corlett, 2020). Namely, the fact that the presence of the DNA of non-indigenous species in the water column does not mean local colonisation of that species. ARMS offer an added advantage for non-indigenous species detection, in that non-indigenous species detected on the ARMS have matured to (and are capable of) settlement and are thus more indicative of acclimation to local conditions and potential for recruitment if they manage to reach maturity. The mid-water suspension of ARMS is practical for artificial structures (e.g. pontoons) and these habitats are known to be commonly exploited by non-indigenous species (Ferrario et al., 2017). Furthermore, moving settlement plates have been shown to recruit more invasive species than fixed settlement plates (Dafforn et al., 2009). Nonetheless, individual settlement plates may be sufficient and of greater practicality for non-indigenous species detection in these habitats (Aschim & Brook, 2019; Ram et al., 2014). Accordingly, further research into the sampling effort required for non-indigenous species detection in these habitats is needed.

Replication is critical to robust ecological research, yet 20% of ARMS deployments lacked replication, and replication could not be confirmed for another 14% of ARMS due to insufficient reporting of metadata. Further, in a singular publication, individual ARMS plates have been treated as the unit of replication. The latter is an uncommon approach, especially as community composition can be influenced by plate surface and position (David et al., 2019; Lee et al., 2024; Steyaert et al., 2022). Where replication of ARMS has been implemented, the spatial arrangement of ARMS was inconsistent. Even small-scale variations in the inter-unit distances of ARMS can introduce biases in the sampling of local biodiversity, especially for species with restricted larval dispersal or rapid settlement behaviour (Jackson, 1986; Todd, 1998). Research into the influence of ARMS' spacing within sites is urgently needed to confirm whether ARMS are serving as independent replicates and also reflecting the patchiness of local biodiversity.

Genetic methods are widely employed in ARMS-based biodiversity assessments but are highly heterogeneous. Most studies employed DNA metabarcoding, with the COI gene as the dominant target, but variation in primer pairs and PCR protocols is notorious for introducing species bias and may produce misleading results (van der Loos & Nijland, 2021). Furthermore, the use of varied bioinformatic pipelines prevents the current integration of datasets across different deployments. The need for standardisation of ARMS processing, preservation, DNA amplification, and sequencing methodologies was highlighted by Ransome et al. (2017) but remains urgent. Open-source, standardised bioinformatic pipelines could promote greater consistency, and facilitate the combined analysis of publicly available raw sequence data (Williams et al., 2024). However, it should be noted that with the current speed of development of sequencing technologies, and associated analysis pipelines, standardisation may not be possible, and the most important aspect is to ensure that all raw data are publicly available, and therefore, can be reanalysed with new bioinformatics tools as these emerge.

Image-based analyses of ARMS are common but underutilised relative to their potential. Image-based analyses were incorporated in 16 of 49 publications, but images of ARMS plates are reported for at least 32 publications. Considering that photography of ARMS

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plates is recommended in all standard protocols, it is likely that photographs have been taken for ARMS from other publications, but these were not described or referred to. Differences in species detected via morphological or image-based methods compared with genetic approaches are likely attributable to limitations of reference databases used for taxonomic assignment during genetic analysis. Greater integration of image-based and genetic analyses can improve the comprehensiveness of ARMS-based biodiversity assessments (Lee et al., 2024; Womacks & Janosik, 2023). Novel machine learning methods could be implemented for the rapid and standardised analysis of this untapped resource. However, public availability of images is currently restricted to five publications (Casey et al., 2021; Daraghmeh et al., 2025; Martaeng et al., 2023; Obst et al., 2020; Pagnier et al., 2025). Nonetheless, it is notable that ARMS-MBON has made images of 171 ARMS publicly available, and this number will increase with continued deployment.

The spatial distribution of ARMS is biased towards the Northern Hemisphere and the Eastern Hemisphere, with deployments notably concentrated around the Tropic of Cancer. The latitudinal bias reflects the relatively high number of ARMS deployments in the Red Sea, while the longitudinal bias is likely due to the large number of deployments in the Red Sea and the high number of deployments in Europe. There is significant underrepresentation in polar regions, which is due to several reasons. These include the logistical constraints of deployment in extreme environments, the need for long deployment times (1–2 years minimum) to ensure reasonable coverage of the plates due to the fact that polar species grow slowly, but also the high probability of physical damage of the stacks due to iceberg impact, especially on such long deployments (Clark, pers. comm). Additionally, most ARMS are deployed in relatively shallow water, due to the depth limitations of SCUBA. Nonetheless, ARMS deployments to 200 m are known but have not been described in the peer-reviewed literature and were only possible with the use of a submarine (https://naturalhistory.si.edu/research/global-arms-program). Expanding ARMS deployments to less-studied biogeographical regions and habitats, including the Arctic and Southern Ocean, would provide a more comprehensive understanding of global marine biodiversity patterns. To isolate the drivers of geographical patterns of biodiversity, ARMS deployments at depths between 5 and 12 m (the most commonly sampled depths to date) should be prioritised.

Although ARMS deployments have been continuous since 2010, temporal coverage is uneven across biogeographical realms. Consistent sampling effort across current sampling sites should be prioritised over the inclusion of novel sites to generate long-term datasets critical to effective biodiversity monitoring (Lindenmayer et al., 2022; Magurran et al., 2010). The timing of deployment and retrieval of ARMS was also inconsistent within and between publications. Inconsistent timing is a critical problem for the standardisation of ARMS research. For settlement plates, terminal community assemblage is known to be dependent on the timing of deployment due to the high-density settlement of initial recruits (Bowden et al., 2006). Recent research has now demonstrated that this pattern is also observed for ARMS; namely, community structure and composition of ARMS in coral reefs is influenced by deployment timing and the length of the immersion period (Couëdel et al., 2024).

4.1 | Recommendations for the future

The adoption of a uniform ARMS method is needed for improved study interoperability. Based on the methodological inconsistencies identified in our review, we propose the following recommendations for future ARMS research.

- In the literature reviewed here, only 21 of 57 publications directly confirmed the use of standard ARMS units. Often the number of ARMS plates varied, or plate dimensions were misreported. Misreporting of ARMS design introduces barriers to cross-study comparison. The Smithsonian Institution, USA, has established the standard ARMS design of nine plates (excluding the base plate) of 22.5 × 22.5 cm. All ARMS should be designed to the standard presented by the Smithsonian Institution. Additionally, future publications should ensure reference is given to the Smithsonian Institution (https://naturalhistory.si.edu/research/global-arms-program), as opposed to 10-plate ARMS (as used in Leray & Knowlton, 2015) or artificial reef matrix structures (Zimmerman & Martin, 2004) as this is a notable error in current literature.
- Approximately, 20% of ARMS deployments have not been replicated. David et al. (2019) identified that individual ARMS' plates provide distinct microhabitats and concluded three replicate ARMS per site are necessary for investigating environmental effects. Individual ARMS units should therefore be considered the unit of replication in all future research and ARMS should be deployed in triplicate, as has been adopted by ARMS-MBON (Obst et al., 2020). Further, as time of deployment and overall deployment duration are known to influence terminal ARMS' community composition (Cecchetto et al., 2024; Sembiring et al., 2023; Womacks & Janosik, 2023), replicate ARMS and redeployments should have consistent deployment and retrieval timings. Where multiple sites are being investigated, an attempt should be made to ensure deployments are synchronised temporally.
- Replicate ARMS deployments have been inconsistently spaced in current research, and no studies have systematically evaluated the effect of spacing on recruitment to ARMS. We recommend the adoption of ARMS-MBON field replicates criteria—replicate ARMS to be spaced 3–10 m apart linearly and within 3 m depth of each other (Obst et al., 2020)—to promote standardisation until experimental evidence for optimal placement becomes available.
- Only 37% of publications reported the use of a mesh-lined crate during retrieval. In studies without proper containment motile fauna are likely to escape leading to biases in species detection. The Smithsonian Institution's Global ARMS Programme protocol describes the use of a milk crate lined with 100 μm mesh (https://naturalhistory.si.edu/research/global-arms-program), whereas ARMS-MBON specifies the use of a plastic container

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lined with 40 μm mesh (Obst et al., 2020). We recommend adopting the smaller 40 μm mesh to maximise capture of motile taxa.
- Photographic records are essential for comprehensive assessment of ARMS' community composition (David et al., 2019; Lee et al., 2024) but are known for only 32 of 49 publications and publicly available for only five publications at present. Once recovered, high-resolution images of both the top and undersides of all ARMS' plates should be taken with all images made publicly available.
- DNA metabarcoding is commonly used to characterise ARMS' community composition, but publications vary in the genetic markers being targeted, primers used, and how the ARMS community is fractionated. The ARMS' biotic community should be divided into standard fractions (motile: >2000, 500–2000, 100–500 μm; sessile: >40 μm). If specific species are being targeted these can be analysed independently, but where resources allow the whole ARMS community should be processed and preserved. For DNA metabarcoding, the COI gene should continue to be targeted, using the mlCOIintF (Leray et al., 2013)—jgHCO2198 (Geller et al., 2013) primer pair so that ARMS studies continue to align with the majority of current research on marine eukaryotic communities. Additionally, 18S should continue to be targeted as part of a multi-marker DNA metabarcoding approach to improve community analysis (Ip et al., 2023; Stoeck et al., 2010). No single primer pair for 18S has been prioritised in current ARMS research, but use of SSU_FO4 (Fonseca et al., 2010) and SSU_R22mod (Sinniger et al., 2016) would align with the molecular standard operating procedures of the European Marine Omics Biodiversity Observation Network (EMO BON).

4.2 | Minimal data standards

Study interoperability is not only dependent on the use of standardised methodologies, but also the availability of FAIR (findable, accessible, interoperable and re-usable) data (Scheffler et al., 2022). To ensure ARMS research aligns with the FAIR data principle, a minimal data standard should be followed. For every site, number of ARMS, distance between ARMS, day of deployment, day of retrieval, depth, and coordinates should be reported. For every ARMS unit, the use of high-resolution photography should be noted, and the fractions analysed recorded. For every fraction, the storage temperature and preservative should be recorded. Where DNA metabarcoding has been implemented, the DNA extraction kit, primers, PCR protocol, and sequencing platform used should be recorded.

A current barrier to the reporting of FAIR data in ARMS research is the lack of a centralised data repository. Multiple repositories have been used across current research but may lack appropriate fields specific to ARMS research. In the absence of an ARMS-specific database, GEOME (Deck et al., 2017) may serve as a suitable metadata repository given users can create custom fields for data storage. Further, inputs to these fields can be standardised (e.g. only numeric values accepted). For any resultant sequence data, a minimal data standard (MIxS: Minimal Information About (X) Any Sequence) should be created specifically for ARMS, as has been implemented for other types of sequence data by the Genomic Standards Consortium (http://www.gensc.org//pages/standards-intro.html), with the most prominent examples being Ocean Sampling Day (Kopf et al., 2015) and the EU MicroB3 project (ten Hoopen et al., 2015). Furthermore, all sequence data should be submitted to partners of the INSDC to ensure global access.

5 | CONCLUSIONS

The use of autonomous reef monitoring structures as a methodology for monitoring marine hard-bottom biodiversity is increasing globally but their comparative potential has been limited by a lack of standardisation. Future research can address some of these methodological differences by exploring temporal and spatial influences on ARMS' terminal biotic communities. Further, images of ARMS plates can be used for novel investigations of biodiversity patterns across ARMS' sites, as these analyses can provide significant added value when conducted alongside genetic analyses of biodiversity. Standardising genetic protocols will also enhance data integration. Moreover, the establishment of a centralised data repository and minimal data standards will help ensure FAIR data principles are followed in ARMS research and improve ARMS capacity to serve as a global biodiversity monitoring tool.

AUTHOR CONTRIBUTIONS

All authors conceived the ideas. Aaron Jessop, Nauras Daraghmeh, Justine Pagnier, and Margaux Steyaert designed the methodology and collected the data. Aaron Jessop analysed the data and led the writing of the manuscript. All authors contributed critically to the drafts and gave final approval for publication.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflict of interest.

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DATA AVAILABILITY STATEMENT

Data and code are available via https://doi.org/10.5281/zenodo.17226696 (Jessop et al., 2025).

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STATEMENT ON INCLUSION

Our study was a global review based on a meta-analysis of secondary data; as such there was no local data collection.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

Table S1: The methodological approaches of publications that have implemented standardised autonomous reef monitoring structures (ARMS) for biodiversity research.

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